Evolution of the hawthorns (*Crataegus*, Rosaceae) of Central Europe

Evolution der mitteleuropäischen Weißdorne (*Crataegus*, Rosaceae)

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Herbis, non verbis.

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List of Abbreviations and Symbols

A	allele
$\bar{A}$	mean of allele sizes
A_R	allelic richness
AMOVA	analysis of molecular variance
ANOVA	analysis of variance
bp	base pairs
BSA	bovine serum albumin
c_{DNA}	concentration of DNA
Ds	Nei's (1978) standard genetic distance based on allele identity under IAM
$(\delta\mu)^2$	Goldstein et al.'s (1995) genetic distance based on allele size under SMM
E	Pielou's (1966) evenness
F_{IS}	inbreeding coefficient or fixation index based on allele identity under IAM
F_{IT}	goodness-of-fit based on allele identity under IAM
F_{ST}	measure of population differentiation based on allele identity under IAM
H'	Shannon's (1948) information index
H_e	expected heterozygosity
H_o	observed heterozygosity
HWE	Hardy-Weinberg-equilibrium
IAM	Kimura and Crow's (1964) infinite allele model
I'	kinship coefficient analogue based on allele sizes
I_A	index of association
IBD	identical-by-descent
LD	linkage disequilibrium
MCMC	Markov Chain Monte Carlo
N_A	number of alleles
N_{Ae}	effective number of alleles
N_{Ap}	number of private alleles
NA	not available
NJ	neighbour-joining
NMDS	non-metrical multidimensional scaling
PIC	polymorphism information content
PVP	polyvinylpyrrolidone
Q	cluster membership coefficient
$\bar{r}_d$	Agapow and Burt's (2001) index of association
r_M	correlation coefficient of the Mantel statistic
R_{IS}	inbreeding coefficient or fixation index based on allele identity under SMM
R_{IT}	goodness-of-fit based on allele identity under SMM
R_{ST}	measure of population differentiation based on allele size under SMM
SE	standard error
SMM	Ohta and Kimura's (1973) stepwise mutation model
SSR	simple sequence repeats
T_a	annealing temperature
TK25	topographical map 1:25,000

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List of Used Software and Software Packages

ArcMap	10.6	ESRI (2011)
CLUMPP	v1.1.2	Jakobsson and Rosenberg (2007)
DISTRUCT	v1.1	Rosenberg (2004)
Peak Scanner™	v2.0	Applied Biosystems
PolyGene	v1.3	Huang, Dunn, Ritland, and Li (2020)
RStudio	v1.3.1093	RStudio Team (2020)
Packages:		
`ape`	v5.4-1	Paradis and Schliep (2019)
`ade4`	v1.7-16	Dray and Dufour (2007), Bougeard and Dray (2018), Thioulouse et al. (2018)
`adegenet`	v2.1.3	Jombart (2008), Jombart and Ahmed (2011)
`cowplot`	v1.1.1	Wilke (2020)
`FD`	v1.0-12	Laliberté and Legendre (2010), Laliberté, Legendre, and Shipley (2014)
`ggfortify`	v0.4.11	Tang, Horikoshi, and Li (2016), Horikoshi and Tang (2018)
`ggplot2`	v3.3.2	Wickham (2016)
`ggVennDiagram`	v1.2.0	Gao (2021)
`graphics`	implemented in R	R Core Team (2020)
`lattice`	v0.20-41	Sarkar (2008)
`pegas`	v0.14	Paradis (2010)
`plotrix`	v3.8-1	Lemon (2006)
`poppr`	v2.9.0	Kamvar, Tabima, and Grünwald (2014), Kamvar, Brooks, and Grünwald (2015)
`stats`	implemented in R	R Core Team (2020)
`vegan`	v2.5-6	Oksanen et al. (2019)
SPAGeDi	v1.5	Hardy and Vekemans (2002)
STRUCTURE	v2.3.4	Pritchard, Stephens, and Donnelly (2000), Falush, Stephens, and Pritchard (2003, 2007)
STRUCTURE HARVESTER	v0.6.94	Earl and vonHoldt (2012)

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1 | Introduction

> “The world is covered with signs that must be deciphered, and those signs, which reveal resemblances and affinities, are themselves no more than forms of similitude. To know must therefore be to interpret: to find a way from the visible mark to that which is being said by it and which, without that mark, would lie like unspoken speech, dormant within things.” (Foucault, 2005)

Applying just a morphological species concept has not always been a constructive method of systematic work as a lot of what makes a species remains unnoticed. In the last few decades contributions of genetic work revealed more and more insights into the taxonomy and phylogeny leading to different impacts on the systematics of plants at each hierarchical level. Despite the groups where nowadays a clearer picture of their phylogeny can be drawn, taxonomically challenging taxa remain unresolved, especially those showing either hybridisation, polyploidisation, apomixis, or combinations of these phenomena. While the former two are regarded as powerful evolutionary factors, the latter fact, reproduction without syngamy (as given in Wagenitz (2003) – at least since Nogler (1984) solely taken as formation of embryos and seeds without prior fertilisation = agamospermy sensu Wagenitz, to exclude vegetative propagation), has been seen as an evolutionary dead end (Darlington, 1939) for long. Since at least the work by Carman (1997) the formerly doomed view on apomixis has emended towards a transition period in the evolution of lineages (Hörandl & Hojsgaard, 2012 and the literature cited therein). This idea appears very comprehensible when thinking of species richness within e.g. Asteraceae, Poaceae, and Rosaceae, where the above mentioned points are likely to occur (Kadereit, 2014). With the latter being a moderately large family with estimated 85 genera (Kalkman, 2004), at least 32 genera exhibit euploid increases in chromosome number (Dickinson, Lo, & Talent, 2007). Among them is the notoriously complex genus *Crataegus* L., an element of the Holarctic (temperate regions of the Northern hemisphere) floral kingdom (Christensen, 1992a), whose taxonomy is challenging due to hybridisation and apomixis (Kalkman, 2004). This certainty culminated in the so-called “*Crataegus*-problem” (Palmer, 1932), where just slight morphological differences were used to provide a myriad of taxonomic descriptions on specific and all infraspecific levels with up to 100 species native to Eurasia and 1,100 to North America (Christensen, 1992a; Krüssmann, 1976; Lippert, 1995; Sell & Murrell, 2014). Depending on species recognition the number of species could be reduced by taxonomic revisions to perhaps 150 (Kalkman, 2004; Phipps, O'Kennon, & Lance, 2003). In fact, numerous studies coping with the morphological and genetic constitution have been carried out by James B. Phipps, Timothy A. Dickinson and colleagues in North America but only few in Europe (see 1.3). As the latest revision of *Crataegus* sect. *Crataegus* was carried out by Christensen (1992a) on morphological characters, an investigation of heredity and phylogeny is in need by applying genetic studies.

1.1 | Study species

All the hawthorns native to the wild in Central Europe belong to *Crataegus* subg. *Crataegus* sect. *Crataegus* ser. *Crataegus* (Christensen, 1992a; Ufimov & Dickinson, 2020). Adopting the nomenclature provided in Schmidt (2019) these species are:

- *C. laevigata* (POIR.) DC. (1825)
- *C. monogyna* JACQ. (1775)
- *C. rhipidophylla* agg.:
    - *C. rhipidophylla* GAND. (1872)
    - *C. lindmanii* HRABĚTOVÁ (1969)
- *C.* ×*media* BECHST. (1797)
- *C.* ×*macrocarpa* agg.:
    - *C.* ×*macrocarpa* HEGETSCHW. (1838/39)
    - *C.* ×*calycina* PETERM. (1846)
- *C.* ×*subsphaerica* agg.:
    - *C.* ×*subsphaerica* GAND. (1872)
    - *C.* ×*domicensis* HRABĚTOVÁ (1969)

These taxa have been treated variably by authors, through geographical space and time. Being different in both, hierarchical levels and applied synonyms, an overview of the different concepts of taxonomic classification of Central European hawthorns is presented in Table 1. The main divergences based upon the constitution of "*C. rhipidophylla*" as a species with two varieties or subspecies or as an aggregate with two species and the dependent taxonomy of the hybridogenous offspring (see 1.2). To maintain clarity among scientific names on a European scale it is seriously advised to consult the respective lists in Christensen (1992a) and the Atlas Florae Europaeae (Kurtto, Sennikov, & Lampinen, 2013) for synonyms. In the latter work the authors deal with broad species concepts despite the particularity of certain non-conformity to Flora Europaea (Franco, 1968). Astonishingly *C. macrocarpa* is not treated as nothospecies in both works although "it is nowadays understood, at least by the majority of Central European botanists, as the (primary) hybrid *C. laevigata* × *rhipidophylla*" (Kurtto et al., 2013).

Table 1 Taxonomic concepts of *Crataegus* ser. *Crataegus* in Central Europe.

Lippert (1978, 1995)	Christensen (1992a)	Schmidt (2005)	Schmidt (2019)
C. laevigata	*C. laevigata*	*C. laevigata*	*C. laevigata*
		ssp. *laevigata*	
		ssp. *palmstruchii* (Lindm.) Franco	
C. monogyna	*C. monogyna*	*C. monogyna*	*C. monogyna*
	var. *monogyna*	ssp. *monogyna*	
	var. *lasiocarpa* (Lange) K .I. Chr.		
C. curvisepala Lindman	*C. rhipidophylla*	*C. rhipidophylla* s. l.	*C. rhipidophylla* agg.
ssp. *curvisepala*	var. *rhipidophylla*	ssp. *rhipidophylla*	*C. rhipidophylla*
ssp. *lindmanii* (Hrabětová) Byatt	var. *lindmanii* (Hrabětová) K .I. Chr.	ssp. *lindmanii* (Hrabětová) P. A. Schmidt	*C. lindmanii*
"C. laevigata × monogyna" *C. ×ovalis* Kit. → *C. ×media*	*C. ×media*	*C. ×media*	*C. ×media*
"C. curvisepala × laevigata" *C. ×macrocarpa*	*C. ×macrocarpa*	*C. ×macrocarpa* s. l.	*C. ×macrocarpa* agg.
	nothovar. *macrocarpa*	nothossp. *macrocarpa*	*C. ×macrocarpa*
	nothovar. *hadensis* (Hrabětová) K .I. Chr.	nothossp. *calciphila* (Hrabětová) Hrabětová	*C. ×calycina*
"C. curvisepala × monogyna" *C. ×heterodonta* Pojark.	*C. ×kyrtostyla* Fingerh.	*C. ×subsphaericea* s. l.*	*C. ×subsphaerica* agg.
	nothovar. *kyrtostyla*	nothossp. *subsphaericea**	*C. ×subsphaerica*
	nothovar. *domicensis* (Hrabětová) K .I. Chr.	nothossp. *domicensis* (Hrabětová) P. A. Schmidt	*C. ×domicensis*

* "*subsphaericea*" with -e- was spuriously applied by authors (Buttler & Kalheber, 2012)

Table 2 Ploidy levels and chromosomal counts of Central European *Crataegus* species. Superscripts indicate if data was presented as a different taxon in literature.

Species	Ploidy level and chromosome count	References
C. laevigata (Poir.) DC.	$2n = 2x = 34$	1, 2, 3, 4, 4[o], 5, 6, 7, 8, 10, 12, 13[o],14, 15
	$2n = 4x$	14
C. monogyna Jacq.	$2n = 2x = 34$	1, 2, 3, 5, 7, 9, 10, 12, 13, 14
	$2n = 3x$	14
C. rhipidophylla Gand.	$2n = 2x = 34$	10[c], 11[r], 12[r]
	$2n = 3x = 51$	10[c], 12[c]
	$2n = 4x = 68$	4[c], 12[d], 13 [c]
C. lindmanii Hrabětová	$2n = 2x = 34$	10, 12
	$2n = 3x = 51$	13
	$2n = 4x = 68$	12
C. ×*media* Bechst.	$2n = 2x = 34$	5, 12[×d, ×i],14
C. ×*macrocarpa* Hegetschw.	$2n = 3x = 51$	12, 12[p], 13, 15
	$2n = 4x = 68$	12[×u]
C. ×*calycina* Peterm.	$2n = 2x = 34$	12[×c]
	$2n = 3x = 51$	12[×r]
C. ×*subsphaerica* Gand.	$2n = 2x = 34$	12[×k, ×s]
	$2n = 51$	4[m]
	$2n = 4x = 68$	12[×f]
C. ×*domicensis* Hrabětová	$2n = 2x = 34$	12[×p]
	$2n = 3x = 51$	12

Note: 1 Moffett (1931a); 2 Moffett (1931b); 3 Tischler (1934); 4 Gladkova (1968); 5 Bradshaw (1975a); 6 Byatt (1975a); 7 Byatt, Ferguson, and Murray (1977); 8 Byatt and Murray (1977); 9 Muniyamma and Phipps (1979b); 10 Baranec (1983); 11 Baranec (1985); 12 Baranec (1986); 13 Ptak (1986); 14 Talent and Dickinson (2005); 15 Lippert (2006).

[c] *C. curvisepala* Lindm.; [×c] *C. calciphila* Hrabětová; [d] *C. dunensis* Cinovskis; [×d] *C.* ×*deltoxyacantha* (Pénzes) Baranec; [×f] *C.* ×*fallacina* Klokov; [×i] *C.* ×*intermixta* (Wenzig) Beck; [×k] *C.* ×*kyrtostyla* Fingerh.; [m] *C. monogyna* s. l. (fide Christensen, 1992a); [o] *C. oxyacantha* L.; [p] *C. palmstruchii* Lindm. (fide Christensen, 1992a); [×p] *C.* ×*plagiosepala* Pojark.; [r] *C. rosiformis* [errore *rosaeformis*] Janka; [×r] *C.* ×*roubalii* Chrtek et Křísa; [×s] *C.* ×*silicensis* (Hrabětová) Baranec; [×u] *C.* ×*uhrovae* Soó.

The chromosomal base number *x* = 17 applies to all of these species (Moffett, 1931a). Apart from some apparent aneuploid miscounts (2*x* = 32 in Meyer, 1915 and Longley, 1924 fide Muniyamma & Phipps, 1979b; *x* = 8, 16 in literature cited in El-Gazzar & Badawi, 1977; 3*x* = 48 in Ptak, 1986 fide Christensen, 1992a) the species display different ploidy levels: diploid (2*n* = 2*x* = 34), triploid (2*n* = 3*x* = 51), or tetraploid (2*n* = 4*x* = 68). Available ploidy and count data from literature is summarised in Table 2. Some have to be "considered unreliable because of uncertain identifications or inadequate taxonomic coverage (Funk, Hoch, Prather, & Wagner, 2005; Merxmüller, 1970; Nelson-Jones, Briggs, & Smith, 2002)" (Talent & Dickinson, 2005).

1.2 | Hybridisation among *Crataegus*

At least since the beginning of the 20th century hybridisation was assumed to be primarily responsible for the systematic difficulties in *Crataegus* (H. B. Brown, 1910; Eggleston, 1908; Standish, 1916). While this opinion changed for North American hawthorns (Phipps, 2005) and classic diploid-diploid hybridisation is proven to occur in two out of three cases between native species and introduced *C. monogyna* (Love & Feigen, 1978; Wells & Phipps, 1989), hybridisation takes place in Eurasia (Bradshaw, 1971; Byatt, 1975a, 1975b, 1976a, 1976b; Christensen, 1982a, 1982b, 1984, 1985, 1992b; Cinovskis, 1971; Gladkova, 1968; Gosler, 1990; Gostyńska-Jakuszewska, 1975; Hellwig, 1997; Hrabětová-Uhrová, 1969b; Pojarkova, 1939). In combination with subsequent polyploidy or introgression this is still supposed to be the main driver of *Crataegus* diversity in Eurasia.

Belonging to a single series, Central European hawthorns are able to form solely interserial hybrids in nature. Interbreeding between species of other series occurs where new species are introduced (see Table S1 and Table S2). Among the above listed taxa (Table 2) the first four are supposed to be the parents of the latter four nothospecies (see Figure 1 and literature subsumed in Fichtner & Wissemann, 2021 and Thomas, Leski, La Porta, Dering, & Iszkuło, 2021). By doing so only one main diagnostic difference of *C. rhipidophylla* and *C. lindmanii* (sepals on ripe fruit deflexed, patent or erecto-patent in the former in contrast to patent, often appressed to another in the latter) results in the same diagnostic character to distinguish their putative hybrids with *C.* ×*calycina* and *C.* ×*domicensis* having erect sepals. However, Zieliński (1977) pointed out that *C. rhipidophylla* [presented as *C. curvisepala* LINDMAN; see Christensen (1992a: 89f.) for a summary of its taxonomy] is "one of the most critical species of hawthorns in Europe" and "views about its systematic rank and taxonomic position are frequently contradictory”. Furthermore, this taxon appears intermediate between *C. monogyna* and *C. lindmanii* [given as *C. calycina* PETERM.] leading Zieliński (1977) to the conclusion of these two taxa being the parents of *C. rhipidophylla* as an old and established hybridogenous species including the call for the need of experimental studies on that topic. Surprisingly this point of view was not regarded at all in the revision by Christensen. At least experimental work on *C.* ×*media* = *C. laevigata* × *C. monogyna* has been carried out (Bradshaw, 1953, 1971; Byatt, 1975b). In fact, the model (Figure 1) presented here is widely accepted among European botanists.

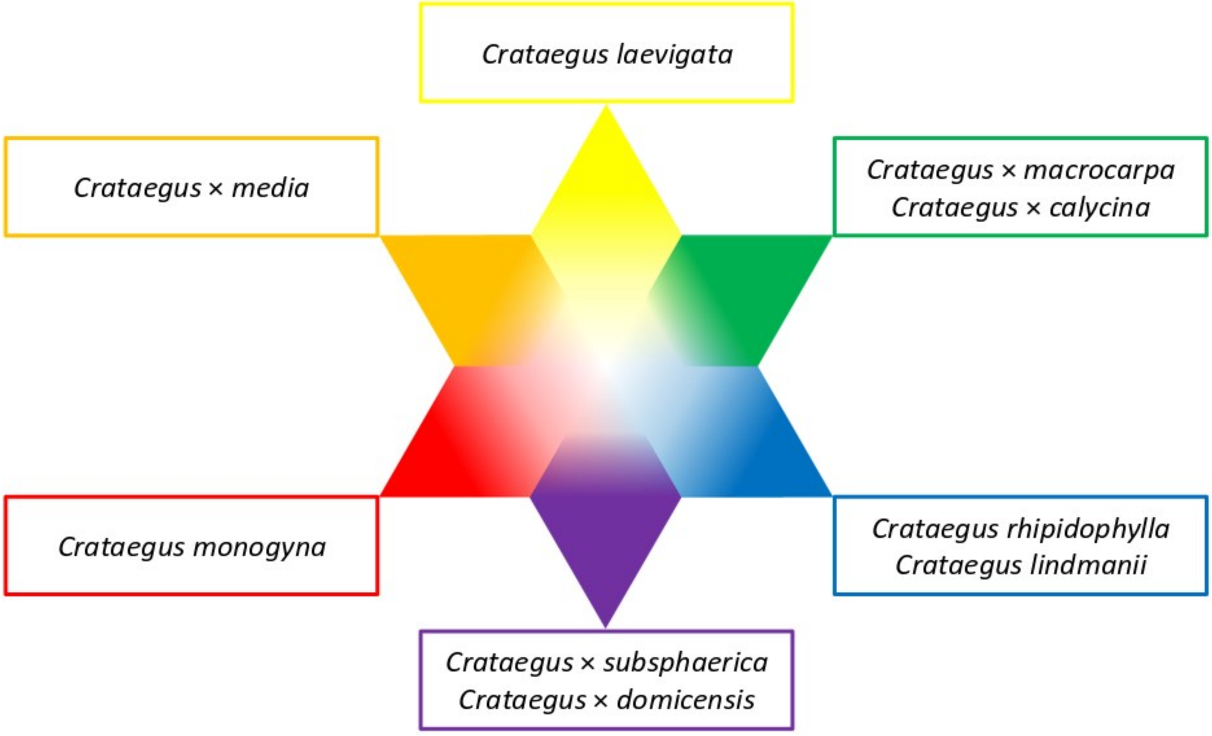


Figure 1 Hypothetic hybridisation model of Central European *Crataegus* taxa. Parents are depicted in primary colours (red, yellow, blue) and the offspring in the respective secondary colours (orange, green, purple). According to their parent taxon of *C. rhipidophylla* agg. the respective hybridogenous offspring is written at the same position of the boxes.

1.3 | Apomixis within *Crataegus*

Apomixis is taken responsible for the evolution of North American taxa (Phipps, 2005; Talent & Dickinson, 2005) and was cytologically proven in the late 20th century by Muniyamma and Phipps (1979a, 1984a, 1984b), Dickinson and Phipps (1986), Smith and Phipps (1988), and Dickinson, Belaoussoff, Love, and Muniyamma (1996). These studies revealed both types of gametophytic apomixis, the diplosporous and the aposporous mechanism, with the latter being more frequent and requiring pollination (Talent & Dickinson, 2007a, 2007b). Further work exposed sexual reproduction being limited to orthoploids while apomixis occurs in triploids and tetraploids (Muniyamma & Phipps, 1985). Fertilisation of egg cells is not restricted to meiotically reduced eggs but leads to polyploidy in apomeiotically unreduced eggs (Talent & Dickinson, 2007c). In contrast, the occurrence of apomixis in Central European hawthorns seemed ambiguous: on the one hand, not experimentally detected in British *C. monogyna* and *C. laevigata* by Gosler (1989) and neglected by Hellwig (2006); on the other hand, reported for Polish triploid taxa (*C. palmstruchii* LINDM., *C. lindmanii*, *C. macrocarpa*) by Ptak (1989) and suggested for Slovakian di- to tetraploid accessions (*C. monogyna*, *C. subsphaerica* s. l. [presented as *C. subsphaericea*], *C. kyrtostyla* Fingerh. = *C. monogyna* × *C. subsphaerica*) by Vašková and Kolarčik (2019).

1.4 | Aim of the study

Up to now several studies dealt morphologically with each putative nothospecies and its parents (*C.* ×*macrocarpa*: Byatt, 1976b; Christensen, 1982a – *C.* ×*subsphaerica*: Byatt, 1976b; Christensen, 1982a, 1984, 1985, 1992b – *C.* ×*media*: Bradshaw, 1953; Byatt, 1975b, 1976b; Christensen, 1982a, 1984; Gosler, 1990; Synnott, 1978). Though most characters can be assumed continuously with overlapping levels among entities, there is certain correlated discontinuity given to call these entities morphospecies according to the morphological species concept. All of this work ended up in the previously depicted model of hybridisation among Central European *Crataegus* spp. (Figure 1). However, by implying hybridisation in this model it has still to be taken hypothetic in most parts. Only the relationship of *C.* ×*media* was experimentally tested and proven to be a product of sexual diploid-diploid hybridisation (see 1.2 and Table 2). Furthermore, because of the different ploidy levels of *C. rhipidophylla* agg. (Table 2) the model also has to take apomictic reproduction into account (see 1.3). Hence, the question arises whether the entities of *C.* ×*macrocarpa* agg. and *C.* ×*subsphaerica* agg. were formed hybridogenously or apomictically. Do they reproduce sexually with the putative ability of backcrossing or asexually and then building swarms? Do these entities fit into the provided model or is an updated model in need? With the challenge of being perennial woody species this phylogenetic approach shall rely on the support of molecular techniques in addition to a morphological reappraisal. This leads to the main hypotheses of this study that are:

(1) The Central European morphotaxa are reproductive isolated,
(2) individuals of these are not only morphologically but also genetically distinct, and
(3) more morphological traits will provide a clearer picture of the morphotaxa.

To test for reproductive isolation several modes are tested including self- and cross-pollination. The consensus of morphology and genetic data is tested by cluster analyses of trait and genetic data. For the latter, sequence data of loci widely regarded as universal DNA barcodes for plants (e.g. *mat*K, *rbc*La, *psb*A-*trn*H, *trn*L-*trn*F, and the internal transcribed spacer 2 (ITS2)) have successfully been used to draw phylogenies of the (maloid) Rosaceae (Potter, Gao, Bortiri, Oh, & Baggett, 2002; Verbylaitė, Ford-Lloyd, & Newbury, 2006). However, as they provided poor resolution at intrageneric level within *Crataegus* (Albarouki & Peterson, 2007; Zarrei et al., 2015), neither nuclear nor plastid sequences seemed the tool of choice to reveal the intraserial relationship of *Crataegus* ser. *Crataegus*. Fortunately the technique of microsatellite markers was shown to be applicable as molecular markers in population genetics (Goldstein et al., 1999) and systematics (Goldstein & Pollock, 1997), and has already been successfully applied to surveys in *Crataegus* (J. A. Brown et al., 2016; Emami, Shabanian, Rahmani, Khadivi, & Mohammad-Panah, 2018; Lo, Stefanović, & Dickinson, 2009; Lo, Stefanović, Ritland, & Dickinson, 2010). Such markers are non-coding nuclear DNA and comprise of short and simple sequence repeats (SSR; e.g. -$(TA)_n$-). The facts of being uninformative combined with high mutation rates, estimated at 10^{-2}-10^{-3} per locus per gamete per generation, make them highly polymorphic with a variable number of repetitions (Tautz, 1989). As microsatellite markers are codominantly inherited and follow the Mendelian laws this technique is expected to elucidate the phylogeny of Central European *Crataegus*.

2 | Material and methods

2.1 | Study sites and sampling

This study dealt with 302 individuals of the genus *Crataegus*. The specimens were sampled in the Botanical Garden of the city of Frankfurt am Main, Germany, (49 individuals) and at natural areas throughout Germany (247 individuals) and Sweden (six individuals) from spring 2017 until spring 2019. These sites were preselected by screening distribution data of the different species and by evaluating aerial photos of raster fields with a high α-diversity of *Crataegus* species for suitable places. For data collection in the field up to twelve individuals per site were chosen by eye to represent both, morphological and species' variation. As all individuals were visited twice, each of them was tagged with its number for an easier visual retrieval and additionally GPS data was noted down (see Table S3). All localities of individuals are depicted in a map drawn with ArcMap 10.6 (ESRI, 2011) (Figure 2).

Among all specimens, 278 samples built up the studies' ingroup which are the representatives of the Central European species of *Crataegus* subg. *Crataegus* sect. *Crataegus* ser. *Crataegus* (as listed in 1.1; species: 53x *C. laevigata*, 82x *C. monogyna*, 22x *C. rhipidophylla*, 7x *C. lindmanii*; hybrids: 9x *C. ×media*, 72x *C. ×macrocarpa* agg., 33x *C. ×subsphaerica* agg.; For the reason of not yet experimentally proven hybridogenous origin the hybrid sign '×' will be discarded in the following.). Identification based on key literature (Schmidt, 2016, 2017a). It arose to be feasible not to differ all aggregates but *C. rhipidophylla* agg. Hence, individuals belonging to the hybridogenous aggregates were treated under their aggregate name. The remaining 24 samples served as outgroup. They belong either to North American taxa ('NAm': 1x *C. arnoldiana* Sarg., 1x *C. intricata* Lange, 2x *C. punctata* Jacq., 3x *C. succulenta* Schrad. ex Link) or Southern and South-eastern European taxa ('EUR': 2x *C. azarolus* L., 1x *C. caucasica* K. Koch, 1x *C. wattiana* Hemsl. & Lace) or are medlars, (10x *C. germanica* (L.) O. Kuntze, syn. *Mespilus germanica* L.; see Talent, Eckenwalder, Lo, Christensen, & Dickinson, 2008), and their graft-chimeras with *C. monogyna* (3x +*Crataegomespilus* Simon-Louis ex Bellair). Where appropriate during analysis, the latter two taxa are grouped as 'Mispel'.

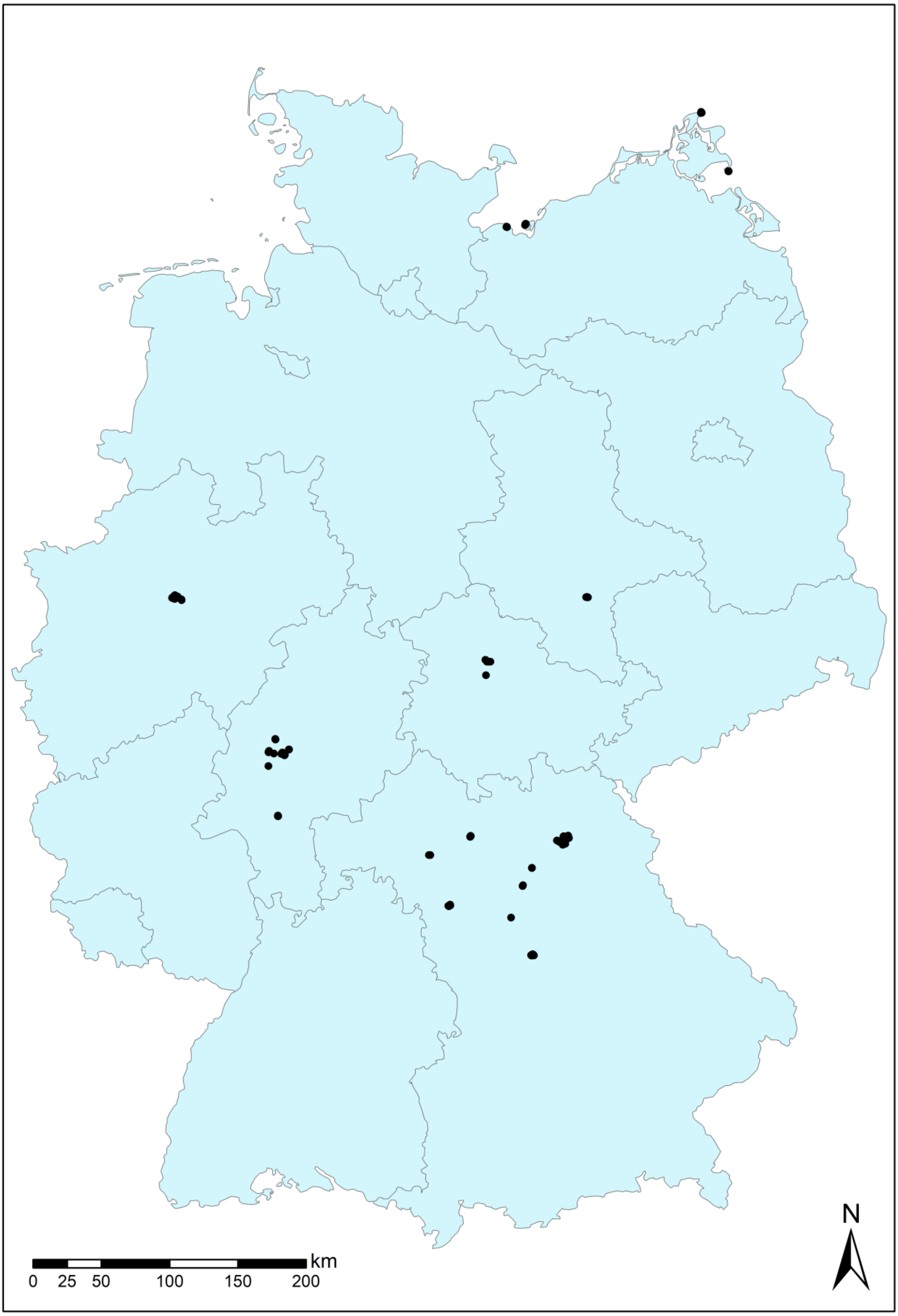


Figure 2 Sites of sampled *Crataegus* individuals in Germany. Note that due to purposes of scaling several individuals may appear as a single spot on the map.

2.2 | Examination of reproductive modes

Amongst the samples in the Botanical Garden of the city of Frankfurt am Main seven individuals representing five different species were selected for testing reproductive modes in spring 2019. In total four ways of breeding were examined: allogamy, autogamy, apogamy, and one mixed way where besides apogamy autogamy and/or allogamy was possible. To test for (**1**) allogamy: The stigma was manually cross-pollinated with previously collected pollen grains of the same or another species and after pollination the flower was covered; (**2**) autogamy: Either the flower was just covered to allow self-pollination or was treated likewise in allogamy but with pollen of the same individual (= geitonogamy); (**3**) apogamy: Each stigma was cut off underneath its base before the flower was finally covered; (**4**) the effect of coverage: The flower remained uncovered in two varieties, either just the petals or both, petals and stamina, had been removed.

Pollen for these experiments was retrieved from indehisced flowers which were collected just before their anthesis from mid-April to early May 2019 according to the individual flowering time of the sampled hawthorns. These flowers were manually depetaled with tweezers and put in a sterile Petri dish individualwise to wilt under room conditions in order to release the pollen from the dried anthers. Released pollen grains were detected as yellow powder in each dish and stored in each dish under room conditions. To avoid biases and contamination all experiments were conducted on indehisced, virgin flowers at the so called 'balloon' stage (see Vašková & Kolarčik, 2019) and all tools, i.e. a pair of tweezers, scissors, and a hook-shaped retractor needle, were sterilised by submergence in ethanol and burning off prior usage. Successful pollen transfer was detected by eye as sticky removal of the yellow pollen grains from the retractor needle onto each stigma. When appropriate according to the tested mode treated flowers were covered with aluminium foil. The number of replicates for testing of allogamy is shown in Figure 3 and for the remaining non-allogamous tests in Table 3. Pollen from ID 1095 was used for interspecific crosses with *C. laevigata*.

Table 3 Number of replicates of the non-allogamous reproduction experiments.

		covered			uncovered	
ID	species	autogamy	geitonogamy	apogamy	depetaled	depetaled & emasculated
1066	*C. laevigata*			16		
1095	*C. laevigata*		15	15	16	
1068	*C. macrocarpa*	19	17	17	24	21
1081	*C. macrocarpa*	19		20	21	21
1094	*C. monogyna*			14		11
1072	*C. subsphaerica*	15	16	14	12	15
1087	*C. rhipidophylla*			10		
	Total	**53**	**48**	**106**	**73**	**68**

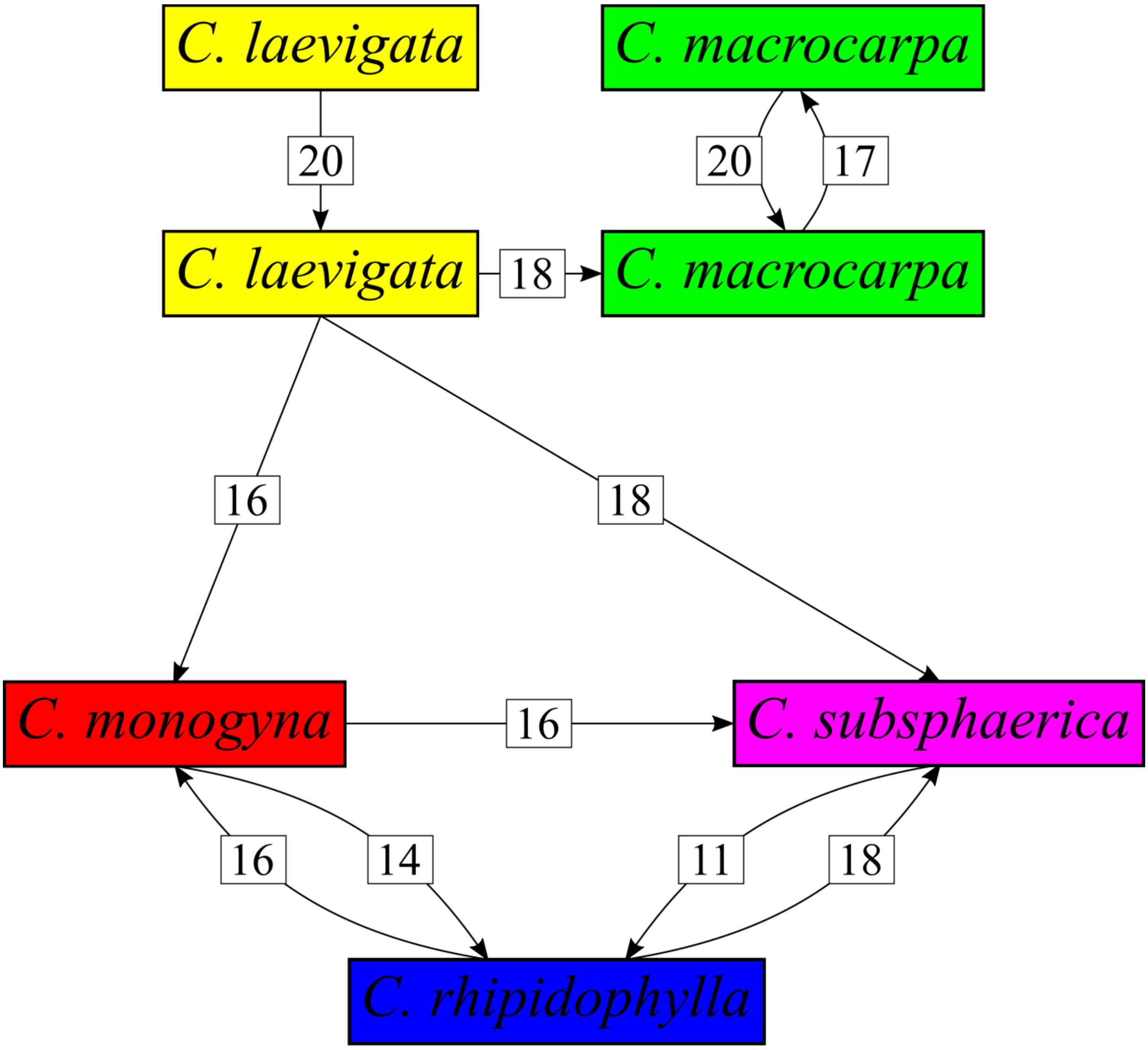


Figure 3 Allogamous breeding experiments in *Crataegus*. Arrows display the direction of pollen transfer from the donor tree to the mother tree, numbers indicate performed crosses.

2.3 | Morphological characterisation

2.3.1 | Morphological traits

Traits were chosen according to species' description and key literature (Lippert, 1978, 1995, 2001; Schmidt, 2016, 2017a, 2017b, 2017c). In total 24 traits of the morphology of leaves, flowers, and fruit were observed. They were grouped into basic traits reflecting those for identification in key literature and additional traits (Table 4). From September 2017 until May 2019 each individual was visited twice (except the six from Sweden) to collect morphological trait data of leaves and flowers in spring and of leaves and fruits in autumn. Data of each trait was observed by eye and on several objects (e.g. five to twenty leaves or fruits) of the same individual considering morphological variability and objectivity. Data was assessed by using classes or, if countable, numeric values. For later data analyses all feature classes of each trait have been transferred to unique numeric values (see Table 4).

Leaf morphology

Leaves are features with the longest appearance throughout a year representing a key role in species recognition of hawthorns. Leaf morphology may vary remarkably within long shoots or short shoots. As agreement of good practice in accordance to advises in key literature only the topmost leaves from short shoots were used for data assessment of the following eight traits: (**1**) Direction of first lateral veins (bending forward, straight, or bending outward), (**2**) presence of hairs on the midrib on the lower surface (yes or no), (**3**) presence of hairs in the axils of veins on the lower surface (yes or no), (**4**) ending points of veins (in sinuses or in teeth), (**5**) depth of lobes (less than ⅓, ⅓ to ½ or more than ½ of half of the width of the leaf), (**6**) margin of leaves (± entire, serrate only on the tip of the lobes, or serrate), (**7**) margin of stipules (entire, little serrate, or serrate), (**8**) amount of glands on stipules' teeth (none, few, or many).

Flower morphology

Flowers are the features with the shortest appearance in a vegetation period with around two to three weeks. Nonetheless they present some key characteristics during the period without fruits. The ten observed flower traits were the following: (**1**) Number of styles (mean of 20 flowers), (**2**) number of stamina (mean of 10 flowers), (**3**) colour of anthers (brown, yellow, pale yellow, white, pale pink, pink, hot pink), (**4**) direction of sepals on flower buds (upright or adjacent), (**5**) direction of sepals during flowering (reflexed or distant), (**6**) presence of hairs on the upper side of sepals (yes or no), (**7**) presence of hairs on the lower side of sepals (yes or no), (**8**) presence of hairs on the hypanthium (yes or no), (**9**) aspect ratio of sepals (1:1, 1:1 to 2:1, more than 2:1), (**10**) shape of the sepal tip (rounded or pointed).

Fruit morphology

As fruit set starts in the mid of the year and ripe fruit remain on plants throughout autumn and early winter, fruit also play a helpful role in identifying of hawthorns. Moreover, some flower traits may be guessed on fruits as well. The six following fruit traits were assessed: (**1**) Direction of sepals on the fruit (reflexed, distant or upright), (**2**) number of nutlets per fruit (mean of 20 fruits), (**3**) shape of fruit (globular or oblong), (**4**) shape of fruit base (rounded or cylindrical), (**5**) colour of fruits (brown, yellow, pale red or deep red), (**6**) presence of hairs on the fruit (yes or no).

Table 4 Morphological traits and respective values. Group reflects **a**dditional and **b**asic traits.

item	**group**	**#**	**trait**	**feature class**	**value**
leaf	**b**	**1**	**direction of 1st lateral veins**	bending forward	1
				straight	3
				bending outward	5
	a	**2**	**veins underneath hairy**	none	0
				few	0.5
				many	1
	a	**3**	**axils of veins hairy**	none	1
				few	3
				many	5
	a	**4**	**ending points of veins**	in sinuses and teeth	0
				in teeth only	1
	b	**5**	**depth of lobes** (… of half of the width of the leaf)	no lobes	0
				less than ⅓	1
				⅓ to ½	3
				more than ½	5
	b	**6**	**margin of leaves**	± entire	1
				serrate only at tip of lobes	3
				serrate	5
	b	**7**	**margin of stipules**	entire	1
				little serrate	3
				serrate	5
	b	**8**	**glands on stipules' teeth**	none	1
				few	3
				many	5

item	group	#	trait	feature class	value
flower	**b**	**1**	**number of styles**	mean of 20 flowers	#
	a	**2**	**number of stamina**	mean of 10 flowers	#
	a	**3**	**colour of anthers**	yellow white pink hot pink	0 1 3 5
	a	**4**	**sepal direction (buds)**	adjacent upright	0 1
	a	**5**	**sepal direction (flowering)**	reflexed distant	0 1
	a	**6**	**upper side of sepals hairy**	no yes	0 1
	a	**7**	**lower side of sepals hairy**	no yes	0 1
	a	**8**	**hypanthium hairy**	no yes	0 1
	b	**9**	**aspect ratio of sepals**	1:1 1:1 to 2:1 more than 2:1	1 3 5
	a	**10**	**shape of the sepal tip**	rounded pointed	0 1
fruit	**b**	**1**	**sepal direction (fruit)**	reflexed distant upright	1 3 5
	b	**2**	**number of nutlets per fruit**	mean of 20 fruits	#
	a	**3**	**shape of fruit**	globular oblong	0 1
	a	**4**	**shape of fruit base**	rounded cylindrical	0 1
	a	**5**	**fruit colour**	brown deep red pale red yellow	−1 0 1 2
	a	**6**	**fruit hairy**	no yes	0 1

Note: If intermediate features applied they were treated as values in between, e.g. if leaves had straight and outward bending lateral veins, the value ‘4’ was denoted. Further subdivisions in quarter steps were used if necessary. In case of countable traits the effective number of items (#) was recorded.

2.3.2 | Multivariate analysis of morphological data

All downstream analyses of the data set including and excluding the outgroup and with just the basic, just the additional and all traits were performed using the programming language R (R Core Team, 2020) in the integrated development environment of RStudio v1.3.1093 (RStudio Team, 2020).

At first, the correlation of the trait data presented in Table S4 was analysed. As being ordinal variables Spearman's rank correlation coefficient ρ was applied and tested via the asymptotic t approximation within the ‘`cor.test`’ function of the implemented ‘`stats`’ package of R. When appropriate these results were plotted by ‘`pairs`’ function of the standard package ‘`graphics`’ with slightly graphically modified visualisation functions ‘`panel.cor`’ and ‘`panel.smooth2`’ by Zuur, Ieno, and Smith (2007).

Then a distance matrix was calculated from the trait data using the ‘`gowdis`’ function of the ‘`FD`’ package v1.0-12 (Laliberté et al., 2014; Laliberté & Legendre, 2010). As most traits are ordinally scaled the setting ‘`ord = "podani"`’ was chosen to treat them not as continuous values but to convert them to ranks. This distance matrix was passed to ‘`metaMDS`’ function of ‘`vegan`’ package v2.5-6 (Oksanen et al., 2019) to perform non-metrical multidimensional scaling (NMDS). Stress values of different runs (i.e. with $k = 1–6$ dimensions and a maximum of 1000 random starts in search of stable solution) were plotted to obtain the optimal k for final analysis by the elbow criterion. A Shepard plot of the chosen k displays ordination distance against observed dissimilarity and additionally two correlation-like statistics on the goodness of fit (R^2) for linear and non-metric fit. After determining the optimal k the NMDS was rerun with ‘`trymax = 1000`’. Obtained results were visualised using the packages ‘`ggplot2`’ v3.3.2 (Wickham, 2016) and ‘`ggfortify`’ v0.4.11 (Horikoshi & Tang, 2018; Tang et al., 2016).

2.4 | Molecular work

2.4.1 | DNA extraction, amplification, and sequencing of microsatellites

DNA extraction

Germplasm acquisition was performed during the morphological observations in spring to avoid contamination with different phytopathogenic fungi increasing during vegetation period. Leaves were collected and stored in tea bags in a silica gel containing jar to ensure fast drying. For genomic DNA isolation the NucleoMag® Plant Kit (Machery-Nagel, Düren, Germany) was used. This original protocol was downscaled by factor two and modified as follows: A self-made magnetic rack fitting to 0.5 µL Eppendorf tubes was used for shaking and separating the magnetic beads from liquid phases. As recommended for dried material an amount of 5–10 mg leaf tissue (Table S6) was weighed in a 2.0 mL Eppendorf tube and homogenised in a mixer mill (MM 400, Retsch GmbH, Haan, Germany) with a 5 mm stainless steel ball for 3 min at 30 Hz. To remove powder from the lid the tube was centrifuged for 1 min at 10.000 rpm. Lysis buffer was supplemented with 0.25 mg/mL proteinase K (Carl Roth GmbH + Co. KG, Karlsruhe, Germany) solved in proteinase buffer (Machery-Nagel, Düren, Germany) and 2% polyvinylpyrrolidone (PVP) K 30 (Carl Roth GmbH + Co. KG, Karlsruhe, Germany). Adding of PVP to the lysis buffer the volume dilates by approx. 33%, thus 350 µL were used for lysis. Lysates were cleared for 5 min at 14680 rpm and 200 µL were transferred to 0.5 mL Eppendorf tubes adding 7.5 µL NucleoMag® C-Beads. After the washing steps according to the protocol tubes were centrifuged for 30 s at 14680 rpm to remove liquid from the lid. Elution was performed for 10 min at 50 °C and 300 rpm in a thermomixer. To get rid of slime in the samples they were centrifuged for 3 min at 14680 rpm before storing the supernatant for later analyses. Concentration and purity of eluted DNA were measured using a spectrometer (Nanophotometer P300, Implen, Munich, Germany).

DNA amplification/PCR conditions

Microsatellite markers designed for the analysis of the domesticated apple *Malus ×domestica* BORKH. (Gianfranceschi, Seglias, Tarchini, Komjanc, & Gessler, 1998; Liebhard et al., 2002), whose transferability to other Rosaceae was proven (Liebhard et al., 2002) and which showed results in several studies in *Crataegus* spp. (Betancourt-Olvera, Nieto-Ángel, Urbano, & González-Andrés, 2018; J. A. Brown et al., 2016; Coughlan, Han, Stefanović, & Dickinson, 2017; Dickinson et al., 2007; Dickinson, Lo, Talent, & Love, 2008; Emami et al., 2018; Khiari, Boussaid, & Messaoud, 2015; Lo, Stefanović, & Dickinson, 2009; Lo, Stefanović, Ritland, & Dickinson, 2010; Piedra-malagón, Albarrán-lara, Rull, Piñero, & Sosa, 2016), were chosen for this study. In total nine SSR loci (CH01D03, CH01F02, CH01F07, CH03C02, CH04F06, CH04G04, CH05D04, CH05G07, and CH05G11) of linkage group (LG) 4, 10, 12, and 14 were tested. These LGs contain perfect dinucleotide tandem repeats except CH05G07 and CH05G11, which contain imperfect dinucleotide repeats (Liebhard et al., 2002). As two loci, CH01D03 and CH01F07, were proven to be hard to amplify they were discarded from further analysis. The remaining seven primer are characterised in Table 5.

Table 5 Information on the selected microsatellite markers. Nucleotide sequences and size range of each locus from two linkage groups (LG) and PCR conditions are provided.

Locus	Maps on LG	Forward primer sequence (5’–3’)	Reverse primer sequence (5’–3’)	T_a (°C)	Cycles 1./2. PCR	Size range (bp)	Pool
CH01D03	4	CCGCTTGGCAATGACTCCTC	ACCCTGAAGCCATGAGGGC			125–149	
CH01F02	12	ACCACATTAGAGCAGTTGAGG	CTGGTTTGTTTTCCTCCAGC	57.4^B	35/–	149–189	1^b
CH01F07	10	CCCTACACAGTTTCTCAACCC	CGTTTTTGGAGCGTAGGAAC			149–263	
CH03C02	12	TCACTATTTACGGGATCAAGCA	GTGCAGAGTCTTTGACAAGGC	57.2^B	35/35^M	108–123	2^b
CH04F06	14	GGCTCAGAGTACTTGCAGAGG	ATCCTTAAGCGCTCTCCACA	55.0	35/35^M	166–187	2^g
CH04G04	12	AGTGGATGATGAGGATGAGG	GCTAGTTGCACCAAGTTCACA	57.0^B	35/–	145–186	1^g
CH05D04	12	ACTTGTGAGCCGTGAGAGGT	TCCGAAGGTATGCTTCGATT	56.4	35/35^M	173–184	2^b
CH05G07^i	12+14^m	CCCAAGCAATATAGTGAATCTCAA	TTCATCTCCTGCTGCAAATAAC	58.3	30+8^M/–	153–173	2^y
CH05G11^i	14	GCAAACCAACCTCTGGTGAT	AAACTGTTCCAACGACGCTA	58.0^B	30+8^M/–	203–271	1^g

Data in the first four columns is represented from Liebhard et al. (2002).
T_a = primer specific annealing temperature;
[B] PCR was performed with additives (betaine and BSA);
[M] primer was end-labelled with the M13-sequence and amplified at T_a = 53 °C (Schuelke, 2000);
[b] PCR products labelled with FAM™;
[g] PCR products labelled with HEX™;
[i] locus contains imperfect dinucleotide repeats;
[m] locus appears as multilocus;
[y] PCR products labelled with NED™.

PCR amplifications were all performed in a 20 µL volume using different modified protocols: (**1**) Loci CH01F02 and CH04G04 were amplified according to Gianfranceschi et al. (1998). Reactions contained ~2 ng of genomic DNA, 0.2 mM of each dNTP, 0.75 M betaine monohydrate, 4.0 ng bovine serum albumin (BSA), 1.25 U of Dream *Taq* Polymerase (Thermo Fisher Scientific, Darmstadt, Germany), 2.0 µL 10x PCR buffer, and 0.2 µM each of the forward and reverse primers, the forward primers end-labelled with the fluorescent dyes FAM™ or HEX™. (**2**) Loci CH05G07 and CH05G11 were amplified according to the 'poor man's approach' of Schuelke (2000). Reactions contained ~2 ng of genomic DNA, 0.2 mM of each dNTP, 2.5 U of Dream *Taq* Polymerase, 2.0 µL 10x PCR buffer,0.04 µM forward primer end-labelled with the M13-sequence, and 0.16 µM each of the M13-forward and reverse primers, the M13-forward primers end-labelled with the fluorescent dyes NED™ or HEX™. The additives betaine and BSA were excluded in CH05G07. (**3**) The remaining loci CH03C02, CH04F06, and CH05D04 failed in the 'poor man's approach' but were able to be amplified in a sequence of both protocols using a 1:100 dilution of first PCR product as template in the second PCR with FAM™, HEX™, and NED™ as dyes of end-labelled M13-forward primers. The additives betaine and BSA were excluded in CH04F06 and CH05D04. Dye colours of each locus were chosen in accordance to the estimated product sizes for post-PCR poolplexing of samples (Table 5).

All amplifications were performed in an Eppendorf Mastercycler nexus GSX1 (Eppendorf, Hamburg, Germany) with an initial denaturation at 94 °C for 2:30 min followed by 35 cycles of 94 °C for 0:30 min, respective annealing temperature (T_a, see Table 5) for 1:00 min, 72 °C for 1:00 min. A final 10 min 72°C extension was included. In case of the 'poor man's approach' the number of cycles was reduced to 30 with another eight cycles of 94 °C for 0:45 min, 53 °C for 0:45 min, 72 °C for 1:00 min added. In the second PCR of the two-step approach the number of cycles was 35.

2.4.2 | Microsatellite marker analysis

Product sizes were measured in capillary electrophoresis with 500 ROX™ as internal size standard at LGC Forensics, Cologne, Germany. Retrieved FASTA data was then analysed with Peak Scanner™ software v2.0 (Applied Biosystems). According to good practice, a subset of samples was screened for each locus at a time to identify possible allele sizes and irregular patterns, such as stutters, pull-ups, minus-adenine peaks, and dinosaur tails (Pan, 2006). As the automated output table of peaks for each primer contained decimal values and a rounding algorithm did not always fit to the peak pattern of visualised FASTA files in Peak Scanner™, both data were compared by eye to pick the true allele sizes and set them to integers. In case of split peaks the true plus-adenine peak was scored even if the height was lower than the minus-adenine peak. These data tables with every peak in a single row were transformed to tables with individuals in rows and the first to the n^{th} allele in columns, with n equal to the maximum allele number of all samples in all loci which was four. If a certain sample showed no alleles in any locus the respective first allele was treated as null allele and thus set to '0'. Any other missing data from the second allele onwards was considered as not available (*NA*). SSR scoring results are presented in Table S7. This data was used to estimate ploidy level of each sample as the maximum number of alleles across the loci based on the expectation that a n-ploid has a maximum of n different alleles per locus (Mishina et al., 2014; Seeber et al., 2014). Due to the ability of the '`poppr`' v2.9.0 package (Kamvar et al., 2014; Kamvar et al., 2015) with its dependencies on '`adegenet`' v2.1.3 package (Jombart, 2008; Jombart & Ahmed, 2011) and '`ade4`' v1.7-16 package (Bougeard & Dray, 2018; Dray & Dufour, 2007; Thioulouse et al., 2018) to deal with both challenges, data of ploidy levels other than two and multiple ploidies, at the same time this was chosen for further analysis. Therefore, raw data was written in GenAlEx file format (Peakall & Smouse, 2006) to be imported by '`read.genalex`' function. Hereby the *NA* status of data had to be coded as '0'. By the fact of CH05G07 being a multilocus marker, this marker was excluded from analysis unless disregarding had only little effect on the outcome.

Hardy-Weinberg-equilibrium

Hardy-Weinberg-equilibrium (HWE) was calculated for all loci of all sample groups by '`hw.test`' of '`pegas`' v0.14 package (Paradis, 2010) with a dependency on '`ape`' v5.4-1 package (Paradis & Schliep, 2019) and then statistically tested under the null hypothesis of no significant difference between observed and expected values. Therefore, a classical chi-squared test and an exact test based on Monte Carlo permutations of alleles (Guo & Thompson, 1992) were considered. By computational burden tests were available for a unique ploidy level only and the latter test solely for data sets of diploids. Thus calculations of HWE were run with subsets by ploidy levels. Tests were also performed by species to assure that the overall outcome is not biased by the structure of the data set. For visualisation '`levelplot`' of '`lattice`' v0.20-41 package (Sarkar, 2008) was used.

Linkage disequilibrium

Genotypic linkage disequilibrium (LD) was calculated as index of association $\bar{r}_d$ (Agapow & Burt, 2001) by function '`ia`' of '`poppr`' package to reveal independence among the SSR markers. '`sample = 999`' was applied as setting to receive p values by a permutation test with null hypothesis of no linkage among loci. Computations were performed for the overall data set, for the ingroup, and for each species of the ingroup, as well as by ploidy level for all of these sets if a single subset had at least four individuals. To ensure that the pattern of linkage disequilibrium seen is not due to a single pair of loci or among a single species calculations were additionally conducted over all pairs of loci and over all seven species of the ingroup with function '`pair.ia`'. For visualisation purposes '`plot_grid`' of '`cowplot`' v1.1.1 package (Wilke, 2020) was applied.

Genotypic variation and molecular diversity

Parameters of genotypic variation and molecular diversity were calculated using SPAGEDI v1.5 (Hardy & Vekemans, 2002) and POLYGENE v1.3 (Huang et al., 2020) as both pieces of software cope with the analysis of data sets containing samples of multiple ploidy levels and the latter is able to manage multiple hierarchies. This functionality was made use of as there is just one unique ploidy level per population allowed. Therefore, samples belonging to the same species had to be split by ploidies into populations 'species_n', with n equal to each of the ploidy levels of the respective species. These populations were bound together as 'species' on the next hierarchical level. This method was applied for all species and samples except members of the outgroup. They have been grouped despite their species level into 'Mispel' (medlars and their graft-chimeras), 'EUR', and 'NAm' (see 2.1). A second level was set up to fuse members of the ingroup and the outgroup into metapopulations 'In' and 'Out', respectively.

Conducted parameters were the total number of individuals genotyped at a locus N_G; the number and proportion of missing or incomplete genotypes $N_{G?}$ and N_{Gi}, respectively; the total number of defined gene copies at a locus N_{GC}; the number of distinct alleles at a locus with non-zero frequency N_A, where the null allele is also considered; the number of private alleles N_{Ap}, where private alleles are the alleles only present in the respective (meta)population; the effective number of alleles, N_{Ae}, as the number of alleles with equal frequencies that would be necessary to provide the same expected heterozygosity, whose value at a locus is $1/\sum_{j=1}^{J}\hat{P}_j^2$, where $\hat{P}_j$ is the frequency of the j^{th} allele A_j at this locus; the mean allele size $\bar{A}$ and the variance of allele size Var(A) at a locus; the allelic richness A_R, as the average number of alleles per locus corrected by sample sizes; the observed heterozygosity H_o, that is the observed average proportion of loci carrying two different alleles at a single locus within an individual; the expected heterozygosity in the current group (gene diversity corrected for sample size) H_e, whose value at a locus is $1 - \sum_{j=1}^{J} \hat{P}_j^2$; the polymorphic information content *PIC*, that is the probability of the marker genotype of the offspring of a heterozygous parent allowing one to deduce which marker allele the offspring inherited from the parent, whose value at a locus is $2\sum_{1 \le i < j \le J} \hat{P}_i \hat{P}_j (1 - \hat{P}_i \hat{P}_j)$; Shannon's information index *H'*, whose value at a locus is $-\sum_{j=1}^{J} \hat{P}_j ln \hat{P}_j$; Pielou's evenness *E*, whose value at a locus is H'/lnN_A; the inbreeding coefficient per group F_{IX}, which is defined as the probability of sampling two identical-by-descent (IBD) alleles from an individual without replacement, whose value is estimated by $1 - H_I/H_X$, where the H_I is the heterozygosity index within individuals (i.e. H_o), H_X is the expected heterozygosity in the current group (i.e. H_e), and $F_{\mathrm{SX}}/F_{\mathrm{C1X}}/F_{\mathrm{C2X}}$, the *F*-statistics among populations or regions within this group (say *X*), which is defined as the probability of sampling two identical-by-descent (IBD) alleles from a population or a region without replacement, whose value is estimated by $1 - H_S/H_X$, where the H_S is the weighted average of expected heterozygosity of populations or regions with the number of allele copies as the weight, and H_X is the expected heterozygosity of this group. These parameters were assessed by locus for the overall and the ingroup data set separately and as multilocus average for each species of the ingroup classified according to morphology a priori and for each genetic group classified according to an a posteriori clustering approach (see next section).

Genetic structure and differentiation

The overall level of genetic differentiation between species was estimated by calculating the ANOVA-based global and pairwise measure of genetic structure and the genetic distance with significant p values of two-sided tests obtained after 9,999 random permutations of allele sizes, genes, individuals, and populations within SPAGEDI. Jackknifed estimates and their standard errors received by the jackknife procedure of deleting each locus at a time were calculated as well. For these computations both models, the infinite allele model (IAM; based on allele identity with all alleles resulting equally likely from a mutation; Cockerham, 1973; Kimura & Crow, 1964) for *F*-statistics (Weir & Cockerham, 1984) and the stepwise mutation model (SMM; based on allele size with allelic evolution by stepwise adding or subtracting single repeat units; Ohta & Kimura, 1973; Slatkin, 1995) for *R*-statistics (Rousset, 1996; Slatkin, 1995) were considered. An overview of the different estimators is presented in Table 6.

To verify whether analysis is affected by the different mutation models the concordance of the respective pair of estimators between the given models was tested by Mantel tests in R. The Mantel statistic r_M was computed as Pearson correlation of 99,999 permutations with the '`mantel`' function of the '`vegan`' package.

As measure of the hierarchical genetic structure the analysis of molecular variance (AMOVA) (Excoffier, Smouse, & Quattro, 1992; Michalakis & Excoffier, 1996) was conducted within the generalised framework of PolyGene for AMOVA with multiple hierarchies and ploidies (Huang et al., 2021). AMOVA was performed for all combinations of data sets ($n = 302$ and $n = 278$) and annotations (morphological and genetic, see next paragraph) by taking IAM and SMM distances under the weight genotype method into account. p values were obtained by significance tests with 99,999 permutations.

Table 6 Parameters of genetic differentiation.

model	measure of genetic structure	genetic distance
based on allele identity under infinite allele model (IAM)	F_{ST} (Wright, 1965)	Ds (Nei, 1978)
based on allele size under step-wise mutation model (SMM)	R_{ST} (Slatkin, 1995)	$(\delta\mu)^2$ (Goldstein et al., 1995)

In addition to AMOVA, genetic clusters were detected by using the Bayesian clustering approach introduced by Pritchard et al. (2000) and extended in sequels by Falush et al. (2003, 2007). Implemented in the program STRUCTURE v2.3.4, this approach tries to identify K groups under varying assumptions about Hardy-Weinberg and linkage equilibria. Therefore, a range of K values (i.e. $K = 1–20$) is applied to estimate posterior probabilities using a Markov chain Monte Carlo (MCMC) method. After a burn-in period of 10,000, 100,000 replicates of each chain were performed for each value of K and 20 repeats per run. The no-admixture model and a ploidy of n (as above) were applied as settings. The most likely K modal distribution, ΔK, a quantity related to the second order rate of change with respect to K of the likelihood function (Evanno, Regnaut, & Goudet, 2005), was identified by using STRUCTURE HARVESTER v0.6.94 (Earl & vonHoldt, 2012). The most probable cluster membership coefficient (Q) among the 20 runs of STRUCTURE and STRUCTURE HARVESTER was verified in CLUMPP v1.1.2 (Jakobsson & Rosenberg, 2007). Corresponding graphs were constructed with DISTRUCT v1.1 (Rosenberg, 2004). As a result of an inhomogeneous picture samples were rearranged by eye to harmonise according to their portions of cluster memberships. This classification into 21 genetic groups was reapplied as different set of annotation or colouring scheme within analyses were appropriate.

Ordination of molecular data

To reveal relationships at species and genetic group level matrices of pairwise *D*s values received from PolyGene were used to build unrooted neighbour-joining (NJ) trees with function '`nj`' of '`ape`' package. Relationships between individuals were visualised by unrooted NJ trees with 1000 bootstraps based on Bruvo's distance. They were constructed from the allelic raw data in '`poppr`' package by '`bruvo.boot`' function with '`replen = 2`', '`tree = "njs"`', '`cutoff = 50`', and '`root = FALSE`' as settings. As some branch lengths of the tree were negative branches were normalised according to Kuhner and Felsenstein (1994). For visualisation purposes the function '`ladderize`' of '`ape`' package and the '`plotrix`' v3.8-1 package (Lemon, 2006) were applied. The morphological and the genetic classification as well as the estimated ploidy level served as graphical parameter for colour and font type of the leaves.

Additionally a NMDS was performed in the same way as those of the morphological analysis (see 2.3.2). The required distance matrix was computed by passing a zero-one matrix of the allelic counts to the '`vegdist`' function of the '`vegan`' package. To avoid an overestimation of double zeroes the Bray-Curtis distance was chosen by setting '`method = bray`'.

2.5 Comparison of morphological and genotypic data and annotations

Mantel test

To examine the correlation of the morphological with the genetic data set of the ingroup a mantel test was conducted. To do so a Gower's distance matrix of the basic morphological trait data (for details see 2.3.2) and a Bray-Curtis distance matrix of the allelic data (for details see previous paragraph) were calculated. Like before r_M of both matrices was obtained as Pearson correlation of 99,999 permutations.

Boxplot

Within the ingroup the genetic annotation drawn from the structure analysis was tested for correlation with the morphological one. As the values of the different annotations are of ordinal nature and exact *p* values could not be computed with ties in the data Kendall's τ was chosen by setting '`method = "kendall"`' in the '`cor.test`' function in R. Results were visualised by a boxplot diagram.

Combined plotting

Plotted results of the multivariate analysis of the morphological data (see 2.3.2, 3.2.2) were supplemented by the genetic annotation (see 2.4.2, 3.3.3) so that points belonging to the same genetic group were connected with the centroids calculated for all these points.

Population assignment

Within POLYGENE the assignment of each individual was performed by calculating the likelihoods for each population according to Paetkau, Slade, Burden, and Estoup (2004). Like for AMOVA this was done for the four combinations of sample size and classification. All these results were compared pairwise according to their annotation to detect outliers which are individuals assigned to the same species or group in the overall and the ingroup data. The quantity of outliers was visualised by their kind, i.e. morphological, genetic or regional (belonging to the ingroup or the outgroup) in a Venn diagram with '`ggVennDiagram`' v1.2.0 package (Gao, 2021).

3 | Results

3.1 | Reproductive modes

The number of developed fruit of the experiments on reproduction is shown in Table 7 and Figure 4. None of the tests in autogamy (53 replicates), geitonogamy (48 replicates) and apogamy (106 replicates) set fruit. Among the uncovered controls only *C. monogyna* (ID 1094) and *C. macrocarpa* (ID 1081) set fruit in depetaled and emasculated conditions, one out of eleven (9%) and three out of 21 (14%) respectively. The other individual of the latter species (ID 1068) set two out of 24 (8%) in depetaled conditions.

In the allogamous experiments (Figure 4) intraspecific crosses showed unequal results. Regardless the involved species fruit set rate was either 0% or about one quarter to one half. While in *C. laevigata* nine out of 20 (45%) flowers converted to fruit, there was no fruit set in reciprocal experiments (20 + 17 replicates) on *C. macrocarpa*. Interspecific pollen transfer of *C. laevigata* (ID 1095) did not lead to fruit set on either *C. monogyna* or *C. subsphaerica*, but on *C. macrocarpa* (ID 1068) with four out of 18 (22%). Pollen transfer among *C. monogyna*, *C. subsphaerica*, and *C. rhipidophylla* resulted in some fruit with fruit conversation rates ranging from 25% (*C. monogyna* → *C. subsphaerica*) to 44% (*C. rhipidophylla* → *C. subsphaerica*). Results of one cross (*C. rhipidophylla* → *C. monogyna*) could unfortunately not be detected as the marked branch with manipulated flowers was removed prior harvest.

Table 7 Fruit set of the non-allogamous reproduction experiments in *Crataegus*. The estimated ploidy level (see Table S7) of individuals and their membership to the respective genetic groups (see 3.3.3) are provided highlighted by colours in compliance with those in Figure 1 and Figure 34, respectively.

				covered			uncovered	
ID	species	group	ploidy	auto-gamy	geitono-gamy	apo-gamy	depetaled	depetaled & emasculated
1066	*C. laevigata*	7	2*x*			16 → 0		
1095	*C. laevigata*	7	2*x*		15 → 0	15 → 0	16 → 0	
1068	*C. macrocarpa*	5.5	3*x*	19 → 0	17 → 0	17 → 0	24 → 2	21 → 0
1081	*C. macrocarpa*	6	3*x*	19 → 0		20 → 0	21 → 0	21 → 3
1094	*C. monogyna*	2.3	2*x*			14 → 0		11 → 1
1072	*C. subsphaerica*	2	3*x*	15 → 0	16 → 0	14 → 0	12 → 0	15 → 0
1087	*C. rhipidophylla*	2	2*x*			10 → 0		
		Total		**53 → 0**	**48 → 0**	**106 → 0**	**73 → 2**	**68 → 4**

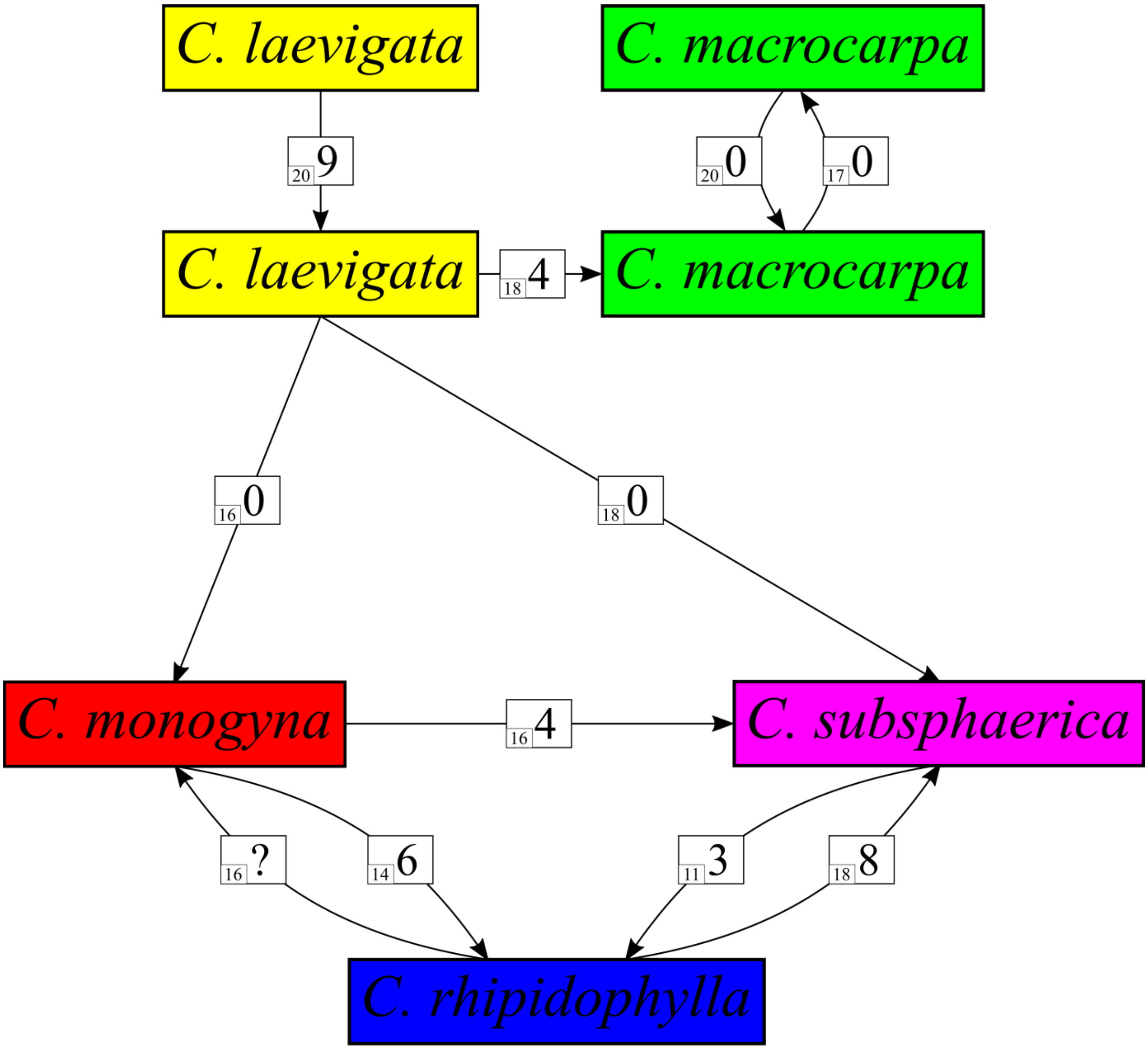


Figure 4 Results of allogamous breeding experiments in *Crataegus*. Arrows display the direction of pollen transfer to the mother tree, numbers indicate the amount of fruit set of a respective cross-pollination while the small numbers indicate performed crosses.

3.2 | Morphological data

3.2.1 | Correlation of trait data

Values of cross correlation of the overall trait data are presented in Table S5. 39 of the 276 combinations of traits show an absolute value of Spearman's ρ greater than 0.5, of which all are highly significant. Among these are 16 pairs of basic traits that take the largest values of correlation among the ingroup (Figure 5) indicating that these traits own the most explanatory power of the morphological *Crataegus* data.

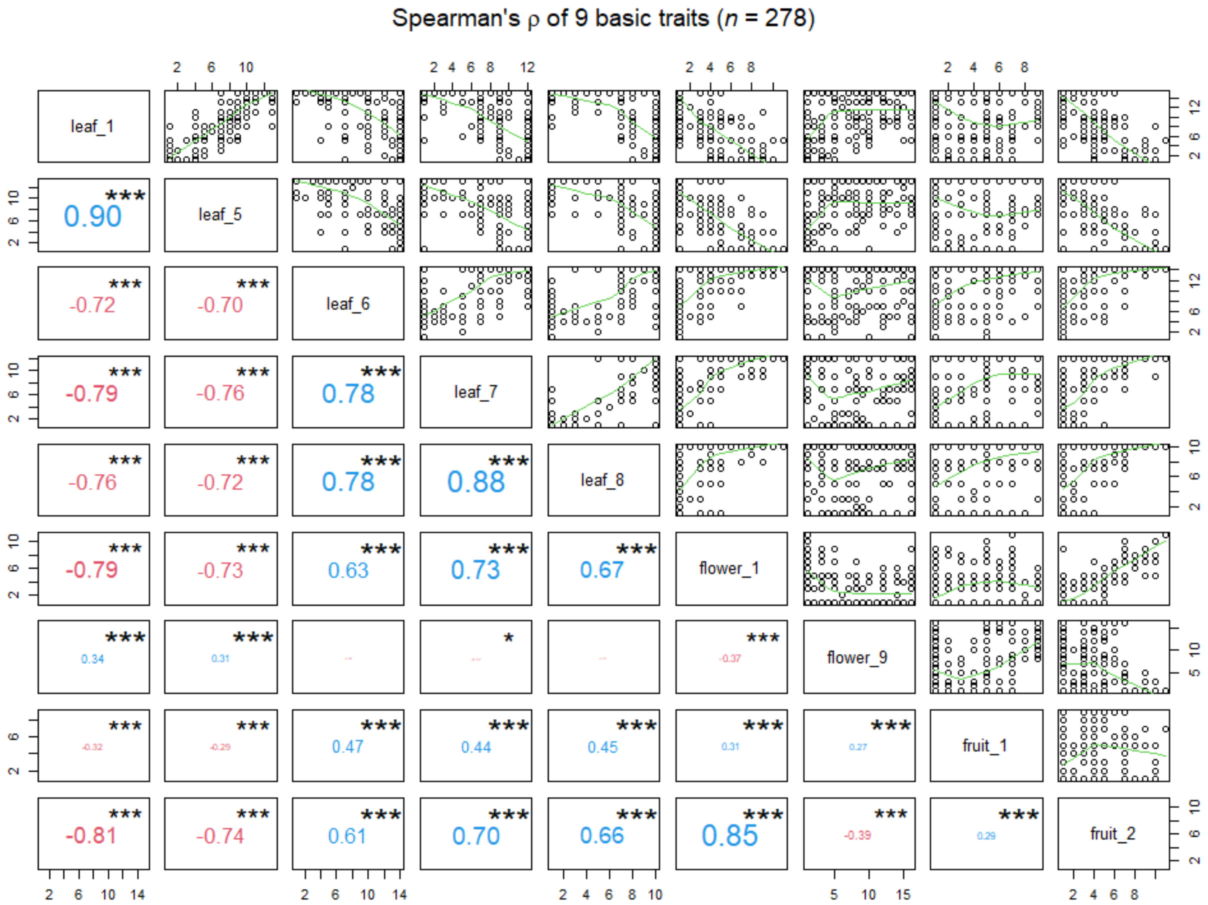


Figure 5 Multi-panel scatterplot of basic trait data (n = 278). Traits are indicated by item and consecutive number in compliance with those in Table 4 and written in the diagonal of the panel matrix. The upper/right panels show pairwise scatterplots with a regression line in green between each pair of traits, and the lower/left panels contain the respective Spearman's rank correlation coefficient ρ. The font size of the correlation coefficient is proportional to its absolute value, negative values are highlighted in red and positive ones in blue. Codes of significance (0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1) are given right above the respective correlation coefficient.

3.2.2 | Ordination of trait data

The value of stress for ordination of the data set in k dimensions via performing NMDS including and excluding the outgroup ranges from lowest 4.43% with just basic traits for six dimensions to 38.12% with just additional traits and one dimension and 4.28% to 39.67%, respectively (Table 8). As calculations show a more or less clear elbow criterion at $k = 3$ (left panels of Figure 6, Figure 8, Figure 9, Figure 12, Figure 13, and Figure 17) this number of dimensions was chosen in every set for further analyses. Although differing in their quality all analyses show similar plot distribution for the main morphological clusters. For the purpose of comparison all three sets of traits of the overall (n = 302) and the ingroup data set (n = 278) are plotted (Figure 7, Figure 10, Figure 11, Figure 14, Figure 15, and Figure 16).

Despite the number and kind of the trait data analysed the plots of the overall data set (Figure 7, Figure 10, and Figure 11) clearly show that the North American outgroup (*C. arnoldiana*, *C. intricata*, *C. punctata*, and *C. succulenta*; depicted by the first letter of the respective specific epithet) and the medlars (*C. germanica*; depicted by brown squares) lie well apart from the other Eurasian taxa. This separation can be seen either along the first, the second or the third dimensional axis in the additional traits (Figure 10, top panel), all traits (Figure 11, top panel), or basic traits data set (Figure 7, bottom panel), respectively. The graft-chimeras (+*Crataegomespilus*; depicted by purple triangles), Southern and South-eastern European taxa (*C. azarolus*, *C. caucasica*, and *C. wattiana*; depicted by diamonds) are more or less located at the edge of the cluster formed by the ingroup set up by the Central European taxa (*C. laevigata*, *C. monogyna*, *C. rhipidophylla*, *C. lindmanii*; *C. media*, *C. macrocarpa* agg., and *C. subsphaerica* agg.; depicted by circles) in each of the plots. This in group is spread along the first dimensional axis in the basic and the all trait data set (Figure 7 and Figure 11) while it can only be assumed along axis two in the additional traits data set (Figure 10). Defined clusters of *C. monogyna*, *C. macrocarpa* agg., and *C. laevigata* appear from left to right along axis one or are not that well separated from each other from bottom to top along axis two, respectively. The samples of *C. subsphaerica* agg. are on the one hand totally overlapping with *C. monogyna* and on the other tending towards *C. macrocarpa* agg., while *C. rhipidophylla* is spread between these two. The small sample of *C. lindmanii* aggregate to a cluster completely sunk in *C. macrocarpa* agg. and *C. media* is located intermediate between its putative parents *C. monogyna* and *C. laevigata* tending more towards the latter, especially in the additional traits data set.

This overall picture remains the same when any of the three trait sets is analysed for the reduced data set with the ingroup only (Figure 14, Figure 15, and Figure 16). Although the additional traits variant (Figure 15) features a higher value of stress (16.59%) compared to the respective value of the overall set of samples (15.67%) this outcome is obvious, too. The lowest value of stress of all six analyses performed is 7.35% for the basic traits data of the ingroup (Figure 16). Therein the additional displayed information of estimated minimum number of ploidy (indirectly received from microsatellite marker analysis, see 3.3, Table S7) shows a clear pattern of distribution: diploids are almost exclusively to be found diametrically opposed along the first dimension within the clusters of *C. laevigata* and *C. monogyna* with the overlapping part of *C. subsphaerica* agg. while tri- and tetraploids appear in *C. lindmanii* and *C. macrocarpa* agg.

Table 8 Stress of NMDS by data sets and groups of traits. Trait groups according to Table 4.

n	*k*	9 basic traits	15 additional traits*	24 all traits*
302	1	20.57%	38.12% [nc]	27.23% [nc]
	2	11.90%	22.84%	17.36% [nc]
	3	8.07%	15.67%	11.96%
	4	6.29%	11.36%	9.14%
	5	5.13%	9.56%	7.66%
	6	4.43%	8.14%	6.74%
278	1	18.64%	39.67% [nc]	27.15%
	2	10.00%	23.38%	16.31%
	3	7.35%	16.59%	12.12%
	4	5.86%	12.72%	9.64%
	5	4.90%	10.59%	8.12%
	6	4.28%	9.00%	7.01%

k Number of dimensions after ordination; *n* number of samples; [nc] the algorithm showed no convergence within 1,000 runs.

Note: * As each of the traits leaf_4 (ending points of veins) and flower_7 (lower side of sepals hairy) have uniform values throughout the ingroup both have been excluded from the analyses of additional traits and all traits in the reduced data set (*n* = 278).

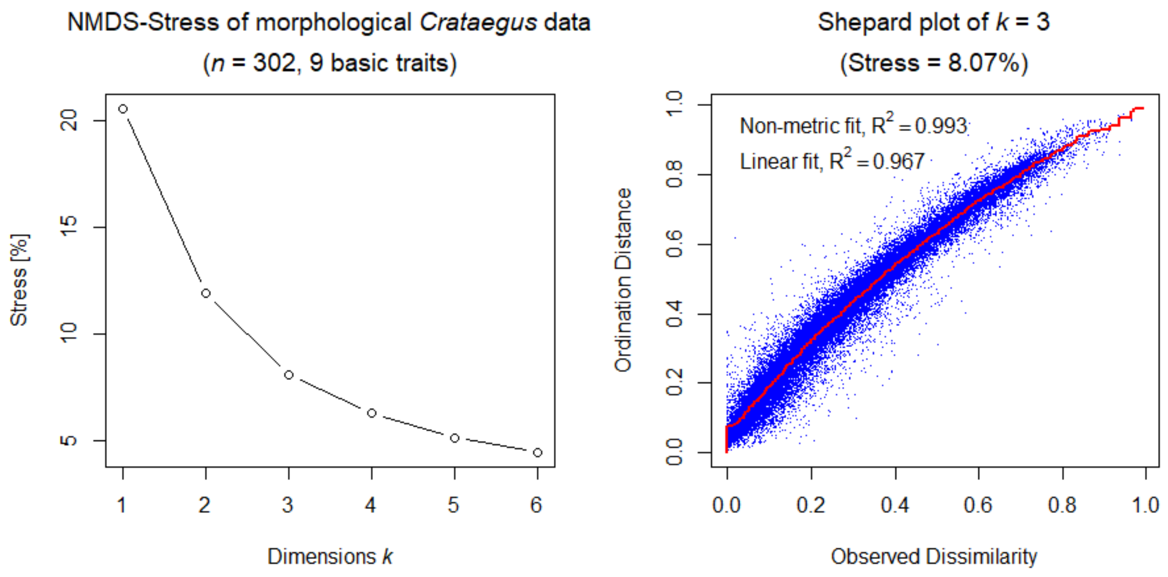
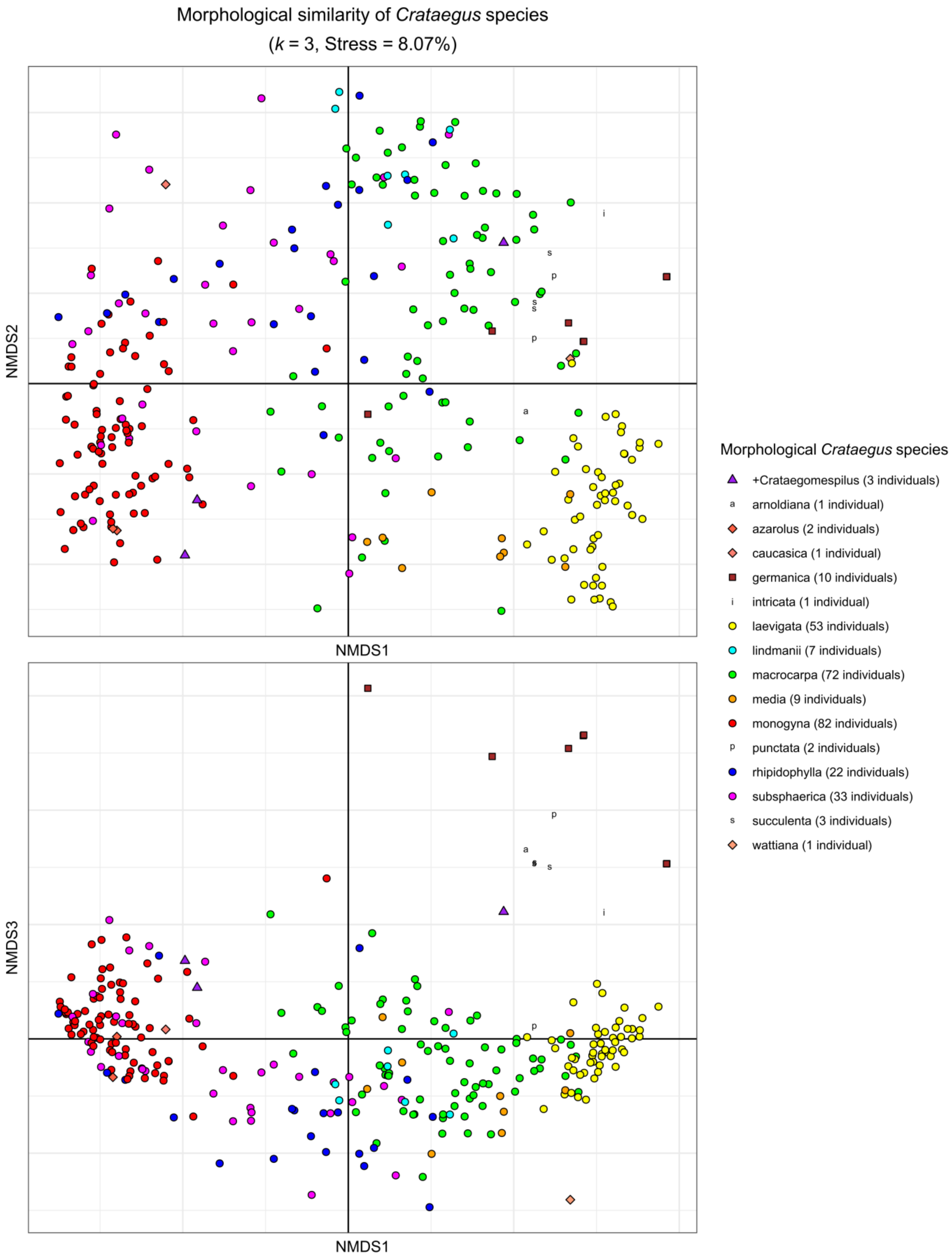


Figure 6 Stress of NMDS of the basic morphological traits data (*n* = 302). Left panel: Stress in relation to number of final dimensions (*k*) after dimensional reduction via NMDS. Right panel: Shepard plot of ordination distance against observed dissimilarity of the optimal *k* = 3 with a stress of 8.07%.



Source: 302 samples, 9 basic traits

Figure 7 NMDS ordination plot of the basic morphological traits data ($n = 302$). North American *Crataegus* are represented by letters while Eurasian *Crataegus* are by coloured symbols (in compliance with those in Figure 1). The ingroup of ser. *Crataegus* is depicted by circles. Number of samples of each group is given in parentheses. Top panel: The first two dimensions are shown. Bottom panel: The first and the third dimension are shown.

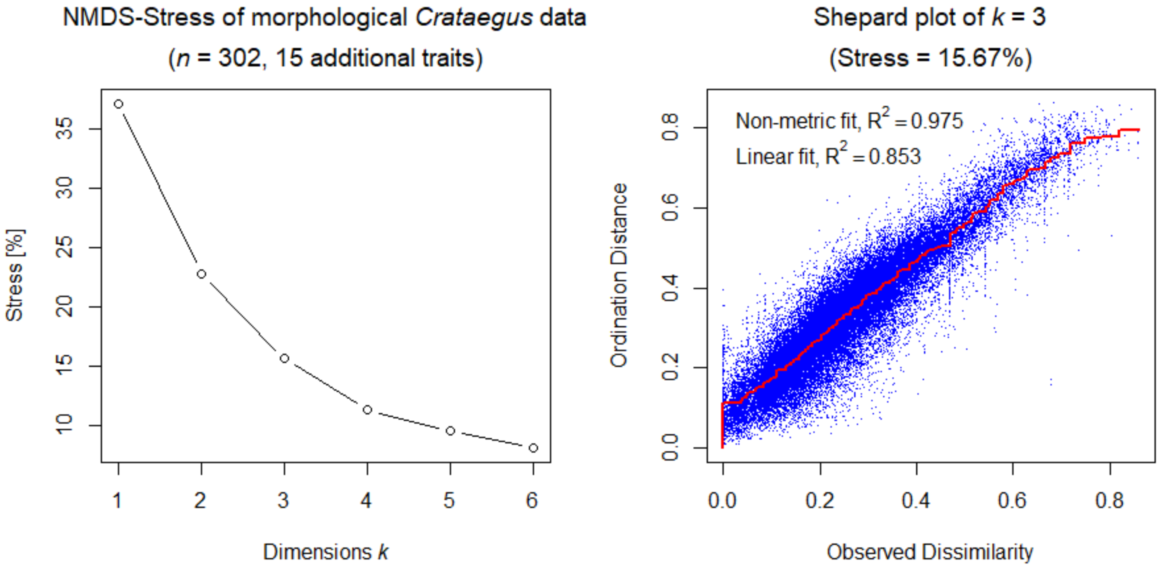


Figure 8 Stress of NMDS of the additional morphological traits data ($n = 302$). Left panel: Stress in relation to number of final dimensions (k) after dimensional reduction via NMDS. Right panel: Shepard plot of ordination distance against observed dissimilarity of the optimal $k = 3$ with a stress of 15.67%.

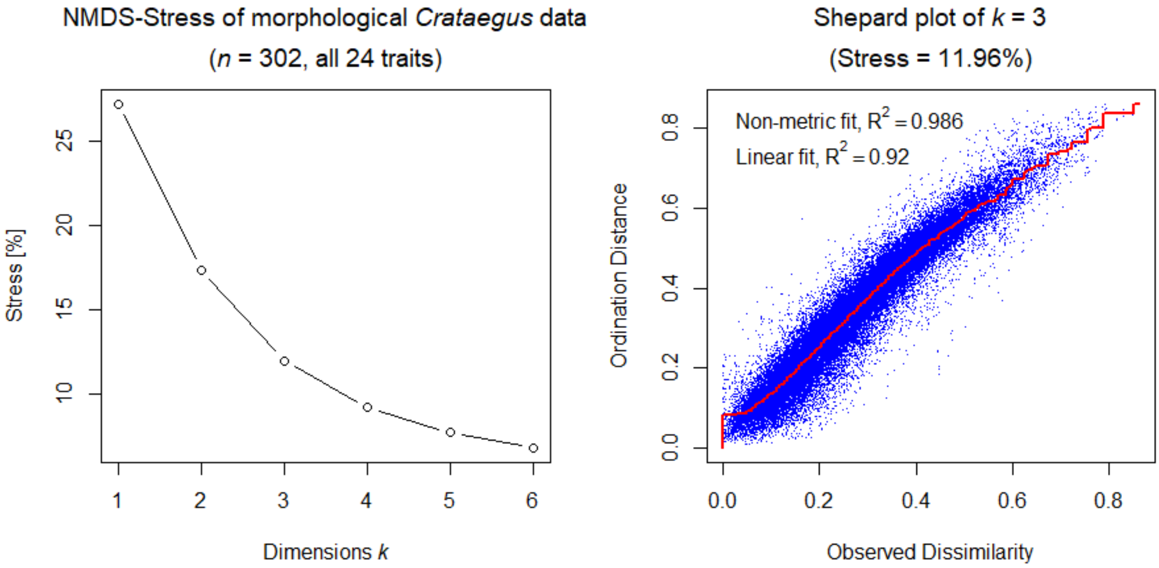
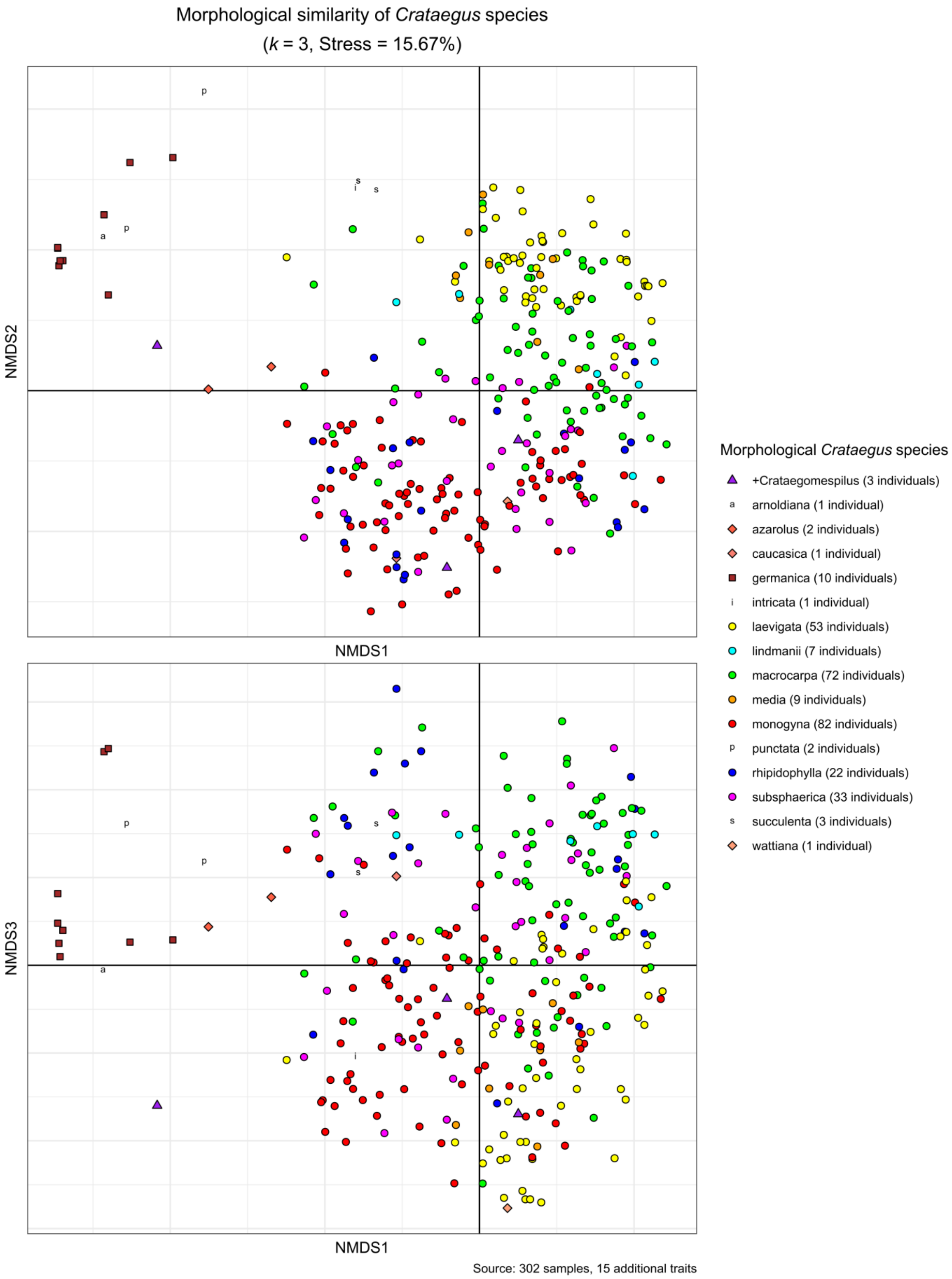
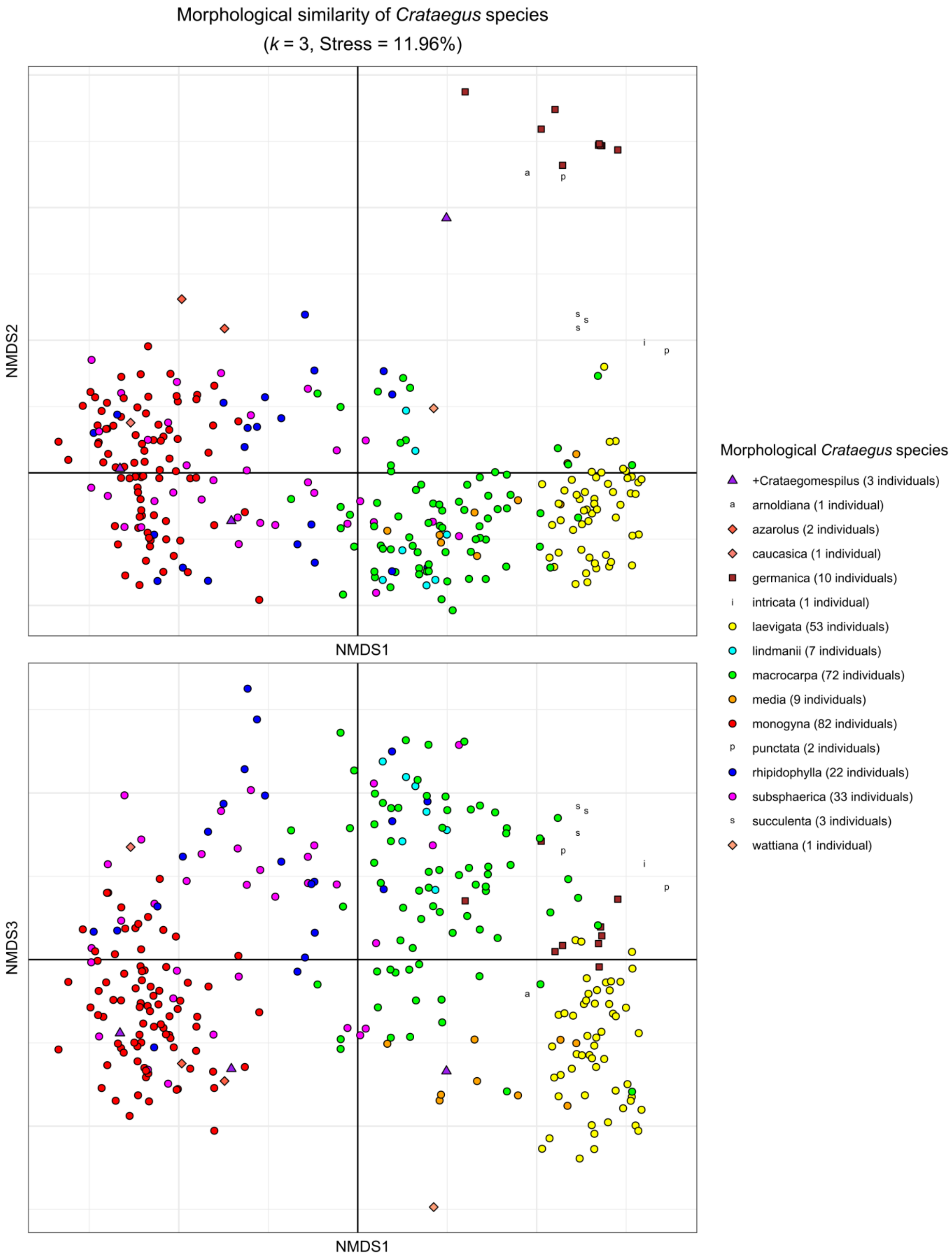


Figure 9 Stress of NMDS of the overall morphological traits data ($n = 302$). Left panel: Stress in relation to number of final dimensions (k) after dimensional reduction via NMDS. Right panel: Shepard plot of ordination distance against observed dissimilarity of the optimal $k = 3$ with a stress of 11.96%.



Source: 302 samples, 15 additional traits

Figure 10 NMDS ordination plot of the additional morphological traits data ($n = 302$). North American *Crataegus* are represented by letters while Eurasian *Crataegus* are by coloured symbols (in compliance with those in Figure 1). The ingroup of ser. *Crataegus* is depicted by circles. Number of samples of each group is given in parentheses. Top panel: The first two dimensions are shown. Bottom panel: The first and the third dimension are shown.



Source: 302 samples, all 24 traits

Figure 11 NMDS ordination plot of the overall morphological traits data ($n = 302$). North American *Crataegus* are represented by letters while Eurasian *Crataegus* are by coloured symbols (in compliance with those in Figure 1). The ingroup of ser. *Crataegus* is depicted by circles. Number of samples of each group is given in parentheses. Top panel: The first two dimensions are shown. Bottom panel: The first and the third dimension are shown.

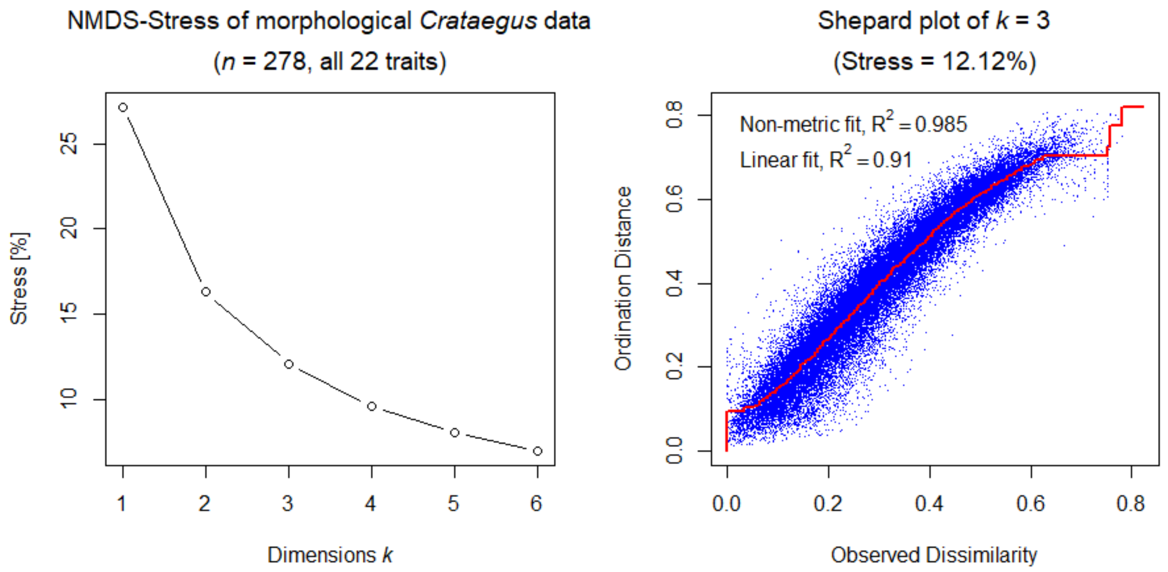


Figure 12 Stress of NMDS of the overall morphological traits data ($n = 278$). Left panel: Stress in relation to number of final dimensions (k) after dimensional reduction via NMDS. Right panel: Shepard plot of ordination distance against observed dissimilarity of the optimal $k = 3$ with a stress of 12.12%.

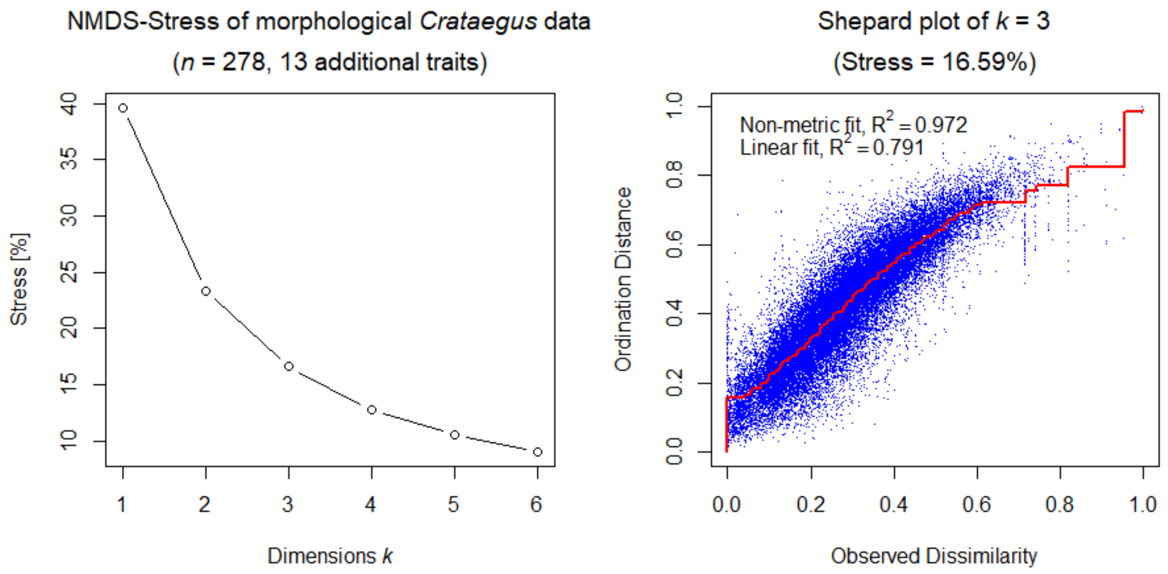
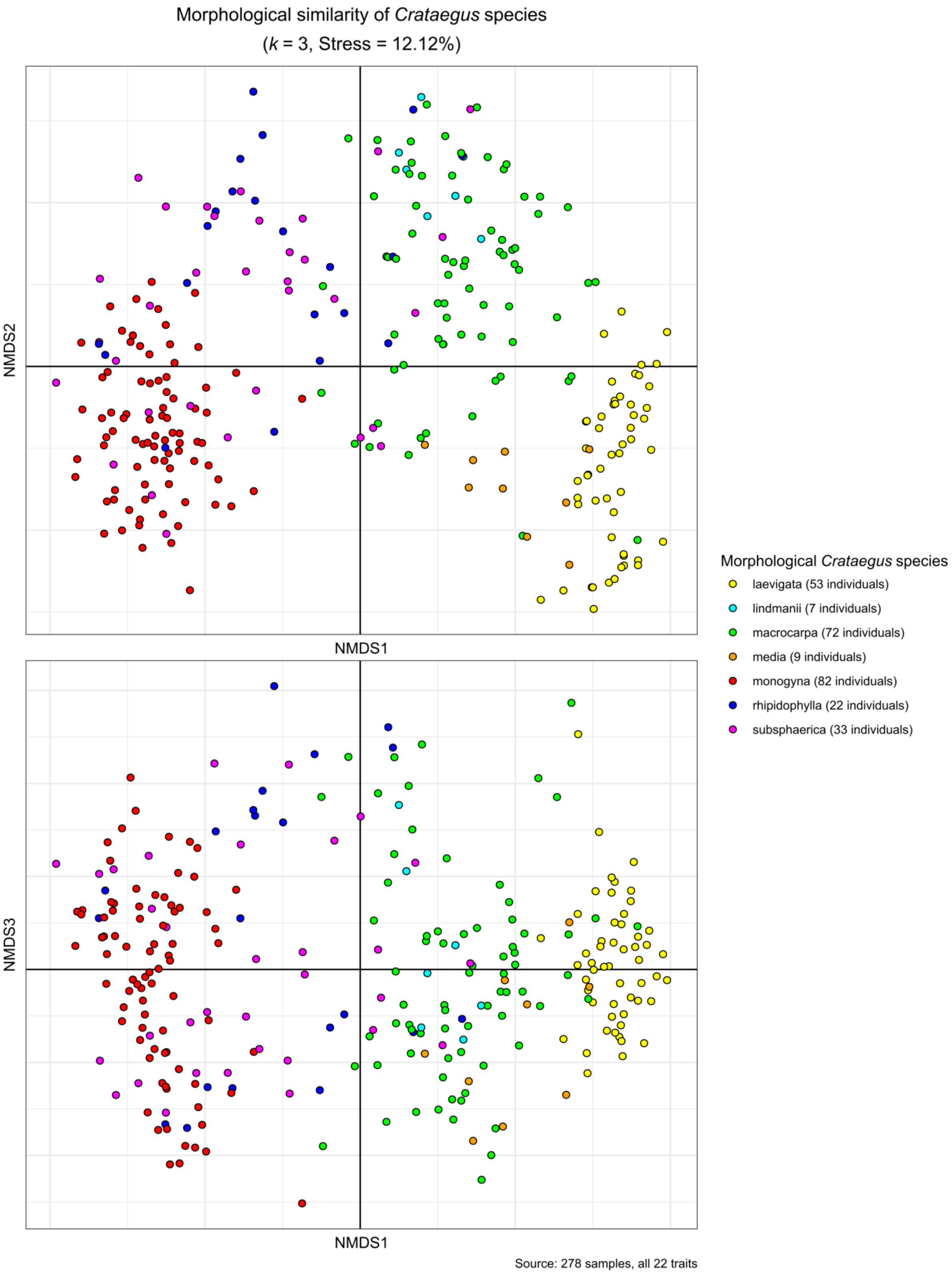
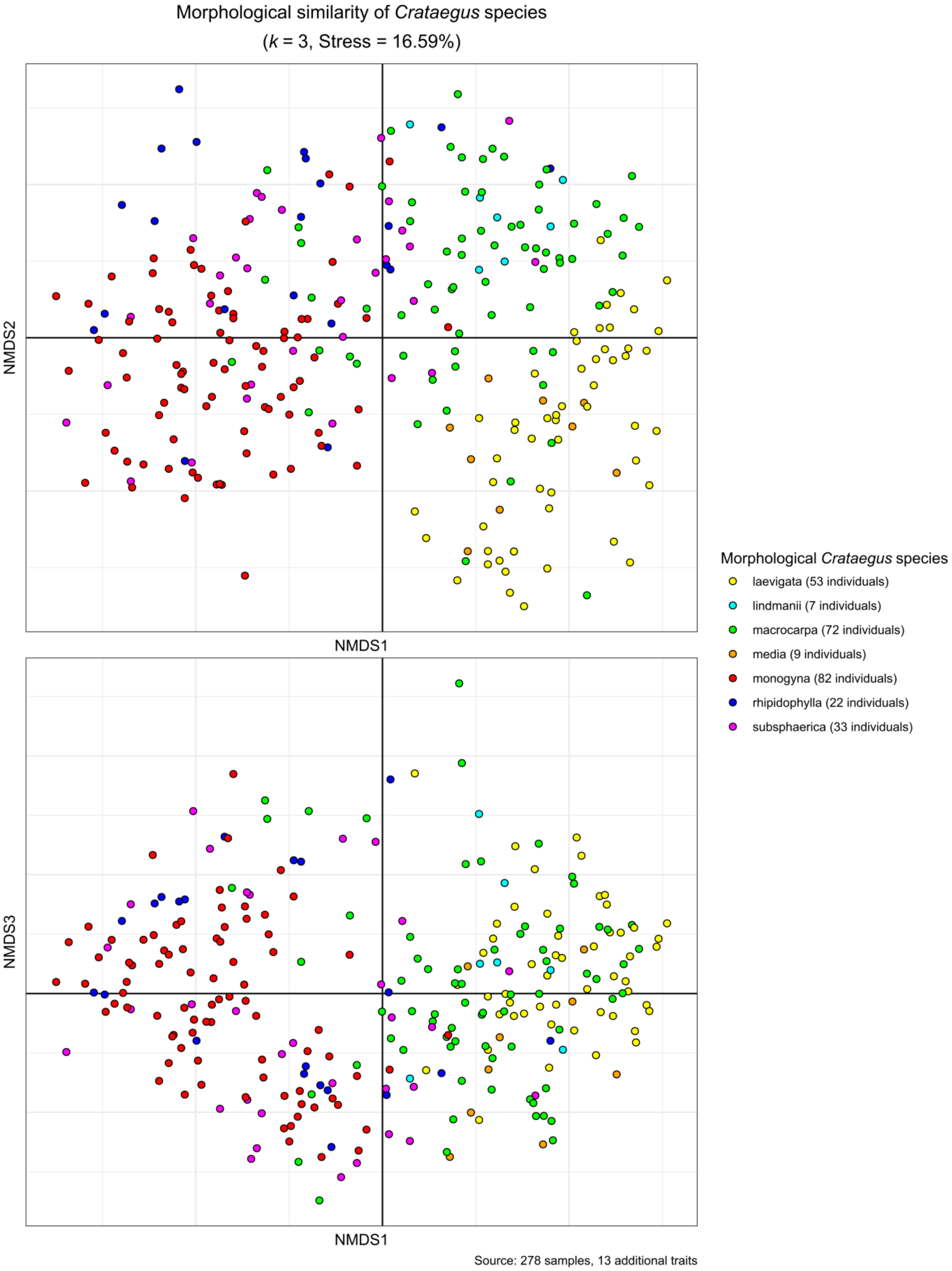


Figure 13 Stress of NMDS of the additional morphological traits data ($n = 278$). Left panel: Stress in relation to number of final dimensions (k) after dimensional reduction via NMDS. Right panel: Shepard plot of ordination distance against observed dissimilarity of the optimal $k = 3$ with a stress of 16.59%.



Source: 278 samples, all 22 traits

Figure 14 NMDS ordination plot of the overall morphological traits data ($n = 278$). The different species of ser. *Crataegus* are represented by colours (in compliance with those in Figure 1). Number of samples of each group is given in parentheses. Top panel: The first two dimensions are shown. Bottom panel: The first and the third dimension are shown.



Source: 278 samples, 13 additional traits

Figure 15 NMDS ordination plot of the additional morphological traits data ($n = 278$). The different species of ser. *Crataegus* are represented by colours (in compliance with those in Figure 1). Number of samples of each group is given in parentheses. Top panel: The first two dimensions are shown. Bottom panel: The first and the third dimension are shown.

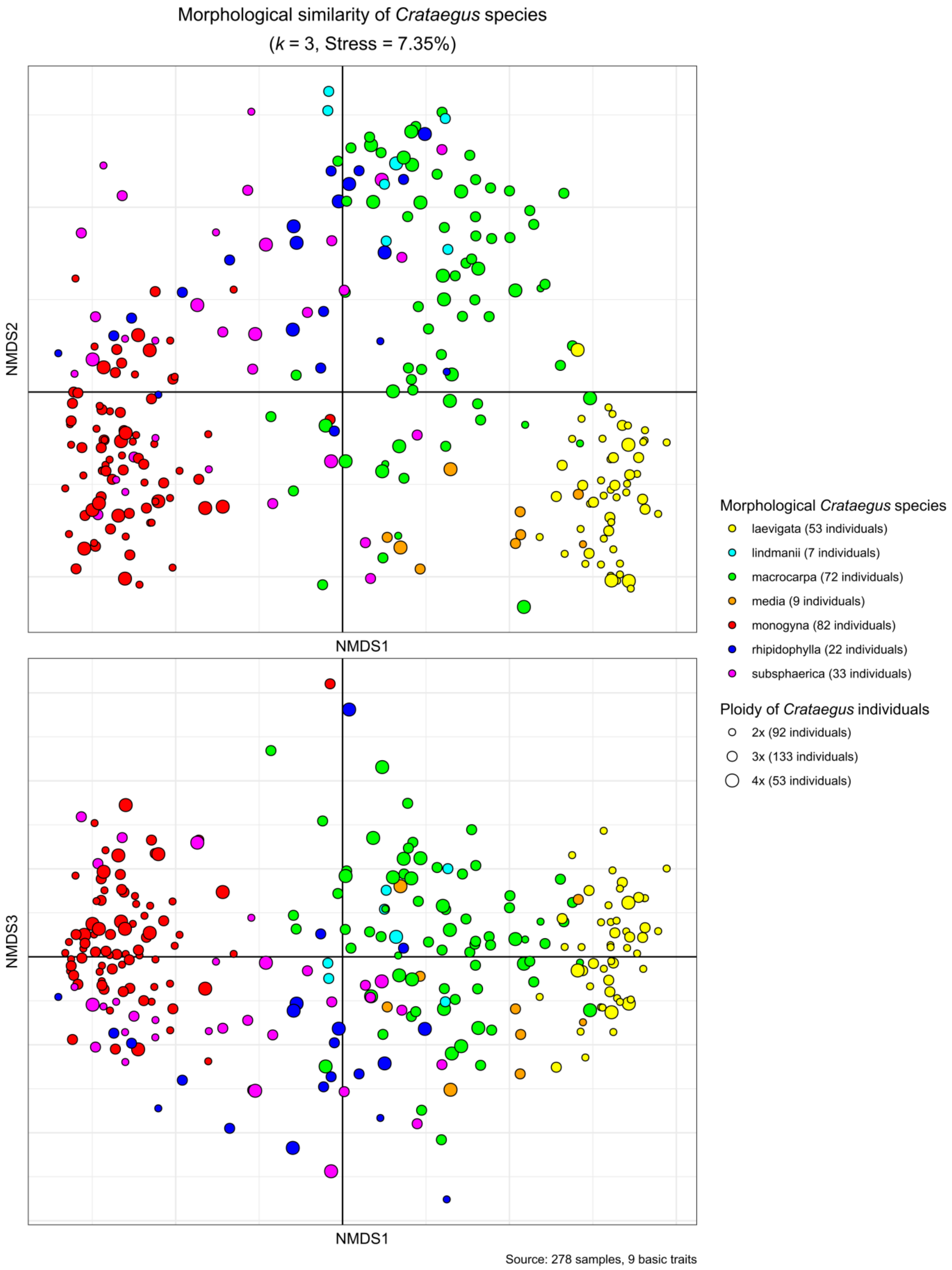


Figure 16 NMDS ordination plot of the basic morphological traits data (*n* = 278). The different species of ser. *Crataegus* are represented by colours (in compliance with those in Figure 1) and size symbolises the estimated minimum ploidy of each sample received from microsatellite marker analysis (see 3.3, Table S7). Number of samples of each group is given in parentheses. Top panel: The first two dimensions are shown. Bottom panel: The first and the third dimension are shown.

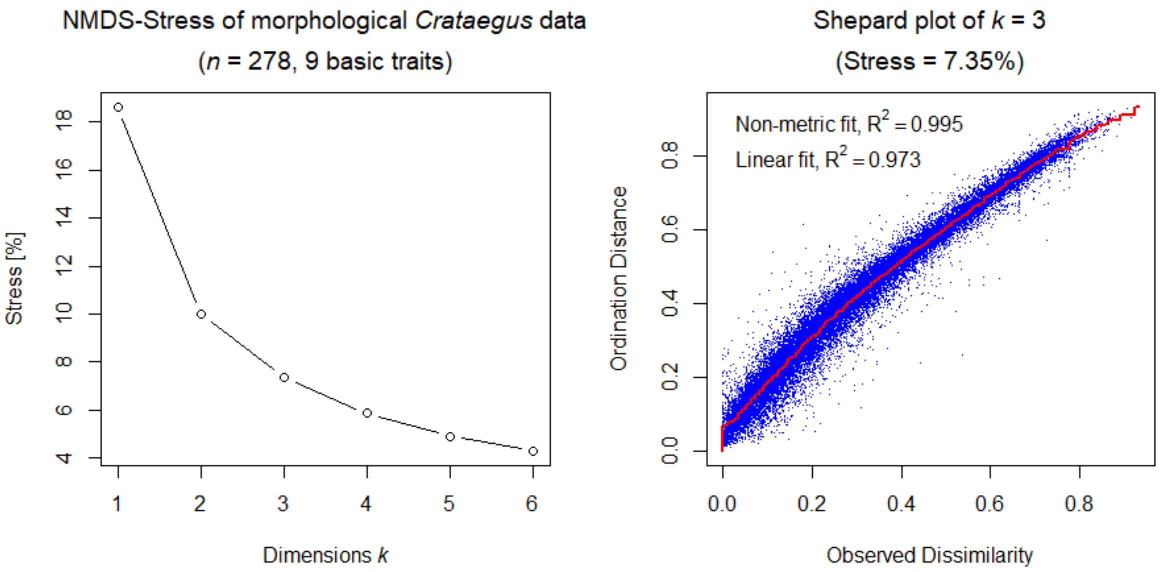


Figure 17 Stress of NMDS of the basic morphological traits data ($n = 278$). Left panel: Stress in relation to number of final dimensions (k) after dimensional reduction via NMDS. Right panel: Shepard plot of ordination distance against observed dissimilarity of the optimal $k = 3$ with a stress of 7.35%.

3.3 | Molecular data

3.3.1 | Analysis of recombination

Results of the test on HWE are presented in Figure 18 and Figure 19. All loci shown in pink are loci suspected of not being in HWE with $p \leq 0.05$. Due to data structure, allelic data from 16 species, it is consistent that neither of the loci is in HWE in any of the data subsets, whereas by the results of the Monte Carlo permutation test of alleles the null hypothesis is rejected for all loci except CH01F02, too, but solely in diploid *C. laevigata* and *C. monogyna* (Figure 18, left panel and right panel, respectively). This means a violation of Hardy-Weinberg principles, probably by genetic drift in disturbed and fragmented habitats and the assumption of non-random mating by the large geographical sampling area. It is conspicuous throughout the results of analytical p values of all data sets (Figure 19) that in several species the loci CH01F02, CH04F06, and CH05D04 appear not under the null expectation of HWE, yet the data contains a lot of combinations below 5 and thus may be taken with caution.

Results of testing on HWE with genetic annotation (see 3.3.3) are in general concordance with those of the morphological annotation. The main difference is the rejection of the null hypothesis only for locus CH05D04 and groups ‘2’, ‘5’, and ‘7’ in all subsets (plots not shown).

Analysis of LD revealed various levels of association among data sets, species and ploidy levels (Figure 20). Values of $\bar{r}_d$ range from lowest −0.153 in *C. rhipidophylla* diploids ($p = 0.895$) to highest 0.202 in *C. subsphaerica* tetraploids ($p = 0.012$). If $\bar{r}_d$ does not lie right inside the re-sampled distribution expected under no linkage it falls either on the right tail in most cases or rarely even outside of the re-sampled distribution with *p* values lower than 0.02. Thus there is significant support for the alternative hypothesis that alleles are linked across loci and the respective analysed sets (*C. monogyna* diploids and tetraploids, *C. rhipidophylla* tetraploids, *C. subsphaerica* tetraploids, and *C. macrocarpa* triploids). Therefore, these sets can be assumed to be clonal. A closer look at the pairwise index of association within the in-group species indicates linkage between loci by support of low *p* values. Hence, the null hypothesis of no linkage among markers is rejected for locus pairs CH04F06 and CH03C02, CH04F06 and CH05G07, and CH04G04 and CH05G11 in four, four, and six species, respectively. These combinations of loci appear with one to four further significant pairings in *C. laevigata*, *C. macrocarpa*, and *C. monogyna*. Despite these significant findings the respective $\bar{r}_d$ for these pairs of loci is low in most cases and the loci are not mapped on the same LG (see Table 5). In total no evidence of consistent linkage disequilibrium (i.e. involving the same loci) was detected between any of the seven SSR marker.

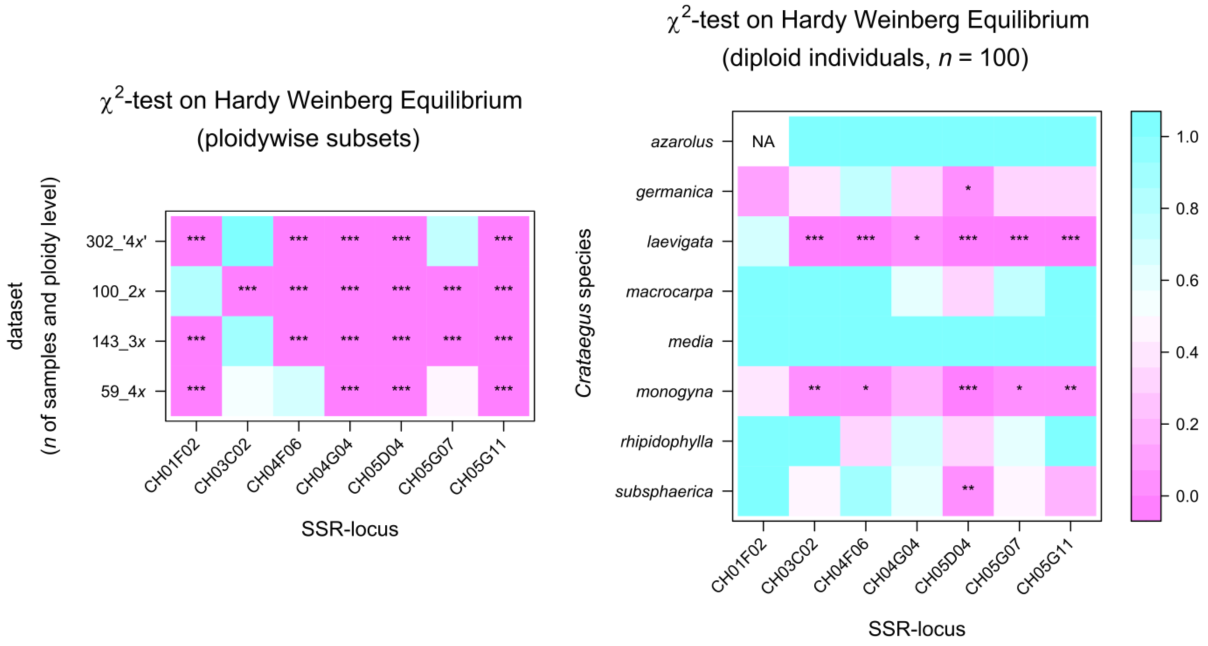


Figure 18 χ^2-test on HWE for diploids with exact *p* values and ploidywise subsets. Subsets and species are presented in rows, loci in columns, tiles are coloured by *p* values and when appropriate codes of significance (0 '***' 0.001 '**' 0.01 '*' 0.05 ' ' 1) are provided per tile. Combinations with too many missing data are indicated by '*NA*'

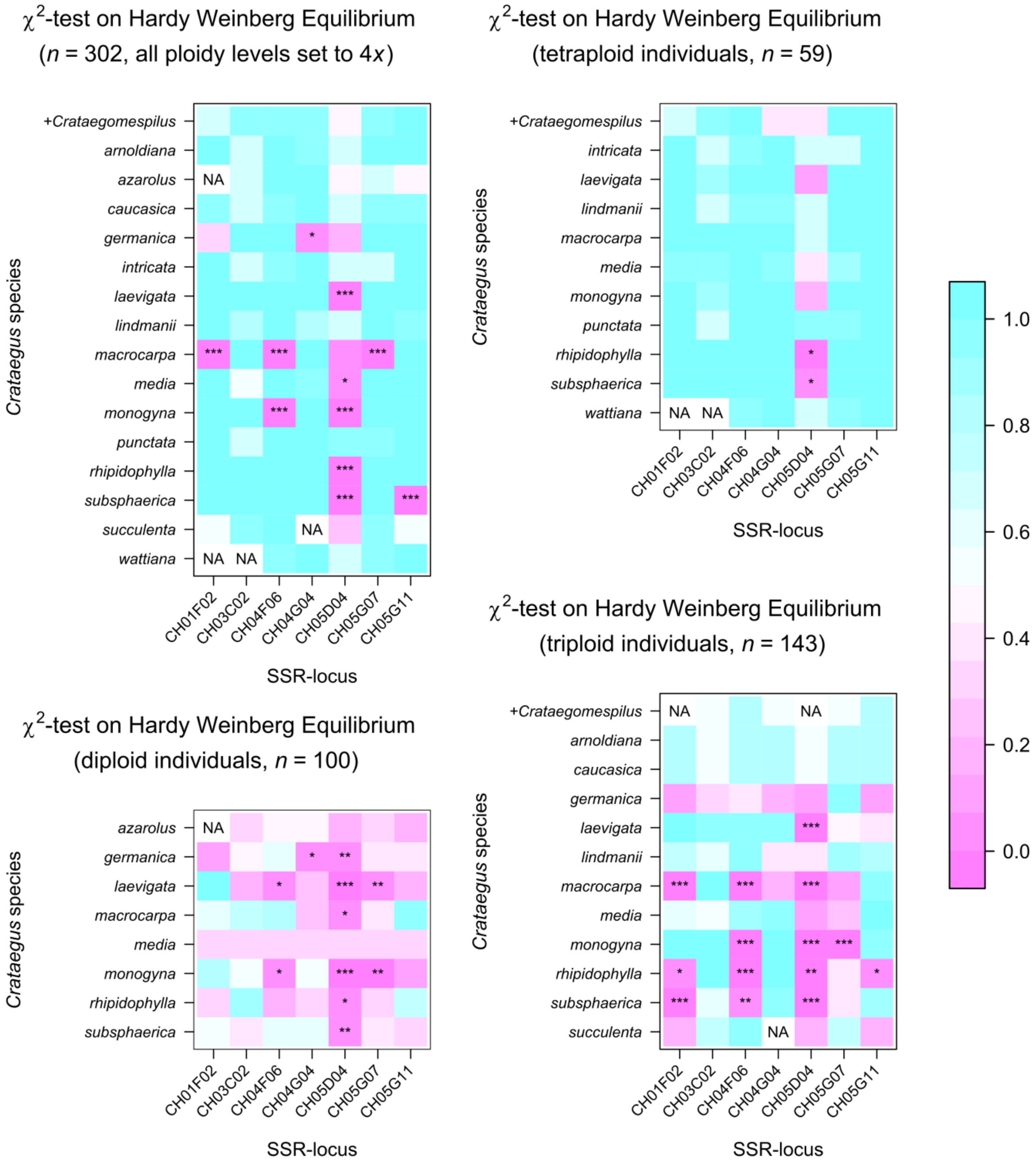
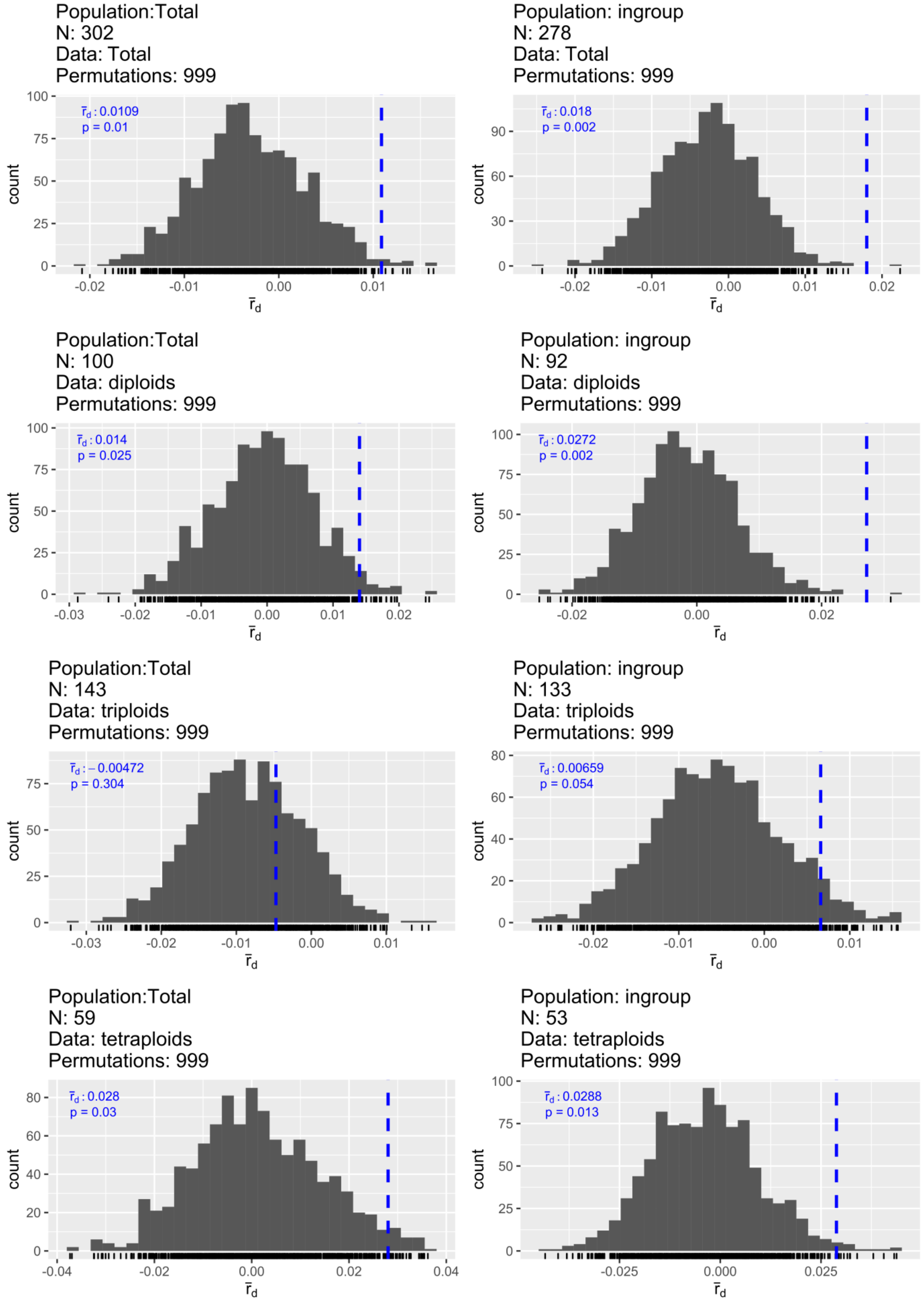


Figure 19 χ^2-test on HWE for the overall dataset and subsets by ploidy level. Species are presented in rows, loci in columns, tiles are coloured by *p* values and when appropriate codes of significance (0 '***' 0.001 '**' 0.01 '*' 0.05 ' ' 1) are provided per tile. Combinations with too many missing data are indicated by '*NA*'.

3.3.2 | Molecular variation and genetic diversity within species

Locus-wise variation

Locus-wise genotypic variation for the overall ($n = 302$) and the ingroup data set ($n = 278$) is presented in Table 9. N_G and $N_{G?}$ sum up to the n of each data set, showing that missing genotypes occur with about 28% in CH01F02 and not at all in CH05G11. In the latter locus N_{Gi} is lowest with approx. 36% and highest in CH05D04 with 92%. In turn N_{GC} behaves



Population:Total
N: 302
Data: Total
Permutations: 999

Population: ingroup
N: 278
Data: Total
Permutations: 999

Population:Total
N: 100
Data: diploids
Permutations: 999

Population: ingroup
N: 92
Data: diploids
Permutations: 999

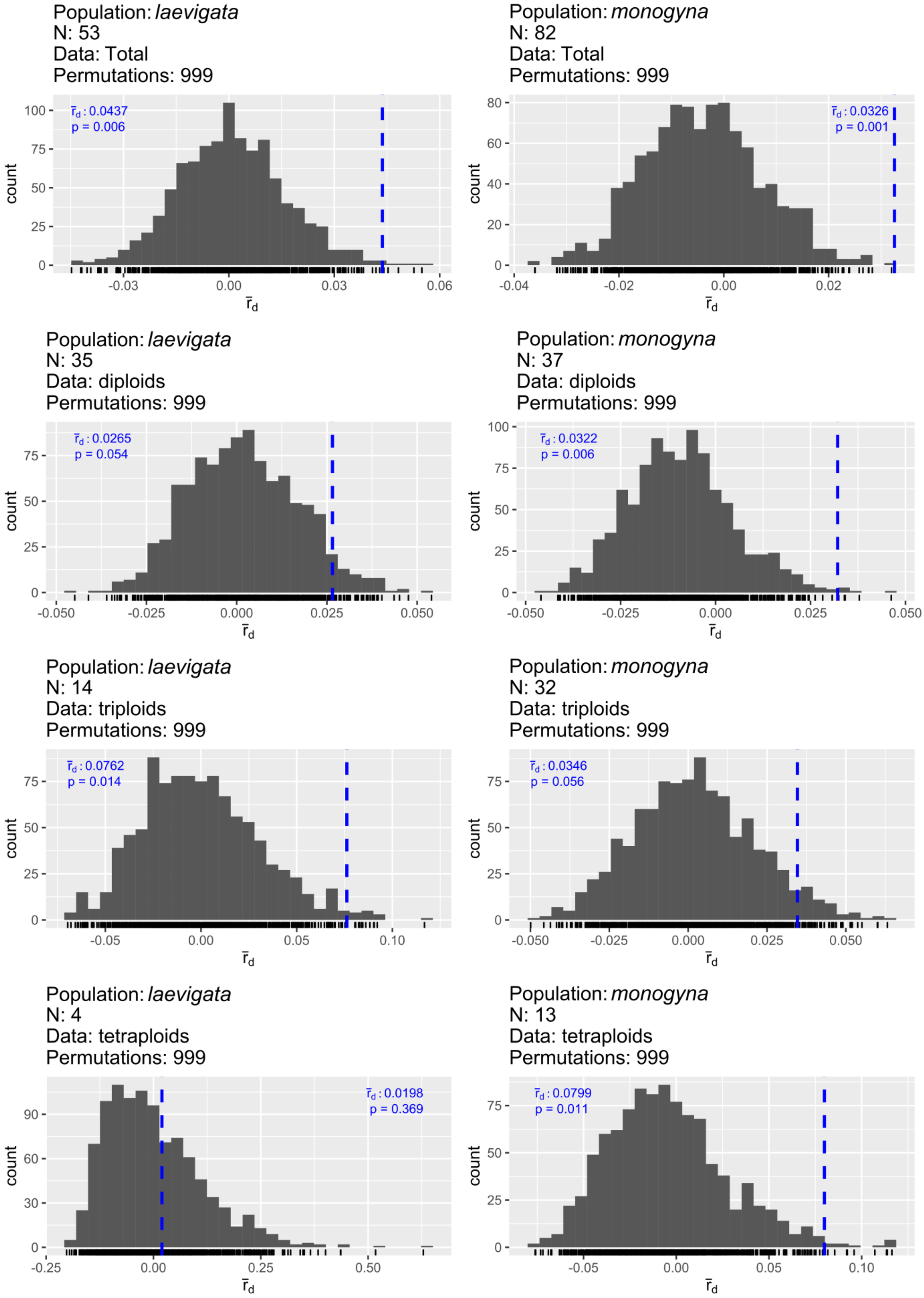
Population:Total
N: 143
Data: triploids
Permutations: 999

Population: ingroup
N: 133
Data: triploids
Permutations: 999

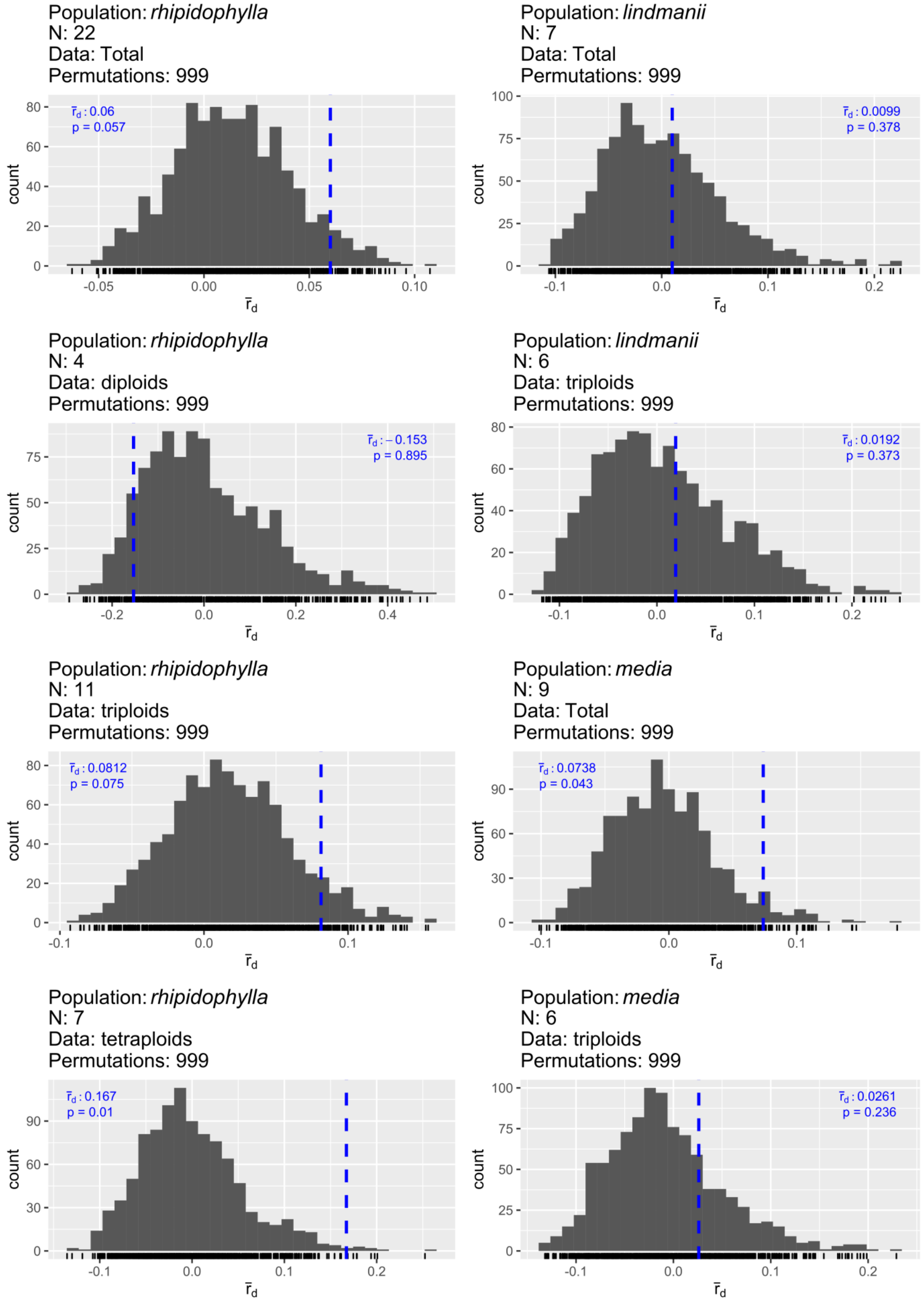
Population:Total
N: 59
Data: tetraploids
Permutations: 999

Population: ingroup
N: 53
Data: tetraploids
Permutations: 999

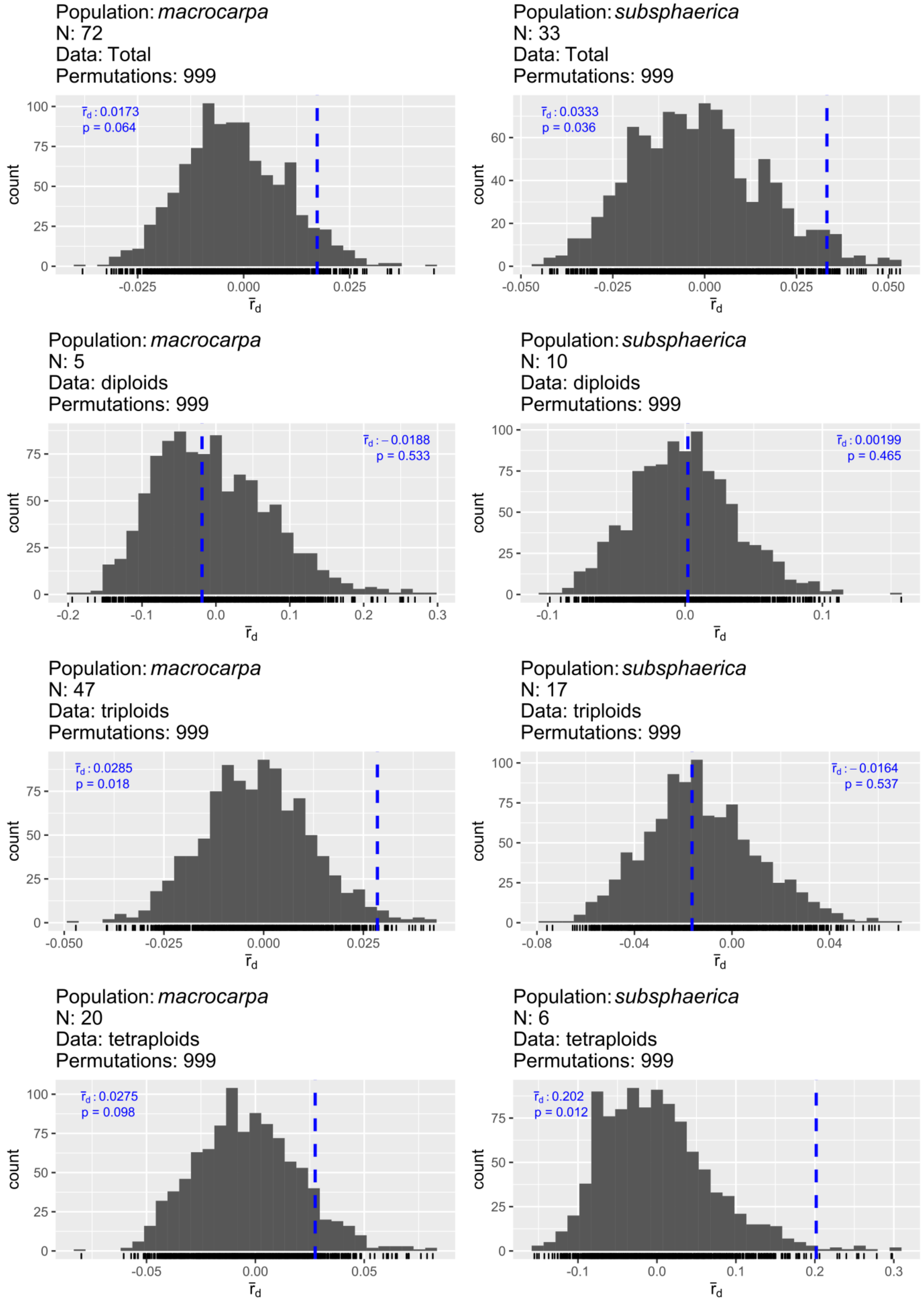
Figure 20 Index of association $\bar{r}_d$ by ploidy level per data set and species. The resampled distribution expected under no linkage is presented, $\bar{r}_d$ is given as dashed line within and as value with the respective p values of a test with 999 permutations.
Note: The figure continues on the following pages.



Continuation of Figure 20.



Continuation of Figure 20.



Population: *macrocarpa*
N: 72
Data: Total
Permutations: 999

Population: *subsphaerica*
N: 33
Data: Total
Permutations: 999

Population: *macrocarpa*
N: 5
Data: diploids
Permutations: 999

Population: *subsphaerica*
N: 10
Data: diploids
Permutations: 999

Population: *macrocarpa*
N: 47
Data: triploids
Permutations: 999

Population: *subsphaerica*
N: 17
Data: triploids
Permutations: 999

Population: *macrocarpa*
N: 20
Data: tetraploids
Permutations: 999

Population: *subsphaerica*
N: 6
Data: tetraploids
Permutations: 999

Continuation of Figure 20.

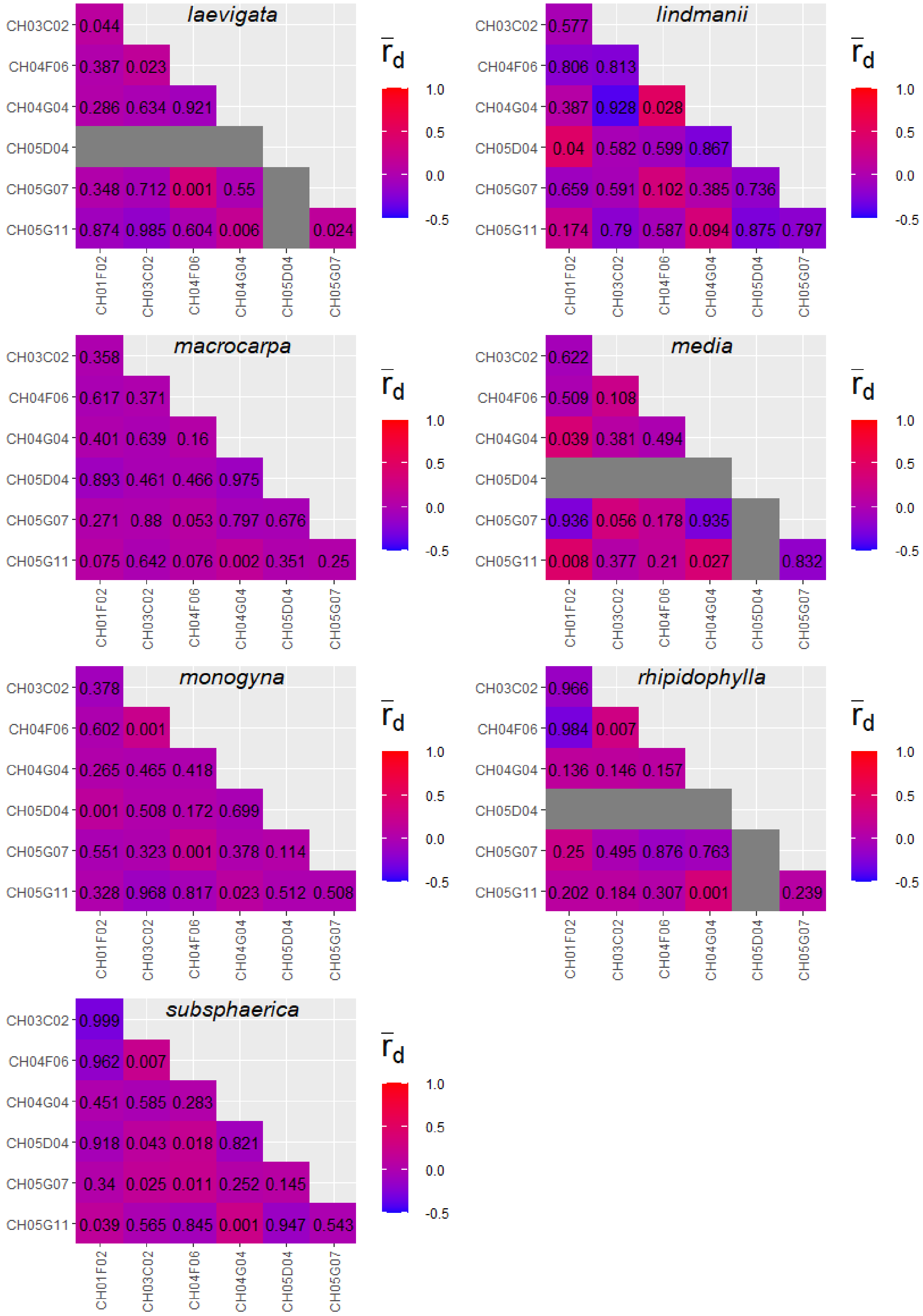


Figure 21 Pairwise index of association $\bar{r}_d$ between loci within ingroup species ($n = 278$). Tiles are grey, if the allelic data is uniform in a locus, otherwise coloured by the respective $\bar{r}_d$ value and contain p values of a test with 999 permutations.

the other way round for these loci with 292 and 268 in CH05D04 and 728 and 672 in CH05G11. N_A ranges from 6 (CH05D04) to 27 (CH01F02), with a total of 116 (mean = 16.6 per locus). Values of N_{Ae} are smaller by definition and vary between 1.9 (CH05D04) and 8.1 (CH04G04). Mean and variance of allele sizes are nearly the same in both analyses except for CH05G11 where the outgroup owns some private alleles (N_A decreases from 24 to 15) of larger size and thus Var(A) falls from 50.0 to 34.5. In total Var(A) ranges from 1.4 (CH05D04) to 70.5 (CH01F02). Between both data sets levels of H_o, H_e, and *PIC* do not vary much either. While the lowest value of both heterozygosities is found in the same locus (CH05D04; $H_o = 0.422$ and $H_e = 0.473$), the highest observed one is 0.802 in CH05G11 and the highest expected one is 0.877 in CH04G04. Multilocus averages are equal to 0.711 and 0.748 for H_o and H_e, respectively. The *PIC* falls between 0.383 and 0.866 of the analogous loci as H_e. The same pair of loci also spans the range of *H'* from 0.765 to 2.371 with a large difference between the data sets in locus CH01F02 of 2.029 and 1.825. The minimum of evenness (0.427 and 0.429) is found again in CH05D04 of both data sets and the maximum is equal to 0.756 in CH05G07 and 0.789 in CH05G11 in the overall and the ingroup data set, respectively.

Annotation-wise variation within the ingroup

Genetic diversity within the ingroup data ($n = 278$) is presented annotation-wise for species and genetic groups in Table 10. The respective number of subsamples n is equal to the sum of N_G and $N_{G?}$. Within genetic groups the lowest and highest proportions are equal to 1.9% in '5.5' and 15.6% in '3' and within species 2.7% in *C. laevigata* and 12.2% in *C. monogyna*, respectively. N_{Gi} varies within annotations throughout the subsamples from 2.0 to 42.0 and 5.0 to 49.4 with proportions in relation to the respective n. The total number of alleles falls between 27 to 57 and 33 to 70 in the genetic and morphological annotations with some groups containing not any private alleles at all or up to four in '2.3' and nine in *C. monogyna*. N_{Ae} ranges overall from 2.8 to 4.9 which is in relation to the respective N_A a part of one out of 9 to 16 and 10 to 19 within the annotation subsets. A_R varies between 10 and 13 per subset which is on average three times higher than the effective number of alleles. All values of observed and expected heterozygosities lie in the interval from 0.505 to 0.778 with a higher minimal values in the morphological subset ($H_o = 0.620$ in *C. media*; $H_e = 0.650$ in *C. monogyna*). Levels of F_{IS} range from lowest −0.362 ('2') and −0.291 (*C. monogyna*) indicating heterozygote excess and thus outbreeding to 0.095 (*C. media*) and 0.230 ('7.7') showing heterozygote deficiency equivalent to inbreeding.

Table 9 Measures of genetic diversity between markers.

Locus	N_G	$N_{G?}$	$\%N_{G?}$	N_{Gi}	$\%N_{Gi}$	N_{GC}	N_A	N_{Ae}	$\bar{A}$	Var(A)	H_o	H_e	PIC	H'	E	F_{SX}	F_{C1X}	F_{C2X}
Overall data set (n = 302)																		
CH01F02	217	85	28.1%	167	55.3%	343	27	4.5	160.8	70.5	0.756	0.776	0.759	2.029	0.616	0.187	0.143	0.030
CH03C02	267	35	11.6%	251	83.1%	327	9	2.7	114.8	6.9	0.672	0.631	0.561	1.259	0.573	0.100	0.032	0.003
CH04F06	299	3	1.0%	195	64.6%	585	12	4.8	170.8	9.5	0.783	0.793	0.762	1.761	0.709	0.057	0.024	0.005
CH04G04	296	6	2.0%	181	59.9%	596	26	8.1	163.0	32.8	0.759	0.877	0.866	2.371	0.728	0.163	0.106	0.009
CH05D04	282	20	6.6%	278	92.1%	292	6	1.9	183.7	1.4	0.422	0.473	0.383	0.765	0.427	0.172	0.104	0.018
CH05G07	295	7	2.3%	171	56.6%	603	12	5.5	163.5	36.9	0.780	0.819	0.795	1.879	0.756	0.069	0.018	0.002
CH05G11	302	0	0.0%	109	36.1%	728	24	7.5	221.4	50.0	0.802	0.867	0.853	2.305	0.725	0.167	0.126	0.016
Average	279.7	22.3	7.4%	193.1	64.0%	496.3	16.6	5.0	168.3	29.7	0.711	0.748	0.711	1.767	0.629	0.131	0.079	0.012
Ingroup data set (n = 278)																		
CH01F02	198	80	28.8%	152	54.7%	310	22	3.9	160.9	70.5	0.776	0.746	0.725	1.825	0.590	0.132	0.103	
CH03C02	249	29	10.4%	234	84.2%	306	9	2.7	114.8	7.0	0.683	0.629	0.559	1.248	0.568	0.075	0.025	
CH04F06	275	3	1.1%	180	64.7%	536	12	4.9	170.8	9.5	0.790	0.796	0.765	1.767	0.711	0.044	0.018	
CH04G04	278	0	0.0%	166	59.7%	566	21	7.6	163.0	30.3	0.768	0.869	0.856	2.288	0.752	0.137	0.097	
CH05D04	259	19	6.8%	256	92.1%	268	6	1.9	183.7	1.4	0.448	0.483	0.386	0.768	0.429	0.144	0.088	
CH05G07	274	4	1.4%	156	56.1%	565	12	5.5	163.5	36.7	0.792	0.820	0.796	1.881	0.757	0.048	0.008	
CH05G11	278	0	0.0%	99	35.6%	672	15	6.7	220.9	34.5	0.816	0.852	0.835	2.137	0.789	0.136	0.111	
Average	258.7	19.3	6.9%	177.6	63.9%	460.4	13.9	4.8	168.3	27.2	0.725	0.742	0.703	1.702	0.647	0.102	0.064	

Measures of genetic diversity at two different levels: overall set and ingroup set. N_G, total number of individuals genotyped at a locus; $N_{G?}$ number of missing genotypes; N_{Gi}, number of incomplete genotypes; N_{GC}, total number of defined gene copies at a locus; N_A, number of distinct alleles (including a null-allele) at a locus; N_{Ae}, effective number of alleles; $\bar{A}$, mean allele size at a locus; Var(A), variance of allele size at a locus; H_o, H_e observed/expected heterozygosity; PIC, polymorphic information content; H', Shannon's information index; E, Pielou's evenness; $F_{SX}/F_{C1X}/F_{C2X}$, F-statistics among populations or regions within this group.

Table 10 Measures of genetic diversity between annotations.

	Morphological annotations ($\sum n = 278$)							Genetic annotations ($\sum n = 278$)												
group	*monogyna*	*subsphaerica*	*rhipidophylla*	*lindmanii*	*macrocarpa*	*laevigata*	*media*	2	2.3	3	4	4.6	5	5.5	6	6.6	7	7.7	1
n	82	33	22	7	72	53	9	71	19	11	3	14	28	22	31	15	53	5	6
N_G	72.0	30.0	20.9	6.7	69.0	51.6	8.6	61.9	16.6	9.3	2.9	13.1	27.1	21.6	30.0	14.6	51.0	4.9	5.9
$N_{G?}$	10.0	3.0	1.1	0.3	3.0	1.4	0.4	9.1	2.4	1.7	0.1	0.9	0.9	0.4	1.0	0.4	2.0	0.1	0.1
$\%N_{G?}$	12.2%	9.1%	5.2%	4.1%	4.2%	2.7%	4.8%	12.9%	12.8%	15.6%	4.8%	6.1%	3.1%	1.9%	3.2%	2.9%	3.8%	2.9%	2.4%
N_{Gi}	48.4	20.0	14.9	5.0	49.4	33.7	6.1	42.0	10.7	5.6	2.0	8.7	19.0	14.7	21.7	9.7	34.9	3.9	4.7
$\%N_{Gi}$	59.1%	60.6%	67.5%	71.4%	68.7%	63.6%	68.3%	59.2%	56.4%	50.6%	66.7%	62.2%	67.9%	66.9%	70.0%	64.8%	65.8%	77.1%	78.6%
N_A	70	67	67	33	66	54	34	57	57	57	27	57	44	46	48	45	47	40	32
N_{Ap}	9	2	4	0	1	4	0	1	4	3	2	3	1	1	1	0	3	0	0
N_{Ae}	3.7	4.6	4.2	3.4	4.1	3.5	3.6	3.5	4.2	4.9	2.9	4.7	3.4	3.8	4.1	4.2	3.5	4.1	2.8
A_R	11.9	12.7	13.0	11.5	12.0	10.9	11.5	10.9	12.1	12.4	12.1	12.6	10.4	11.4	11.1	11.9	10.0	12.4	11.7
H_o	0.751	0.738	0.674	0.713	0.764	0.675	0.620	0.738	0.778	0.750	0.505	0.725	0.716	0.685	0.736	0.683	0.668	0.551	0.552
H_e	0.650	0.701	0.652	0.662	0.725	0.673	0.680	0.624	0.691	0.715	0.576	0.738	0.660	0.704	0.720	0.681	0.682	0.691	0.525
F_{IX}	-0.291	-0.074	-0.018	-0.078	-0.060	-0.003	0.095	-0.362	-0.147	-0.037	0.153	0.008	-0.081	0.032	-0.023	0.027	0.016	0.230	-0.032
F_{SX}	0.030	0.073	0.042	0.070	0.013	0.052	0.181	0.027	0.090	0.209	0.296	0.070	0.046	0.081	0.042	0.099	0.070	0.332	0.075

Measures of genetic diversity at two different levels: morphological and genetic annotation. n, number of samples; N_G, total number of individuals genotyped at a locus; $N_{G?}$ number of missing genotypes; N_{Gi}, number of incomplete genotypes; N_A, number of distinct alleles (including a null-allele) at a locus; N_{Ap}, number of private alleles; N_{Ae}, effective number of alleles; A_R, allelic richness; H_o, H_e observed/expected heterozygosity; F_{IX}, inbreeding coefficient per group; F_{SX}, F-statistics among populations within this group.

3.3.3 | Genetic structure and divergence among species

ANOVA-based global *F*- and *R*-statistics

Global *F*- and *R*-statistics are presented in Table 12. While there are only slight differences between the respective values of the overall and the ingroup data set, there is a discrepancy between the respective values of the *F*- and *R*-statistics. Most *p* values of the respective permutation tests are at least significant with $p < 0.05$ (77 of 96), despite of testing permutations of allele sizes among alleles within each locus (11 of 48). The most extreme goodness-of-fit values of both models, IAM and SMM, are found in CH05D04 and CH01F02, respectively. Locus CH05D04 indicates the highest rate of outbreeding by F_{IS} and R_{IS} values much lower than −1 throughout all analyses. The smallest rates of outbreeding under IAM are found in CH05G07 (−0.251) and CH01F02 (−0.236) for the overall and the ingroup data, respectively. However, for the SMM, the locus CH04F06 shows even small positive values in both sets (0.145 and 0.166) and thus inbreeding. For both data sets the lowest F_{ST} equal to 0 is found in CH05G07 and the lowest, even negative R_{ST} in CH03C02 (−0.011). The highest level of differentiation can be seen in locus CH01F02 (0.135, 0.490, 0.535) in all analyses, except for F_{ST} in the ingroup where the maximum is found in CH05G11 (0.109). Values of the multilocus average are not differing much from the respective jackknifed mean over loci, e.g. 0.055 and 0.056±0.022 for F_{ST} and 0.258 and 0.287±0.156 for R_{ST} of the ingroup data set.

ANOVA-based pairwise *F*- and *R*-statistics of the ingroup

Pairwise statistics of the ingroup were performed for both classifications. Results of the morphological annotations are presented in Table 13, those of the genetic annotations for genetic structure in Table 14 and for genetic distances in Table 15.

Within the morphological annotations (Table 13) pairwise F_{ST} falls between 0.009 (*C. subsphaerica* ↔ *C. rhipidophylla*) and 0.127 (*C. monogyna* ↔ *C. lindmanii*). Levels of *Ds* range from 0.008 to 0.298 within the same pairs. The pairwise R_{ST} values lie in the interval from 0.021 (*C. macrocarpa* ↔ *C. rhipidophylla*) to 0.586 (*C. monogyna* ↔ *C. laevigata*) and the $(\delta\mu)^2$ distances vary between −0.538 (*C. laevigata* ↔ *C. lindmanii*) and 62.397 (*C. monogyna* ↔ *C. lindmanii*). Most estimates, 73 of 84, are at least significant ($p < 0.05$) except for all values of *C. subsphaerica* ↔ *C. rhipidophylla* and *C. macrocarpa* ↔ *C. lindmanii*. Both estimates under SMM are insignificant for *C. laevigata* ↔ *C. lindmanii* and *C. subsphaerica* ↔ *C. media* and just R_{ST} for *C. macrocarpa* ↔ *C. media*. In contrast most values of SMM appear to be insignificant under permutations of allele sizes among alleles within each locus (33 of 42). Nearly all of the topmost and highly significant values among all pairwise measures of genetic differentiation within the morphological annotations are found in pairs with *C. monogyna*, *C. laevigata* or *C. lindmanii* indicating those are the most differentiated species.

Within the genetic annotations (Table 14) pairwise F_{ST} ranges from 0.004 (‘4.6’ ↔ ‘6.6’ and ‘7.7’) to 0.157 (‘2’ ↔ ‘5’) while the interval for pairwise R_{ST} is enlarged to −0.286 (‘3’ ↔ ‘4’) to 0.767 (‘2’ ↔ ‘1’). The percentage of insignificant values ($p > 0.05$) is higher compared to the estimates in Table 13 (302% in F_{ST} and 115% in R_{ST}). Similar to the morphological annotation nearly all of the topmost highly significant values among all pairwise measures of genetic differentiation within the genetic annotations (Table 14) are found in pairs with either ‘2’, ‘5’ or ‘7’ indicating those groups as the most differentiated ones. Within R_{ST} also groups ‘1’, ‘2.3’ and ‘6’ have to be considered that way. The genetic distances of the genetic classification (Table 15) vary between −15.00 (‘3’ ↔ ‘4’) and 113.3 (‘2’ ↔ ‘1’) and between −0.027 (‘2.3’ ↔ ‘4’) and 0.343 (‘2’ ↔ ‘5’) for Goldstein et al.’s and Nei’s standard genetic distance, respectively. Like for the measures of genetic differentiation the percentage of significant distance estimates ($p < 0.05$) is lower in the genetic than in the morphological annotations (45 of 132 compared to 6 of 42).

Mantel test of pairwise *F*- and *R*-statistics of the ingroup

The mantel test for concordance of estimates of genetic structure and distances under both models revealed slightly moderate positive correlations. The respective mantel statistics are presented for both classifications is presented in Table 11.

Table 11 Mantel statistic r_{M} of concordance of IAM and SMM of measures of genetic structure and genetic distance.

pair of measures	morphological classification	genetic classification
$\boldsymbol{F_{\mathrm{ST}} \leftrightarrow R_{\mathrm{ST}}}$	0.518^{**}	0.623^{***}
$\boldsymbol{Ds \leftrightarrow (\delta\mu)^2}$	0.675^{*}	0.631^{***}

Note: Codes of significance (0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 'ns' 1) are presented right above each value. *p* values were obtained by 5,039 and 99,999 permutations due to sample size of annotations among the morphological and the genetic classification, respectively.

AMOVA

According to the AMOVA (see Table 16 and Table 17 for the summary table of the morphological and genetic classification, respectively, and Table S10 for the sum of squares), most of the variation, namely 76.7% up to 91.3% with the lower four values under SMM, is found within ‘populations’ representing a group of individuals of the same annotation with the same estimated level of ploidy. The variation among these ‘populations’ varies between 3.8% and 6.5% under the IAM and between 5.1% and 9.9% under the SMM. While the variation among ‘regions level 1’, displaying annotations of any estimated ploidy level, is around 5% under IAM, irrespective of the classification and the number of samples, it is higher under SMM. To be specific around 8.5% of the overall data set and around 11.0% of the ingroup data set, likewise for both classifications. The *F*-statistic value of interest is F_{C1T}, which is the F_{ST} equivalent of differentiation among species in this study. The values are lower in the ingroup data set than in the overall data set, higher under SMM than under IAM, and nearly identical over classifications. The differentiation between species belonging to the ingroup or the outgroup (F_{C1C2}) ranges from around 0.05 to 0.09 under the respective model. All values are highly significant in case of a two-sided permutation test.

Structure analysis

The $\ln[\Pr(X|K)]$ values for the analysis of all individuals keep increasing with higher K until values drop at $K = 9$ and $K = 8$, respectively, in concordance with larger standard errors from thereon (Figure 22, left panels). When applying the posterior ΔK statistics (Evanno et al., 2005) both analyses share their highest ΔK for K equal to 2. Further values vary tremendously when discarding CH05G07 as multilocus marker from the analysis (Figure 22, right panels). In view of the aim to reveal any genetic pattern of speciation, hybridisation, and apomixis and by the fact of another clear, yet local maximum at $K = 7$ and an equal ΔK for $K = 3$ the reduced data seemed appropriate for further investigations. The obtained results of the hierarchical structure analysis for all of these values of K are presented in Figure 23. Obviously the membership of single individuals does not fit to the respective assigned species. Although providing insight in the overall genetic structure of the sampled individuals, the lower values for K solely show the separation of *C. laevigata*, *C. lindmanii*, *C. macrocarpa*, and *C. media* from the outgroup members, *C. monogyna*, with the majorities of *C. rhipidophylla*, and *C. subsphaerica*. By adding another posterior cluster samples of *C. monogyna* and *C. subsphaerica* may be excluded from the latter group. The former group is not split up until the number of genetic clusters reaches seven. From there $K = 7$ was chosen for further analysis. While the North American *C. succulenta* and the medlars, *C. germanica* are identified as representing a single cluster (‘red’) with high membership coefficient values, the remaining members of the outgroup belong entirely (*C. arnoldiana*, *C. intricata*, *C. punctata*) or partly (*C. azarolus*, *C. caucasica*, *C. wattiana*) to the same cluster (‘magenta’). However, the alleles giving rise to this cluster are shared with individuals throughout all species of the ingroup. The rest of clusters is partitioned into two groups. Clusters ‘orange’ and ‘green’ occur together with almost equal rates of Q within most individuals of +*Crataegomespilus*, *C. monogyna*, *C. subsphaerica*, and *C. rhipidophylla*. Clusters ‘blue’, ‘cyan’, and ‘yellow’ co-occur to a lesser extend within *C. subsphaerica* and *C. rhipidophylla* but predominantly within *C. lindmanii*, *C. macrocarpa*, *C. laevigata*, and *C. media*. However, the respective Q is varying with high proportions of either ‘blue’ or ‘yellow’ complemented with each other and ‘cyan’, except for *C. laevigata* where ‘cyan’ prevails.

As due to possible misidentification there are outliers likely to appear in the data set, especially individuals 1036 and 1238 within *C. monogyna* and 1032 within *C. macrocarpa*. Additionally there are patterns indicating a specific membership caused by allelic composition. Taking these points into account the results were rearranged to reduce heterogeneity among groups. This harmonised sorting is illustrated in Figure 24. For comparability the morphological annotation of any individual is represented by the colour of sample IDs left of the cluster analysis while the so built group is indicated by an assumed name on species level with a correspondent number on the right-hand side. Integers index unique morpho-genetic groups. Decimals are used to refer to an appropriate mixture of those (‘2.3’ and ‘4.6’) or when there are differences to the main group not giving rise to a complete separate group on their own (‘5.5’, ‘6.6’, and ‘7.7’). In contrast ‘1’ is used for a homogenous group not fitting into this system at all. In doing so a second set of annotations is formed and applied for the re-calculation of parameters of genetic diversity and differentiation.

Clusters, except ‘red’, are split into two major groups: (A) ‘magenta’, ‘orange’, and ‘green’ within groups ‘2’ to ‘4.6’ and ‘9’ to ‘15’ (assumed *C. monogyna*, *C. subsphaerica*, *C. rhipidophylla*, possible hybrids, and the outgroup except *C. germanica* and *C. succulenta*) and (B) ‘blue’, ‘cyan’, and ‘yellow’ within groups ‘5’ to ‘7.7’ (assumed *C. lindmanii*, *C. macrocarpa*, *C. laevigata*, and possible hybrids). As individuals of *C. media* are divided up into other groups, predominantly ‘7’ and also ‘5.5’ and ‘7.7’, there is no equivalent among the genetic groups. By comparing both assignments with each other outliers can be detected. Crosswise outliers are: individual 1032 within group ‘2’ (assumed *C. monogyna*); 1023, 1141, 1154, 1183, 1110, and 1123 within ‘4.6’ (assumed *C. rhipidophylla* hybrid); 1151 and 1196 in ‘5’ (assumed *C. lindmanii*); 1036, 1035, 1038B, 1150, 1181, 1202, 1203, 1245, 1128, 1133, and 1152 within ‘6’ (assumed *C. macrocarpa*); 1238, 1069, 1195, 1114, 1145, and 1252 within ‘6.6’ (assumed *C. macrocarpa* hybrid); and 1135 within ‘7.7’ (assumed *C. laevigata* hybrid).

Table 12 Global F- and R-statistics of the overall and the ingroup data set.

		Global F-statistics			Global R-statistics		
	Locus	F_{IT}	F_{IS}	F_{ST}	R_{IT}	R_{IS}	R_{ST}
Overall data set ($n = 302$)	CH01F02	-0.097^{***}	-0.267^{***}	0.135^{***}	$0.236^{*/ns}$	$-0.496^{***/ns}$	$0.490^{***/**}$
	CH03C02	-0.773^{***}	-0.782^{***}	0.005^{ns}	$-0.836^{***/ns}$	$-0.816^{***/ns}$	$-0.011^{ns/ns}$
	CH04F06	-0.315^{***}	-0.316^{***}	0.001^{ns}	$0.141^{*/**}$	$0.145^{*/**}$	$-0.004^{ns/ns}$
	CH04G04	-0.115^{***}	-0.261^{***}	0.116^{***}	$0.149^{*/ns}$	$-0.338^{***/ns}$	$0.364^{***/*}$
	CH05D04	-6.288^{***}	-6.410^{***}	0.016^{ns}	$-7.274^{***/ns}$	$-7.472^{***/ns}$	$0.023^{ns/ns}$
	CH05G07	-0.251^{***}	-0.251^{***}	0.000^{ns}	$-0.250^{***/ns}$	$-0.257^{***/ns}$	$0.005^{ns/ns}$
	CH05G11	-0.123^{***}	-0.288^{***}	0.128^{***}	$-0.138^{**/ns}$	$-0.410^{***/.}$	$0.193^{***/ns}$
	All loci	-0.411^{***}	-0.517^{***}	0.070^{***}	$-0.069^{ns/ns}$	$-0.454^{***/**}$	$0.265^{***/**}$
	Jackknifed estimators (over loci)						
	Mean	-0.382	-0.490	0.071	-0.036	-0.438	0.282
	SE	0.195	0.197	0.028	0.158	0.105	0.115
Ingroup data set ($n = 278$)	CH01F02	-0.124^{***}	-0.236^{***}	0.091^{***}	$0.402^{**/*}$	$-0.287^{***/ns}$	$0.535^{***/***}$
	CH03C02	-0.769^{***}	-0.776^{***}	0.004^{ns}	$-0.778^{***/ns}$	$-0.770^{***/ns}$	$-0.005^{ns/ns}$
	CH04F06	-0.313^{***}	-0.316^{***}	0.002^{ns}	$0.170^{*/**}$	$0.166^{*/**}$	$0.005^{ns/ns}$
	CH04G04	-0.126^{***}	-0.249^{***}	0.098^{***}	$0.093^{ns/ns}$	$-0.309^{***/ns}$	$0.307^{***/.}$
	CH05D04	-6.765^{***}	-6.922^{***}	0.020^{ns}	$-8.130^{***/ns}$	$-8.466^{***/ns}$	$0.036^{ns/ns}$
	CH05G07	-0.249^{***}	-0.249^{***}	0.000^{ns}	$-0.242^{***/ns}$	$-0.244^{***/ns}$	$0.001^{ns/ns}$
	CH05G11	-0.141^{***}	-0.282^{***}	0.109^{***}	$-0.217^{***/ns}$	$-0.349^{***/ns}$	$0.098^{***/ns}$
	All loci	-0.425^{***}	-0.509^{***}	0.055^{***}	$-0.036^{ns/.}$	$-0.397^{***/ns}$	$0.258^{***/***}$
	Jackknifed estimators (over loci)						
	Mean	-0.396	-0.480	0.056	0.022	-0.374	0.287
	SE	0.197	0.199	0.022	0.243	0.120	0.156

Note: Codes of significance (0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 'ns' 1) are presented right above each value. p values were obtained by 9,999 permutations each with gene copies among all individuals for goodness-of-fit (F_{IT}, R_{IT}), gene copies among individuals within population for fixation indices (F_{IS}, R_{IS}), and individuals among all populations for measures of population differentiation (F_{ST}, R_{ST}). For R-statistics a second set of p values is provided by permutation of allele sizes among alleles within each locus after the slash.

Continuation of note to Table 13 (next page): The upper half contains pairwise measures of genetic differentiation F_{ST} and R_{ST}, the lower half pairwise genetic distances Ds and $(\delta\mu)^2$. The respective upper/right triangular matrices provide values under SMM, while the lower/left shows values under IAM. Codes of significance (0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 'ns' 1) of a two-sided test by 9,999 permutations of individuals between a pair of populations are given right above the respective value. Under SMM a second set of p values is provided by 9,999 permutations of allele sizes among alleles within each locus after the slash.

Table 13 Pairwise F- and R-statistics of the ingroup (n = 278, morphological annotation).

IAM	*monogyna*	*subsphaerica*	*rhipidophylla*	*lindmanii*	*macrocarpa*	*laevigata*	*media*	R_{ST}
monogyna		$0.424^{***/***}$	$0.491^{***/***}$	$0.535^{***/**}$	$0.545^{***/***}$	$0.586^{***/***}$	$0.430^{***/.}$	*monogyna*
subsphaerica	0.030^{***}		$0.029^{./\mathrm{ns}}$	$0.138^{***/\mathrm{ns}}$	$0.043^{***/\mathrm{ns}}$	$0.119^{***/\mathrm{ns}}$	$0.027^{\mathrm{ns/ns}}$	*subsphaerica*
rhipidophylla	0.035^{***}	0.009^{ns}		$0.064^{*/\mathrm{ns}}$	$0.021^{*/\mathrm{ns}}$	$0.087^{***/\mathrm{ns}}$	$0.065^{*/\mathrm{ns}}$	*rhipidophylla*
lindmanii	0.127^{***}	0.062^{**}	0.063^{**}		$0.037^{./\mathrm{ns}}$	$0.027^{\mathrm{ns/ns}}$	$0.124^{*/\mathrm{ns}}$	*lindmanii*
macrocarpa	0.076^{***}	0.022^{***}	0.027^{***}	0.017^{ns}		$0.028^{***/\mathrm{ns}}$	$0.031^{./\mathrm{ns}}$	*macrocarpa*
laevigata	0.123^{***}	0.062^{***}	0.074^{***}	0.077^{***}	0.035^{***}		$0.111^{**/\mathrm{ns}}$	*laevigata*
media	0.107^{***}	0.057^{**}	0.070^{***}	0.103^{**}	0.054^{***}	0.066^{***}		*media*
F_{ST}	*monogyna*	*subsphaerica*	*rhipidophylla*	*lindmanii*	*macrocarpa*	*laevigata*	*media*	$(\delta\mu)^2$
monogyna		$37.524^{***/**}$	$54.671^{***/**}$	$62.397^{***/.}$	$53.241^{***/*}$	$54.611^{***/*}$	$40.191^{**/\mathrm{ns}}$	*monogyna*
subsphaerica	0.061^{***}		$1.056^{./\mathrm{ns}}$	$6.314^{***/\mathrm{ns}}$	$1.744^{***/\mathrm{ns}}$	$4.643^{***/\mathrm{ns}}$	$1.024^{./\mathrm{ns}}$	*subsphaerica*
rhipidophylla	0.072^{***}	0.008^{ns}		$3.268^{*/\mathrm{ns}}$	$0.580^{*/\mathrm{ns}}$	$3.352^{***/\mathrm{ns}}$	$3.673^{*/\mathrm{ns}}$	*rhipidophylla*
lindmanii	0.298^{***}	0.107^{**}	0.110^{**}		$0.673^{\mathrm{ns/ns}}$	$-0.538^{\mathrm{ns/ns}}$	$4.158^{*/\mathrm{ns}}$	*lindmanii*
macrocarpa	0.186^{***}	0.041^{***}	0.050^{***}	$0.010^{.}$		$1.048^{***/\mathrm{ns}}$	$1.463^{*/\mathrm{ns}}$	*macrocarpa*
laevigata	0.273^{***}	0.103^{***}	0.127^{***}	0.098^{***}	0.054^{***}		$3.445^{**/\mathrm{ns}}$	*laevigata*
media	0.240^{***}	0.106^{**}	0.133^{***}	0.139^{**}	0.103^{***}	0.092^{***}		*media*
Ds	*monogyna*	*subsphaerica*	*rhipidophylla*	*lindmanii*	*macrocarpa*	*laevigata*	*media*	**SMM**

Note: Explanation for reasons of space on the bottom of the previous page.

Table 14 Pairwise genetic differentiation of the ingroup (n = 278, genetic annotation).

IAM	2	2.3	3	4	4.6	5	5.5	6	6.6	7	7.7	1	R_{ST}
2		$0.154^{*/\mathrm{ns}}$	$0.294^{./.}$	$0.377^{*/\mathrm{ns}}$	$0.634^{***/***}$	$0.655^{***/**}$	$0.688^{***/***}$	$0.661^{***/***}$	$0.654^{***/**}$	$0.719^{***/***}$	$0.663^{***/***}$	$0.767^{***/***}$	2
2.3	$0.027^{.}$		$-0.038^{\mathrm{ns}/\mathrm{ns}}$	$-0.106^{\mathrm{ns}/\mathrm{ns}}$	$0.289^{***/*}$	$0.402^{***/\mathrm{ns}}$	$0.407^{***/*}$	$0.378^{***/**}$	$0.312^{**/.}$	$0.497^{***/**}$	$0.289^{*/.}$	$0.450^{***/*}$	2.3
3	0.063^{**}	0.006^{ns}		$-0.286^{\mathrm{ns}/**}$	$0.101^{*/\mathrm{ns}}$	$0.260^{***/\mathrm{ns}}$	$0.217^{***/\mathrm{ns}}$	$0.199^{***/\mathrm{ns}}$	$0.102^{\mathrm{ns}/\mathrm{ns}}$	$0.328^{***/.}$	$0.045^{\mathrm{ns}/\mathrm{ns}}$	$0.227^{\mathrm{ns}/.}$	3
4	$0.083^{.}$	0.014^{ns}	0.028^{ns}		$0.156^{*/\mathrm{ns}}$	$0.271^{***/\mathrm{ns}}$	$0.256^{**/\mathrm{ns}}$	$0.213^{**/.}$	$0.154^{./\mathrm{ns}}$	$0.384^{***/*}$	$0.193^{./\mathrm{ns}}$	$0.376^{*/.}$	4
4.6	0.091^{***}	0.046^{**}	0.046^{**}	0.041^{ns}		$0.035^{**/\mathrm{ns}}$	$0.026^{\mathrm{ns}/\mathrm{ns}}$	$0.061^{**/\mathrm{ns}}$	$0.026^{\mathrm{ns}/\mathrm{ns}}$	$0.052^{*/\mathrm{ns}}$	$-0.003^{\mathrm{ns}/\mathrm{ns}}$	$0.130^{**/\mathrm{ns}}$	4.6
5	0.157^{***}	0.137^{***}	0.156^{***}	0.127^{**}	0.094^{***}		$0.041^{**/\mathrm{ns}}$	$0.093^{***/\mathrm{ns}}$	$0.091^{***/\mathrm{ns}}$	$0.021^{*/\mathrm{ns}}$	$0.042^{*/\mathrm{ns}}$	$0.131^{***/\mathrm{ns}}$	5
5.5	0.128^{***}	0.087^{***}	0.081^{***}	0.055^{ns}	0.043^{***}	0.035^{***}		$0.079^{***/\mathrm{ns}}$	$0.044^{./\mathrm{ns}}$	$0.036^{*/\mathrm{ns}}$	$0.062^{\mathrm{ns}/\mathrm{ns}}$	$0.177^{***/\mathrm{ns}}$	5.5
6	0.077^{***}	0.067^{***}	0.100^{***}	0.046^{ns}	0.039^{**}	0.051^{***}	0.047^{***}		$0.029^{./\mathrm{ns}}$	$0.070^{***/\mathrm{ns}}$	$0.038^{\mathrm{ns}/\mathrm{ns}}$	$0.248^{***/**}$	6
6.6	0.075^{***}	0.045^{***}	0.059^{**}	0.053^{ns}	0.004^{ns}	0.091^{***}	0.045^{***}	0.023^{*}		$0.115^{***/*}$	$0.065^{\mathrm{ns}/\mathrm{ns}}$	$0.172^{**/\mathrm{ns}}$	6.6
7	0.144^{***}	0.120^{***}	0.146^{***}	0.101^{*}	0.056^{***}	0.070^{***}	0.051^{***}	0.044^{***}	0.043^{***}		$0.050^{\mathrm{ns}/\mathrm{ns}}$	$0.279^{***/\mathrm{ns}}$	7
7.7	0.117^{**}	$0.045^{.}$	0.032^{ns}	0.031^{ns}	0.004^{ns}	0.092^{***}	0.028^{ns}	0.053^{*}	0.029^{ns}	0.049^{*}		$0.175^{**/\mathrm{ns}}$	7.7
1	0.074^{*}	0.065^{*}	$0.067^{.}$	$0.105^{.}$	0.055^{*}	0.114^{***}	0.096^{***}	0.049^{**}	$0.049^{.}$	0.117^{***}	0.107^{*}		1
F_{ST}	2	2.3	3	4	4.6	5	5.5	6	6.6	7	7.7	1	SMM

Note: Pairwise measures of genetic differentiation are provided as R_{ST} under SMM and as F_{ST} under IAM in the upper/right and lower/left triangular matrix, respectively. Codes of significance (0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 'ns' 1) of a two-sided test by 9,999 permutations of individuals between a pair of populations are given right above the respective value. Under SMM a second set of p values is provided by 9,999 permutations of allele sizes among alleles within each locus after the slash.

Table 15 Pairwise genetic distance of the ingroup ($n = 278$, genetic annotation).

IAM	2	2.3	3	4	4.6	5	5.5	6	6.6	7	7.7	1	$(\delta\mu)^2$
2		$7.323^{./\mathrm{ns}}$	$18.34^{./\mathrm{ns}}$	$15.80^{**/\mathrm{ns}}$	$66.28^{***/*}$	$81.75^{***/*}$	$75.70^{***/*}$	$59.99^{***/**}$	$61.42^{***/*}$	$73.90^{***/**}$	$64.78^{***/*}$	$113.3^{***/*}$	2
2.3	$0.038^{.}$		$-6.461^{\mathrm{ns/ns}}$	$-6.671^{\mathrm{ns/ns}}$	$24.66^{***/\mathrm{ns}}$	$38.53^{***/\mathrm{ns}}$	$32.09^{***/\mathrm{ns}}$	$22.43^{***/.}$	$21.56^{**/\mathrm{ns}}$	$32.44^{***/.}$	$24.37^{*/\mathrm{ns}}$	$57.33^{**/*}$	2.3
3	$0.097^{.}$	-0.019^{ns}		$-15.00^{\mathrm{ns/ns}}$	$4.379^{\mathrm{ns/ns}}$	$16.76^{***/\mathrm{ns}}$	$9.623^{**/\mathrm{ns}}$	$4.202^{**/\mathrm{ns}}$	$2.582^{\mathrm{ns/ns}}$	$11.10^{***/\mathrm{ns}}$	$4.436^{\mathrm{ns/ns}}$	$29.94^{\mathrm{ns/ns}}$	3
4	$0.089^{.}$	-0.027^{ns}	0.035^{ns}		$6.758^{./\mathrm{ns}}$	$16.81^{***/\mathrm{ns}}$	$9.070^{*/\mathrm{ns}}$	$1.985^{./\mathrm{ns}}$	$0.776^{\mathrm{ns/ns}}$	$10.82^{**/\mathrm{ns}}$	$6.884^{./\mathrm{ns}}$	$27.73^{*/\mathrm{ns}}$	4
4.6	0.205^{***}	0.108^{**}	0.105^{**}	0.041^{ns}		$1.383^{**/\mathrm{ns}}$	$0.731^{\mathrm{ns/ns}}$	$1.792^{**/\mathrm{ns}}$	$0.483^{\mathrm{ns/ns}}$	$1.116^{*/\mathrm{ns}}$	$-1.932^{\mathrm{ns/ns}}$	$8.235^{**/\mathrm{ns}}$	4.6
5	0.343^{***}	0.276^{***}	0.301^{***}	0.088^{**}	0.145^{***}		$1.719^{***/\mathrm{ns}}$	$4.184^{***/\mathrm{ns}}$	$4.763^{***/\mathrm{ns}}$	$0.498^{*/\mathrm{ns}}$	$0.848^{*/\mathrm{ns}}$	$8.209^{***/\mathrm{ns}}$	5
5.5	0.328^{***}	0.225^{***}	0.197^{***}	0.044^{ns}	0.085^{***}	0.030^{***}		$2.671^{***/\mathrm{ns}}$	$1.406^{./\mathrm{ns}}$	$0.851^{*/\mathrm{ns}}$	$1.659^{\mathrm{ns/ns}}$	$8.800^{***/\mathrm{ns}}$	5.5
6	0.162^{***}	0.136^{***}	0.212^{***}	-0.017^{ns}	0.052^{**}	0.070^{***}	0.081^{***}		$0.536^{\mathrm{ns/ns}}$	$1.994^{***/\mathrm{ns}}$	$-0.56^{\mathrm{ns/ns}}$	$10.27^{***/*}$	6
6.6	0.152^{**}	0.094^{***}	0.125^{**}	0.041^{ns}	-0.022^{ns}	0.142^{***}	0.085^{***}	0.023^{*}		$3.245^{***/.}$	$1.141^{\mathrm{ns/ns}}$	$7.362^{**/\mathrm{ns}}$	6.6
7	0.309^{***}	0.227^{***}	0.273^{***}	0.041^{ns}	0.056^{***}	0.098^{***}	0.065^{***}	0.061^{***}	0.041^{***}		$-0.459^{\mathrm{ns/ns}}$	$10.66^{***/\mathrm{ns}}$	7
7.7	0.259^{**}	$0.090^{.}$	0.059^{ns}	-0.007^{ns}	-0.026^{ns}	0.081^{***}	0.020^{ns}	0.058^{*}	0.028^{ns}	-0.001^{ns}		$8.851^{*/\mathrm{ns}}$	7.7
1	0.129^{*}	0.118^{*}	0.088^{ns}	$0.061^{.}$	$0.082^{.}$	0.159^{***}	0.191^{***}	0.068^{**}	$0.066^{.}$	0.177^{***}	0.157**		1
Ds	2	2.3	3	4	4.6	5	5.5	6	6.6	7	7.7	1	SMM

Note: Pairwise genetic distances are provided as $(\delta\mu)^2$ under SMM and as *Ds* under IAM in the upper/right and lower/left triangular matrix, respectively. Codes of significance (0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 'ns' 1) of a two-sided test by 9,999 permutations of individuals between a pair of populations are given right above the respective value. Under SMM a second set of p values is provided by 9,999 permutations of allele sizes among alleles within each locus after the slash.

Table 16 Summary of AMOVA tables and F-statistics for the morphological classification.

		IAM					SMM				
	source	d.f.	SS	MS	var	%	d.f.	SS	MS	var	%
$n = 302$	Within Populations	5416	1855.15	0.343	0.343	86.2	5416	177094.11	32.698	32.698	77.5
	Among Populations	141	108.48	0.769	0.019	4.7	141	16719.91	118.581	3.731	8.8
	Among Regions lv. 1	56	136.28	2.434	0.019	4.8	56	24376.84	435.301	3.602	8.5
	Among Regions lv. 2	7	22.31	3.187	0.017	4.3	7	3160.58	451.511	2.183	5.2
	Total	5620	2122.22	0.378	0.397	100	5620	221351.43	39.386	42.215	100
$n = 278$	Within Populations	5058	1758.94	0.348	0.348	91.3	5058	149725.09	29.602	29.602	83.9
	Among Populations	91	74.25	0.816	0.014	3.8	91	8046.53	88.423	1.812	5.1
	Among Regions lv. 1	42	117.35	2.794	0.019	5.0	42	20223.83	481.52	3.862	10.9
	Total	5191	1950.54	0.376	0.381	100	5191	177995.46	34.289	35.276	100

		IAM					SMM				
	F-statistics	value	mean	var	1-sided p	2-sided p	value	mean	var	1-sided p	2-sided p
$n = 302$	F_{SC1}	0.051					0.102				
	F_{SC2}	0.099					0.183				
	F_{ST}	0.138					0.225				
	F_{C1C2}	0.050	-0.008	0	0	0	0.090	-0.016	0.001	0	0
	F_{C1T}	0.091	-0.013	0.003	0.005	0	0.137	-0.030	0.008	0.006	0
	F_{C2T}	0.043	-0.003	0	0	0	0.052	-0.008	0.002	0.099	0
$n = 278$	F_{SC1}	0.040					0.058				
	F_{ST}	0.087					0.161				
	F_{C1T}	0.050	-0.005	0	0	0	0.109	-0.003	0.001	0	0

d.f. degrees of freedom; SS sum of squares; MS mean of squares; var variance; % proportion of explained variance; 1-sided p P(random > observation); 2-sided p P(random = observation) Note that 'population' refers to a set of individuals of the same species with identical ploidy level, 'region lv. 1' reflects species level, and 'region lv. 2' depicts in- and outgroup.

Table 17 Summary of AMOVA tables and F-statistics for the genetic classification.

		IAM					SMM				
	source	d.f.	SS	MS	var	%	d.f.	SS	MS	var	%
$n = 302$	Within Populations	5326	1772.76	0.333	0.333	84.7	5326	169414.41	31.809	31.809	76.7
	Among Populations	196	148.43	0.757	0.026	6.5	196	19551.77	99.754	4.090	9.9
	Among Regions lv. 1	91	175.01	1.923	0.020	5.0	91	28071.60	308.479	3.569	8.6
	Among Regions lv. 2	7	20.38	2.912	0.015	3.9	7	2877.78	411.111	2.013	4.9
	Total	5620	2116.58	0.377	0.393	100	5620	219915.56	39.131	41.481	100
$n = 278$	Within Populations	4968	1676.55	0.337	0.337	89.1	4968	141725.31	28.528	28.528	82.0
	Among Populations	146	114.20	0.782	0.022	5.8	146	11425.34	78.256	2.449	7.0
	Among Regions lv. 1	77	156.08	2.027	0.020	5.2	77	24043.15	312.249	3.817	11.0
	Total	5191	1946.83	0.375	0.379	100	5191	177193.80	34.135	34.794	100

	F-statistics	value	mean	var	1-sided p	2-sided p	value	mean	var	1-sided p	2-sided p
$n = 302$	F_{SC1}	0.071					0.114				
	F_{SC2}	0.120					0.194				
	F_{ST}	0.153					0.233				
	F_{C1C2}	0.052	-0.010	0	0	0	0.090	-0.020	0.001	0	0
	F_{C1T}	0.088	-0.010	0.001	0.013	0	0.135	-0.024	0.003	0.013	0
	F_{C2T}	0.039	-0.001	0	0.009	0	0.049	-0.008	0.001	0.061	0
$n = 278$	F_{SC1}	0.061					0.079				
	F_{ST}	0.109					0.180				
	F_{C1T}	0.052	-0.007	0	0	0	0.110	-0.008	0.001	0	0

d.f. degrees of freedom; SS sum of squares; MS mean of squares; var variance; % proportion of explained variance; 1-sided p P(random > observation); 2-sided p P(random = observation) Note that 'population' refers to a set of individuals of the same genetic group with identical ploidy level, 'region lv. 1' reflects genetic groups, and 'region lv. 2' depicts in- and outgroup.

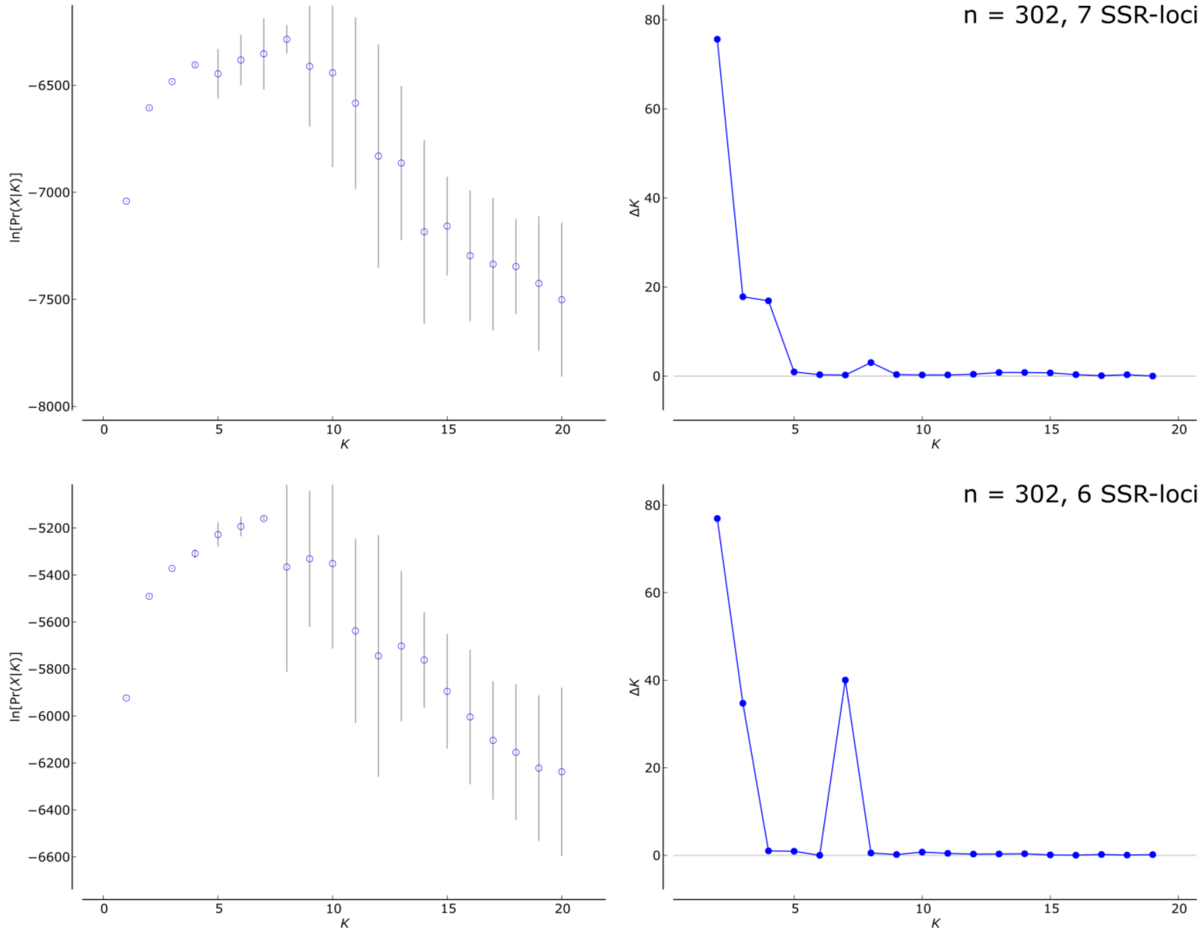


Figure 22 Bayesian inferences of the *K* clusters estimated by STRUCTURE using the no admixture model among individuals. Plots of ln[Pr(X|K)] with error bars and Δ*K* values against *K* are shown in the left and the right panels, respectively, to identify the most probable *K* in each data set. Plots in the upper row present the overall SSR data and in the lower row a reduced data set with just six SSR loci after discarding CH05G07 as multilocus marker from analysis.

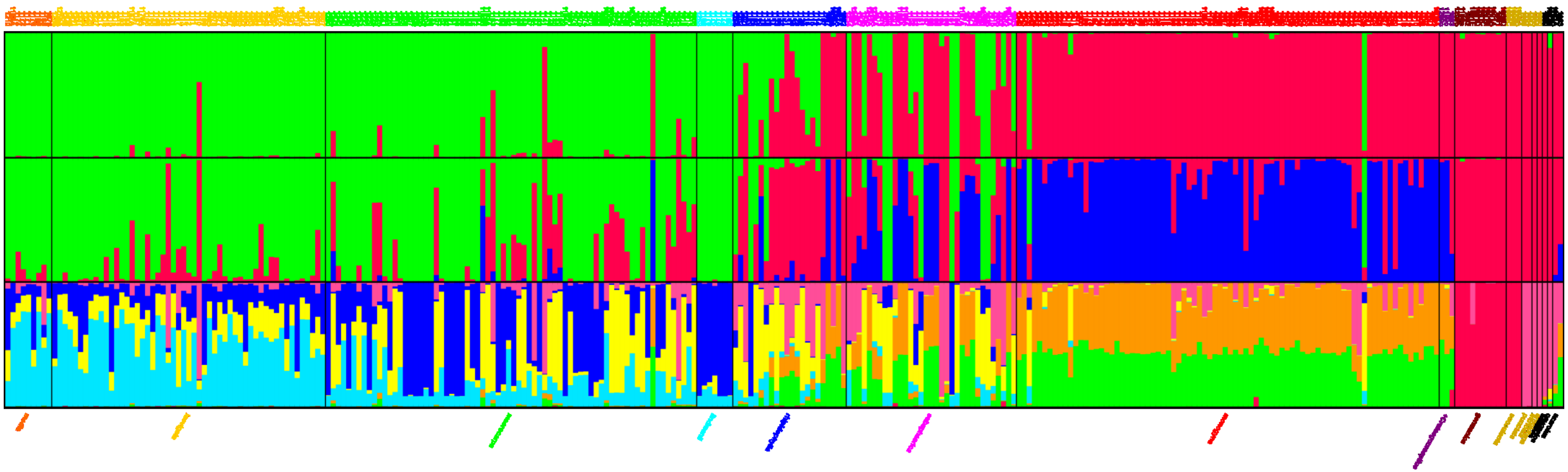


Figure 23 Hierarchical structure analysis obtained by using STRUCTURE (Pritchard et al., 2000), with $K = 2$, 3, and 7 (from top to bottom), based on data for 6 SSRs of 302 unique genotypes of *Crataegus* spp. Clusters are represented by colours, and individuals are represented as columns. Within each column (individual), the extent of the component colours indicates the magnitude of the membership coefficient (Q) corresponding to each cluster. Individuals are arranged by morphological annotations; IDs atop and morphological annotation on below in colours (in compliance with those in Figure 1).

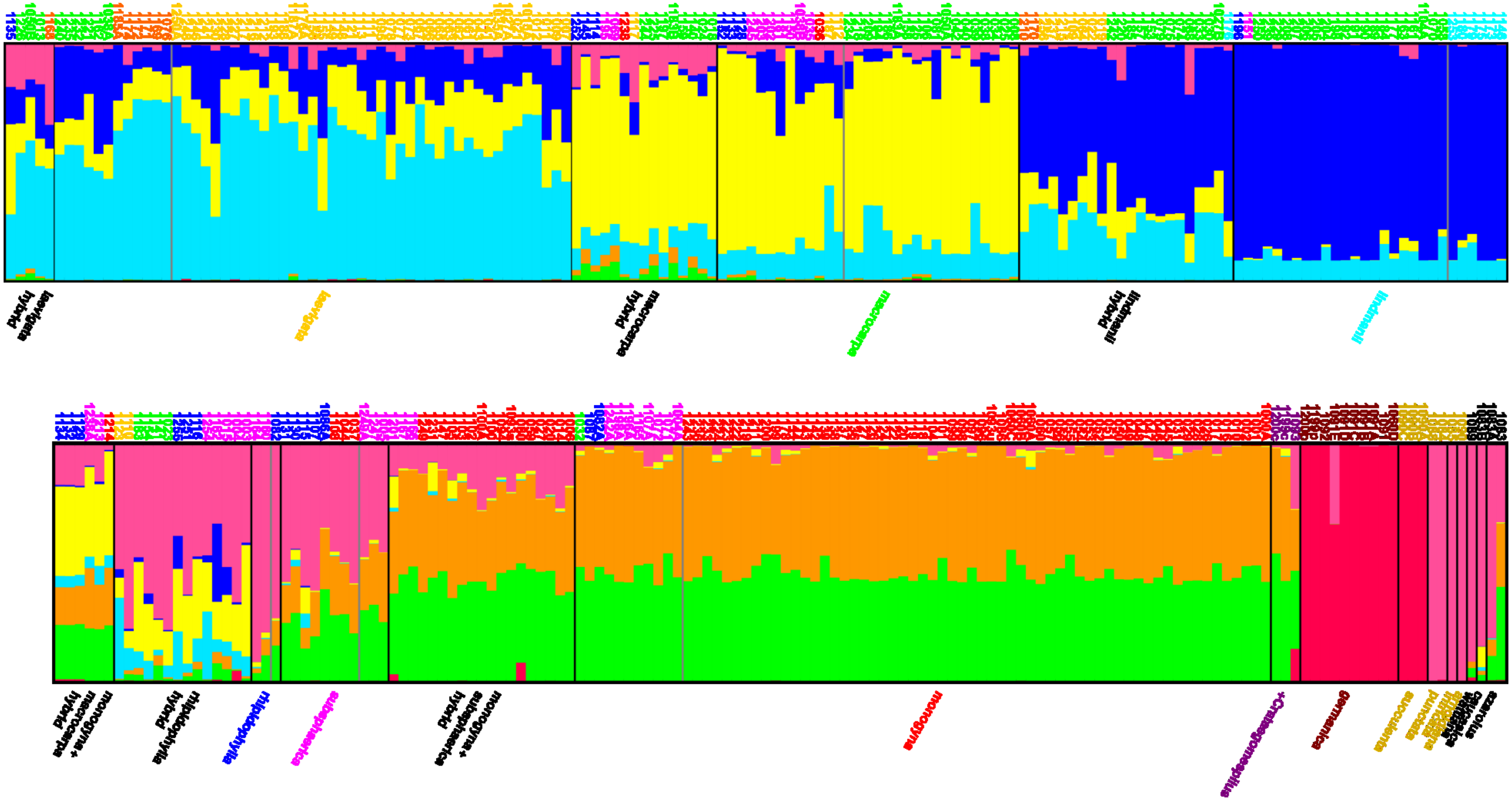


Figure 24 Rearranged hierarchical structure analysis of the lowest panel of Figure 23 obtained by using STRUCTURE (Pritchard et al., 2000), with $K = 7$, based on data for 6 SSRs of 302 unique genotypes of *Crataegus* spp. Individuals were sorted to harmonise according to their genetic structure analysis; IDs presented in the colour of the respective morphological annotation on the left (in compliance with those in Figure 1), genetic group annotation on the right. Genetic annotations are framed by black lines, grey lines separate individuals of morphological noncorfirmity to the supposed morphological equivalent within a group.

3.3.4 | Ordination of molecular data

Neighbour-joining trees

According to the *D*s-based unrooted NJ trees at species and genetic group level extracted from PolyGene (Figure 25) there are three distinct branches: First the outgroup, second the group of *C. lindmanii*, *C. macrocarpa*, and *C. laevigata* or the assumed genetic groups ‘5’, ‘6’, and ‘7’ at the opposed site, and third the group of *C. monogyna*, *C. subsphaerica*, and *C. rhipidophylla* or the assumed genetic groups ‘2’, ‘3’, and ‘4’ in between. The position of *C. media* seems reasonable intermediate between *C. monogyna* and *C. laevigata*. The intermediate group ‘1’ with almost equal proportions of both sets of genetic clusters (A) and (B) (see previous section and Figure 24) is located towards the outgroup. In contrast group ‘6.6’ with cluster membership coefficients similar to ‘6’ is found intermediate between the two main branches of the ingroup. Additionally group ‘4.6’, seen as mixture of groups ‘4’ and ‘6’, is as sister branch to ‘6’ far apart from group ‘4’. The remaining groups with only slight differences from others (‘5.5’, ‘7.7’) or with intermediate status (‘2.3’) are placed next to their concerned groups.

For a closer look at the relationships at individual level unrooted NJ trees based on Bruvo’s distance are provided for the overall (Figure 26) and the ingroup data set (Figure 27). As obvious from both dendrograms there are no monophyletic groups and, moreover, nearly all branches suffer support by bootstrapping.

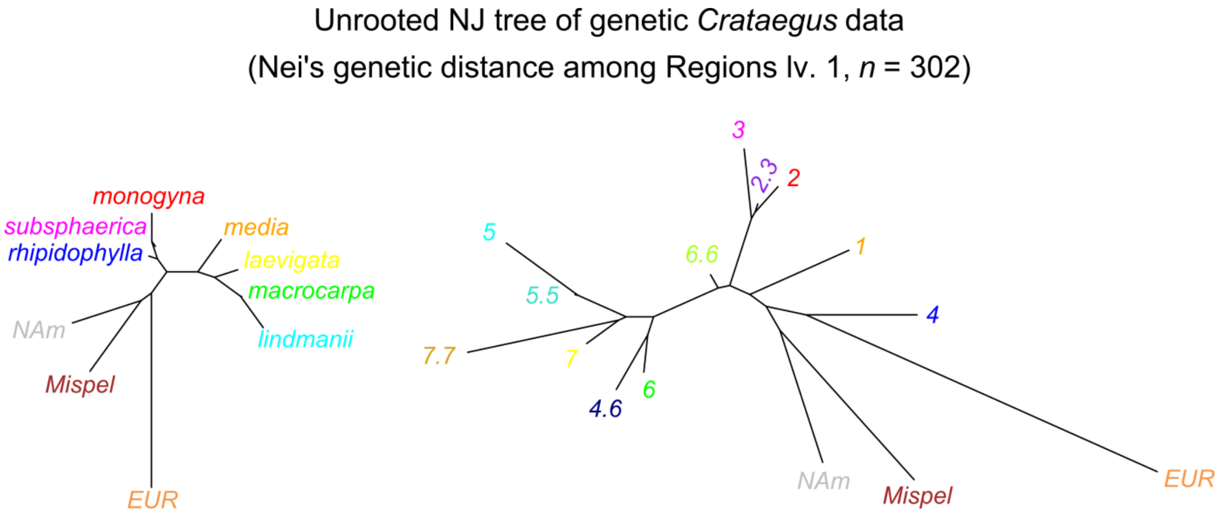


Figure 25 Unrooted dendrograms of the overall data based on *D*s distances between different classifications at Region level 1. Left panel: morphological annotations; right panel: genetic annotations.

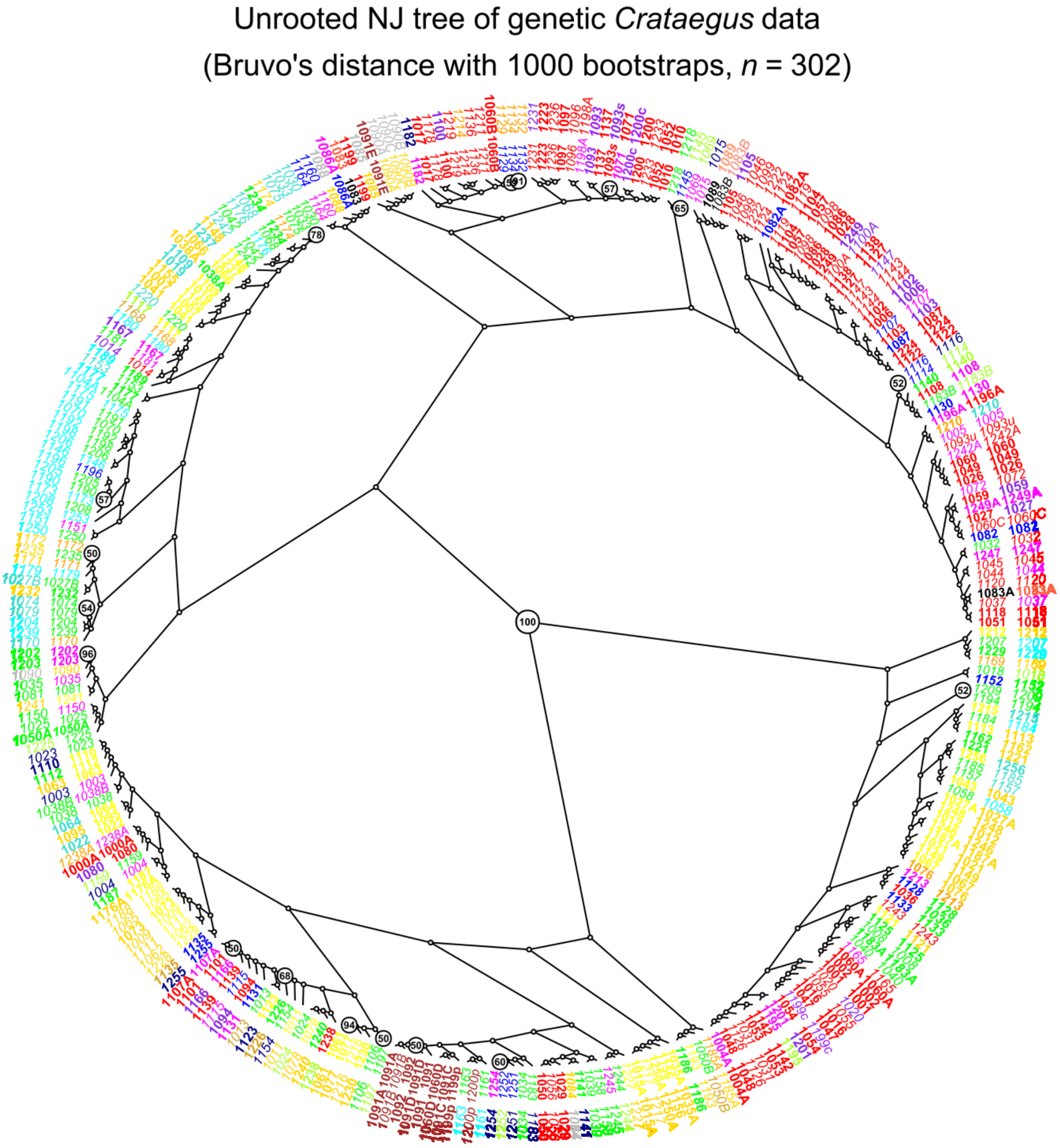


Figure 26 Unrooted dendrogram of the overall data set based on Bruvo’s distance between individuals. Sample IDs coloured according to morphological and genetic annotation are written as leaves in an inner and an outer ring, respectively, with font type representing the estimated ploidy level (see Table S7): 2*x* in **bold**, 3*x* in *italics*, and 4*x* in ***bold italics***. Bootstrap values are presented as integers at nodes if higher than 50%.

NMDS

The ordination of the overall and the ingroup allelic data as zero-one matrix produces stress values between 11.22% and 37.91% by performing a NMDS up to six dimensions (Table 18). Despite a weak elbow criterion at $k = 3$ (left panels of Figure 28 and Figure 29) this number of dimensions was chosen for further analyses. The ordination of both data sets (Figure 30 and Figure 31) shows similar tendencies of clustering. The species *C. monogyna*,

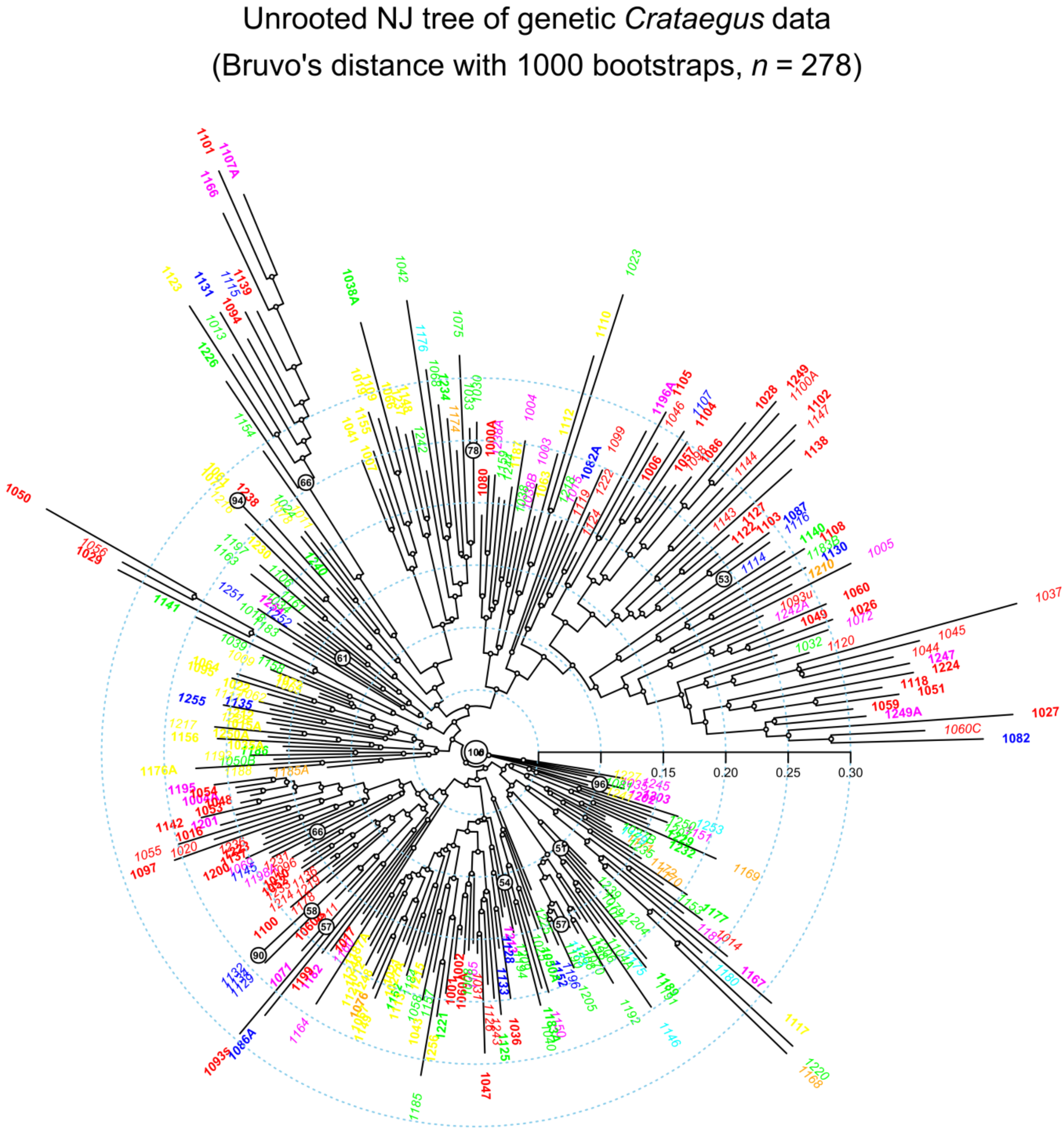


Figure 27 Unrooted dendrogram of the ingroup data set based on Bruvo's distance between individuals. Sample IDs coloured according to morphological annotation are written as leaves with font type representing the estimated ploidy level (see Table S7): 2*x* in **bold**, 3*x* in *italics*, and 4*x* in ***bold italics***. Bootstrap values are presented as integers at nodes if higher than 50%. For purposes of recognisability circles of equal distances are drawn at a 0.05 interval.

C. subsphaerica, and *C. rhipidophylla* (including the European outgroup and the graft-chimeras in the overall data set) map together left of axes two and three while *C. lindmanii*, *C. macrocarpa*, *C. laevigata*, and *C. media* are located right of those axes. Members of the North American outgroup and the medlars are found in between the other two main cluster along axis two. No further division pattern of clusters can be announced for sure.

Table 18 Stress of NMDS by data sets of allelic data.

k	1	2	3	4	5	6
***n* = 302**	39.77% $^{\text{nc}}$	25.28% $^{\text{nc}}$	19.15%	15.65%	13.16%	11.37% $^{\text{nc}}$
***n* = 278**	37.91% $^{\text{nc}}$	24.74% $^{\text{nc}}$	18.99%	15.53%	13.08%	11.22% $^{\text{nc}}$

k Number of dimensions after ordination; *n* number of samples; $^{\text{nc}}$ the algorithm showed no convergence within 1,000 runs.

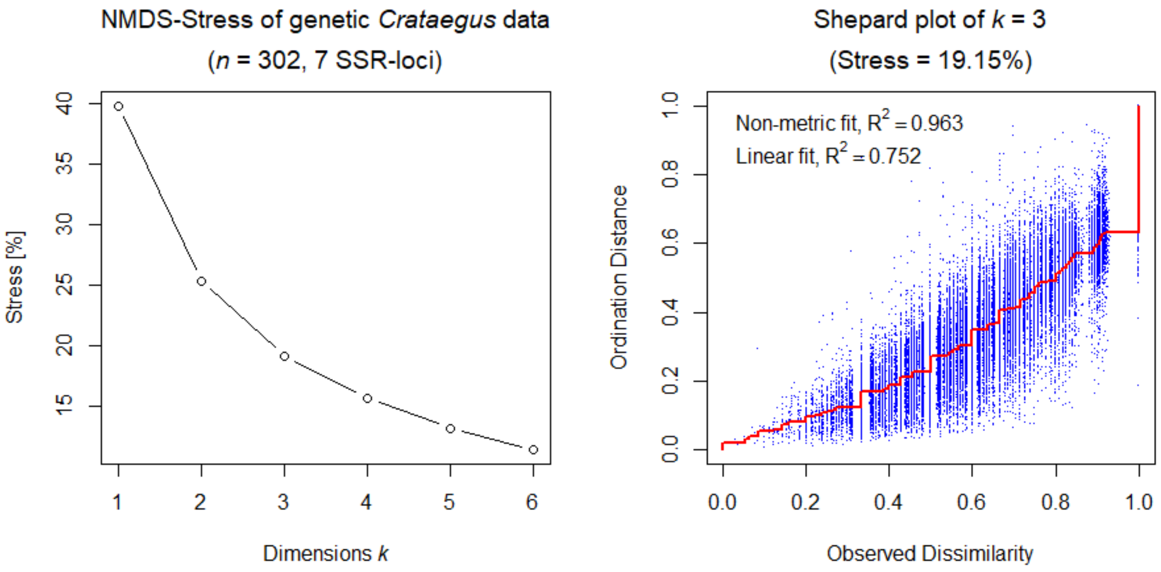


Figure 28 Stress of NMDS of the allelic data ($n = 302$). Left panel: Stress in relation to number of final dimensions (k) after dimensional reduction via NMDS. Right panel: Shepard plot of ordination distance against observed dissimilarity of the optimal $k = 3$ with a stress of 19.15%.

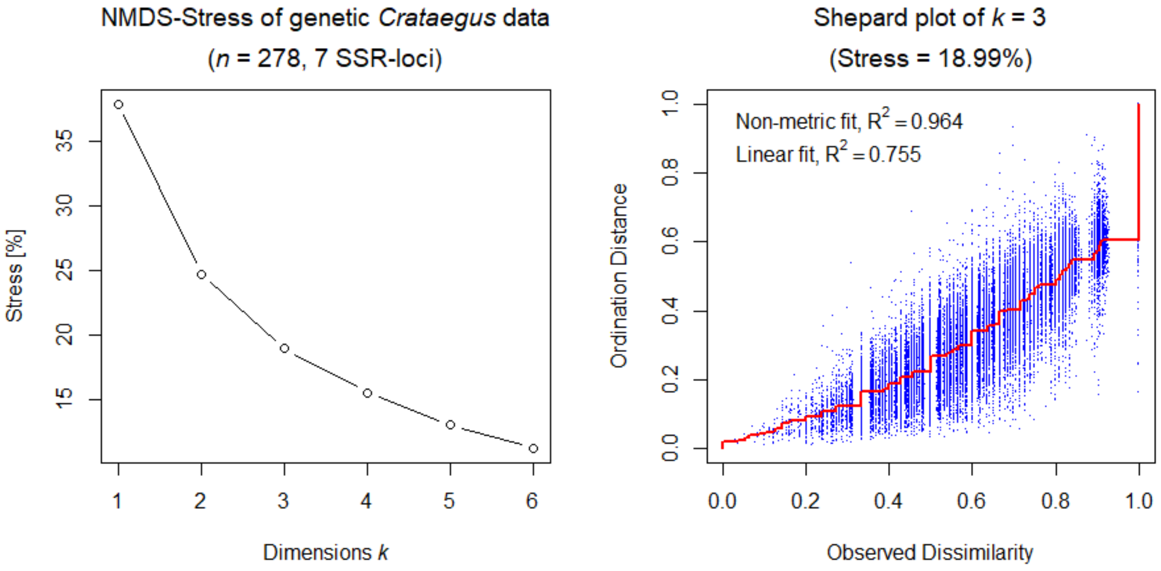
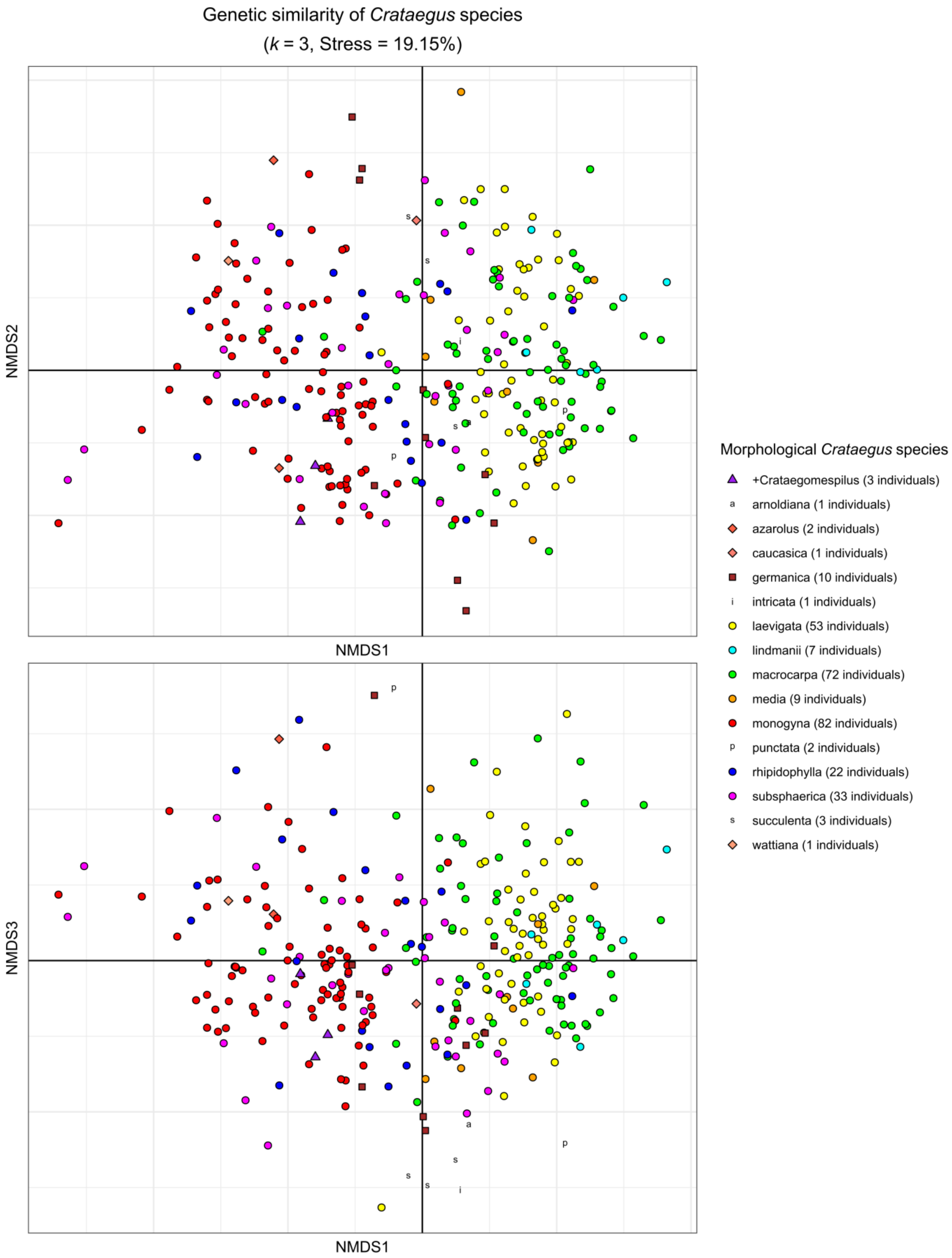
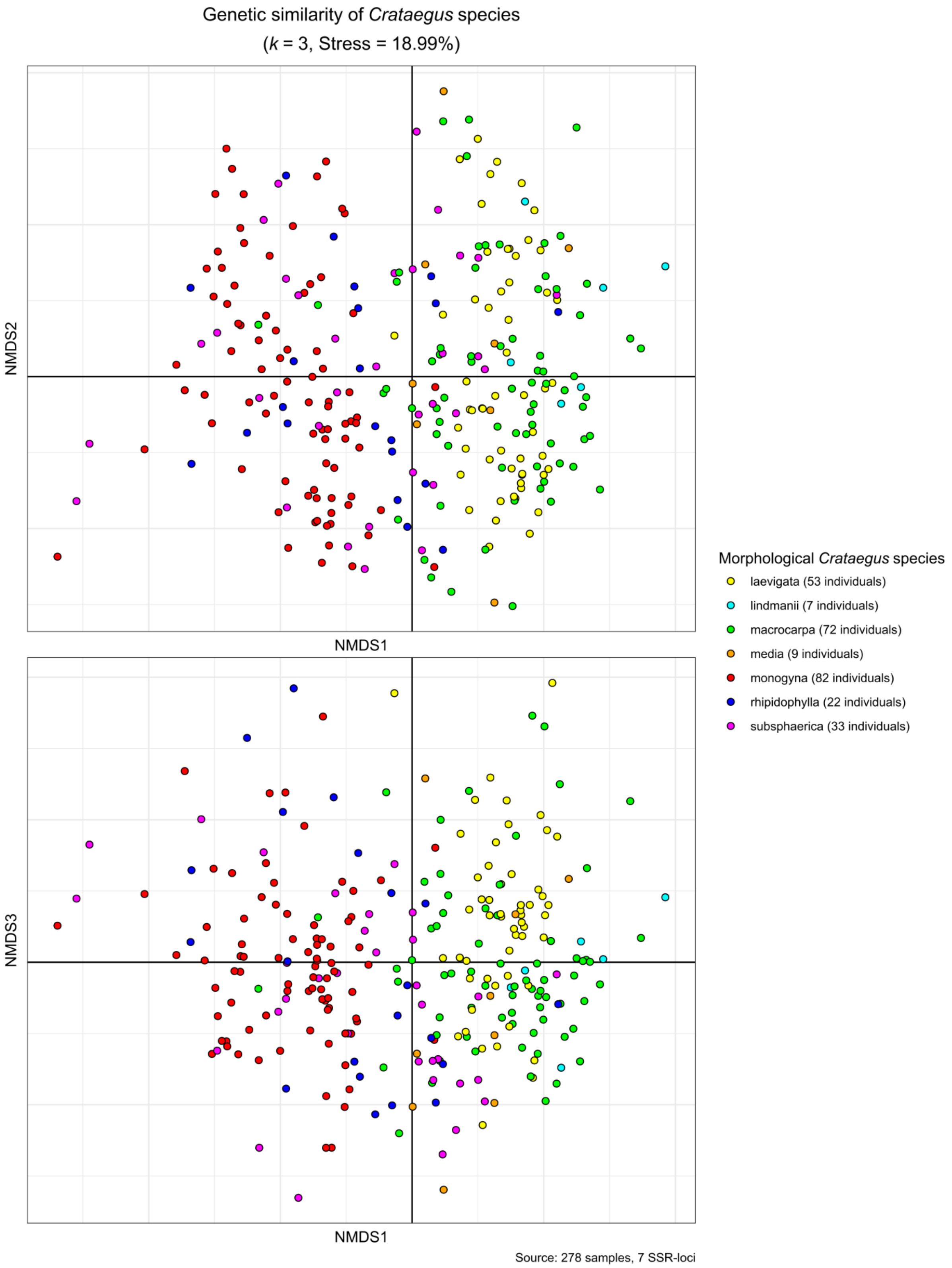


Figure 29 Stress of NMDS of the allelic data ($n = 278$). Left panel: Stress in relation to number of final dimensions (k) after dimensional reduction via NMDS. Right panel: Shepard plot of ordination distance against observed dissimilarity of the optimal $k = 3$ with a stress of 18.99%.



Source: 302 samples, 7 SSR-loci

Figure 30 NMDS ordination plot of the allelic data ($n = 302$). North American *Crataegus* are represented by letters while Eurasian *Crataegus* are by coloured symbols (in compliance with those in Figure 1). The ingroup of ser. *Crataegus* is depicted by circles. Number of samples of each group is given in parentheses. Top panel: The first two dimensions are shown. Bottom panel: The first and the third dimension are shown.



Source: 278 samples, 7 SSR-loci

Figure 31 NMDS ordination plot of the allelic data ($n = 278$). The different species of ser. *Crataegus* are represented by colours (in compliance with those in Figure 1). Number of samples of each group is given in parentheses. Top panel: The first two dimensions are shown. Bottom panel: The first and the third dimension are shown.

3.4 | Comparison of morphological and genotypic data

The comparison of distance matrices of the morphological and the allelic raw data revealed a highly significant and slightly positive correlation (overall group: $r_M = 0.38$; ingroup: $r_M = 0.37$; both $p < 0.0001$). However, Kendall's τ of comparing the different classifications of the ingroup resulted in a highly significant and clearly positive correlation ($\tau = 0.70$, $p < 0.001$; Figure 33).

The combined plotting in Figure 34 is an extension of Figure 16 with assignment of every ingroup sample to its genetic group. As recognisable from the 'Rearranged hierarchical structure analysis' (Figure 24) and the 'Boxplot of different *Crataegus* annotations' (Figure 33) the genetic groups '1', '2', '2.3', '3', and '4' are presented left of axes two and three and samples right of these axes are found within groups '5', '5.5', '6', '6.6', '7', and '7.7'. Although most genetic groups are well defined and appear condensed some have outliers that are far apart from the centre. The majority of these outliers belongs to groups '3', '4.6', '6', and '6.6'. The centroids of groups '2' and '2.3' fall almost together on both planes of the ordination space while those of groups '5', '6', and '6.6' are close to each other only in the lower panel of the first and third dimension. The remaining centroids are separated from each other.

The outlier detection by population assignment revealed in total 80 individuals with an unconfirmed annotation (Figure 32; for details see Table S8 and Table S9). Amongst them two third (54 individuals) showed divergences in the morphological classification and about 40% (34 individuals) in the genetic classification. Yet, six individuals (7.5%) were assigned to the respective other in concerns of in- and outgroup. Within the ingroup (right Venn) there are eight individuals, namely 1027, 1032, 1038, 1038A, 1060A, 1071, 1158, and 1213, that were assigned neither to their morphological nor their genetic classification.

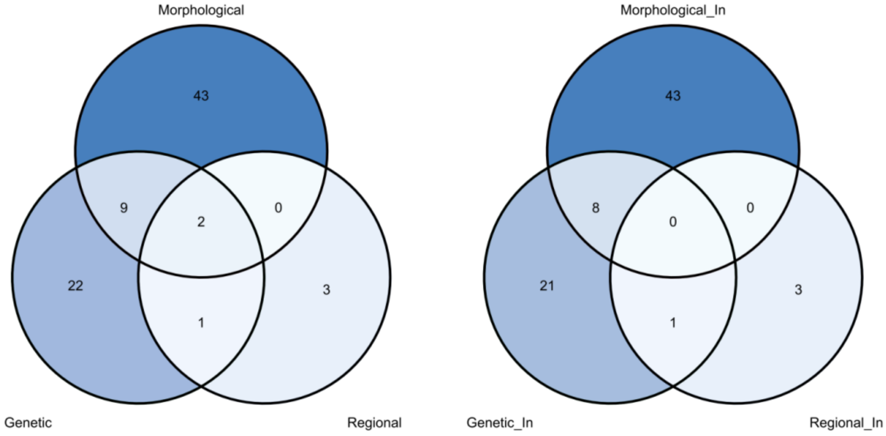


Figure 32 Number of individuals with divergences under population assignment of the overall (left Venn) and the ingroup data set (right Venn).

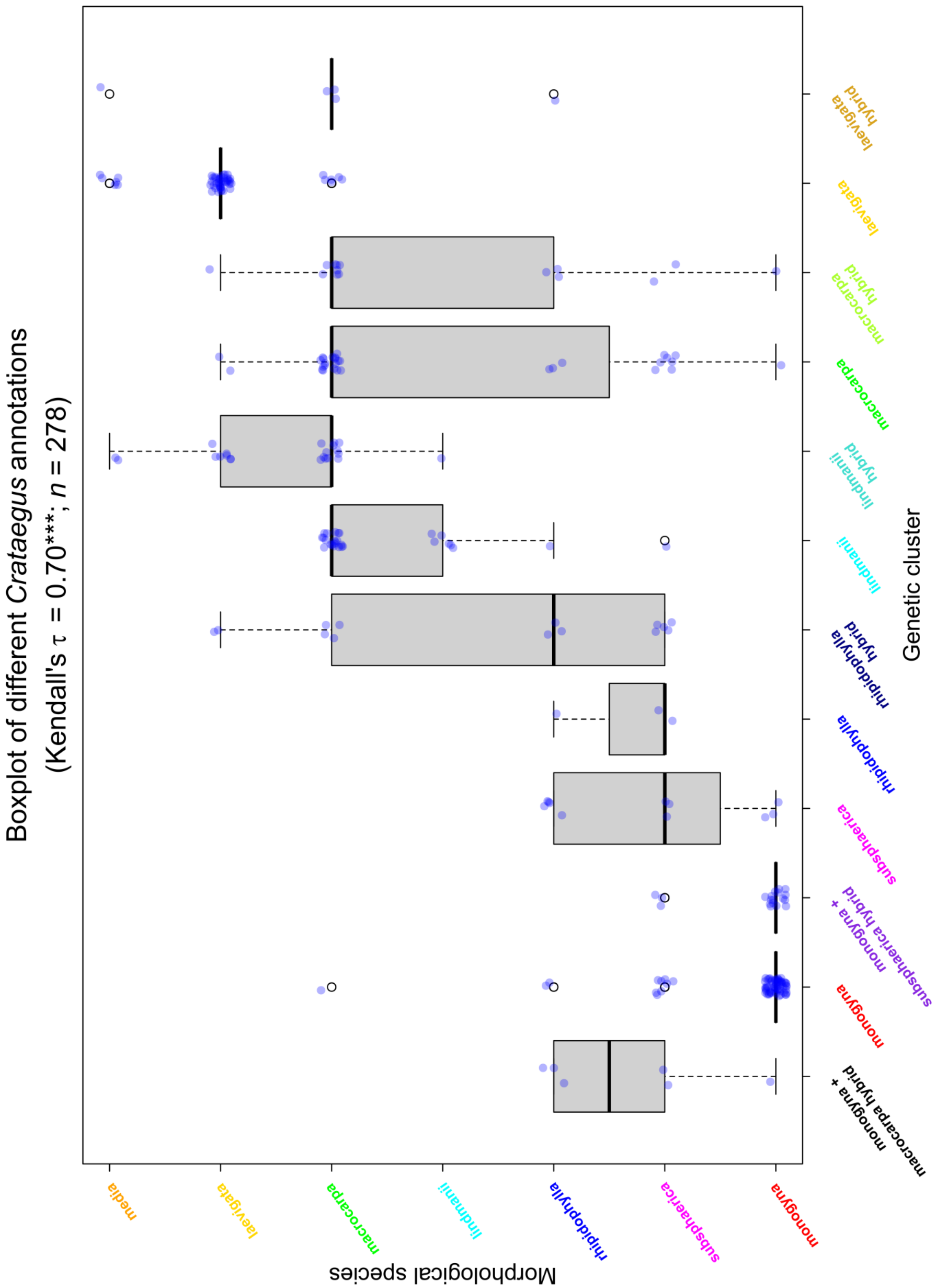
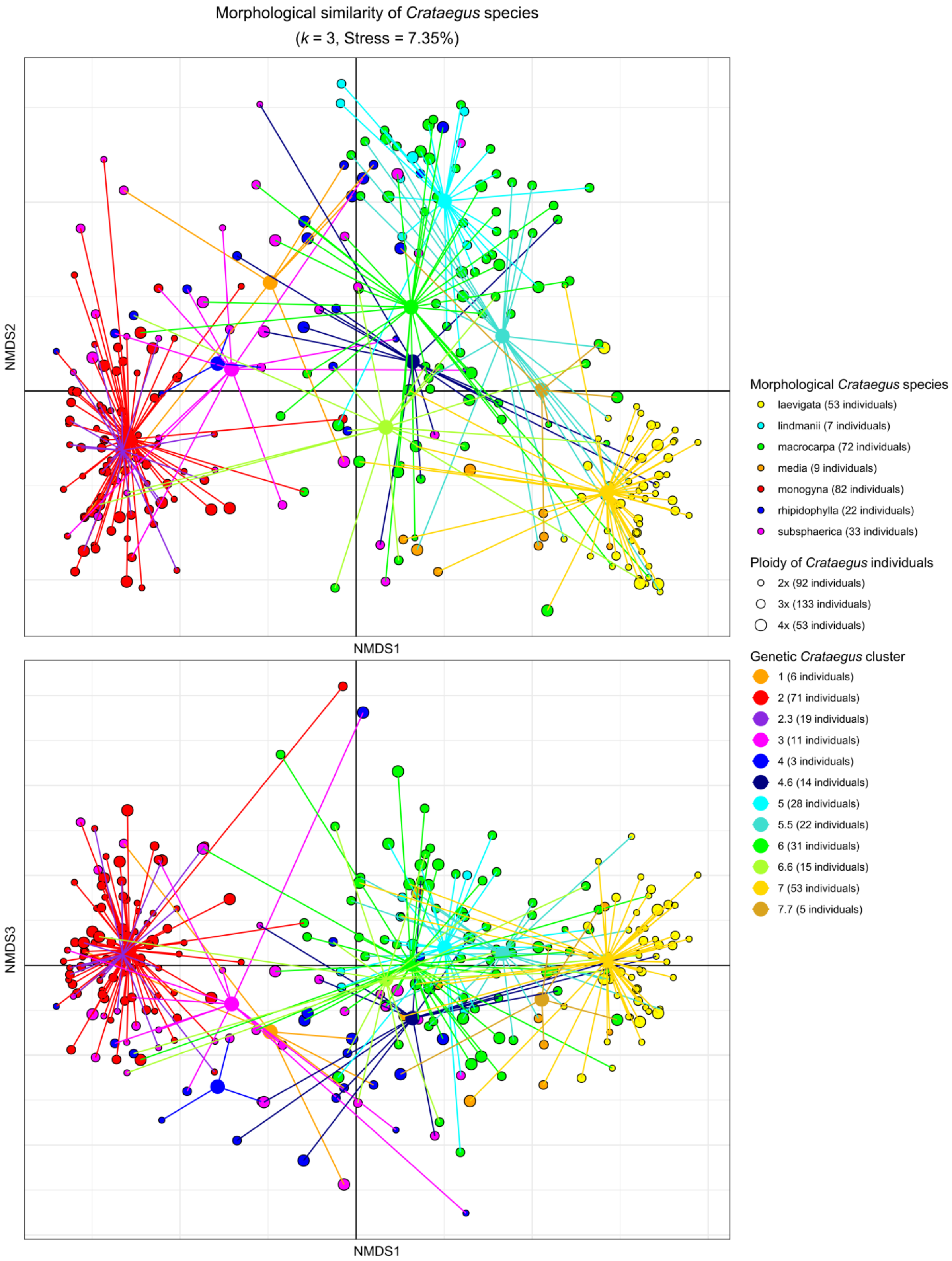


Figure 33 Boxplot of different *Crataegus* annotations.



Source: 278 samples, 9 basic traits

Figure 34 NMDS ordination plot of the basic morphological traits data ($n = 278$) with membership to genetic groups. For description see Figure 16 as identical to except points belonging to the same genetic group are connected with the centroids calculated for all these points. Top panel: The first two dimensions are shown. Bottom panel: The first and the third dimension are shown.

4 | Discussion

4.1 | Reproductive modes

Despite of the eventual mechanism, the ability of reproduction is an essential point in every species life history. In literature there are several mechanisms reported for the genus *Crataegus*, ranging from obligate outbreeding in diploids (Bradshaw, 1971; Vašková & Kolarčik, 2019), possible and rare (depending on authorities) autogamy via self-pollination (Dau, 1941; Guitián & Fuentes, 1992; Gyan & Woodell, 1987; Kalkman, 2004; Knuth, 1898; Talent & Dickinson, 2007b), autonomous apomixis, that does not require fertilisation of the endosperm (Talent & Dickinson, 2007b), to pseudogamous apospory requiring pollination to fertilise the endosperm (Dickinson & Phipps, 1986; Pelc & Ptak, 1981; Smith & Phipps, 1988; Talent & Dickinson, 2007a). In this context the ambiguous findings on polyspermy and gametophytic apomixis were emphasised by Scott (2007) and Talent (2009). Although male-sterility is reported for triploid taxa (Campbell, Greene, & Dickinson, 1991; Dickinson, 1983; Dickinson & Phipps, 1986; Muniyamma & Phipps, 1979b), Vašková and Kolarčik (2019) stated that triploids "are also capable of utilising pollen from 2*x*, 3*x*, or 4*x* donors for pseudogamous formation of endosperm". Previous findings of RNase-based gametophytic self-incompatibility in *Crataegus* (Love & Feigen, 1978; Nettancourt, 1977; Raspé & Kohn, 2002) as well as a general breakdown of self-incompatibility in pseudogamous apomicts (Hörandl, 2010) have to be considered in this case.

This study's results of experiments on reproductive modes show little fruit set in the uncovered but treated flowers and no fruit set at all under the applied apogamous, autogamous, and geitonogamous conditions (Table 7). These results seem to be in line with xenogamic cross-pollination of Central European *Crataegus* spp. by insects being the rule, even if selfing was reported as a resort to lack of allogamous pollination (Knuth, 1898) or as real alternative with half of the fruit set rate of freely-exposed flowers (Guitián & Fuentes, 1992). On the other hand these results contradict previous findings of self-incompatibility (Love & Feigen, 1978; Nettancourt, 1977; Raspé & Kohn, 2002). If the little fruit set in treated but open flowers may be a result of rare autogamy (Kalkman, 2004) with a selfing rate of 2% (Bradshaw, 1971; Talent & Dickinson, 2007b), this does not explain the fact of bearing fruits in those cases where selfing was inhibited by emasculation. Although lacking their visual attractant depetaled flowers may still be appealing pollinators fond of putrefying substances by their scent of herring brine due to a trimethylamine component (Kugler, 1970). Alternatively, seeds might have developed apomictically. One possibility out of many methods to test for apomixis is cutting each stigma off (V. Wissemann, pers. comm.) which resulted in zero fruit set in this study. At least for examined diploids this cannot be harmonised with the statement concerning autonomous apomixis of Talent and Dickinson (2007b).

However, earlier experiments on seed formation in apomictic tetraploid *Crataegus* (Dickinson & Phipps, 1986; Smith & Phipps, 1988) have given rise to another favoured mechanism of apomixis in *Crataegus*: pseudogamous apospory requiring pollination (Talent & Dickinson, 2007a). Both possible apomictic mechanisms may also matter in the allogamous breeding experiments were potential hybrids were assumed to be artificially made. Crosses involving individuals assigned to different species set fruit. Surprisingly that single cross of the totally interfertile obligate outbreeders *C. laevigata* and *C. monogyna* supposed to form the only so far proven hybrid of diploid-diploid origin, *C. media* (Bradshaw, 1953, 1971; Byatt, 1975b), produced no fruit. On the other hand, Bradshaw (1971) found a fruit set rate of 30%–59% in a series of interspecific cross-pollination between *C. laevigata* and *C. monogyna*. By the facts of being protogynous (Knuth, 1898) and differing remarkably in their begin of flowering of about 1-2 weeks (Clapham, Tutin, & Moore, 1989; Hegi, 1923), the most promising direction of pollen transfer is, as applied in this study, from *C. laevigata* as pollen donor to *C. monogyna* as pistillate parent. Thus pollen of *C. laevigata* had to be stored for the pollination of later flourishing *C. monogyna*. Despite the possibility of erroneous storage condition inside a Petri dish at room temperature, the question for how long pollen is germinable under natural conditions to perform the supposed cross remains unanswered. At least pollen from freshly harvested flowers germinates readily on several media (Th. Reimann, pers. comm.: Feng, An, Tan, Hou, & Wang, 2000; Lord & Heslop-Harrison, 1984; Tansengco et al., 2004). Other striking points are the possibility to form viable pollen via microsporogenesis and their ability to fertilise the egg cell. This might be irrelevant in diploids, e.g. in *C. monogyna* were pollen viability is c. 70% (Muniyamma & Phipps, 1979b) or 45 to 90% of pure species and hybrids (Lippert, 1995), but crucial in those cases were the ploidy level exceeds two and especially when equal to an odd number. In fact, Vašková and Kolarčik (2019) suggest that *C. monogyna* (2*x*), *C. subsphaerica* (3*x* and 4*x*), and *C. kyrtostyla* (2*x*, interpreted as *C. monogyna* × *C. subsphaerica*) produce reduced pollen irrespective of ploidy level but apparently aneuploid pollen grains as a result of irregular meiosis in triploids. Male-sterility is reported for other triploid taxa (Campbell et al., 1991; Dickinson, 1983; Dickinson & Phipps, 1986; Muniyamma & Phipps, 1979b). This in mind the zero fruit set in reciprocal crosses of *C. macrocarpa* might not be that devious as both individuals are estimated triploids (Table 7 and Table S7). At the same time the autonomous endosperm formation and both pathways of pseudogamous apomixis, i.e. self-compatible pseudogamy via geitonogamy or selfincompatible pseudogamy via reciprocal xenogamy (Hörandl, 2010), did not happen. Both individuals appear morphologically alike but not genetically. The failure of setting any fruit at all can be seen either under the light of a gametophytic incompatibility or reproductive isolation. Contrastingly pollen transfer from *C. laevigata* to *C. macrocarpa* resulted in 22% fruit set regardless apomictic or sexual and thus challenging the option of reproductive isolation as well as assuming pseudogamous apomixis in this case. The viability of pollen should be given as flowering of *C. macrocarpa* started unambiguously earlier than that of *C. monogyna* and cross pollination happened two days after harvesting pollen from *C. laevigata*. The remaining individuals of *C. monogyna*, *C. subsphaerica*, and *C. rhipidophylla* were in bloom at the same time so that their pollen had not to be stored for over one week for reciprocal pollination purposes. Although the individual assigned to *C. subsphaerica* turned out to be an estimated triploid, fruit set on this plant ranged from 25% to 44%. Crosses with this individual as pollen donor yielded 27% fruit. Therefore, a reduced pollen fertility or even male-sterility was a vague conclusion. On the other hand fruit set may be due to autonomous or pseudogamous apomixis.

As the morphological variation of these three plants is little (Table S4) and their genetic clustering result is similar (Figure 24) crosses have to be considered more intra- than interspecific. Hence, the amount of fruit set between these individuals and the cross between the individuals of *C. laevigata* is in line with the rate of natural and open pollinated flowers (20% to 60%) reported by Bradshaw (1971), Guitián and Fuentes (1992) and Guitián, Sánchez, and Guitián (1992). These values also fit the overall visually but not quantifiably subjective perception during field season.

4.2 | Morphology

Morphology played a crucial role in species recognition ever since and comparison of traits led to the morphological species concept. Therein species are distinguished by the highly correlated discontinuity of features of traits. The set of basic traits provides a lot of highly significant and strongly correlated pair of traits (Figure 5). The highest correlations among traits are those pairs that appear to bear autocorrelation, i.e. the direction of first lateral veins and the depth of lobes (leaf_1 and leaf_5), the appearance of glands on teeth of stipules (leaf_7 and leaf_8), and the number of styles and the number of nutlets (flower_1 and fruit_2). The first pair may be auto correlated by constraints of geometry and leaf architecture to build laminae that are not self-overlapping, the second due to the definition of these traits as glands exist on tips of teeth if the margin is serrate, and the third by the developmental process that, in fact, each one-celled ovary contains two ovules but only the lower of the them is pregnable leading to an identity in the number of styles and eggs and thus nutlets (Hegi, 1923). However, there are other highly correlated traits without causal relationship within this set providing feasible values for identification of groups of individuals. So it is no wonder that discarding traits leaf_5, leaf_8, and fruit_2 from the analysis leads to the same picture in ordination with even lower stress (data not shown). Hence, these traits are rightly used in hawthorn key literature throughout the centuries (de Candolle, 1825; Lippert, 1978; Petermann, 1849; Schmidt, 2019; Vollmann, 1914; Wenzig, 1874). Despite the historically inherited usage of these traits morphological characteristics are subjective and the assessment of traits as key traits depends on 'expert' opinion (Aldhebiani, 2018; Regan, 1926).

By the fact of initial hybridisation followed by backcrossing and introgression it may happen that individuals are not exactly intermediate between but show much more characteristics of either of the parental species (Lippert, 1995; Timmermann & Müller, 1994). Stace (1989) stated to attain more characters of equal weight in phenetic taxonomy which was again emphasised by Wiens (2004). Following the work of Pforr (2017) additional describing traits were denoted that were taken from species descriptions and after testing them for a certain degree of variability in the field. However, it was shown by values of stress after NMDS (Table 8) that simply more traits do not automatically lead to a better resolution of a given data set. Although the plotting results appeared similar, in cases of stress the opposite finding was detected. Stress decreased by subsetting data to the traditionally handed down characteristics. In a subsequent study the power of explanation of each set among all combination of the *k*–permutations of *n* traits may be analysed which is

$$\sum_{k=1}^{n} \binom{n}{k} = \sum_{k=0}^{n} \binom{n}{k} - 1 = 2^n - 1$$

that equals 16,777,215 combinations for the considered $n = 24$ traits. In spite of these theoretical implications and by neglecting former assignment the analysis of the morphological data separates the outgroup taxa from the ingroup (Figure 7, Figure 10, and Figure 11) mainly by reflecting the different subgenera with their main differing traits of incised leaves and veins ending solely in teeth (El-Gazzar, 1980; Ufimov & Dickinson, 2020). Within the ingroup the multivariate analysis leads to two distinct groups of phenotypes which are expected to cover the description of *C. laevigata* and *C. monogyna* (Figure 16). Further clustering among the remaining individuals is not detectable until the former assignment is taken into account. The pattern of not facing distinct morphological discontinuities yet a smooth transition between the considered taxa has given rise to the calling for hybridogenous behaviour among them. Thus Palmer's 1932 invented term of the "*Crataegus*-problem" among North American taxa swapped across the Atlantic Ocean and endorsed European taxonomists to carry on in postulating hybrids and describing species, microspecies and varieties as the easy way out explanation of blurred morphological discontinuities (Hrabětová-Uhrová, 1969a, 1973a, 1973b, 1976, 1978, 1980; Petauer, 1980). A peak of that period is preserved in Doll's (1976) key to *Crataegus* species in Germany with 20 microspecies, eleven of them assumed as primary hybrids. At the same time Doll himself classified all these taxa into two distinct aggregates, that are the formerly mentioned species of this study's analysis. Although a plenty of studies on the hybridogenous species and their putative parents (*C. subsphaerica*: Byatt, 1976b; Christensen, 1982a, 1984, 1985, 1992b; *C. macrocarpa*: Byatt, 1976b; Christensen, 1982a; *C. media*: Bradshaw, 1953; Byatt, 1975b, 1976b; Christensen, 1982a, 1984; Gosler, 1990; Synnott, 1978) on the British Isles (Bradshaw, 1953; Byatt, 1975b; Gosler, 1990; Synnott, 1978), in Belgium (Byatt, 1976b; Depypere et al., 2009), Denmark (Christensen, 1982a), Poland (Gostyńska-Jakuszewska, 1975; Oklejewicz, Chwastek, Szewczyk, Bobiec, & Mitka, 2013; Zaraś-Januszkiewicz, 2008), and the Balkan Peninsula (Christensen, 1984, 1992b) has been performed, their hybridogenous formation could not be proven as the investigations were always designed from a morphometric point of view. Another crucial point is the fact of herbarium material used in these studies lacking reliable identification (Loos, 1994). Furthermore, some species seem to be absent in certain areas and published distribution maps have to be considered very critically (Gregor, 2015).

4.3 | Molecular characterisation

Even the phylogeny of morphotaxa, where the (dis)similarity of morphological features is used to identify any single individual belonging to a certain species, is ultimately based on the individual's genetic composition. The (supressed) expression of genes leads to the finally recognised morphological appearance of any given individual. Non-coding SSRs are also part of the genome. They are polymorphic and thus were considered to elucidate the phylogeny of Central European *Crataegus* taxa in this study. Although number of private alleles (Table 10) presents evidence for differentiation processes, the ordination of the genetic data revealed no clustering until a previous assignment is applied (Figure 31). Thus, the AMOVA-based overall level of differentiation (Table 16) is only slightly moderate according to the classification provided by Hartl and Clark (1997). A closer look at the results in Table 13 and Table 14 reveals there is at least relatively higher differentiation between some attributed groups supported by pairwise F_{ST} or R_{ST} values. Belonging to those attributions *C. laevigata* and *C. monogyna* are under the first species to be clustered separately as obvious from the structure analysis (Figure 23). With higher *K* the third group that features high pairwise values, *C. lindmanii*, is apparently differentiated. These findings are also supported by the unrooted dendrogram (Figure 25, left panel). The heterogeneity of gene pools among groups increases also with higher *K* (Figure 24, 'orange' and 'green' or 'yellow', 'cyan', and 'blue', respectively). This could be either an underlying biological cause or is an artefact caused by using STRUCTURE for different ploidy levels (Lo, Stefanović, & Dickinson, 2009). However, the robustness of STRUCTURE is greater in simulated mixed-ploidy populations than other clustering methods (Stift, Kolář, & Meirmans, 2019). Another breakdown of the analysis may be the fact of dealing with a lot of missing values. The probable appearance of a null allele in CH01F02 in the *C. monogyna*-related group can be postulated from the raw allelic data (Table S7). Moreover, the usage of the no admixture model is debatable. Pritchard, Wen, and Falush (2010) specify this option in the documentation for STRUCTURE as follows: "Each individual comes purely from one of the *K* populations" and "this model is appropriate for studying fully discrete populations and is often more powerful than the admixture model at detecting subtle structure." Yet, this model was exactly chosen for the latter reason to investigate the possibly underlying structure.

To avoid bias caused by the a priori morphological assignment of individuals the structure analysis was rearranged to set up an alternative set of classification. These annotations were reapplied in an iteration of analyses to overcome the chicken or the egg causality dilemma. Thereby all respective values increased (Table 17; Table 13 and Table 14; Figure 25, right panel) and thus support the picture of underlying genetic differentiation among individuals in this study. This also indicates linkage between morphological and molecular characterisation to a certain degree, however, this picture is not exactly congruent. *C. laevigata* and *C. monogyna* are 'well'-defined morphotaxa, show in most cases diploidy and can be easily assigned to one of the genetic groups. Only samples of the latter share the same membership coefficients of genetic clusters ('orange' and 'green') throughout the respective individuals, thus building a morpho-genetic entity. This entity also contains some individuals of those assigned to *C. subsphaerica*. In contrast, samples of *C. laevigata* seem genetically more heterogeneous. Moreover, they share the same genetic clusters ('yellow', 'cyan', and 'blue') with *C. lindmanii* and *C. macrocarpa*. These three taxa can be split apart from each other by the membership coefficients of their genetic clusters. Although the species of the *C. macrocarpa* agg. were not discriminated, those samples with erect sepals on fruit share the same high amount of 'blue' like *C. lindmanii*. These samples are consistently triploids and are likely to build another morpho-genetic entity. Following the argumentation of Christensen (1992a) entities differing in just a single character should not be treated as different on species rank. Hence, *C. macrocarpa* agg. represents two groups, one that is morphologically and genetically close to *C. lindmanii* and one that also contains tetraploids and is more morphologically variable between the putative parents. This might be the explanation for the seldom recognition of *C. calycina* (Gregor, 2015).

From the results of the structure analysis it is vague to separate the hybrid *C. media*. The only group representing half and half genetic clusters of both parent species is '1' that is morphologically absolutely not intermediate between its parents. Moreover, this group shares proportions of the genetic cluster assigned to *C. macrocarpa*. This ambiguity between these two taxa has already been stated by Christensen (1982a).

The neither morphologically nor genetically distinct appearance of *C. rhipidophylla* supports the opinion of Zieliński (1977) that *C. rhipidophylla* might be an old and established hybridogenous species of *C. monogyna* and *C. lindmanii*. However, this cannot be documented from the structure analysis where the respective genetic clusters do not appear with high proportions at the same time in any individual. Instead, 'magenta' is also shared with members of the outgroup raising evidence for a geographical signal of Southern and Eastern European relationship. Contrastingly, by accepting Zieliński's theory the assumed hybrid of *C. monogyna* and *C. rhipidophylla*, *C. subsphaerica*, might be a result from backcrossing with the more frequent parent *C. monogyna*. The morphological variability seen in *C. subsphaerica* could have originated by consecutive backcrossing events. On the one hand, this might have led to an introgression of *C. rhipidophylla* (i.e. *C. lindmanii* in the end) into *C. monogyna* and enlarging its morphological variability, and on the other, the greater similarity of *C. subsphaerica* and *C. monogyna* could have supported the range expansion by man due to propagation in nurseries.

4.4 | Limitations and perspectives

The morphological species concept in mind handed down traits were used for the sake of comparability to the various studies on the morphology of Central European *Crataegus* taxa (see 4.2). The novelty was an additional set of traits that has not been used in hawthorn identification by now. Nearly all of the basic and additional traits are lacking a biological dimension. At most the general tendency of reduction of organs in higher plants can be considered in the little number of styles. Taxa of *C.* subg. *Crataegus* have on average fewer styles per flower than North American (Phipps et al., 2003) or East Asian taxa (Cuizhi & Spongberg, 2003), although the subgenus native to Europe is dated the oldest one, i.e. the least derived of all subgenera (Liston et al., 2021; Ufimov & Dickinson, 2020). However, neither of the other subgenera (according to Ufimov and Dickinson (2020): *C.* subg. *Americanae* El-Gazzar, *C.* subg. *Sanguineae* Ufimov, *C.* subg. *Mespilus* (L.) Ufimov and T. A. Dickinson, and *C.* subg. *Brevispinae* (Beadle) Ufimov and T. A. Dickinson, of which the last two are monotypic) is that conservative to express exactly five styles, the postulated base number in Rosaceae (Kalkman, 2004), but the reduction seems not that derived. All in all the examined traits represent a set of correlated discontinuities, that are simply inherited together. Up to now there is no evidence of biological selection for or against any of these traits, e.g. con- or diverging veins and the orientation or the length/width-ratio of sepals. Thus, they seem stochastically distributed.

In the light of Mayr's biological species concept (1942) species are defined as groups of actually or potentially interbreeding natural populations, which are reproductively isolated from other such groups. There are two breakdowns when focussing on Central European haws: The concept is limited if species reproduce asexually, e.g. apomictic, and if there is substantial gene flow between species by hybridisation. Therefore the breeding experiments were performed to evaluate the possible modes and barriers of reproduction. Results have to be taken with care. All experiments have been performed within the framework of a botanical garden that offers not only all considered species, at favourably small distances to each other, but also minimises possible vandalism in the field. However, working with individuals in horticulture implies on the one hand that the number of individuals to work with was limited and on the other that the question of their regional origin has to be addressed. While three individuals were received from natural populations (*C. rhipidophylla*, ID 1087, from Upper Lusatia, Saxony, Germany and *C. laevigata*, IDs 1066 and 1095, from the Franconian Jura, Bavaria, Germany) the remaining four plants (*C. monogyna*, *C. subsphaerica*, and *C. macrocarpa*) were inventory of unknown origin. Anyhow it is likely that the source of the two most frequent hawthorn species is most likely from the nearer surroundings and thus right from the centre of the distribution area than from any edge (see Kurtto et al., 2013). Hence and by the fact that partial mantel tests revealed no correlation between genetic and geographical distance (data not shown), crosses without fruit set should not be seen due to the incompatibility of locally adapted genotypes. Apart from that the ranges of any local genotypes, especially of

C. monogyna and *C. subsphaerica*, have been blurred completely as both taxa appear as stock in nurseries indiscriminated and solely labelled as *C. monogyna* (Gatterer & Nezadal, 2003). This might be recognised from the certain uniformity in the structure analysis of those samples (group '2' in Figure 24). Contrastingly group '5', attributed (together with some probably misidentified samples) to the less frequent species *C. lindmanii*, that has not been in the focus of propagation in nurseries, appears almost homogenously and with high proportions of a single cluster. Instead, group '7' (assigned to *C. laevigata*, that is available in nurseries but to a lesser extent) presents itself with some variation within its genetic structure. Plantings with any stock led to an enormous and unbalanced rise in individual number and an unselected distribution of genotypes through space. Moreover, a shift of the natural species composition and in some cases an expansion of the natural habitat took and still takes place (Lippert, 1978). The considered species are realised to be ecologically separated (Lippert, 2001; Oklejewicz et al., 2013). While hybridisation is usually low in undisturbed woodlands, "disturbance has allowed *C. monogyna* to spread more effectively into woodlands and woodland margins" (Thomas et al., 2021) facilitating hybridisation in such manmade secondary contact zones as the natural barrier to it seems spatial separation (Stace, 1975).

Additionally, in those contact zones or in triploids, that are either formed by syngamy with unreduced gametes or a result of autopolyploidisation and backcrossing with diploids, pseudogamous apomixis may also be reinforced. Tests with sterilised pollen have to be object of further investigations, as this was not considered in the current study. Nevertheless the results already indicate that autonomous apomixis is not likely to happen in Central European hawthorn. To draw further conclusions from the breeding experiments this study is in need of measuring ploidy levels and ratios of endosperm and embryo of developing fruit with the technique of flow cytometry (Talent & Dickinson, 2007b). So the deviation from the normal sexual 3:2-ratio to autonomous 4:2, pseudogamous apomictic 5:2, or sexual/apomictic 5:3-ratios (Hojsgaard & Hörandl, 2019) is detectable. As the seed is destroyed thereby this cannot be the technique of choice to elucidate hybridisation among *Crataegus* spp. So the intention was to let the ripened seeds germinate to compare the progeny's SSR constitution with those of the parent individuals. Due to the double dormancy of embryo and endocarp (Davies, Geneve, & Wilson, 2017; Phipps, 1998, pers. comm. as cited in Lasseigne & Blazich, 2008) the seeds have not germinated yet and ongoing investigations were not possible up to now.

Furthermore, the exact ploidy level of each individual is important to obtain a more complete picture of the frequency of polyploids among samples and their geographical distribution. Moreover, the ploidy level is necessary to tell the right allelic dosage in polyploids and to avoid errors in genetic studies such as allelic dropout (Gagneux, Boesch, & Woodruff, 1997; Pompanon, Bonin, Bellemain, & Taberlet, 2005). Contrary to the findings of Doležel, Greilhuber, and Suda (2007) the recording of ploidy levels was not determinable by flow cytometry from the collected silica-dried specimen. Thus, an estimation was the way out to receive any data on ploidies. Therefore, the maximum number of alleles in any of the analysed loci was used as proxy for the minimum level of ploidy. Nevertheless, the effective ploidies are in need to be measured from fresh material to guarantee results. Presumably leaf laminae will be the tissue of choice. However, leaves may not yield the best results due to phytochemical compounds and other tissues not of first glance should be tested, like buds, petals, or petioles. A combination of lamina and petiole was used by Vašková and Kolarčik (2019) following the protocol by Loureiro, Rodriguez, Doležel, and Santos (2007).

Missing genetic data, i.e. uncertain ploidy level, unknown allelic dosage, the fact of allelic dropout, and null-alleles, is likely to decrease the ability to recover correct population clusters (Reeves, Bowker, Fettig, Tembrock, & Richards, 2016). Also some computational burdens due to data bearing different ploidy levels between and even within species (Lo, Stefanović, & Dickinson, 2009) draws the focus to other techniques such as chloroplast DNA. In a group of species with evidence to apomixis the analysis of the maternally inherited plastids in comparison to the findings in nuclear DNA of this study may offer further insights in the lineages of the considered taxa (J. A. Brown et al., 2016; Lo, Stefanović, Christensen, & Dickinson, 2009; Lo, Stefanović, Ritland, & Dickinson, 2010).

Another point that influences data evaluation is the uneven number of samples per species. This is due to an inequality of accessions per species caused by different frequencies of distribution of the hawthorn taxa. However, the sampling strategy of choosing individuals of a certain variability in an area displays the relative frequencies of the considered taxa. Additionally, difficulties in identification and thus erroneous attribution led to this partition of samples. Ongoing investigations should try to take specimen especially from the more rare taxa to overcome this disparity. A larger number of samples per assignment will contribute to increase the reliability and statistical power. Furthermore, genotypes from conserved areas with potentially pure populations should be taken into account to calibrate the molecular marker analysis. By extending the geographical range of sampling areas the question of a monotope or a polytope evolution of possible hybrids can be elucidated.

4.5 | Conclusion

Despite the eventual species concept, evolutionary speciation studies may reveal the truth but are somehow limited, if the outcome is hardly comprehensible in the field. Findings are the more memorable the easier they are visually detectable. Besides the question of standing variation across lineages or hybridisation in secondary contact zones evolution is anything and in between bifurcating or reticulate (Lo, Stefanović, & Dickinson, 2010). The morphological variation of the taxonomically complex genus *Crataegus* in Central Europe was object of several morphological studies with observations in the field and comparison of herbarium material have been conducted in several parts of Europe in the second half of the 20th century. All this work contributed to the until now favoured system of three parent species hybridising with each other (Figure 1; Lippert, 1978 and publications of several authors thereafter). Traits from identification literature reproduce this common picture very well. In fact, the pictures does not become more detailed by applying more characters. Erroneous attributions can be identified with trait checks (Pforr, 2017) or by ordination methods like NMDS. However, the molecular analyses do not document morphological attribution in total concordance to genetic attribution. This combination revealed that the provided system has to be modified.

Although the breeding experiments did not cover all possibilities of apomictic seed set, the findings already indicate that autonomous apomixis is not likely in the considered species. Nevertheless, results have to be quantified with local genotypes in the field, to finally evaluate their mode of reproduction. The two (nearly) ever since distinguished diploid and thus sexual species *C. laevigata* and *C. monogyna* together with the triploid *C. lindmanii* represent the cornerstones of Central European hawthorn diversity. The genetic structure analysis points out that *C. monogyna*, together with individuals of other misidentified samples, is well differentiated from the other two species. As the latter two share the same genetic clusters, although in different proportions, the question of their relationship remains unanswered and has be addressed in further investigations. In spite of these three morpho-genetic entities there are still individuals that cannot be assigned to any of those by neither the morphological nor the genetic constitution. Analysing subsets with these samples only as well as applying other molecular techniques such as sequences of the plastid DNA might shed more light on this problem.

5 | Summary

Hawthorn species of *Crataegus* L. subg. *Crataegus* sect. *Crataegus* ser. *Crataegus* (Rosaceae) are abundant shrubs in European scrub, hedges, and forest margins, yet the taxonomy of these plants said-to-be hybridizing freely is only based on morphological traits. To investigate the relationship of the Central European hawthorn species (i.e. *C. laevigata* (Poir.) DC., *Crataegus monogyna* Jacq., *C. rhipidophylla* Gand. s. l. = *C. rhipidophylla* Gand. s. str. and *C. lindmanii* Hrabětová, *C.* ×*macrocarpa* Hegetschw. s. l. = *C.* ×*macrocarpa* Hegetschw. s. str. and *C.* ×*calycina* Peterm., *C.* ×*media* Bechst., *C.* ×*subsphaerica* Gand. s. l. = *C.* ×*subsphaerica* Gand. s. str. and *C.* ×*domicensis* Hrabětová) a suite of handed down and novel morphological traits (morphology of leaves, flowers, and fruits) was assessed and compared to their genetic constitution for the first time in this study. Genetic analyses based on seven unlinked SSR markers of two linkage groups. In addition breeding experiments were performed to gather insight in the reproductive behaviour. The results of the present study do not provide better resolution of morphotaxa with an increased number of traits analysed. Instead, a small subset of the handed down traits was confirmed sufficient to sift out the groups of the inherited speciation model of Central European haws. Three extreme and concordant morphological and genetic phenotypes among the considered taxa with smooth transition stages between them can be reported. There is high level of morphological but also genetic diversity within all of the *Crataegus* species. Although they share a lot of alleles there are also private alleles for species and groups, respectively. In total the level of genetic differentiation is moderate. No final conclusion whether the considered species reproduce facultatively or mandatorily sexually or apomictically can be drawn from the breeding experiments. Further investigations in pseudogamous apomixis with sterilised pollen and the analysis especially of developing seeds with flow cytometric measurement is required. Yet, the results grant more insight in the reproductive modes of Central European hawthorns.

6 | Zusammenfassung (Summary in German)

Weißdorne (*Crataegus* L. subg. *Crataegus* sect. *Crataegus* ser. *Crataegus*, Rosaceae) sind häufig anzutreffende Sträucher an Waldrändern, in Gebüschen und Hecken. Die Taxonomie dieser Arten, die frei miteinander kreuzbar sein sollen, basiert lediglich auf morphologischen Merkmalen. Um die verwandtschaftlichen Beziehungen der mitteleuropäischen Weißdorn-Arten (*C. laevigata* (Poir.) DC., *Crataegus monogyna* Jacq., *C. rhipidophylla* Gand. s. l. = *C. rhipidophylla* Gand. s. str. und *C. lindmanii* Hrabětová, *C.* ×*macrocarpa* Hegetschw. s. l. = *C.* ×*macrocarpa* Hegetschw. s. str. und *C.* ×*calycina* Peterm., *C.* ×*media* Bechst., *C.* ×*subsphaerica* Gand. s. l. = *C.* ×*subsphaerica* Gand. s. str. und *C.* ×*domicensis* Hrabětová) zu untersuchen wurden tradierte und neu etablierte morphologische Merkmale von Blättern, Blüten und Früchten untersucht und erstmals mit molekularen Merkmalen verglichen. Die genetischen Analysen basieren auf sieben ungekoppelten Mikrosatelliten-Markern von zwei Kopplungsgruppen. Um Einsicht in die Reproduktionsbiologie der Arten zu erhalten wurden zusätzlich Kreuzungsexperimente durchgeführt. Die Ergebnisse der vorliegenden Arbeit belegen keine höhere Auflösung der Morphospezies mit gesteigerter Anzahl an Merkmalen. Stattdessen wurde eine ausreichende Unterscheidung der mitteleuropäischen Weißdorne gemäß dem akzeptierten Artbild schon mit einer geringen Anzahl der tradierten Merkmale bestätigt. Aus den untersuchten Individuen können drei sowohl morphologisch als auch molekular einheitliche Phänotypen mit fließenden Übergängen zwischen diesen ausgewiesen werden. Morphologisch wie auch genetisch herrscht eine große Variabilität innerhalb der untersuchten Weißdorn-Arten. Obwohl es neben ubiquitären auch gruppenspezifische Allele gibt, ist die genetische Differenzierung mäßig. Ein finaler Schluss, ob die betrachteten Arten nun fakultativ oder obligat sexuell oder apomiktisch sind, ist nicht möglich. In weiteren Studien sollte die Möglichkeit pseudogamer Apomixis mit sterilisiertem Pollen untersucht werden. Auch werden die Aussagen durchflusszytometrischer Messungen an sich entwickelnden Samen weitere Erkenntnisse in der Biologie der mitteleuropäischen Weißdorne liefern.

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9 | Appendix

9.1 | Table S1 Putative hybrids of Crataegus monogyna

Table S1 Putative hybrids of *Crataegus monogyna*

Parents	Hybrid	References
Hybrids with species of **sect. *Crataegus***	Intrasectional hybrids	
Hybrids with species of **ser. *Crataegus***	Intraserial hybrids	
C. m. Jacq. × *C. laevigata* (Poir.) DC.	*C.* ×*media* Bechst.	1, 4, 6, 8, 9, 10, 16
C. m. Jacq. × *C. rhipidophylla* Gand.	*C.* ×*subsphaerica* Gand. s. str.	8, 9, 10, 11, 12, 14, 16
C. m. Jacq. × *C. lindmanii* Hrabětová	C. ×*domicensis* Hrabětová	8, 9, 10
C. m. Jacq. × *C. meyeri* Pojarkova	*C.* ×*armena* Pojarkova	2, 10
C. m. Jacq. × *C. nevadensis* Christensen	*C.* ×*inexpectans* Christensen	14
C. m. Jacq. × *C. heterophylla* Flüggé		17
Hybrids with species of **ser. *Orientales*** (Zabel ex. Schneid.) Pojarkova	Hybrids of **nothoser. *Orientaegus*** Christensen	10
C. m. Jacq. × *C. azarolus* L.	C. ×*sinaica* Boiss.	10, 12, 13, 14
C. m. Jacq. × *C. heldreichii* Boiss.	*C.* ×*killinica* Christensen	10, 11
C. m. Jacq. × *C. orientalis* Pallas ex Bieb.	*C.* ×*albanica* Pojarkova	10, 11
Hybrids with species of **ser. *Pentagynae*** (Schneid.) Rus.	Hybrids of **nothoser. *Crataegynae*** Christensen	10
C. m. Jacq. × *C. pentagyna* Waldst. & Kit ex Willd.	*C.* ×*rubinervis* Lange (= *C. dipyrena* Pojarkova)	2, 10, 12, 14
Hybrids with species of **ser. *Tanacetifoliae*** Christensen	Hybrids of **nothoser. *Crataegifoliae*** Christensen	10
C. m. Jacq. × *C. tanacetifolia* L.	*C.* ×*yosgatica* Christensen	10, 12, 14
	Intersectional hybrids	
Hybrids with species of **sect. *Sanguineae*** Zabel ex. Schneid.	Hybrids of **nothosect. *Crataeguineae*** Christensen	10
C. m. Jacq. × *C. nigra* Waldst. & Kit.	C. ×*lambertiana* Lange	10
Hybrids with species of **sect. *Coccineae*** Loud.	Hybrids of **nothosect. *Coccitaegus*** Christensen & Dickinson	15

C. m. Jacq. × *C. punctata* Jacq.	*C.* ×*ninae-celottiae* Christensen & Dickinson	15
Hybrids with species of **sect. *Douglasia*** Loud.	Hybrids of **nothosect. *Crataeglasia*** Christensen & Dickinson	15
C. m. Jacq. × *C. suksdorfii* (Sarg.) Kruschke	*C.* ×*cogswellii* Christensen & Dickinson	15
Hybrids with different ‘genera’	‘Intergeneric’ hybrid	
C. m. Jacq. × *Crataegus germanica* (L.) O. Kuntze	×*Crataemespilus gillotii* Beck	1, 3, 5*, 7, 16, 17

C. m. = Crataegus monogyna

1. Hegi (1923); 2. Pojarkova (1939); 3. Browicz (1970); 4. Bradshaw (1975a); 5. Bradshaw (1975b); 6. Byatt (1975b); 7. Byatt et al. (1977); 8. Lippert (1978); 9. Schmidt (1981); 10. Christensen (1992a); 11. Christensen (1992b); 12. Dönmez (2004); 13. Albarouki and Peterson (2007); 14. Christensen and Zieliński (2008); 15. Christensen et al. (2014); 16. Stace, Preston, and Pearman (2015); 17. Phipps (2016).

* Bradshaw (1975b) applied ×*Crataemespilus grandiflora* (Sm.) E. G. Camus for this sexual medlar-hawthorn hybrid, which refers to *C. laevigata* as the hawthorn-parent (Byatt et al., 1977).

9.2 | Table S2 Putative hybrids of *Crataegus laevigata*

Table S2 Putative hybrids of *Crataegus laevigata*

Parents	Hybrid	References
Hybrids with species of **sect. *Crataegus***	Intrasectional hybrids	
Hybrids with species of **ser. *Crataegus***	Intraserial hybrids	
C. l. (Poir.) DC. × *C. monogyna* Jacq.	*C.* ×*media* Bechst.	1, 3, 4, 6, 7, 8, 9
C. l. (Poir.) DC. × *C. rhipidophylla* Gand.	*C.* ×*macrocarpa* Gand. s. str.	8, 9
C. l. (Poir.) DC. × *C. lindmanii* Hrabětová	*C.* ×*calycina* Peterm.	8
C. l. (Poir.) DC. × *C. microphylla* Pojarkova	*C.* ×*hafniensis* Christensen	8
Hybrids with different ‘genera’	‘Intergeneric’ hybrid	
C. l. (Poir.) DC. × *Crataegus germanica* (L.) O. Kuntze	×*Crataemespilus grandiflora* (Sm.) E. G. Camus	1, 2, 5, 9, 10

C. l. = Crataegus laevigata

1. Hegi (1923); 2. Browicz (1970); 3. Bradshaw (1975a); 4 Byatt (1975b); 5. Byatt et al. (1977); 6. Lippert (1978); 7. Schmidt (1981); 8. Christensen (1992a); 9. Stace et al. (2015); 10. Phipps (2016).

9.3 | Table S3 Geographical data of sampled Crataegus individuals

Table S3 Geographical data of sampled *Crataegus* individuals. Coordinates of WGS 84 datum in decimal degrees, the elevation above sea level, and the number of the topographical map 1:25,000 (TK25) each individual is located in are provided. Therein the six samples from Sweden are indicated by a ‘S’.

#	**ID**	**Species**	**Latitude [°]**	**Longitude [°]**	**Elevation [m]**	**TK25**
1	1000A	*C. monogyna*	49.441004	11.017234	307.0	6532
2	1001	*C. monogyna*	49.984445	10.629656	225.1	6029
3	1002	*C. monogyna*	49.984308	10.628159	225.4	6029
4	1003	*C. subsphaerica*	49.984691	10.626921	235.0	6029
5	1004A	*C. subsphaerica*	49.979541	10.625422	253.0	6029
6	1004	*C. subsphaerica*	49.978609	10.622278	278.5	6029
7	1005	*C. subsphaerica*	49.978850	10.622289	283.2	6029
8	1006	*C. monogyna*	49.980228	10.622443	291.2	6029
9	1007	*C. laevigata*	49.980324	10.622652	290.2	6029
10	1008	*C. macrocarpa*	49.980350	10.622668	293.0	6029
11	1009	*C. laevigata*	49.980540	10.623530	284.1	6029
12	1010	*C. monogyna*	49.980621	10.623855	280.6	6029
13	1011	*C. laevigata*	49.980338	10.624289	272.2	6029
14	1012	*C. laevigata*	49.980410	10.624397	272.6	6029
15	1013	*C. macrocarpa*	49.980872	10.625024	273.3	6029
16	1014	*C. monogyna*	49.186834	11.236134	414.5	6833
17	1015	*C. subsphaerica*	49.187258	11.234998	414.5	6833
18	1015A	*C. laevigata*	49.187692	11.234439	423.0	6833
19	1016	*C. monogyna*	49.191444	11.233620	405.9	6833
20	1017	*C. monogyna*	49.195458	11.224658	402.9	6833
21	1018	*C. macrocarpa*	49.187166	11.231493	427.7	6833
22	1019	*C. laevigata*	49.190288	11.211794	411.4	6833
23	1020	*C. monogyna*	49.189683	11.208351	416.8	6833
24	1021	*C. laevigata*	49.189688	11.208342	417.4	6833
25	1022	*C. laevigata*	49.189146	11.211636	422.2	6833
26	1023	*C. macrocarpa*	49.189165	11.211652	422.3	6833
27	1024	*C. macrocarpa*	49.188719	11.211819	422.2	6833
28	1025	*C. macrocarpa*	49.185673	11.213425	428.8	6833
29	1026	*C. monogyna*	49.529118	10.406943	287.6	6428
30	1027	*C. monogyna*	49.531351	10.405598	333.4	6428
31	1027A	*C. laevigata*	49.531826	10.405394	339.0	6428
32	1027B	*C. macrocarpa*	49.532186	10.405094	342.0	6428
33	1028	*C. monogyna*	49.533813	10.405686	357.7	6428
34	1029	*C. monogyna*	49.534300	10.405668	369.7	6428
35	1030	*C. macrocarpa*	49.532883	10.403478	362.7	6428
36	1031	*C. monogyna*	49.525272	10.393540	352.5	6428
37	1032	*C. macrocarpa*	49.525142	10.392779	360.8	6428
38	1033	*C. macrocarpa*	49.524981	10.392346	363.3	6428
39	1034	*C. macrocarpa*	49.525292	10.390215	368.8	6428
40	1035	*C. subsphaerica*	49.525708	10.389119	371.2	6428
41	1035A	*C. laevigata*	49.525822	10.388913	363.0	6428
42	1036	*C. monogyna*	49.526852	10.387780	370.1	6428
43	1037	*C. monogyna*	49.527385	10.387181	366.6	6428
44	1038	*C. macrocarpa*	49.645868	11.142772	396.9	6332

#	ID	Species	Latitude [°]	Longitude [°]	Elevation [m]	TK25
45	1038A	*C. macrocarpa*	49.645896	11.142814	434.0	6332
46	1038B	*C. subsphaerica*	49.645989	11.142916	435.0	6332
47	1039	*C. macrocarpa*	49.646029	11.143120	437.5	6332
48	1040	*C. macrocarpa*	49.647638	11.144570	462.4	6332
49	1041	*C. laevigata*	49.647970	11.144550	461.9	6332
50	1042	*C. macrocarpa*	49.649461	11.145843	489.3	6332
51	1043	*C. laevigata*	49.649485	11.145831	488.1	6332
52	1044	*C. monogyna*	49.650822	11.148315	514.9	6332
53	1045	*C. monogyna*	51.532315	11.914724	103.5	4437
54	1046	*C. monogyna*	51.533122	11.914010	103.1	4437
55	1047	*C. monogyna*	51.534374	11.913090	103.4	4437
56	1048	*C. monogyna*	51.534759	11.912622	101.2	4437
57	1049	*C. monogyna*	51.534804	11.911184	94.2	4437
58	1050	*C. monogyna*	51.534646	11.910497	91.4	4437
59	1050A	*C. macrocarpa*	51.534242	11.907392	88.0	4437
60	1050B	*C. macrocarpa*	51.534128	11.901062	80.0	4437
61	1051	*C. monogyna*	51.533228	11.911070	100.7	4437
62	1052	*C. monogyna*	51.531325	11.920140	85.2	4437
63	1053	*C. monogyna*	51.142296	10.820848	308.1	4830
64	1054	*C. monogyna*	51.140828	10.825004	292.5	4830
65	1055	*C. monogyna*	51.140749	10.825329	195.4	4830
66	1056	*C. monogyna*	51.140453	10.826221	192.2	4830
67	1057	*C. monogyna*	51.130297	10.839331	177.9	4831
68	1058	*C. macrocarpa*	51.130225	10.838357	173.8	4831
69	1059	*C. monogyna*	51.130153	10.838217	166.8	4831
70	1060	*C. monogyna*	51.130466	10.839867	174.5	4831
71	1060A	*C. monogyna*	51.129364	10.863624	155.0	4831
72	1060B	*C. monogyna*	51.129394	10.865857	153.0	4831
73	1060C	*C. monogyna*	51.128765	10.873238	153.0	4831
74	1060D	*C. germanica*	51.041231	10.824339	255.0	4930
75	1061	*C. laevigata*	50.126790	8.657050	113.0	5817
76	1062	*C. laevigata*	50.126794	8.657101	113.0	5817
77	1063	*C. laevigata*	50.127169	8.657279	144.0	5817
78	1064	*C. laevigata*	50.127234	8.657526	116.0	5817
79	1065	*C. laevigata*	50.127235	8.657543	116.0	5817
80	1066	*C. laevigata*	50.126714	8.657664	113.0	5817
81	1067	*C. laevigata*	50.127298	8.657511	123.8	5817
82	1068	*C. macrocarpa*	50.127351	8.657597	123.3	5817
83	1069	*C. subsphaerica*	50.127301	8.657869	123.0	5817
84	1070	*C. macrocarpa*	50.127601	8.657611	126.6	5817
85	1071	*C. subsphaerica*	50.127684	8.657655	121.2	5817
86	1072	*C. subsphaerica*	50.127710	8.657737	122.2	5817
87	1073	*C. laevigata*	50.127193	8.657143	117.6	5817
88	1074	*C. macrocarpa*	50.127511	8.657086	116.6	5817
89	1075	*C. macrocarpa*	50.127720	8.657039	117.2	5817
90	1076	*C. media*	50.127764	8.656984	118.9	5817
91	1077	*C. laevigata*	50.127865	8.656929	118.9	5817
92	1078	*C. laevigata*	50.128051	8.656933	119.7	5817
93	1079	*C. macrocarpa*	50.127804	8.657055	111.9	5817
94	1080	*C. monogyna*	50.127778	8.657157	111.9	5817

#	ID	Species	Latitude [°]	Longitude [°]	Elevation [m]	TK25
95	1081	*C. macrocarpa*	50.128030	8.657530	113.7	5817
96	1082	*C. rhipidophylla*	50.127327	8.659306	113.7	5817
97	1082A	*C. rhipidophylla*	50.127341	8.659263	117.0	5817
98	1083	*C. azarolus*	50.127211	8.659116	112.4	5817
99	1083A	*C. azarolus*	50.127349	8.658665	122.0	5817
100	1083B	*C. caucasica*	50.125836	8.658447	109.0	5817
101	1084	*C. punctata*	50.128893	8.657734	120.1	5817
102	1085	*C. intricata*	50.128985	8.657690	120.8	5817
103	1086	*C. monogyna*	50.129128	8.657208	120.7	5817
104	1086A	*C. rhipidophylla*	50.129125	8.657196	120.7	5817
105	1087	*C. rhipidophylla*	50.129121	8.657178	120.0	5817
106	1088	*C. punctata*	50.129089	8.657167	119.5	5817
107	1089	*C. wattiana*	50.129040	8.657138	122.5	5817
108	1090	*C. arnoldiana*	50.128991	8.657126	120.8	5817
109	1090A	*C. succulenta*	50.125869	8.659305	109.0	5817
110	1090B	*C. succulenta*	50.125876	8.659219	109.0	5817
111	1090C	*C. succulenta*	50.125762	8.659152	109.0	5817
112	1091	*C. germanica*	50.127365	8.659351	120.9	5817
113	1091A	*C. germanica*	50.127326	8.659257	117.0	5817
114	1091B	*C. germanica*	50.127434	8.659046	117.0	5817
115	1091C	*C. germanica*	50.127272	8.659451	125.0	5817
116	1091D	*C. germanica*	50.127219	8.659037	121.0	5817
117	1091E	*C. germanica*	50.127485	8.659154	127.0	5817
118	1092	*C. germanica*	50.127302	8.659479	119.4	5817
119	1093	*+Crataegomespilus*	50.125840	8.658374	111.3	5817
120	1093s	*C. monogyna*	50.125840	8.658374	111.3	5817
121	1093u	*C. monogyna*	50.125840	8.658374	111.3	5817
122	1094	*C. monogyna*	50.126313	8.659748	115.4	5817
123	1095	*C. laevigata*	50.126295	8.659700	115.5	5817
124	1096	*C. monogyna*	50.536716	8.689176	185.6	5418
125	1097	*C. monogyna*	50.536798	8.691881	187.4	5418
126	1098	*C. monogyna*	50.536818	8.692617	185.3	5418
127	1099	*C. monogyna*	50.536865	8.693217	184.7	5418
128	1100	*C. monogyna*	50.536161	8.694693	179.9	5418
129	1100A	*C. monogyna*	50.536200	8.694688	179.0	5418
130	1101	*C. monogyna*	50.536418	8.695963	178.1	5418
131	1102	*C. monogyna*	50.538670	8.697316	177.5	5418
132	1103	*C. monogyna*	50.539084	8.698966	175.2	5418
133	1104	*C. monogyna*	50.543693	8.698447	178.7	5418
134	1104A	*C. macrocarpa*	50.543852	8.698719	179.0	5418
135	1105	*C. monogyna*	50.543902	8.699213	179.0	5418
136	1106	*C. macrocarpa*	50.545387	8.699834	178.4	5418
137	1107	*C. rhipidophylla*	49.863427	10.198273	200.1	6127
138	1107A	*C. subsphaerica*	49.863320	10.211447	220.0	6127
139	1108	*C. monogyna*	53.988008	11.179511	15.4	2033
140	1109	*C. laevigata*	53.989014	11.182287	14.6	2033
141	1110	*C. laevigata*	53.989004	11.182512	10.5	2033
142	1111	*C. laevigata*	53.989083	11.182660	14.1	2033
143	1112	*C. laevigata*	53.988775	11.182961	13.5	2033
144	1113	*C. laevigata*	53.988891	11.183699	11.2	2033

#	ID	Species	Latitude [°]	Longitude [°]	Elevation [m]	TK25
145	1114	*C. rhipidophylla*	53.988879	11.184027	2.4	2033
146	1115	*C. rhipidophylla*	53.988833	11.184200	4.5	2033
147	1116	*C. rhipidophylla*	53.986648	11.184524	1.7	2033
148	1117	*C. laevigata*	53.986688	11.184564	1.8	2033
149	1118	*C. monogyna*	53.995742	11.387149	44.9	1934
150	1119	*C. monogyna*	54.000648	11.388745	1.6	1934
151	1120	*C. monogyna*	54.001499	11.391838	5.8	1934
152	1121	*C. laevigata*	54.005476	11.397498	9.9	1934
153	1122	*C. monogyna*	54.005050	11.396824	7.8	1934
154	1123	*C. laevigata*	54.004852	11.396355	11.3	1934
155	1124	*C. monogyna*	54.004412	11.395436	6.9	1934
156	1125	*C. macrocarpa*	54.004432	11.395361	8.1	1934
157	1126	*C. monogyna*	54.004408	11.395245	7.9	1934
158	1127	*C. monogyna*	54.003224	11.393103	6.4	1934
159	1128	*C. rhipidophylla*	54.282671	13.694526	-3.0	1748
160	1129	*C. rhipidophylla*	54.283042	13.694576	10.5	1748
161	1130	*C. rhipidophylla*	54.283263	13.694467	20.7	1748
162	1131	*C. rhipidophylla*	54.283303	13.694676	21.8	1748
163	1132	*C. rhipidophylla*	54.283245	13.693537	31.1	1748
164	1133	*C. rhipidophylla*	54.283021	13.693183	26.8	1748
165	1134	*C. rhipidophylla*	54.283128	13.692853	31.2	1748
166	1135	*C. rhipidophylla*	54.283158	13.692306	29.9	1748
167	1136	*C. monogyna*	54.681976	13.430644	38.7	1346
168	1137	*C. monogyna*	54.682377	13.431209	45.8	1346
169	1138	*C. monogyna*	54.682522	13.430975	43.9	1346
170	1139	*C. monogyna*	54.682577	13.430922	43.0	1346
171	1140	*C. macrocarpa*	54.684152	13.428520	39.8	1346
172	1141	*C. macrocarpa*	54.678419	13.435370	44.8	1346
173	1142	*C. monogyna*	54.678067	13.434696	39.6	1346
174	1143	*C. monogyna*	54.676256	13.425575	28.1	1346
175	1144	*C. monogyna*	50.532516	8.725350	205.6	5418
176	1145	*C. rhipidophylla*	50.529017	8.726300	216.5	5418
177	1146	*C. lindmanii*	50.528986	8.725945	216.3	5418
178	1147	*C. monogyna*	50.528958	8.725073	217.4	5418
179	1148	*C. laevigata*	50.527392	8.722381	218.4	5418
180	1149	*C. laevigata*	50.527292	8.722695	221.3	5418
181	1150	*C. subsphaerica*	49.763818	11.243210	454.6	6233
182	1151	*C. subsphaerica*	49.763426	11.243149	476.3	6233
183	1152	*C. rhipidophylla*	49.762395	11.242270	478.1	6233
184	1153	*C. macrocarpa*	50.565423	8.768459	270.2	5418
185	1154	*C. macrocarpa*	50.565398	8.768540	269.1	5418
186	1155	*C. laevigata*	50.565355	8.768584	268.7	5418
187	1156	*C. laevigata*	50.565100	8.767843	274.5	5418
188	1157	*C. macrocarpa*	50.564880	8.767358	273.5	5418
189	1158	*C. macrocarpa*	49.938236	11.507456	433.5	6035
190	1159	*C. macrocarpa*	49.938271	11.507484	435.8	6035
191	1160	*C. subsphaerica*	49.938340	11.507436	433.1	6035
192	1161	*C. macrocarpa*	49.938405	11.507466	431.0	6035
193	1162	*C. macrocarpa*	49.938473	11.507453	430.6	6035
194	1163	*C. macrocarpa*	49.938875	11.507366	429.6	6035

#	ID	Species	Latitude [°]	Longitude [°]	Elevation [m]	TK25
195	1164	*C. subsphaerica*	49.938969	11.507295	432.2	6035
196	1165	*C. subsphaerica*	49.929678	11.530798	358.9	6035
197	1166	*C. subsphaerica*	49.930782	11.532290	357.9	6035
198	1167	*C. subsphaerica*	49.930818	11.532355	357.2	6035
199	1168	*C. media*	49.964847	11.577514	384.7	6035
200	1169	*C. media*	49.964874	11.577290	384.6	6035
201	1170	*C. media*	49.964877	11.577130	386.3	6035
202	1171	*C. media*	49.964854	11.576937	387.4	6035
203	1172	*C. media*	49.963843	11.574790	377.1	6035
204	1173	*C. lindmanii*	49.963826	11.574821	377.6	6035
205	1174	*C. media*	49.963840	11.574754	378.9	6035
206	1175	*C. lindmanii*	49.963629	11.574364	374.3	6035
207	1176	*C. lindmanii*	49.963623	11.574380	373.8	6035
208	1176A	*C. laevigata*	49.962310	11.573629	377.0	6035
209	1177	*C. macrocarpa*	49.968001	11.622613	382.7	6035
210	1178	*C. monogyna*	49.967951	11.622635	381.9	6035
211	1179	*C. lindmanii*	49.954776	11.628691	400.0	6035
212	1180	*C. lindmanii*	49.952573	11.629425	402.0	6035
213	1181	*C. subsphaerica*	49.916225	11.589874	364.8	6035
214	1182	*C. subsphaerica*	49.916192	11.589831	363.2	6035
215	1183	*C. macrocarpa*	49.909530	11.565349	426.5	6035
216	1183A	*C. macrocarpa*	49.910182	11.563851	388.0	6035
217	1183B	*C. macrocarpa*	49.911679	11.563154	388.0	6035
218	1184	*C. macrocarpa*	49.909172	11.566270	424.5	6035
219	1185	*C. macrocarpa*	49.914908	11.569604	370.1	6035
220	1185A	*C. media*	49.914944	11.569356	364.0	6035
221	1186	*C. macrocarpa*	49.914532	11.570355	371.9	6035
222	1187	*C. laevigata*	50.630455	8.628416	193.6	5317
223	1187A	*C. laevigata*	50.630468	8.628436	194.0	5317
224	1188	*C. laevigata*	50.632431	8.627270	232.2	5317
225	1189	*C. macrocarpa*	50.632499	8.627273	233.0	5317
226	1190	*C. macrocarpa*	50.632533	8.627246	233.3	5317
227	1191	*C. macrocarpa*	50.632568	8.627203	238.1	5317
228	1192	*C. macrocarpa*	50.632634	8.626963	238.7	5317
229	1193	*C. laevigata*	50.633274	8.626769	239.6	5317
230	1194	*C. macrocarpa*	50.633286	8.626777	240.0	5317
231	1195	*C. subsphaerica*	50.633554	8.626807	238.9	5317
232	1196	*C. rhipidophylla*	50.634052	8.626691	240.3	5317
233	1196A	*C. subsphaerica*	50.634036	8.626694	240.0	5317
234	1197	*C. macrocarpa*	50.633612	8.629594	254.6	5317
235	1198	*C. macrocarpa*	50.632210	8.628733	240.0	5317
236	1198A	*C. subsphaerica*	50.631804	8.629104	228.0	5317
237	1199	*C. monogyna*	50.538394	8.613127	186.0	5417
238	1199p	*C. germanica*	50.538394	8.613127	186.0	5417
239	1199c	+*Crataegomespilus*	50.538394	8.613127	186.0	5417
240	1200	*C. monogyna*	50.538354	8.612994	186.0	5417
241	1200p	*C. germanica*	50.538354	8.612994	186.0	5417
242	1200c	+*Crataegomespilus*	50.538354	8.612994	186.0	5417
243	1201	*C. subsphaerica*	50.556321	8.563244	237.1	5417
244	1202	*C. subsphaerica*	50.546586	8.558631	210.9	5417

#	ID	Species	Latitude [°]	Longitude [°]	Elevation [m]	TK25
245	1203	*C. subsphaerica*	50.546548	8.557485	214.0	5417
246	1204	*C. macrocarpa*	50.547132	8.556405	226.1	5417
247	1205	*C. macrocarpa*	50.548079	8.558793	232.8	5417
248	1206	*C. macrocarpa*	50.548166	8.558772	233.2	5417
249	1207	*C. macrocarpa*	50.548539	8.558558	241.2	5417
250	1208	*C. macrocarpa*	50.548592	8.558535	245.6	5417
251	1209	*C. macrocarpa*	50.549404	8.558089	255.5	5417
252	1210	*C. media*	50.455043	8.556411	331.8	5517
253	1211	*C. monogyna*	51.541931	7.628786	71.0	4411
254	1212	*C. laevigata*	51.542632	7.629313	74.3	4411
255	1213	*C. subsphaerica*	51.543333	7.629200	71.5	4411
256	1214	*C. monogyna*	51.546543	7.628514	72.3	4411
257	1215	*C. laevigata*	51.546601	7.627517	74.2	4411
258	1216	*C. laevigata*	51.546669	7.627474	77.8	4411
259	1217	*C. laevigata*	51.546913	7.626986	80.2	4411
260	1218	*C. macrocarpa*	51.546798	7.626714	76.2	4411
261	1219	*C. monogyna*	51.546682	7.626547	80.3	4411
262	1220	*C. macrocarpa*	51.546716	7.626447	75.5	4411
263	1221	*C. macrocarpa*	51.546375	7.625746	78.5	4411
264	1222	*C. monogyna*	51.544662	7.625716	73.6	4411
265	1223	*C. monogyna*	51.544231	7.627488	70.0	4411
266	1224	*C. monogyna*	51.555032	7.528504	68.6	4411
267	1225	*C. macrocarpa*	51.557260	7.530271	69.0	4411
268	1226	*C. macrocarpa*	51.557311	7.530981	71.8	4411
269	1227	*C. laevigata*	51.557334	7.531080	72.6	4411
270	1228	*C. laevigata*	51.557368	7.531684	71.7	4411
271	1229	*C. macrocarpa*	51.557560	7.533720	72.0	4411
272	1230	*C. laevigata*	51.557573	7.534180	73.3	4411
273	1231	*C. monogyna*	51.556930	7.535503	74.5	4411
274	1232	*C. macrocarpa*	51.569755	7.552071	80.9	4411
275	1233	*C. monogyna*	51.571988	7.555810	77.0	4411
276	1234	*C. macrocarpa*	51.573122	7.558245	67.9	4411
277	1235	*C. macrocarpa*	51.573289	7.558305	66.7	4411
278	1236	*C. monogyna*	51.550583	7.552635	69.4	4411
279	1237	*C. laevigata*	51.550132	7.553430	71.1	4411
280	1238	*C. monogyna*	51.550128	7.553429	72.0	4411
281	1238A	*C. subsphaerica*	51.549796	7.553529	72.0	4411
282	1239	*C. macrocarpa*	51.550018	7.556835	69.8	4411
283	1240	*C. macrocarpa*	51.549069	7.557228	71.0	4411
284	1241	*C. laevigata*	51.552801	7.563139	67.1	4411
285	1242	*C. macrocarpa*	51.552863	7.563155	70.9	4411
286	1242A	*C. subsphaerica*	51.552495	7.561395	70.0	4411
287	1243	*C. monogyna*	51.553623	7.558528	74.7	4411
288	1244	*C. macrocarpa*	51.553672	7.558407	71.6	4411
289	1245	*C. subsphaerica*	51.553601	7.558392	70.4	4411
290	1246	*C. laevigata*	51.562511	7.580115	68.6	4411
291	1247	*C. subsphaerica*	51.563450	7.576687	73.5	4411
292	1248	*C. laevigata*	51.564474	7.578568	75.5	4411
293	1249	*C. monogyna*	51.566527	7.581506	79.1	4411
294	1249A	*C. subsphaerica*	51.566460	7.581429	79.0	4411

#	ID	Species	Latitude [°]	Longitude [°]	Elevation [m]	TK25
295	1250	*C. macrocarpa*	51.563370	7.587948	80.4	4411
296	1250A	*C. laevigata*	51.563263	7.589472	79.0	4411
297	1251	*C. rhipidophylla*	55.66249	14.274772	98.8	S
298	1252	*C. rhipidophylla*	55.66249	14.274743	98.3	S
299	1253	*C. lindmanii*	55.66546	14.272207	29.8	S
300	1254	*C. subsphaerica*	55.65992	14.276571	14.9	S
301	1255	*C. rhipidophylla*	55.65743	14.269711	33.3	S
302	1256	*C. laevigata*	55.66282	14.270341	41.0	S

9.4 | Table S4 Morphological data of sampled Crataegus individuals

Table S4 Morphological data of sampled *Crataegus* individuals.

ID	direction of 1^{st} lateral veins	veins underneath hairy	axils of veins hairy	ending points of veins	depth of lobes	margin of leaves	margin of stipules	glands on stipules' teeth	number of styles	number of stamina	colour of anthers	sepal direction (buds)	sepal direction (flowering)	upper side of sepals hairy	lower side of sepals hairy	hypanthium hairy	aspect ratio of sepals	shape of the sepal tip	sepal direction (fruit)	number of nutlets per fruit	shape of fruit	shape of fruit base	fruit colour	fruit hairy
1000A	5	1	3	0	3	2	1	1	1	20	3	0	0	1	0	1	2	1	1	1	0	0	0	1
1001	5	0	3	0	5	2	1	1	1	20	3	0	0	0	0	1	1.5	0.5	3	1	1	1	0	1
1002	5	0	3	0	5	2	1	1	1		3	0	0	0	0	0.5	1	0	1	1	0	0	0	0.5
1003	4.5	0.5	2	0	3	4	4	3	1	20	5	0	0.5	1	0	1	3	1	3	1	1	1	0	0.5
1004A	4	0	2	0	3	3	1.5	2	1	20	2	0	0	0	0	1	2.5	0.5	1	1	0.25	0	0	1
1004	2	0.5	2	0	3.5	5	3	3	1.5	20	3	0	0	1	0	1	1	1	2	1	1	1	0	0.5
1005	4.5	0	2	0	3.5	5	2.5	3	1	18	3	0	0	0	0	0.5	1	0.5	2	1	1	1	0	0.5
1006	5	0	1	0	5	3	3	1						1	0		1	1	2	1	0	0	0	1
1007	1.5	1	1	0	1	5	5	5	2.25	20	1	0	0	1	0	0	1	0.5	2	2	1	1	1	0.5
1008	4.5	0	3	0	3	5	3	3	1.5	20	5	1	0	0	0	0	4	1	3	1.5	0	0	0.5	0
1009	1.5	1	1	0	1	5	5	5	2.25	20.5	2	0	0	1	0	0	1	1	2	2	1	1	1	0.5
1010	4.5	0.5	2	0	5	2.5	1	3	1	19	3	0	0	0	0	1	1.5	0.5	2	1	1	0	0	1
1011	1	1	1	0	1	5	5	5	1.75	20.5	3	0	0	1	0	0	1	0.5	4	2	1	1	0.5	0.5
1012	1	1	1	0	1.5	5	5	5	2.25	20.5	3	0	0	1	0	0	1	0.5	4	2	1	0	1	0.5
1013	2	1	3	0	3	5	5	5	1.75	20	4	0	1	1	0	0	2	0.5	4	2.25	1	1	1	0.5
1014	5	0	3	0	5	2	1.5	1.5	1	20	2	0	0	0	0	0.5	2	0.5	3	1	1	0	0.5	0.5
1015	3.5	0	3	0	3	5	5	5	1	20	5	0	0	1	0	0	1	1	2	1	1	1	0.5	0.5
1015A	3	1	2	0	3	5	5	5	2.25	21	3	0	0	1	0	0	1.5	0	1.5	2.5	0	0	0	0
1016	4.5	0	3	0	5	3	1	1	1	19	3	0	0	0	0	1	2	0.5	2	1	0	0	0	1

ID	direction of 1st lateral veins	veins underneath hairy	axils of veins hairy	ending points of veins	depth of lobes	margin of leaves	margin of stipules	glands on stipules' teeth	number of styles	number of stamina	colour of anthers	sepal direction (buds)	sepal direction (flowering)	upper side of sepals hairy	lower side of sepals hairy	hypanthium hairy	aspect ratio of sepals	shape of the sepal tip	sepal direction (fruit)	number of nutlets per fruit	shape of fruit	shape of fruit base	fruit colour	fruit hairy
1017	5	0	2	0	5	3	1	1	1	20	3	0	0	0	0	0.5	2	0.5	2	1	0	0	0	1
1018	2.5	1	3.5	0	3	3	4	4	1.5	20	4	0	0	1	0	1	1.5	0.5	3	1.75	1	0	0.5	1
1019	1	1	1	0	1	5	5	5	1.75	20	4	0	0	1	0	0	1	0	3	2	1	0	0.5	0.5
1020	4.5	0	3	0	3	3	1	1	1	20	2	0	0	0	0	1	1.5	0.5	3	1	1	1	0.5	0.5
1021	2	1	1	0	1	5	5	5	3	20.5	2	0	0	1	0	0	1	1	4	2.75	0	0	0.5	0.5
1022	1.5	1	1	0	1	5	5	5	1.75	20	3	0	0	1	0	0	1.5	0.5	2.5	2	1	0	1	0
1023	2.5	1	2	0	3	4.5	5	5	1.5	20	3	0	0	0	0	0	2	0.5	2.5	1.5	1	0	1	0.5
1024	1.5	1	2	0	2	4	5	5	2	20	3	0	0	1	0	0	2	1	4	1.5	1	0	1	0
1025	3.5	0	3	0	3.5	5	5	5	1.75	20	5	0	0	1	0	0	2	1	2	1.5	1	0	1	0
1026	5	0	3	0	5	2.5	2	2	1	20	3	0	0	1	0	1	1	0.5	2	1	0	0	0.5	1
1027	5	0	3	0	5	2	1	1	1	19.5	3	0	0	0	0	1	2.5	1	4	1	0	0	0	1
1027A	1	1	1	0	1	5	5	5	2.5	20.5	3	0	0	1	0	0	2	0.5	3	2.25	1	0	0	0
1027B	3.5	0.5	4	0	4	5	4.5	5	1.75	19.5	5	0	1	1	0	0	2.5	1	3	1.5	1	0.5	0.5	0
1028	5	0	2.5	0	5	2	1	1	1	20	3	0	0	0	0	0	3	1	1	1	1	0	0.5	0.5
1029	5	0.5	3	0	5	4	1	1	1	20	3	0	0	1	0	1	2	0.5	2	1	1	0	0.5	1
1030	3.5	1	3	0	3.5	5	4	5	1.5	20	5	0	1	1	0	0	2	1	2	1.5	1	1	1	0.5
1031	5	0	2.5	0	4.5	2	1	1	1	18	3	0	0	0	0	0	1.5	0.5	2	1	1	0	0	0.5
1032	5	0.5	2	0	3	5	2	2	1.5	20	4	0	0.5	1	0	1	2	0.5	2	1.5	1	1	0.5	1
1033	3	0.5	3	0	3	5	5	5	1.5	20	5	0	0.5	1	0	0	2	1	4	1.5	1	1	1	0
1034	3.5	0.5	3	0	3.5	4.5	1	1	1.5	20	5	0	0.5	1	0	0	1.5	1	4	1.25	1	1	1	0
1035	3.5	0	1.5	0	3	5	4	4	1	20	5	1	0.5	0.5	0	0	4.5	1	4	1	1	1	0	0.5
1035A	1.5	0.5	1	0	1	5	5	5	2.5	20	3	0	0.5	1	0	0	1.5	0	3	2.25	0	0	1	0

ID	direction of 1st lateral veins	veins underneath hairy	axils of veins hairy	ending points of veins	depth of lobes	margin of leaves	margin of stipules	glands on stipules' teeth	number of styles	number of stamina	colour of anthers	sepal direction (buds)	sepal direction (flowering)	upper side of sepals hairy	lower side of sepals hairy	hypanthium hairy	aspect ratio of sepals	shape of the sepal tip	sepal direction (fruit)	number of nutlets per fruit	shape of fruit	shape of fruit base	fruit colour	fruit hairy
1036	5	0	2	0	5	2	2	3	1	18	5	1	0	0	0	0.5	4	1	1	1.25	1	0	0	0.5
1037	5	0	3	0	4	2	2	2	1	20	3	0	0	0	0	1	3	0.5	4	1	1	1	0.5	1
1038	3.5	0.5	2	0	3	5	5	5	1.5	20	5	0	0	0	0	0.5	3	1	4	1	1	1	0	0.5
1038A	2.5	0.5	1.5	0	2	5	5	5	1.5	19	3	0	0	0.5	0	0	3	0.5	4	1.75	1	0	0.5	0
1038B	4.5	0.5	5	0	4	5	5	3	1					0	0	0	3.5	1	3	1.5	1	0.5	0	0.5
1039	3	0.5	1	0	2	4	3	3	1.5	20	4	0	0	1	0	0	2	0.5	4	1.5	1	0	0	0.5
1040	3.5	0.5	3	0	4	5	5	5	2	20	5	0	0	0.5	0	0	3	1	4	1.5	1	0	1	0.5
1041	1	1	1	0	2	5	5	5	2.5	20			0	1	0	0	1	0.5	4	2	1	0	1	0.5
1042	3	0.5	2.5	0	2	5	5	5	2	20	5	0	0	1	0	0	3	1	4	1.5	1	0	0.5	0
1043	2	1	1	0	2	5	5	5	2	20	4	0	0	1	0	0	1	0.5	4	2	1	0	1	0
1044	5	0	3	0	5	2	2	2	1	19	2	0	0	0	0	0.5	1	0	1	1	1	0	0	0.5
1045	5	0	3	0	3.5	3	1	1	1	20	3	0	0	0	0	0	4	0.5	1	1	1	0	1	0
1046	5	0	3	0	4.5	3	2	3	1	20	3	0	0	1	0	1	3	0.5	1	1	1	0	0	0
1047	5	0	3	0	5	3	2	3	1	20	4	0	0	0	0	1	2	0.5		1	0	0	0	0.5
1048	5	0.5	3	0	5	3	2	2	1	20	4	0	0	0.5	0	1	2	1	1	1	0	0	0.5	1
1049	5	0	3	0	5	3	1	1.5	1	20	4	0	0	0	0	1	2	1	1	1	1	0	0.5	0.5
1050	5	0	3	0	5	3	1	3	1.25	20	3	0	0	1	0	1	1.5	0.5	1	1	0	0	0.5	0.5
1050A	4	0	2	0	3	5	5	5	1.5	20	5	1	0	0	0	0	5	1						
1050B	1	0	2	0	1	5	5	5	1.5	19.5	4	0	0	0	0	0	2	1						
1051	5	0	3	0	5	3	1	1.5	1	17	4	0	0	1	0	1	2.5	0.5	3	1	0	0	0.5	1
1052	4.5	0	2	0	3	3	2	2	1	20	4	0	0	0	0	0.5	1	0		1	1	0	0.5	1
1053	5	0	3	0	5	3	1	1.5	1	20	3	0	0	0.5	0	1	1	0.5	1	1	0	0	0	1

ID	direction of 1st lateral veins	veins underneath hairy	axils of veins hairy	ending points of veins	depth of lobes	margin of leaves	margin of stipules	glands on stipules' teeth	number of styles	number of stamina	colour of anthers	sepal direction (buds)	sepal direction (flowering)	upper side of sepals hairy	lower side of sepals hairy	hypanthium hairy	aspect ratio of sepals	shape of the sepal tip	sepal direction (fruit)	number of nutlets per fruit	shape of fruit	shape of fruit base	fruit colour	fruit hairy
1054	5	0	3	0	5	3	1	1.5	1.25	20	4	0	0	0.5	0	1	1.5	0.5	2	1	1	0	0	1
1055	5	0	2	0	4	3	1	1	1.25	20	4	0	0	0.5	0	1	1.5	0.5	1.5	1	1	0	0.5	1
1056	5	0	3	0	5	3	1	1.5			3	0.5		0	0	0	2.5	0.5	1	1	1	1	1	0
1057	5	0	2	0	5	3	1	3	1.25	20	4	0	0	0.5	0	0	1.5	0.5	2	1	0	0	0	0
1058	3.5	0	2.5	0	2	5	5	5	1.5	19.5	5	0	0	1	0	0	3	1	1	1	1	0	1	0
1059	5	0	3	0	5	5	2	3	1	20	3		0	0	0	1	2	1	1	1	1	0	0	0
1060	5	0	3	0	5	4.5	3	3	1	20	4.5	0	0	0.5	0	1	3	1	3	1	0	0	0.5	0.5
1060A	5	0.5	3	0	5	3	1	1	1	20	2	0	0	0.5	0	1	2	0.5						
1060B	5	0	2	0	4.5	3	1	3	1	19.5	4	0	0	0	0	1	2.5	1						
1060C	2	0	2	0	1	3	1	3	1	20	2.5	0	0	0	0	0	3.5	1						
1060D	1	1	5	1	0	1	1	1	5	45	0	1	1	1	1	1	5	1						
1061	1	1	1	0	1	5	5	5	2.5	20	2		0	1	0	0	1.5	0.5	1	2	0	0	0	0
1062	1	1	1	0	1	5	5	5	2.25	20			0	1	0	0	1	0.5	1	2.25	0	0	0	0
1063	1	1	1	0	1	5	5	5	2.25	20.5			0	1	0	0	1	0.5	3	2.5	0	0	0	0
1064	1	1	1	0	1	5	5	5	2.25	20.5			0	0.5	0	0	1	0.5	1	2.5	0	0	1	0
1065	1	1	1	0	1	5	5	5	2.25	20			0	1	0	0	1	0.5	3	2.5	0	0	0	0
1066	1.5	1	1	0	1	5	5	5	2	20			0	1	0	0	1	0	4	2	0	0	0	0
1067	1	1	1	0	1	5	5	5	2	20	2		0	0.5	0	0	1	0	1	2.25	0	0	0.5	0
1068	3	0	2	0	3	5	5	5	1.5	20	5	1	0	0.5	0	0	4.5	0.5	5	1.5	1	1	1	0
1069	3	0	3	0	3	5	2.5	4	1	19.5	5	1	0	1	0	0.5	4	1	2.5	1	1	0	0	1
1070	3	0.5	2.5	0	3	5	5	5	1	20			1	0.5	0	0	4.5	1	5	1.5	1	1	1	0
1071	5	0	3	0	5	2.5	1	2	1	20	3	1	0	0.5	0	1	4	1	1	1	1	0	0	1

ID	direction of 1st lateral veins	veins underneath hairy	axils of veins hairy	ending points of veins	depth of lobes	margin of leaves	margin of stipules	glands on stipules' teeth	number of styles	number of stamina	colour of anthers	sepal direction (buds)	sepal direction (flowering)	upper side of sepals hairy	lower side of sepals hairy	hypanthium hairy	aspect ratio of sepals	shape of the sepal tip	sepal direction (fruit)	number of nutlets per fruit	shape of fruit	shape of fruit base	fruit colour	fruit hairy
1072	5	0	2.5	0	5	2	1	3	1	20	3	1	0	0	0	1	5	1	1	1	0	0	0	1
1073	1	1	1	0	2	5	5	5					0	1	0	0	1.5	0	1	2	0	0	0	0
1074	4.5	1	4	0	4	5	5	5	1	20			0	1	0	1	3	1	5	1.25	1	1	1	0
1075	3.5	1	4	0	3.5	5	5	5																
1076	2	1	1	0	1.5	5	5	5	2	20			0	1	0	0	1	0.5	1	2	0	0	0	0.5
1077	1	0.5	1	0	1	5	5	5	2	19.5			0	1	0	0	1	0	1	2	1	0	1	0
1078	1.5	1	1	0	1	5	5	5	2.5	20.5			0	1	0	0	1	0	3	2.25	0	0	0.5	0
1079	4	0.5	3	0	3.5	5	3.5	5	1	20			0	0.5	0	0.5	3	1	5	1	1	1	1	0
1080	5	0	4	0	5	3	1	1	1	20	2	0	0	0.5	0	1	3	0.5	1	1	1	0	0	0.5
1081	4	0.5	4	0	3	4	5	5	1.5	20	5	1	0	0.5	0	1	5	1	5	1	1	1	1	1
1082	4.5	0	2.5	0	3	3	1	1	1	20			0	0	0	1	4.5	1	1	1.25	1	0	0	1
1082A	5	0	3	0	5	3																		
1083	5	1	4	0	4	3	1	1	1	19.5	5		0	1	1	1	1	0.5	1	1	1	0	0	1
1083A	5	1	3	0	5	2			1	19.5	4	0	0	1	1	1	1	0.75	1	1	1	0.5	0.25	1
1083B	4.5	0	5	01	5	4	3	1	1	17	5		0		0	1	5	1						
1084	3	1	3	1	1	5	3	5																
1085	3	1	5	1	0.5	5	3	5	4	6.5	5		0	0.5	0	0	5	1	5	3.5	0	0	1	0
1086	5	0	4	0	5	2	1	2	1	20	3	0	0	0.5	0	1	2	0.5	1	1	0	0	0	1
1086A	5	0.5	4	0	5	5	5	2	1.75	19.5	4	0	0	0.5	0	1	5	1	3.5	1.875	0	0	0	1
1087	5	0	3	0	5	2.5	1	1	1	20	3	0	0	0.5	0	0	5	1	1	1	0	0	0	0
1088	1.5	1	5	1	0.5	5	1	3	3.5	18	4	1	1	1	1	1	5	1	5	3.5	0	0	2	1
1089	4	0	2	0	2	5	5	5	4	17	1	0	0	0	0	0	4	1	1	4.5	0	0	2	1

ID	direction of 1st lateral veins	veins underneath hairy	axils of veins hairy	ending points of veins	depth of lobes	margin of leaves	margin of stipules	glands on stipules' teeth	number of styles	number of stamina	colour of anthers	sepal direction (buds)	sepal direction (flowering)	upper side of sepals hairy	lower side of sepals hairy	hypanthium hairy	aspect ratio of sepals	shape of the sepal tip	sepal direction (fruit)	number of nutlets per fruit	shape of fruit	shape of fruit base	fruit colour	fruit hairy
1090	4.5	1	4	1	1	5		5	4.5	12.5	0.5		1	1	1	1	5	1	1.5	4.5	0	0	0	1
1090A	3	0	3	1	1	5	1	5	3	10	3	1	0.75	1	0	0	5	1	3.5	2.875	0	0	1	0
1090B	3	0	3	1	1	5	1	5	3	10	3	1	0.75	1	0	0	5	1	3	2.875	0	0	1	0
1090C	3	0	3	1	1	5	1	5	3.25	10	4	1	0.75	1	0	0	5	1	3	2.875	0	0	1	0
1091	1	1	5	1	0	5			5	42.5	0	1	1	1	1	1	5	1	5	5	0	0	-1	1
1091A	1	1	5	1	0	5			5			1	1	1	1	1	5	1	5	5	0	0	-1	1
1091B	1	1	5	1	0	5			5			1	1	1	1	1	5	1	5	5	0	0	-1	1
1091C	1	1	5	1	0	1			5		0.5	1	1	1	1	1	5	1	5	5	0	0	-1	1
1091D	1	1	5	1	0	5			5	30	0.5	1	1	1	1	1	5	1	5	5	0	0	-1	1
1091E	1	1	5	1	0	1			5			1	1	1	1	1	5	1	5	5	1	0	-1	1
1092	1	1	5	1	0	5			5	45	0	1	1	1	1	1	5	1	5	5	0	0	-1	1
1093	1	1	4	0	0	5			1.75	19.5	1	1	0	1	1	1	4.5	0.5	3	1	0	0	-1	1
1093s	5	0.5	3	0	5	3	1	3	1	20	4	0	0	0	0	1	1	0.5						
1093u	5	0	3	0	5	3																		
1094	5	0	3	0	5	3	1	1	1	20	1	0	0	0.5	0	1	2	0.5	1	1	1	0	0	0
1095	1	0.5	1	0	1	5	5	5	2.5	20	3	0	0	0.5	0	0	1	0	1.5	2	0	1	0	0
1096	5	0	2	0	5	3	1	1	1	20	4	0	0	0	0	0	2	0.5	2.5	1	1	0	0	0
1097	5	0	2	0	5	2	1	1.5	1	19.5	3	0	0	0	0	1	2	1	2.5	1	1	0	0	1
1098	5	0	3	0	5	2	1	1.5	1	20	2	0	0	0	0	1	1	1	1	1	1	0	0	0.5
1099	5	0	2	0	5	2	1	1	1.25	20	3.5	0	0	0	0	1	2	0.5	2.5	1	1	0	0	1
1100	5	0	2	0	5	2	1	1	1	20	3	0	0	0	0	0.5	1	0.5	1	1	1	0	0	0
1100A	4.75	0	2.5	0	5	2.5	1	1	1	19	4	0	0	0	0	0	2.25	0.75	1	1	1	0	0	0

ID	direction of 1^{st} lateral veins	veins underneath hairy	axils of veins hairy	ending points of veins	depth of lobes	margin of leaves	margin of stipules	glands on stipules' teeth	number of styles	number of stamina	colour of anthers	sepal direction (buds)	sepal direction (flowering)	upper side of sepals hairy	lower side of sepals hairy	hypanthium hairy	aspect ratio of sepals	shape of the sepal tip	sepal direction (fruit)	number of nutlets per fruit	shape of fruit	shape of fruit base	fruit colour	fruit hairy
1101	5	0	3	0	5	1.5	1	1	1	20	3	0	0	0.5	0	1	2	1	1	1	1	0	0	0
1102	5	0	2	0	5	2	1	1	1	20	3	0	0	0.5	0	1	2.5	1	1	1	1	0	0	1
1103	5	0.5	4	0	5	2	1.5	1.5	1	20	4	0	0	0	0	1	2	1	1	1.125	1	0	0.5	0.5
1104	5	0	3	0	5	2	1	1	1	20	4	0	0	0	0	0	2	0.5	1	1.125	1	0	0	0
1104A	3	0.5	3	0	3	5	4	5	1.5	20	5	0	0.5	1	0	0	3	0.5	4.5	1.5	1	1	1	0
1105	4.5	0.5	3.5	0	4	3	1	1.5	1	17	3	0	0	0	0	1	1.5	0.5	1	1	0	0	0	1
1106	3.5	0.5	4.5	0	3	5	5	5	1.75	20	4	0	0	0.5	0	1	2	0.5	1	1.75	1	0	0.5	1
1107	4.75	0	2.75	0	4.5	2			1				0	0	0	1	4	0.75	1	1	1	0	0.5	1
1107A	4.5	0	3	0	4.5	2.5	2	2	1					0	0	0	4.25	1	1	1	1	0	0	0.5
1108	5	0	3	0	5	1	1	1	1	20	2	0	0	0	0	0	1.5	0.5	1	1	1	0		0
1109	1.25	1	1	0	2.5	5	5	5	1.75	16	3	0	1	1	0	0	1.75	0.75	3	2	0	0		0
1110	1.25	1	1	0	2	5	4.5	5	2.5	17	5	0	1	1	0	1	1.5	0.75	3	2	0	0		1
1111	2	1	1	0	2	4.75	5	5	2.75	19	4	0	1	0.75	0	0.25	1	1	3	2	0.5	0		1
1112	1.75	1	1	0	3	4.75	5	5	2.5	18	3	0	0.5	1	0	0	1	0.75	1	2.25	0.5	0		0
1113	2	1	1	0	3.25	4.75	5	5	2.25	19.5	3	0	0.25	1	0	0	1.5	0.75	3	2.25	0	0		0
1114	5	0	3	0	5	2.5	2	3	1	20	2	0	0	0	0	0	4.5	1	1	1	1	1		0
1115	5	0	4	0	4.75	3.25	3	3	1	20	2	0.5	0.25	0	0	0	4.75	1	1	1	1	1		0
1116	5	0	5	0	5	3.25	4	4	1	20	2	0.5	0.25	0	0	0	4.75	1	1	1	1	1		0
1117	1	1	1	0	1.25	5	4	5	2.25	20.5	3	0	1	1	0	0	1	0	2	2.5	0	0		0
1118	5	0	3	0	4	2.5	1.75	2.5	1	20.5	2	0	0.25	0.5	0	1	1.5	1	1	1	1	0		0.5
1119	5	0	3	0	5	2.75	1	1	1	17	3	0.5	0.5	0	0	0.25	3.25	1	1	1	1	0		0
1120	5	0	2.5	0	4	2	1.25	1.5	1	17	3.5	0	0.5	0	0	1	2	0.75	1	1	1	0		0.5

ID	direction of 1st lateral veins	veins underneath hairy	axils of veins hairy	ending points of veins	depth of lobes	margin of leaves	margin of stipules	glands on stipules' teeth	number of styles	number of stamina	colour of anthers	sepal direction (buds)	sepal direction (flowering)	upper side of sepals hairy	lower side of sepals hairy	hypanthium hairy	aspect ratio of sepals	shape of the sepal tip	sepal direction (fruit)	number of nutlets per fruit	shape of fruit	shape of fruit base	fruit colour	fruit hairy
1121	1	1	1	0	1	4.75	4.75	5	2	17.5	3	0	0.5	1	0	0	1	0.5	3	2	0	1		0
1122	5	0	3	0	5	2.75	1.25	1.25	1	21	3	0	0.25	0	0	0	3.25	1	1	1	1	1		0
1123	1.5	1	1	0	1	5	5	5	2.5	18.5	3	0	1	0.75	0	0	1	0.75	3	2	1	0		0
1124	5	0	3	0	4	1.25	2	2	1	21.5	2	0	0.75	0	0	1	2	0.5	3	1	1	0		1
1125	2.5	0	1.5	0	3	5	2	4	1.25	18	3	0	0.25	1	0	0	1	0.75	2	1.5	1	0		0
1126	5	0	5	0	4	2.5	1.25	1	1	22	3	0	1	0.5	0	1	3	1	3	1	1	0		1
1127	5	0	3	0	4	1	1	1	1	20	2	0.5	0	0.25	0	1	5	1	3	1	1	0		1
1128	4.75	0	4.5	0	4	4.5	4	4	1		5	0.5	1	0.25	0	1	3.5	1	3	1	1	0		1
1129	4	0.25	5	0	3.5	5	4	4	1	20	5	0.5	1	0.25	0	1	5	1	3	1	1	0		1
1130	1.75	0.25	5	0	1	5	4	5	1	20	5	0	0.25	1	0	1	3.5	1	1	1	1	0		0
1131	3.25	0.25	4.5	0	3	5	4	5	1	20	5	0	0.5	0.75	0	1	3	1	1	1	1	0		1
1132	4	0.25	5	0	4	5	5	5	1	20	5	1	0.25	0.25	0	1	5	1	3	1	1	1		1
1133	5	0	4.5	0	4	4.5	4	4	1	20	4	1	1	0.25	0	1	4	1	3	1	1	0		0
1134	5	0	4.5	0	3.5	4.5	4.5	4.5	1	20	5	1	1	0	0	1	5	1	3	1	1	1		1
1135	4.5	0.75	5	0	3	5	5	5	1	20	1	0	0.5	0.75	0	1	3	1	3	1	1	1		0.5
1136	5	0	2.5	0	4	2	1	1	1			0		0.25	0	1	1.75	0.25	1	1.25	1	0		1
1137	5	0.5	3	0	4	2	1	2	1			1		1	0	1	3	0.75	1	1	1	0		1
1138	5	0	2.5	0	5	2	1	1	1		3	0		1	0	0	1.5	0.75	1	1	1	0		0
1139	5	0	3	0	5	3	2	3	1	19.5	4	1	0.25	0	0	1	3.75	0.25	1	1.25	1	0		1
1140	3	1	1	0	1	5	5	5						1	0		1	0	3	2	0	0		0
1141	3	0.25	3	0	3	4	4	4	1.5	17	5	0	1	1	0	1	2	1	3	2	1	0		1
1142	5	0	3	0	5	2.5	1	1	1	20	3	0	0.5	0.5	0	0	1	0.25	1	1	1	0		1

ID	direction of 1st lateral veins	veins underneath hairy	axils of veins hairy	ending points of veins	depth of lobes	margin of leaves	margin of stipules	glands on stipules’ teeth	number of styles	number of stamina	colour of anthers	sepal direction (buds)	sepal direction (flowering)	upper side of sepals hairy	lower side of sepals hairy	hypanthium hairy	aspect ratio of sepals	shape of the sepal tip	sepal direction (fruit)	number of nutlets per fruit	shape of fruit	shape of fruit base	fruit colour	fruit hairy
1143	5	0	3	0	5	3	1	1						1	0		1	1	1	1.25	1	0		1
1144	4.5	0	2.5	0	4.5	2.5	1	1	1	20	3	0	0	0	0	1	2	0.5	1	1	0	0	0	1
1145	3	0	3	0	3.5	4.5	3	3	1	20	4	0	0	0.5	0	0	2	0.5	3	1	1	1		0
1146	3.5	0.25	2.5	0	3	5	4	3	1.5	19.5	5	0.5	0.5	1	0	0	3	1	5	1	1	1		0
1147	5	0	3	0	5	2	1	1.25	1	20	3	0.5	0.25	0.25	0	1	3	1	1	1	1	0		1
1148	1.25	1	1	0	1	5	4.5	4.5	2.25	20	3	0	0	1	0	0	1	0.5	3	2	1	0		0
1149	1	1	1	0	1	5	5	5	2.25	17.5	3	0	0	0	0	0	1	0.5	3	2	1	0		0
1150	3.25	0	1.5	0	3.5	5	4	4	1.75	20			1	0.75	0	0	3.5	1	3	1	1	0		0
1151	4	0	3	0	3	5	4	4	2.5				1	0.75	0	0	5	1	4	1	1	1		0
1152	4	0	2.5	0	3.5	5	4.5	5	1.75	14.5	5		0.75	0.25	0	0	5	1	4	1	1	1		0
1153	4	1	2.5	0	3	5	3	3	1	20	5		1	0	0	0	4	1	5	1.5	1	0	1	0.5
1154	2.75	1	3	0	2.5	4.5			1	20	5		1	0.75	0	0	1.5	0.75	3	1.25	1	0	1	0
1155	1.5	0.75	1	0	1	5	5	5	2	19	3	0	1	1	0	0	1.5	0.75	2	2	0	0	1	0
1156	1	0.75	1	0	1	5	5	5	2	20	3	0	1	0.5	0	0	1.5	0.75	3	2.5	1	0	1	0
1157	3	1	2.5	0	3	5	5	4	1.5	19.5	5		1	0.25	0	0	5	1	5	2	1	0	1	0.5
1158	1.75	0.25	2.5	0	3	4	5	4	1.25	17	4	0	0.5	0.5	0	0	3	1	3.5	1.5	1	1	0	0
1159	2	0	3	0	3	4.75	3	3	1.25	17	4	0.5	0.5	0.5	0	0	2	1	4	1.5	1	1	0	0
1160	4.75	0	3	0	4	4	3	3	1	15.5	4	1	0.5	0.25	0	0	3.5	1	1.5	1	1	0	1	0
1161	2.75	0.25	2	0	3	4	4	4	1.5	16	4	0.5	0.75	0.75	0	0	3.5	1	3	1.5	1	0	0.5	0
1162	1.5	1	1	0	1.25	5			1.75	15.5	3.5	0	0.25	1	0	0	1.25	0.5	1.5	1.75	0.5	0	0	0
1163	2.75	0.25	1.25	0	3.25	4	5	5	1.5	16	3.5	1	0.5	0.5	0	0	3.5	0.75	3	1.5	1	0	0.5	0
1164	4.5	0.5	3	0	3	4.25	2.5	3	1	15.5	3	1	0.25	0.25	0	0	3.25	1	1	1	1	0	1	0

ID	direction of 1^{st} lateral veins	veins underneath hairy	axils of veins hairy	ending points of veins	depth of lobes	margin of leaves	margin of stipules	glands on stipules' teeth	number of styles	number of stamina	colour of anthers	sepal direction (buds)	sepal direction (flowering)	upper side of sepals hairy	lower side of sepals hairy	hypanthium hairy	aspect ratio of sepals	shape of the sepal tip	sepal direction (fruit)	number of nutlets per fruit	shape of fruit	shape of fruit base	fruit colour	fruit hairy
1165	4.25	0	3	0	4	2.5	1.5	1.5	1.125	19.5	3	1	0.5	0.5	0	1	2.25	0.75	1	1	0	0	0	0.5
1166	5	0	2.5	0	4.5	2.5	1	1	1	20	5	0	0.5	0	0	1	4	0.75	1	1	0	0	1	0
1167	5	0	3	0	4	2.5	2	3	1	20	5	0.5	0.75	0	0	0.5	4	1	1	1	0	0	1	0
1168	1.25	0.25	1	0	2	4.5	5	5	1.5	16	4	0	1	0.5	0	0	1	0.75	1.5	1.5	0	0	0	0
1169	3	0.75	1.5	0	2.75	5	3	3	1.5	15.5	4	0	1	0.25	0	0	1	1	1	1.75	0	0	0.5	0
1170	1.5	1	1	0	2	5	4	5	1.5	17	4	0	1	1	0	0	1	1	1	1.75	0	0	0	0
1171	3	0.25	1	0	3	5			1.25	14.5	4	0	0	0.75	0	0	1.25	1	1	1.5	0.5	0	1	0
1172	3.25	0.75	1	0	3	5	5	5	1.25	15.5	3.5	0	0.25	0.25	0	0	1.25	1	1	1.5	0	0	0.5	0
1173	3	0.5	1.25	0	4	5	4	5	1	19	5		1	0.25	0	0	3.5	0.5	5	1.25	1	1	1	0
1174	2	0.75	1	0	2	5	5	5	1.75	18.5	3.5	0	0.25	1	0	0	1.25	1	1	1.25	0	0	0	0
1175	3	0.25	2	0	3	5	3	5	1.75	18.5	5	0	0.25	0.75	0	0	3	0.75	5	1.25	1	1	1	0
1176	3.5	0.75	2	0	3	5	3	5	1	20	5	0.5	0.75	0.5	0	0	3.25	0.75	5	1.25	1	1	0	0
1176A	1	1	1	0	1	5	5	5	2.75	21.5	3		0	1	0	0	1	0.5	3	2.5	0	0	0.25	0
1177	4.5	0.25	3	0	3.25	4.75	4.5	5	1.5	17.5	5	1	1	0.75	0	0	3.5	1	4.5	1.25	1	1	0	0
1178	5	0	1.75	0	5	2.75	1.5	1.5	1	18.5	2	0	0	0	0	0.5	3	0.5	1	1	1	0	0	0
1179	4.25	1	4	0	4	5	3.5	5	1	16.5	5		1	1	0	0.5	4.75	1	5	1	1	0	1	0.5
1180	4.25	1	4	0	3.5	5	3	5	1	17	4		1	0.75	0	0.25	4.5	1	5	1	1	0.5	0.5	0.5
1181	5	0	4	0	5	4	3.5	4	1	18.5	5	1	0	0.75	0	1	4.75	1	3	1	1	0	1	1
1182	5	0	3	0	5	5	2	5	1	16.5	5	0.5	1	0.5	0	1	3.75	1	5	1	1	0.5	0.5	1
1183	2	0.75	1.25	0	2.5	4.75	5	5	1.5	16.5	3	1	0	1	0	0	4.75	1	3.5	1.5	1	0	0	0
1183A	3.5	0	1	0	4	5	3	5	1.75	19	5	1	0	0.5	0	0	4	1	4	1.75	1	0	1	0
1183B	3.5	0	3	0	3	5	5	5	1.5	19	3.5	0	0.5	1	0	0	2	1	4	1.5	1	0.5	1	0

ID	direction of 1st lateral veins	veins underneath hairy	axils of veins hairy	ending points of veins	depth of lobes	margin of leaves	margin of stipules	glands on stipules' teeth	number of styles	number of stamina	colour of anthers	sepal direction (buds)	sepal direction (flowering)	upper side of sepals hairy	lower side of sepals hairy	hypanthium hairy	aspect ratio of sepals	shape of the sepal tip	sepal direction (fruit)	number of nutlets per fruit	shape of fruit	shape of fruit base	fruit colour	fruit hairy
1184	2	1	1	0	3	5	5	5	1.875	18.5	1.5	1	0.75	1	0	0.5	5	1	5	1.75	0	0	0	0.5
1185	3.5	1	2.5	0	3.25	5	3	3	1.25	20	5	1	1	1	0	0	5	1	5	1.25	1	1	1	0
1185A	1.5	1	1	0	2	5	4	5	1.75	17	3	0	0	1	0	0	1	1	3	2.5	0.5	0	1	0
1186	4	0.5	1.75	0	2	5	4	4	1.75	19.5	5	1	0	1	0	0	4.5	1	3	1.75	1	0.5	1	0
1187	1	1	1	0	1	5			2.25	18.5		0	1	0.75	0	0	1	0.5	3	2.125	1	0	1	0
1187A	3	1	1	0	2	5	5	5	2.25	20	4	0		1	0	0	1	1						
1188	1	1	1	0	1	5			2	19.5	3	0	1	1	0	0	1	0.75	3	2	1	0	1	0
1189	3	0.75	2	0	2.5	5			1	20	5		1	0.5	0	0	4	1	4.5	1.25	1	1	1	0
1190	3.25	0.25	2.5	0	3.25	5	3	5	1	19	5		1	0.5	0	0	4.25	1	5	1.75	1	1	1	0
1191	2.75	0.75	1.25	0	2.75	5	3	5	1.25	20	5		1	0.75	0	0	3.25	1	4	1.75	1	1	1	0
1192	3	0.25	1.25	0	3	5	3	5	1.125	20	5		1	0.5	0	0	4.5	1	4.5	1.75	1	0.5	1	0
1193	1	1	1	0	1	5	5	5	1.875	20	3	0	0	1	0	0	1	0.75	1	2.125	1	1	1	0
1194	3.25	1	2	0	3	4.5	5	5	1.875	19.5	5	0.5	0.5	0	0	0	4.5	1	3.5	1.875	1	0	0.5	0
1195	5	0	2	0	5	2	1	2	1	20	4	0	0.5	0	0	1	2.5	0.25	1.5	1.75	1	0	0	1
1196	3	0.5	1.25	0	3	5	4	4	1	20	5		1	0.25	0	0	4	1	4.5	1	1	1	1	0
1196A	5	0	3	0	5	1.5	1	5	1		5	1	0	0	0	0	4	1						
1197	3	0.75	3	0	3	5								0.5	0		4	1	1.5	1.75	1	0	0	0.5
1198	3.25	0	1.25	0	3.5	4.5		5	1.25	20	5	0.5	1	0.25	0	0	4	1	5	1.25	1	1	1	0
1198A	5	0	3	0	5	3	1	1	1	20	3	0	0	1	0	1	1	0.5						
1199	5	0	3	0	5	2	1.25	1.75	1	18.5	4	0	1	0	0	1	1.25	0.5	2.5	1.125	0.25	0	0	0.5
1199p	1.25	1	3	1	1	1	2	3	5		0.5	1	1	1	1	1	5	1	5	5	0.25	0	-1	0
1199c	4.5	0.25	3	0	3	2	1.5	2	1.25	19	3	0	0.5	0	0	0	2	0.5	1	1.5	0.25	0	-0.5	0

ID	direction of 1st lateral veins	veins underneath hairy	axils of veins hairy	ending points of veins	depth of lobes	margin of leaves	margin of stipules	glands on stipules' teeth	number of styles	number of stamina	colour of anthers	sepal direction (buds)	sepal direction (flowering)	upper side of sepals hairy	lower side of sepals hairy	hypanthium hairy	aspect ratio of sepals	shape of the sepal tip	sepal direction (fruit)	number of nutlets per fruit	shape of fruit	shape of fruit base	fruit colour	fruit hairy
1200	4.75	0	3.5	0	4	3	1	1	1	20	5	0	0	0	0	1	2	0.5	1.5	1.125	1	0	0	1
1200p	1.25	1	5	1	1	1			5		0.5	1	1	1	1	1	5	1	5	5	0	0	-1	0
1200c	4	0	4	0	3	3	1	1	1	19.5	4	0	0	0	0	1	1	0.5						
1201	5	0	3	0	4.75	3.25	1	1	1	19.5	3	0	0	0	0	0.5	2	0.75	1	1	0.5	0	0.5	0
1202	4	0.75	3	0	4.5	4.5								0.25	0		3.5	1	3	1.125	1	0	0.5	0
1203	4.5	0.75	3	0	4	5	1	1.5						0.25	0		3.5	1	2.5	1.25	1	0	0.5	0
1204	3.5	0.75	2.5	0	4	5	5	5	1.25	18	4	0	1	0.25	0	0	5	1	5	1.75	0.25	0	1	0
1205	3.5	0	2	0	3.5	5	3.5	4	1.25	18.5	5	0	0.5	0.5	0	0	5	1	5	1.25	1	1	1	0
1206	3	0	2	0	3.25	5	5	5	1.5	18	5	0.5	0.75	0	0	0	4	1	5	1.5	1	0.75	1	0
1207	3.25	0.5	3.25	0	3.25	5	4	4	1.75	17.5	4	0	1	0	0	0	3	1	5	1.875	1	0.75	0	0
1208	4	0	2.5	0	3.25	5	3	3	1.75	19	5	0.5	1	0.5	0	0	4	1	5	1.5	1	1	1	0
1209	3.5	0.75	1.5	0	3.25	4			1.875	20	5	0	0.75	0	0	0	4	1	4	1.75	1	0	0.5	0
1210	3	1	1	0	2	3	3	3	1.5	19	4	0	0.5	1	0	0	1	0.5						
1211	4.5	0	3	0	5	2	1.5	2	1	20	3	0	0	0.5	0	0.5	2	0.5	1	1	0	0	0.5	0
1212	1	0.5	1	0	1	5	5	5	2	19	2	0	1	0.5	0	0	1	0.5	4	1.5	1	1	1	0
1213	4	0.5	3	0	4.5	4	5	5	1	19		0	0	0.5	0	0	1	0.5	1	1.125	0.5	0	1	0
1214	5	0	3.5	0	5	2	1	1	1	20	3	0	0	0.5	0	0	1.5	0	1	1	1	1	0.5	0
1215	1.5	1	1	0	2.5	5	5	5	2	17.5	3	0	0.5	1	0	0	3	0.5	3	1.875	1	1	0.5	0
1216	1	1	1	0	1	5	5	5	2.25	19	4	0	0	1	0	0	1.5	0.75	2	2	1	1	1	0
1217	2	1	1	0	1.5	5	5	5	2	20	3	0	1	1	0	0	1	0.75	2.5	2	1	0	1	0
1218	4	0.75	2	0	4	4			1.25	19.5	5	0	1	0.75	0	1	2	1	3	1.5	1	1	1	0
1219	5	0	3.5	0	5	3.5	2	1	1	20	3	0	0	0	0	1	2	0	1.5	1	0	0	0	1

ID	direction of 1st lateral veins	veins underneath hairy	axils of veins hairy	ending points of veins	depth of lobes	margin of leaves	margin of stipules	glands on stipules' teeth	number of styles	number of stamina	colour of anthers	sepal direction (buds)	sepal direction (flowering)	upper side of sepals hairy	lower side of sepals hairy	hypanthium hairy	aspect ratio of sepals	shape of the sepal tip	sepal direction (fruit)	number of nutlets per fruit	shape of fruit	shape of fruit base	fruit colour	fruit hairy
1220	3	0.75	2.5	0	3	3.5	5	4	1.25	17.5	5	0	1	0	0	0	2.5	0.75	3.5	1.25	1	0	1	0
1221	3.5	0.5	3	0	3	4	3	3	1.75	20	5	0	0	0.5	0	0	2.5	1	2	2	1	0	1	0
1222	4.5	0	1.5	0	4	1	1	1	1	18	3	0	0	0	0	0	3.5	1	1	1	0	0	0	0
1223	4	0	2.5	0	3	3	1.5	1.5	1	20	2	0	0	0	0	0	2	0.5	1	1	0	0	0	0
1224	4.5	0	3	0	5	2.5	1	1	1	22.5	3	0	1	0.5	0	0	1.5	0.5	3.5	1	1	0	0	0
1225	3	0.5	5	0	5	4.5	3	1	1.75	18	5	0	0	0.5	0	0	1	1	2.5	1.5	0.5	0	0.5	0
1226	1.5	0.5	1	0	3	5	4.5	4.5	1.5	17.5		0	1	1	0	0	1.5	1	3	1.875	1	1	1	0
1227	1	1	1	0	1	5	5	5	2	18	3	0	0.5	1	0	0	1	0.5	3	2	1	1	1	0
1228	2	1	1	0	2.5	5	4	5	2	19.5		0	0.5	1	0	0	1	0.5	3	2	0.5	0	1	0
1229	3.5	0	2.5	0	3	5	5	5	1.75	20	5	0	1	0.5	0	0	2.5	0.5	3.5	1.875	1	1	0.5	0
1230	1.5	1	1	0	2	5	5	5	2	20	3	0	1	1	0	0	1	0.5	3.5	2.125	0.5	1	1	0
1231	5	0	2.5	0	5	2.5	1	2	1.25	20	5	0	0	0	0	1	1.5	0	1	1.125	0	0	0	0
1232	2.5	0.5	1.5	0	3	3	4	4	1.5	19	4	0	0.5	1	0	1	2	1	2	1.25	1	1	1	0
1233	5	0	3	0	5	2	1	1	1	20	4	0	0	0	0	0	3	1	3	1.25	0	0	0	0
1234	2	0.5	1	0	2	2	3	3	1.25	18	5	0	1	1	0	0	2.5	1	3	1.75	0.5	1	0	0
1235	3	1	2.5	0	3.5	2.5	4	5	1.5	18.5	5	0	1	1	0	0	2	1	3	1.5	1	1	0.5	0
1236	5	0	2	0	5	2	1	1	1	20	3	0	0	0	0	1	1.5	0.5	1.5	1.125	0.5	0	0	0.5
1237	1	1	1	0	1	3	5	5	2	20		0	1	1	0	0	1	0.5	3.5	2	1	1	1	0
1238	5	0	3	0	5	2.5	1	1	1	20	4	0	0	0	0	0	1.5	0.5	1.5	1	0.5	0	0	0
1238A	5	0	1	0	5	3	1.5	1.5						0	0		5	1	5	1	1	0	1	0.25
1239	2.5	1	2.5	0	3	3	3	3	1.5	19.5	5	0	0.5	1	0	0	3.5	0.5	1.5	1.125	0.5	1	1	0
1240	3	0.5	1.5	0	3	2.5	3	3	1.5	19.5		0	0	1	0	0	3	1	2	1.75	1	1	1	0

ID	direction of 1st lateral veins	veins underneath hairy	axils of veins hairy	ending points of veins	depth of lobes	margin of leaves	margin of stipules	glands on stipules' teeth	number of styles	number of stamina	colour of anthers	sepal direction (buds)	sepal direction (flowering)	upper side of sepals hairy	lower side of sepals hairy	hypanthium hairy	aspect ratio of sepals	shape of the sepal tip	sepal direction (fruit)	number of nutlets per fruit	shape of fruit	shape of fruit base	fruit colour	fruit hairy
1241	1.5	1	1	0	1	5	5	5	2	20	3	0	0	1	0	0	1	0.5	3.5	2.125	1	1	1	0
1242	3	0	2	0	3	5	4	5	1.75	20	5	0	1	1	0	0	3.5	1	5	1.875	1	1	1	0
1242A	5	0	3	0	5	2.5	1	1						0	0		4.5	1	4.5	1	0.75	0	0	0
1243	5	0	2.5	0	4.5	1	1	1	1	20	4	0	0	0	0	0	1	0.5	1	1	0	0	1	0
1244	2.5	0	4	0	2	5	3	3	1	18.5	5	0	0	0.5	0	0	1.5	0.5	1	1.25	0.5	0	0.5	0
1245	2.5	0.5	3.5	0	2.5	4	3	3	1.25	19.5	4	0	0	0.5	0	0	1	0.5	1	1.25	0.5	0	0.5	0
1246	1	1	1	0	1	5	5	5	2	20		0		1	0	0	1	1	2	2	1	1	0.5	0
1247	4.5	0	3	0	4.5	4	1.5	1	1	17.5	3	0	0	0.5	0	0.5	2.5	1	1	1.25	0	0	1	0
1248	1	1	1	0	1.5	5	4	4	2	18	3	0	1	0.5	0	0	1	1	2	2	0.5	0	1	0
1249	5	0	2.5	0	5	3	1	1	1	18.5	3	0	0	0.25	0	1	3	0.5	1	1	1	1	0.5	0
1249A	5	0	4	0	5	4.5								0	0		3.5	1	3	1	1	0	1	0
1250	2.5	0.5	2.5	0	3.5	5	4	4	1.5	19.5		0	1	0.5	0	0	3	1	4	1.5	0.25	0	1	0
1250A	1	1	1	0	1	5	5	5						1	0		1	0	2.5	2	0	0	1	0
1251	4	0	3	0	3	4	4	4	1					0.5	0	0	4	1	1.5	1	0.75	0		0
1252	4	0	3	0	4	4	3	5	1.5					0	0	0	2	0.5	1	1.5	0.5	0		0
1253	3	0	3	0	3	5	5	5	1					0	0	0	5	1	5	1	1	1	1	0
1254	4	0	3	0	5	4	3	3	1.5					0.5	0	0	4	1	1		1	0		0
1255	3	0.5	5	0	3	4			1					0.5	0		5	1	1	1	1	0.5	1	1
1256	1	1	1	0	2	5	4	4	2					1	0	0	2	0.5	1	2	0	0	1	0

9.5 | Table S5 Spearman’s ρ of cross correlation of the overall trait data

Table S5 Spearman’s ρ of cross correlation of the overall trait data.

trait[i]	**trait[j]**	**ρ**	**trait[i]**	**trait[j]**	**ρ**	**trait[i]**	**trait[j]**	**ρ**
leaf_1	leaf_2	-0.74^{***}	leaf_5	flower_4	-0.19^{**}	flower_2	fruit_6	0.22^{***}
leaf_1	leaf_3	0.42^{***}	leaf_5	flower_5	-0.30^{***}	flower_3	flower_4	-0.01^{ns}
leaf_1	leaf_4	-0.26^{***}	leaf_5	flower_6	-0.58^{***}	flower_3	flower_5	0.14^{*}
leaf_1	leaf_5	0.89^{***}	leaf_5	flower_7	-0.36^{***}	flower_3	flower_6	-0.04^{ns}
leaf_1	leaf_6	-0.57^{***}	leaf_5	flower_8	0.33^{***}	flower_3	flower_7	-0.41^{***}
leaf_1	leaf_7	-0.72^{***}	leaf_5	flower_9	0.04^{ns}	flower_3	flower_8	-0.21^{**}
leaf_1	leaf_8	-0.71^{***}	leaf_5	flower_10	0.05^{ns}	flower_3	flower_9	0.10^{ns}
leaf_1	flower_1	-0.64^{***}	leaf_5	fruit_1	-0.34^{***}	flower_3	flower_10	0.21^{**}
leaf_1	flower_2	$-0.11^{\cdot}$	leaf_5	fruit_2	-0.72^{***}	flower_3	fruit_1	0.23^{***}
leaf_1	flower_3	0.14^{*}	leaf_5	fruit_3	0.22^{***}	flower_3	fruit_2	-0.39^{***}
leaf_1	flower_4	-0.05^{ns}	leaf_5	fruit_4	-0.06^{ns}	flower_3	fruit_3	0.30^{***}
leaf_1	flower_5	-0.29^{***}	leaf_5	fruit_5	-0.05^{ns}	flower_3	fruit_4	0.23^{***}
leaf_1	flower_6	-0.61^{***}	leaf_5	fruit_6	0.20^{**}	flower_3	fruit_5	0.45^{***}
leaf_1	flower_7	-0.25^{***}	leaf_6	leaf_7	0.78^{***}	flower_3	fruit_6	-0.15^{*}
leaf_1	flower_8	0.43^{***}	leaf_6	leaf_8	0.79^{***}	flower_4	flower_5	0.25^{***}
leaf_1	flower_9	0.18^{**}	leaf_6	flower_1	0.25^{***}	flower_4	flower_6	0.07^{ns}
leaf_1	flower_10	0.08^{ns}	leaf_6	flower_2	-0.13^{*}	flower_4	flower_7	0.45^{***}
leaf_1	fruit_1	-0.33^{***}	leaf_6	flower_3	0.28^{***}	flower_4	flower_8	0.14^{*}
leaf_1	fruit_2	-0.63^{***}	leaf_6	flower_4	0.05^{ns}	flower_4	flower_9	0.74^{***}
leaf_1	fruit_3	0.19^{**}	leaf_6	flower_5	0.26^{***}	flower_4	flower_10	0.38^{***}
leaf_1	fruit_4	-0.09^{ns}	leaf_6	flower_6	0.44^{***}	flower_4	fruit_1	0.34^{***}
leaf_1	fruit_5	-0.09^{ns}	leaf_6	flower_7	-0.10.	flower_4	fruit_2	0.33^{***}
leaf_1	fruit_6	0.31^{***}	leaf_6	flower_8	-0.45^{***}	flower_4	fruit_3	-0.06^{ns}
leaf_2	leaf_3	-0.28^{***}	leaf_6	flower_9	0.02^{ns}	flower_4	fruit_4	-0.03^{ns}
leaf_2	leaf_4	0.23^{***}	leaf_6	flower_10	$0.11^{\cdot}$	flower_4	fruit_5	-0.21^{**}
leaf_2	leaf_5	-0.69^{***}	leaf_6	fruit_1	0.41^{***}	flower_4	fruit_6	0.16^{*}
leaf_2	leaf_6	0.47^{***}	leaf_6	fruit_2	0.27^{***}	flower_5	flower_6	0.23^{***}
leaf_2	leaf_7	0.62^{***}	leaf_6	fruit_3	0.01^{ns}	flower_5	flower_7	0.25^{***}
leaf_2	leaf_8	0.58^{***}	leaf_6	fruit_4	0.24^{***}	flower_5	flower_8	-0.12^{*}
leaf_2	flower_1	0.55^{***}	leaf_6	fruit_5	0.40^{***}	flower_5	flower_9	0.31^{***}
leaf_2	flower_2	$0.12^{\cdot}$	leaf_6	fruit_6	-0.30^{***}	flower_5	flower_10	0.34^{***}
leaf_2	flower_3	-0.13^{*}	leaf_7	leaf_8	0.87^{***}	flower_5	fruit_1	0.51^{***}
leaf_2	flower_4	-0.01^{ns}	leaf_7	flower_1	0.43^{***}	flower_5	fruit_2	0.33^{***}
leaf_2	flower_5	0.28^{***}	leaf_7	flower_2	-0.06^{ns}	flower_5	fruit_3	0.05^{ns}
leaf_2	flower_6	0.60^{***}	leaf_7	flower_3	0.21^{**}	flower_5	fruit_4	0.21^{**}
leaf_2	flower_7	0.31^{***}	leaf_7	flower_4	-0.01^{ns}	flower_5	fruit_5	0.11^{ns}
leaf_2	flower_8	-0.24^{***}	leaf_7	flower_5	0.25^{***}	flower_5	fruit_6	$-0.12^{\cdot}$
leaf_2	flower_9	-0.18^{**}	leaf_7	flower_6	0.47^{***}	flower_6	flower_7	0.25^{***}
leaf_2	flower_10	-0.08^{ns}	leaf_7	flower_7	-0.13^{*}	flower_6	flower_8	-0.16^{**}
leaf_2	fruit_1	0.31^{***}	leaf_7	flower_8	-0.51^{***}	flower_6	flower_9	-0.17^{**}
leaf_2	fruit_2	0.56^{***}	leaf_7	flower_9	-0.07^{ns}	flower_6	flower_10	0.00^{ns}
leaf_2	fruit_3	-0.16^{**}	leaf_7	flower_10	0.05^{ns}	flower_6	fruit_1	0.24^{***}
leaf_2	fruit_4	0.03^{ns}	leaf_7	fruit_1	0.40^{***}	flower_6	fruit_2	0.44^{***}
leaf_2	fruit_5	0.07^{ns}	leaf_7	fruit_2	0.47^{***}	flower_6	fruit_3	-0.12^{*}
leaf_2	fruit_6	-0.14^{*}	leaf_7	fruit_3	0.04^{ns}	flower_6	fruit_4	$0.11^{\cdot}$

trait[i]	trait[j]	ρ	trait[i]	trait[j]	ρ	trait[i]	trait[j]	ρ
leaf_3	leaf_4	0.39^{***}	leaf_7	fruit_4	0.28^{***}	flower_6	fruit_5	0.09^{ns}
leaf_3	leaf_5	0.29^{***}	leaf_7	fruit_5	0.38^{***}	flower_6	fruit_6	$-0.12^{.}$
leaf_3	leaf_6	-0.27^{***}	leaf_7	fruit_6	-0.34^{***}	flower_7	flower_8	0.32^{***}
leaf_3	leaf_7	-0.39^{***}	leaf_8	flower_1	0.48^{***}	flower_7	flower_9	0.30^{***}
leaf_3	leaf_8	-0.37^{***}	leaf_8	flower_2	-0.21^{**}	flower_7	flower_10	0.13^{*}
leaf_3	flower_1	0.04^{ns}	leaf_8	flower_3	0.25^{***}	flower_7	fruit_1	0.24^{***}
leaf_3	flower_2	0.20^{**}	leaf_8	flower_4	0.16^{*}	flower_7	fruit_2	0.66^{***}
leaf_3	flower_3	-0.05^{ns}	leaf_8	flower_5	0.33^{***}	flower_7	fruit_3	-0.23^{***}
leaf_3	flower_4	0.35^{***}	leaf_8	flower_6	0.50^{***}	flower_7	fruit_4	-0.12^{*}
leaf_3	flower_5	0.06^{ns}	leaf_8	flower_7	-0.06^{ns}	flower_7	fruit_5	-0.46^{***}
leaf_3	flower_6	-0.21^{***}	leaf_8	flower_8	-0.50^{***}	flower_7	fruit_6	0.29^{***}
leaf_3	flower_7	0.40^{***}	leaf_8	flower_9	0.04^{ns}	flower_8	flower_9	0.13^{*}
leaf_3	flower_8	0.52^{***}	leaf_8	flower_10	0.10.	flower_8	flower_10	0.01^{ns}
leaf_3	flower_9	0.48^{***}	leaf_8	fruit_1	0.45^{***}	flower_8	fruit_1	-0.15^{*}
leaf_3	flower_10	0.28^{***}	leaf_8	fruit_2	0.54^{***}	flower_8	fruit_2	-0.07^{ns}
leaf_3	fruit_1	0.03^{ns}	leaf_8	fruit_3	0.01^{ns}	flower_8	fruit_3	-0.07^{ns}
leaf_3	fruit_2	0.02^{ns}	leaf_8	fruit_4	0.27^{***}	flower_8	fruit_4	-0.21^{**}
leaf_3	fruit_3	0.05^{ns}	leaf_8	fruit_5	0.45^{***}	flower_8	fruit_5	-0.45^{***}
leaf_3	fruit_4	-0.06^{ns}	leaf_8	fruit_6	-0.35^{***}	flower_8	fruit_6	0.74^{***}
leaf_3	fruit_5	-0.30^{***}	flower_1	flower_2	0.30^{***}	flower_9	flower_10	0.57^{***}
leaf_3	fruit_6	0.40^{***}	flower_1	flower_3	-0.42^{***}	flower_9	fruit_1	0.41^{***}
leaf_4	leaf_5	-0.44^{***}	flower_1	flower_4	0.36^{***}	flower_9	fruit_2	0.16^{**}
leaf_4	leaf_6	-0.02^{ns}	flower_1	flower_5	0.32^{***}	flower_9	fruit_3	0.10^{ns}
leaf_4	leaf_7	-0.15^{*}	flower_1	flower_6	0.48^{***}	flower_9	fruit_4	$0.11^{.}$
leaf_4	leaf_8	0.08^{ns}	flower_1	flower_7	0.68^{***}	flower_9	fruit_5	-0.05^{ns}
leaf_4	flower_1	0.80^{***}	flower_1	flower_8	-0.06^{ns}	flower_9	fruit_6	$0.11^{.}$
leaf_4	flower_2	0.21^{**}	flower_1	flower_9	0.18^{**}	flower_10	fruit_1	0.29^{***}
leaf_4	flower_3	-0.38^{***}	flower_1	flower_10	0.10^{ns}	flower_10	fruit_2	0.06^{ns}
leaf_4	flower_4	0.52^{***}	flower_1	fruit_1	0.38^{***}	flower_10	fruit_3	0.20^{**}
leaf_4	flower_5	0.31^{***}	flower_1	fruit_2	0.96^{***}	flower_10	fruit_4	0.15^{*}
leaf_4	flower_6	0.24^{***}	flower_1	fruit_3	-0.36^{***}	flower_10	fruit_5	0.10^{ns}
leaf_4	flower_7	0.76^{***}	flower_1	fruit_4	$-0.12^{.}$	flower_10	fruit_6	0.00^{ns}
leaf_4	flower_8	0.20^{**}	flower_1	fruit_5	-0.22^{**}	fruit_1	fruit_2	0.36^{***}
leaf_4	flower_9	0.41^{***}	flower_1	fruit_6	0.00^{ns}	fruit_1	fruit_3	0.14^{*}
leaf_4	flower_10	0.20^{***}	flower_2	flower_3	-0.34^{***}	fruit_1	fruit_4	0.34^{***}
leaf_4	fruit_1	0.30^{***}	flower_2	flower_4	$0.12^{.}$	fruit_1	fruit_5	$0.12^{.}$
leaf_4	fruit_2	0.78^{***}	flower_2	flower_5	0.03^{ns}	fruit_1	fruit_6	-0.08^{ns}
leaf_4	fruit_3	-0.32^{***}	flower_2	flower_6	0.06^{ns}	fruit_2	fruit_3	-0.36^{***}
leaf_4	fruit_4	-0.15^{*}	flower_2	flower_7	0.49^{***}	fruit_2	fruit_4	-0.13^{*}
leaf_4	fruit_5	-0.31^{***}	flower_2	flower_8	0.22^{***}	fruit_2	fruit_5	-0.20^{**}
leaf_4	fruit_6	0.15^{**}	flower_2	flower_9	0.05^{ns}	fruit_2	fruit_6	0.00^{ns}
leaf_5	leaf_6	-0.55^{***}	flower_2	flower_10	-0.05^{ns}	fruit_3	fruit_4	0.39^{***}
leaf_5	leaf_7	-0.65^{***}	flower_2	fruit_1	0.09^{ns}	fruit_3	fruit_5	0.30^{***}
leaf_5	leaf_8	-0.69^{***}	flower_2	fruit_2	0.21^{**}	fruit_3	fruit_6	-0.04^{ns}
leaf_5	flower_1	-0.73^{***}	flower_2	fruit_3	0.00^{ns}	fruit_4	fruit_5	0.29^{***}
leaf_5	flower_2	$-0.11^{.}$	flower_2	fruit_4	0.01^{ns}	fruit_4	fruit_6	-0.21^{***}
leaf_5	flower_3	0.19^{**}	flower_2	fruit_5	-0.34^{***}	fruit_5	fruit_6	-0.37^{***}

Codes of significance (0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 'ns' 1) are given right above the respective value.

9.6 | Table S6 Mass of Crataegus samples for DNA extraction

Table S6 Mass of *Crataegus* samples for DNA extraction. The concentration of extracted DNA and two ratios of absorbances at certain wave lengths (230, 260, and 280 nm) with a Nanophotometer P300 (Implen, Munich, Germany) to estimate the purity are provided.

#	**ID**	**m_{sample} [mg]**	**c_{DNA} [ng/µL]**	**A260/A280**	**A260/A230**
1	1000A	7.4	46.5	1.576	0.727
2	1001	8.0	96.5	1.990	1.990
3	1002	8.4	202	1.952	1.734
4	1003	7.6	77	1.974	1.638
5	1004A	8.0	175	1.966	1.913
6	1004	8.6	129	1.940	1.612
7	1005	8.6	125	1.953	1.852
8	1006	7.9	64.5	1.792	0.866
9	1007	7.9	43.5	2.023	2.417
10	1008	7.8	62	2.033	2.296
11	1009	8.4	75.5	1.987	1.911
12	1010	7.2	198	1.985	1.829
13	1011	7.6	78	2.000	2.400
14	1012	8.5	271	1.964	1.813
15	1013	8.4	67	1.974	2.161
16	1014	7.7	277	1.979	1.884
17	1015	8.7	49	2.000	2.390
18	1015A	7.4	50.5	1.942	1.980
19	1016	7.6	209	1.953	1.659
20	1017	8.8	81.5	2.037	2.117
21	1018	7.8	325	1.994	1.821
22	1019	7.8	242	2.012	2.235
23	1020	7.7	106	1.963	1.876
24	1021	7.4	61	2.000	1.968
25	1022	8.4	250	1.957	1.692
26	1023	8.6	176	1.908	1.569
27	1024	7.6	195	1.940	1.500
28	1025	7.7	252	1.942	1.587
29	1026	8.6	329	2.000	1.880
30	1027	7.6	290	1.956	1.651
31	1027A	8.4	224	1.965	1.404
32	1027B	8.2	201	1.985	1.865
33	1028	7.6	155	1.890	1.281
34	1029	7.9	239	1.975	1.707
35	1030	7.8	160	1.945	1.500
36	1031	7.9	170	1.926	1.319
37	1032	8.7	243	1.960	1.642
38	1033	8.2	112	1.948	1.736
39	1034	7.7	328	1.988	1.918
40	1035	7.9	206	1.976	1.764
41	1035A	7.2	97	1.830	1.228
42	1036	8.7	145	1.908	1.551
43	1037	8.1	154	1.822	1.189
44	1038	8.0	186	1.874	1.416
45	1038A	7.8	193	1.901	1.233

#	**ID**	**m_{sample} [mg]**	**c_{DNA} [ng/µL]**	**A260/A280**	**A260/A230**
46	1038B	8.2	78	1.717	0.918
47	1039	7.3	257	1.940	1.616
48	1040	8.0	150	1.857	1.251
49	1041	8.7	59	1.553	0.724
50	1042	7.6	69.5	1.805	0.986
51	1043	7.8	84.5	1.837	1.000
52	1044	7.6	44.5	1.816	1.271
53	1045	8.4	80	1.951	1.684
54	1046	8.3	69	1.865	1.190
55	1047	7.2	88.5	1.903	1.221
56	1048	8.6	122	1.877	1.196
57	1049	8.1	132	1.821	1.039
58	1050	8.1	162	1.994	1.994
59	1050A	8.2	114	1.900	1.140
60	1050B	8.9	73.5	1.909	1.633
61	1051	8.4	131	1.782	1.236
62	1052	8.0	179	1.972	1.840
63	1053	8.4	176	1.892	1.294
64	1054	7.7	123	1.892	1.309
65	1055	8.3	158	1.975	1.827
66	1056	7.8	132	1.948	1.719
67	1057	8.2	141	1.945	1.659
68	1058	8.0	94.5	1.871	1.056
69	1059	8.1	136	1.896	1.282
70	1060	7.6	83	1.844	1.248
71	1060A	7.5	112	1.851	1.258
72	1060B	7.9	174	1.923	1.475
73	1060C	8.5	97.5	1.912	1.168
74	1060D	9.0	344	1.946	1.172
75	1061	8.3	104	1.683	0.920
76	1062	7.4	89	1.728	0.848
77	1063	8.4	63	1.881	1.340
78	1064	8.8	72	1.946	1.485
79	1065	8.2	108	1.593	0.793
80	1066	8.0	57.5	1.949	1.667
81	1067	8.5	64.5	1.483	0.514
82	1068	8.0	99	1.833	1.021
83	1069	8.2	113	1.965	1.421
84	1070	8.5	97	1.940	1.590
85	1071	8.2	159	1.975	1.598
86	1072	8.8	103	1.962	1.661
87	1073	7.7	74.5	1.840	1.355
88	1074	8.8	121	1.928	1.545
89	1075	8.0	108	1.955	1.483
90	1076	8.5	65	1.912	1.548
91	1077	8.4	69	1.865	1.408
92	1078	8.4	64	1.910	1.471
93	1079	7.5	98	1.941	1.543
94	1080	7.6	113	1.982	1.932
95	1081	7.8	61.5	2.016	1.864

#	ID	m_{sample} [mg]	c_{DNA} [ng/µL]	A260/A280	A260/A230
96	1082	7.2	77.5	1.987	1.535
97	1082A	7.8	43.5	1.642	0.719
98	1083	7.9	95	1.900	1.105
99	1083A	7.4	80.5	1.988	1.059
100	1083B	8.8	55	1.833	1.048
101	1084	7.6	95	1.810	1.092
102	1085	9.5	109	1.863	1.463
103	1086	7.5	77.5	1.914	1.422
104	1086A	8.1	78.5	1.805	0.751
105	1087	9.1	142	1.959	1.587
106	1088	9.3	63	1.969	1.703
107	1089	8.7	94	1.979	1.757
108	1090	8.2	135	1.888	1.298
109	1090A	8.3	143	1.723	0.688
110	1090B	9.4	211	1.754	0.710
111	1090C	9.7	130	1.877	0.906
112	1091	9.1	93	1.898	1.431
113	1091A	8.0	59	1.815	0.702
114	1091B	9.6	66.5	1.684	0.532
115	1091C	8.9	103	1.640	0.621
116	1091D	9.3	140	1.701	0.566
117	1091E	7.3	75	1.765	0.595
118	1092	9.0	69.5	1.904	1.086
119	1093	9.2	122	1.869	1.272
120	1093s	8.3	130	1.831	1.390
121	1093u	8.0	78	1.835	1.076
122	1094	7.8	114	1.846	1.071
123	1095	8.3	172	1.782	0.770
124	1096	7.3	90.5	1.757	0.923
125	1097	8.2	135	1.929	1.256
126	1098	7.5	106	1.812	0.951
127	1099	7.9	135	1.849	1.149
128	1100	9.4	132	1.927	1.228
129	1100A	8.6	122	1.960	1.512
130	1101	8.9	191	1.949	1.431
131	1102	7.6	137	1.877	1.046
132	1103	8.0	106	1.945	1.462
133	1104	8.4	157	2.006	1.820
134	1104A	8.1	128	1.855	0.924
135	1105	7.4	117	1.857	0.992
136	1106	8.0	102	1.744	0.927
137	1107	10.6	140	2.029	1.818
138	1107A	10.0	92	1.937	1.150
139	1108	7.6	70	1.818	0.927
140	1109	8.1	74.5	1.886	1.221
141	1110	8.1	73.5	1.909	1.301
142	1111	8.5	71	1.919	1.268
143	1112	8.6	89.5	1.925	1.377
144	1113	8.6	71	1.945	1.495
145	1114	9.5	68	1.971	1.744

#	ID	m_{sample} [mg]	c_{DNA} [ng/µL]	A260/A280	A260/A230
146	1115	8.6	79	1.951	1.491
147	1116	8.9	100	1.942	1.481
148	1117	9.0	85	1.910	1.149
149	1118	7.9	121	2.008	1.734
150	1119	9.5	127	2.024	1.782
151	1120	7.6	95.5	1.929	1.436
152	1121	8.6	106	1.991	1.249
153	1122	7.7	85	1.954	1.417
154	1123	7.9	78.5	1.847	0.987
155	1124	8.4	99	1.960	1.623
156	1125	7.9	130	1.904	1.408
157	1126	8.9	137	1.971	1.539
158	1127	9.2	102	2.000	1.789
159	1128	9.1	93	1.979	1.691
160	1129	8.1	87	1.977	1.626
161	1130	7.9	107	2.000	1.769
162	1131	8.3	87	1.891	1.208
163	1132	8.3	87.5	1.923	1.207
164	1133	8.8	99	1.904	1.286
165	1134	9.4	102	1.971	1.735
166	1135	8.7	91.5	1.968	1.649
167	1136	7.6	100	2.010	1.795
168	1137	8.4	72	2.028	1.846
169	1138	7.5	107	1.991	1.821
170	1139	7.2	132	2.023	1.977
171	1140	7.7	56	1.836	1.047
172	1141	8.2	86	2.024	1.933
173	1142	8.3	97	2.000	1.883
174	1143	8.2	160	1.697	0.742
175	1144	8.8	117	2.000	1.741
176	1145	8.2	104	1.971	1.643
177	1146	8.3	116	1.863	1.249
178	1147	8.0	106	1.945	1.158
179	1148	8.5	87.5	1.620	1.036
180	1149	9.0	97	1.930	1.386
181	1150	6.8	96.5	1.569	0.808
182	1151	7.8	82	1.843	1.123
183	1152	8.4	108	1.955	1.569
184	1153	8.2	78	1.880	1.418
185	1154	9.0	87.5	1.902	1.232
186	1155	7.5	93	1.918	1.563
187	1156	8.3	73	1.933	1.526
188	1157	8.4	81.5	1.918	1.552
189	1158	8.8	109	1.982	1.546
190	1159	8.8	108	1.938	1.382
191	1160	9.3	110	1.991	1.810
192	1161	8.1	91.5	2.011	1.926
193	1162	8.0	75	1.899	1.163
194	1163	9.5	134	1.978	1.768
195	1164	8.3	130	1.912	1.538

#	ID	m_{sample} [mg]	c_{DNA} [ng/µL]	A260/A280	A260/A230
196	1165	7.8	121	1.952	1.833
197	1166	7.6	100	1.879	1.163
198	1167	7.5	97.5	1.931	1.596
199	1168	9.5	129	1.969	1.792
200	1169	7.8	78.5	1.938	1.670
201	1170	7.7	100	1.844	1.248
202	1171	7.3	103	1.971	1.694
203	1172	8.1	107	1.954	1.732
204	1173	7.8	91	1.896	1.583
205	1174	7.6	87.5	2.035	1.989
206	1175	7.7	161	1.928	1.406
207	1176	7.6	95	1.810	1.098
208	1176A	8.0	138	1.930	1.321
209	1177	8.3	158	1.951	1.827
210	1178	8.8	127	1.939	1.337
211	1179	8.5	78	1.902	1.660
212	1180	9.1	108	1.946	1.895
213	1181	8.1	90.5	1.905	1.645
214	1182	7.8	120	1.832	1.341
215	1183	7.7	100	1.896	1.689
216	1183A	7.7	67.5	1.875	1.607
217	1183B	8.9	165	1.947	1.582
218	1184	8.1	137	1.890	1.473
219	1185	8.0	98.5	1.913	1.407
220	1185A	8.2	103	1.881	1.331
221	1186	7.9	59.5	1.831	1.280
222	1187	7.4	104	1.883	1.174
223	1187A	7.7	107	1.894	1.427
224	1188	8.6	92.5	1.814	1.178
225	1189	7.5	78	1.773	1.130
226	1190	7.5	114	1.795	1.219
227	1191	7.8	107	1.754	1.014
228	1192	7.6	68.5	1.851	1.412
229	1193	8.8	79.5	1.987	1.674
230	1194	7.7	70.5	1.855	1.396
231	1195	8.2	75	1.786	1.027
232	1196	7.2	66.5	1.822	1.304
233	1196A	8.5	106	1.963	1.752
234	1197	7.8	54	1.862	1.598
235	1198	8.1	117	2.000	1.683
236	1198A	8.8	93.5	1.870	1.406
237	1199	8.8	98.5	1.950	1.775
238	1199p	8.7	58.5	1.857	1.170
239	1199c	8.3	100	1.933	1.661
240	1200	7.7	91	1.957	1.936
241	1200p	9.4	112	1.898	1.295
242	1200c	7.9	125	1.984	2.101
243	1201	9.4	114	1.983	1.900
244	1202	7.9	73	1.869	1.505
245	1203	7.6	75.5	1.887	1.573

#	ID	m_{sample} [mg]	c_{DNA} [ng/µL]	A260/A280	A260/A230
246	1204	8.5	130	1.825	1.220
247	1205	7.5	80.5	1.894	1.677
248	1206	9.1	92	1.917	1.643
249	1207	7.6	86	1.911	1.686
250	1208	7.7	65.5	1.871	1.409
251	1209	8.6	97	1.980	1.717
252	1210	8.6	77	1.974	1.925
253	1211	7.5	97.5	2.074	2.378
254	1212	8.3	56	1.836	1.455
255	1213	8.4	74	1.947	1.805
256	1214	7.3	46	1.878	1.804
257	1215	7.3	42.5	1.604	0.955
258	1216	7.6	49.5	1.868	1.833
259	1217	9.0	89.5	1.946	1.178
260	1218	7.9	69	2.091	1.816
261	1219	8.3	48	1.882	2.043
262	1220	8.7	51.5	1.907	2.020
263	1221	7.5	44	1.600	0.838
264	1222	8.0	58.5	1.918	1.983
265	1223	7.4	79	1.951	1.411
266	1224	8.0	126	1.961	1.579
267	1225	7.6	110	1.904	1.327
268	1226	8.3	77.5	1.845	0.969
269	1227	8.7	77.5	2.013	1.598
270	1228	8.8	80.5	1.894	1.150
271	1229	8.5	150	1.929	1.230
272	1230	7.6	106	1.918	1.529
273	1231	8.9	195	2.016	1.801
274	1232	7.4	138	1.822	1.057
275	1233	9.1	103	2.010	1.798
276	1234	7.8	90	1.957	1.552
277	1235	8.0	100	1.923	1.389
278	1236	8.2	122	2.008	1.976
279	1237	8.3	110	1.982	1.630
280	1238	8.8	158	2.000	1.775
281	1238A	8.3	99	1.784	0.510
282	1239	7.9	75.5	1.987	1.756
283	1240	8.7	67.5	1.929	1.452
284	1241	7.7	118	2.009	1.794
285	1242	8.8	176	1.972	1.792
286	1242A	8.5	68.5	1.827	0.714
287	1243	8.3	137	2.000	1.839
288	1244	8.0	87.5	1.966	1.683
289	1245	8.9	61.5	2.016	1.685
290	1246	7.3	68.5	1.986	1.575
291	1247	8.6	90	1.895	1.176
292	1248	8.5	117	2.009	1.726
293	1249	7.5	83.5	1.835	1.136
294	1249A	8.0	53.5	1.621	0.615
295	1250	7.4	77.5	1.824	1.084

#	**ID**	**m_{sample} [mg]**	**c_{DNA} [ng/µL]**	**A260/A280**	**A260/A230**
296	1250A	7.7	45.5	1.596	0.595
297	1251	8.6	112	1.792	0.806
298	1252	9.4	115	1.862	1.009
299	1253	9.7	174	1.599	0.684
300	1254	7.4	43.5	1.933	1.225
301	1255	8.9	136	1.784	0.760
302	1256	7.8	66.5	1.529	0.689

9.7 | Table S7 Allelic SSR data and estimated ploidy level of sampled Crataegus individuals

Table S7 Allelic SSR data and estimated ploidy level of sampled *Crataegus* individuals. Values given in bp. Missing data is presented as 0 for a putative null-allele and from the second allele onwards as *NA* (not available). Estimated ploidy level is drawn from the maximum number of detected alleles in any locus per individual.

ID	**CH01F02**	**CH03C02**	**CH04F06**	**CH04G04**	**CH05D44**	**CH05G07**	**CH05G11**	**ploidy**
1000A	0/NA/NA/NA	114/116/NA/NA	168/NA/NA/NA	164/170/NA/NA	184/NA/NA/NA	167/NA/NA/NA	218/222/NA/NA	2*x*
1001	0/NA/NA/NA	114/NA/NA/NA	170/NA/NA/NA	159/164/NA/NA	184/NA/NA/NA	155/157/NA/NA	218/220/NA/NA	2*x*
1002	0/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	159/164/NA/NA	184/NA/NA/NA	157/NA/NA/NA	218/220/NA/NA	2*x*
1003	157/NA/NA/NA	114/NA/NA/NA	172/174/176/NA	158/162/170/NA	184/NA/NA/NA	167/169/NA/NA	218/222/243/NA	3*x*
1004A	0/NA/NA/NA	114/NA/NA/NA	170/NA/NA/NA	164/170/NA/NA	184/NA/NA/NA	157/NA/NA/NA	218/220/NA/NA	2*x*
1004	157/NA/NA/NA	0/NA/NA/NA	168/NA/NA/NA	145/156/168/NA	184/NA/NA/NA	167/169/NA/NA	216/224/NA/NA	3*x*
1005	0/NA/NA/NA	116/NA/NA/NA	172/174/176/NA	152/176/NA/NA	184/NA/NA/NA	167/169/NA/NA	218/NA/NA/NA	3*x*
1006	0/NA/NA/NA	114/120/NA/NA	0/NA/NA/NA	168/170/NA/NA	184/NA/NA/NA	157/169/NA/NA	218/222/NA/NA	2*x*
1007	161/165/NA/NA	114/118/NA/NA	168/NA/NA/NA	158/162/NA/NA	184/NA/NA/NA	167/169/NA/NA	224/NA/NA/NA	2*x*
1008	158/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	158/164/NA/NA	184/NA/NA/NA	157/NA/NA/NA	214/218/220/NA	3*x*
1009	157/NA/NA/NA	114/123/NA/NA	168/170/172/NA	158/NA/NA/NA	184/NA/NA/NA	157/167/169/NA	224/NA/NA/NA	3*x*
1010	0/NA/NA/NA	114/NA/NA/NA	168/172/NA/NA	170/NA/NA/NA	184/NA/NA/NA	153/157/169/NA	218/220/NA/NA	3*x*
1011	157/165/NA/NA	114/122/NA/NA	168/170/178/NA	158/NA/NA/NA	184/NA/NA/NA	157/165/169/NA	224/NA/NA/NA	3*x*
1012	157/165/NA/NA	114/NA/NA/NA	170/172/NA/NA	158/NA/NA/NA	184/NA/NA/NA	157/NA/NA/NA	224/226/NA/NA	2*x*
1013	154/159/165/NA	108/NA/NA/NA	178/180/NA/NA	158/162/NA/NA	184/NA/NA/NA	165/NA/NA/NA	216/224/NA/NA	3*x*
1014	0/NA/NA/NA	114/116/NA/NA	168/NA/NA/NA	162/186/NA/NA	184/NA/NA/NA	167/169/NA/NA	216/218/220/NA	3*x*
1015	162/NA/NA/NA	114/NA/NA/NA	168/172/NA/NA	162/168/172/NA	184/NA/NA/NA	167/171/NA/NA	214/218/224/NA	3*x*
1015A	154/157/NA/NA	114/NA/NA/NA	168/170/NA/NA	160/NA/NA/NA	184/NA/NA/NA	153/157/169/NA	224/NA/NA/NA	3*x*
1016	0/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	170/172/NA/NA	184/NA/NA/NA	157/NA/NA/NA	216/218/NA/NA	2*x*
1017	0/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	168/184/NA/NA	184/NA/NA/NA	153/157/169/171	214/216/218/220	4*x*
1018	157/NA/NA/NA	114/NA/NA/NA	172/NA/NA/NA	158/166/NA/NA	184/NA/NA/NA	157/NA/NA/NA	214/218/228/NA	3*x*
1019	165/NA/NA/NA	118/120/NA/NA	172/NA/NA/NA	158/162/NA/NA	184/NA/NA/NA	169/NA/NA/NA	224/NA/NA/NA	2*x*
1020	0/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	147/174/NA/NA	184/NA/NA/NA	157/NA/NA/NA	216/218/226/NA	3*x*
1021	154/157/NA/NA	114/NA/NA/NA	170/172/NA/NA	158/162/NA/NA	184/NA/NA/NA	157/NA/NA/NA	224/NA/NA/NA	2*x*
1022	157/NA/NA/NA	114/NA/NA/NA	168/174/NA/NA	158/162/NA/NA	184/NA/NA/NA	153/167/169/NA	224/NA/NA/NA	3*x*

ID	CH01F02	CH03C02	CH04F06	CH04G04	CH05D44	CH05G07	CH05G11	ploidy
1023	157/NA/NA/NA	116/NA/NA/NA	170/176/NA/NA	158/166/NA/NA	179/NA/NA/NA	169/NA/NA/NA	224/228/237/NA	3*x*
1024	157/NA/NA/NA	114/122/NA/NA	170/172/178/NA	158/162/NA/NA	178/184/NA/NA	157/167/NA/NA	218/220/224/NA	3*x*
1025	158/161/168/NA	114/NA/NA/NA	168/170/174/NA	158/164/NA/NA	184/NA/NA/NA	153/157/167/169	214/220/224/NA	4*x*
1026	181/NA/NA/NA	0/NA/NA/NA	168/172/NA/NA	164/170/NA/NA	184/NA/NA/NA	167/NA/NA/NA	220/NA/NA/NA	2*x*
1027	0/NA/NA/NA	122/NA/NA/NA	176/NA/NA/NA	147/166/NA/NA	184/NA/NA/NA	167/169/NA/NA	212/220/NA/NA	2*x*
1027A	157/161/NA/NA	114/NA/NA/NA	170/NA/NA/NA	158/162/NA/NA	184/NA/NA/NA	157/NA/NA/NA	224/NA/NA/NA	2*x*
1027B	159/NA/NA/NA	114/NA/NA/NA	168/170/NA/NA	158/160/162/NA	184/NA/NA/NA	153/157/167/169	216/220/224/NA	4*x*
1028	175/181/NA/NA	0/NA/NA/NA	170/172/NA/NA	170/NA/NA/NA	184/NA/NA/NA	171/NA/NA/NA	216/218/NA/NA	2*x*
1029	171/181/NA/NA	114/NA/NA/NA	168/170/NA/NA	164/NA/NA/NA	179/NA/NA/NA	157/167/NA/NA	216/218/NA/NA	2*x*
1030	159/NA/NA/NA	120/NA/NA/NA	168/172/NA/NA	158/160/162/NA	184/NA/NA/NA	167/171/NA/NA	216/220/224/NA	3*x*
1031	0/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	164/170/NA/NA	184/NA/NA/NA	157/NA/NA/NA	218/222/224/NA	3*x*
1032	0/NA/NA/NA	114/118/NA/NA	166/168/NA/NA	162/164/168/NA	184/NA/NA/NA	167/NA/NA/NA	218/220/NA/NA	3*x*
1033	159/NA/NA/NA	120/NA/NA/NA	168/172/NA/NA	158/160/162/NA	184/NA/NA/NA	169/NA/NA/NA	216/220/224/NA	3*x*
1034	157/NA/NA/NA	114/118/NA/NA	170/NA/NA/NA	158/162/166/NA	184/NA/NA/NA	157/169/NA/NA	214/222/NA/NA	3*x*
1035	154/159/NA/NA	114/NA/NA/NA	168/170/NA/NA	158/162/168/NA	184/NA/NA/NA	153/157/167/169	216/222/NA/NA	4*x*
1035A	157/162/NA/NA	114/NA/NA/NA	170/172/NA/NA	160/162/NA/NA	184/NA/NA/NA	157/167/NA/NA	224/NA/NA/NA	2*x*
1036	159/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	158/162/168/NA	0/NA/NA/NA	157/NA/NA/NA	216/218/220/222	4*x*
1037	187/NA/NA/NA	0/NA/NA/NA	166/168/NA/NA	152/164/NA/NA	0/NA/NA/NA	167/169/NA/NA	214/216/218/NA	3*x*
1038	157/NA/NA/NA	114/NA/NA/NA	168/170/174/NA	158/162/168/NA	0/NA/NA/NA	153/167/169/NA	214/218/224/NA	3*x*
1038A	154/NA/NA/NA	118/NA/NA/NA	168/NA/NA/NA	158/162/NA/NA	0/NA/NA/NA	167/NA/NA/NA	224/NA/NA/NA	2*x*
1038B	157/NA/NA/NA	114/NA/NA/NA	168/172/NA/NA	158/162/168/NA	0/NA/NA/NA	169/NA/NA/NA	214/218/224/NA	3*x*
1039	157/NA/NA/NA	114/NA/NA/NA	170/NA/NA/NA	156/160/164/NA	0/NA/NA/NA	157/169/NA/NA	218/224/NA/NA	3*x*
1040	158/161/168/NA	114/NA/NA/NA	170/NA/NA/NA	158/164/NA/NA	0/NA/NA/NA	157/NA/NA/NA	214/220/224/NA	3*x*
1041	161/NA/NA/NA	0/NA/NA/NA	168/NA/NA/NA	158/NA/NA/NA	184/NA/NA/NA	167/169/NA/NA	224/NA/NA/NA	2*x*
1042	154/157/158/NA	122/NA/NA/NA	168/172/NA/NA	158/164/NA/NA	179/NA/NA/NA	167/NA/NA/NA	214/218/224/NA	3*x*
1043	154/161/NA/NA	114/118/NA/NA	170/NA/NA/NA	158/NA/NA/NA	184/NA/NA/NA	157/NA/NA/NA	224/NA/NA/NA	2*x*
1044	187/NA/NA/NA	0/NA/NA/NA	168/170/NA/NA	162/184/NA/NA	184/NA/NA/NA	169/NA/NA/NA	212/216/218/NA	3*x*
1045	187/NA/NA/NA	118/NA/NA/NA	172/NA/NA/NA	164/184/NA/NA	184/NA/NA/NA	169/NA/NA/NA	216/218/220/NA	3*x*
1046	0/NA/NA/NA	112/NA/NA/NA	168/NA/NA/NA	168/170/NA/NA	184/NA/NA/NA	169/171/NA/NA	216/218/224/NA	3*x*
1047	181/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	152/170/NA/NA	184/NA/NA/NA	157/NA/NA/NA	218/224/NA/NA	2*x*

ID	CH01F02	CH03C02	CH04F06	CH04G04	CH05D44	CH05G07	CH05G11	ploidy
1048	0/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	164/170/NA/NA	184/NA/NA/NA	157/NA/NA/NA	218/220/NA/NA	2*x*
1049	0/NA/NA/NA	116/NA/NA/NA	168/172/NA/NA	170/NA/NA/NA	184/NA/NA/NA	169/NA/NA/NA	218/220/NA/NA	2*x*
1050	175/181/NA/NA	0/NA/NA/NA	168/NA/NA/NA	164/170/NA/NA	179/NA/NA/NA	167/169/NA/NA	218/NA/NA/NA	2*x*
1050A	158/168/NA/NA	114/NA/NA/NA	168/172/NA/NA	158/164/NA/NA	184/NA/NA/NA	153/157/169/NA	214/218/220/228	4*x*
1050B	157/165/NA/NA	114/NA/NA/NA	168/170/172/NA	158/174/NA/NA	184/NA/NA/NA	153/157/169/171	218/226/NA/NA	4*x*
1051	187/NA/NA/NA	112/118/NA/NA	168/NA/NA/NA	168/170/NA/NA	184/NA/NA/NA	167/169/NA/NA	218/220/NA/NA	2*x*
1052	0/NA/NA/NA	114/NA/NA/NA	168/172/NA/NA	168/170/NA/NA	184/NA/NA/NA	153/157/167/169	218/220/NA/NA	4*x*
1053	0/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	164/172/NA/NA	184/NA/NA/NA	157/NA/NA/NA	218/220/NA/NA	2*x*
1054	0/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	170/NA/NA/NA	184/NA/NA/NA	157/NA/NA/NA	218/220/NA/NA	2*x*
1055	0/NA/NA/NA	114/118/NA/NA	170/NA/NA/NA	170/174/NA/NA	184/NA/NA/NA	157/NA/NA/NA	214/216/218/NA	3*x*
1056	0/NA/NA/NA	116/NA/NA/NA	168/170/172/NA	166/170/NA/NA	179/NA/NA/NA	157/167/169/NA	218/220/NA/NA	3*x*
1057	0/NA/NA/NA	114/118/NA/NA	172/NA/NA/NA	168/170/NA/NA	184/NA/NA/NA	167/NA/NA/NA	218/NA/NA/NA	2*x*
1058	149/154/159/NA	114/118/NA/NA	170/172/NA/NA	158/NA/NA/NA	184/NA/NA/NA	157/NA/NA/NA	214/216/224/NA	3*x*
1059	0/NA/NA/NA	0/NA/NA/NA	168/176/NA/NA	166/168/NA/NA	184/NA/NA/NA	169/NA/NA/NA	218/NA/NA/NA	2*x*
1060	181/NA/NA/NA	116/NA/NA/NA	168/172/NA/NA	168/NA/NA/NA	184/NA/NA/NA	167/NA/NA/NA	218/224/NA/NA	2*x*
1060A	0/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	162/164/NA/NA	184/NA/NA/NA	157/NA/NA/NA	220/NA/NA/NA	2*x*
1060B	0/NA/NA/NA	114/NA/NA/NA	168/170/NA/NA	164/166/NA/NA	184/NA/NA/NA	153/157/167/169	218/NA/NA/NA	4*x*
1060C	0/NA/NA/NA	122/NA/NA/NA	168/170/178/NA	166/174/NA/NA	184/NA/NA/NA	165/167/169/NA	218/220/NA/NA	3*x*
1060D	155/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	0/NA/NA/NA	179/181/NA/NA	157/NA/NA/NA	235/NA/NA/NA	2*x*
1061	154/NA/NA/NA	0/NA/NA/NA	168/176/NA/NA	158/NA/NA/NA	184/NA/NA/NA	167/171/NA/NA	224/228/NA/NA	2*x*
1062	157/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	158/NA/NA/NA	184/NA/NA/NA	153/157/169/171	228/NA/NA/NA	4*x*
1063	154/157/NA/NA	114/NA/NA/NA	172/NA/NA/NA	162/NA/NA/NA	184/NA/NA/NA	167/169/NA/NA	224/NA/NA/NA	2*x*
1064	157/NA/NA/NA	114/NA/NA/NA	166/168/NA/NA	158/162/NA/NA	184/NA/NA/NA	169/171/NA/NA	224/NA/NA/NA	2*x*
1065	157/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	158/NA/NA/NA	184/NA/NA/NA	153/157/169/NA	224/NA/NA/NA	3*x*
1066	157/161/NA/NA	120/NA/NA/NA	170/172/NA/NA	162/NA/NA/NA	184/NA/NA/NA	169/171/NA/NA	224/NA/NA/NA	2*x*
1067	154/NA/NA/NA	114/NA/NA/NA	170/NA/NA/NA	160/162/NA/NA	184/NA/NA/NA	157/NA/NA/NA	224/226/NA/NA	2*x*
1068	149/159/165/NA	0/NA/NA/NA	168/170/NA/NA	158/162/NA/NA	179/181/184/NA	167/169/NA/NA	214/224/243/NA	3*x*
1069	165/NA/NA/NA	114/NA/NA/NA	168/172/NA/NA	162/166/170/NA	184/NA/NA/NA	153/157/169/NA	218/220/224/NA	3*x*
1070	149/159/165/NA	114/NA/NA/NA	170/174/NA/NA	158/162/NA/NA	184/NA/NA/NA	157/167/171/NA	214/224/241/NA	3*x*
1071	0/NA/NA/NA	114/122/NA/NA	168/170/172/178	162/170/NA/NA	184/NA/NA/NA	157/165/167/169	218/220/NA/NA	4*x*

ID	CH01F02	CH03C02	CH04F06	CH04G04	CH05D44	CH05G07	CH05G11	ploidy
1072	171/NA/NA/NA	0/NA/NA/NA	170/NA/NA/NA	164/NA/NA/NA	184/NA/NA/NA	169/NA/NA/NA	216/218/222/NA	3*x*
1073	157/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	158/NA/NA/NA	184/NA/NA/NA	157/167/NA/NA	224/NA/NA/NA	2*x*
1074	149/154/159/NA	114/NA/NA/NA	172/NA/NA/NA	158/160/162/NA	184/NA/NA/NA	153/157/167/169	214/216/226/NA	4*x*
1075	149/154/159/NA	120/NA/NA/NA	170/172/NA/NA	158/160/162/NA	173/184/NA/NA	167/169/NA/NA	214/216/226/NA	3*x*
1076	154/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	158/160/NA/NA	184/NA/NA/NA	157/NA/NA/NA	224/226/NA/NA	2*x*
1077	154/NA/NA/NA	114/118/NA/NA	168/176/NA/NA	158/NA/NA/NA	184/NA/NA/NA	169/171/NA/NA	224/228/NA/NA	2*x*
1078	157/NA/NA/NA	114/122/NA/NA	170/172/178/NA	158/162/NA/NA	184/NA/NA/NA	157/167/NA/NA	228/NA/NA/NA	3*x*
1079	149/154/159/NA	114/NA/NA/NA	166/170/172/NA	158/160/162/NA	184/NA/NA/NA	157/167/169/NA	214/216/226/NA	3*x*
1080	155/NA/NA/NA	114/NA/NA/NA	168/172/NA/NA	164/174/NA/NA	184/NA/NA/NA	167/NA/NA/NA	218/224/NA/NA	2*x*
1081	157/159/NA/NA	114/NA/NA/NA	168/170/172/NA	158/168/NA/NA	184/NA/NA/NA	153/157/169/NA	218/224/NA/NA	3*x*
1082	173/NA/NA/NA	122/NA/NA/NA	168/NA/NA/NA	166/176/NA/NA	184/NA/NA/NA	169/NA/NA/NA	216/218/NA/NA	2*x*
1082A	0/NA/NA/NA	114/118/NA/NA	166/172/NA/NA	164/168/NA/NA	184/NA/NA/NA	157/167/169/NA	218/220/NA/NA	3*x*
1083	0/NA/NA/NA	0/NA/NA/NA	170/174/NA/NA	166/174/NA/NA	184/NA/NA/NA	0/NA/NA/NA	212/NA/NA/NA	2*x*
1083A	0/NA/NA/NA	120/NA/NA/NA	166/168/NA/NA	169/NA/NA/NA	184/NA/NA/NA	167/NA/NA/NA	212/NA/NA/NA	2*x*
1083B	170/173/NA/NA	112/NA/NA/NA	168/172/NA/NA	158/162/166/NA	184/NA/NA/NA	169/171/NA/NA	214/218/NA/NA	3*x*
1084	157/159/163/NA	114/NA/NA/NA	168/170/NA/NA	148/158/NA/NA	179/NA/NA/NA	157/169/NA/NA	207/209/216/261	4*x*
1085	153/173/179/NA	114/NA/NA/NA	168/170/NA/NA	146/150/156/160	184/NA/NA/NA	169/NA/NA/NA	212/216/243/265	4*x*
1086	181/NA/NA/NA	114/NA/NA/NA	172/NA/NA/NA	170/NA/NA/NA	184/NA/NA/NA	169/171/NA/NA	218/220/NA/NA	2*x*
1086A	149/NA/NA/NA	114/122/NA/NA	170/172/178/NA	147/158/164/174	184/NA/NA/NA	157/167/NA/NA	212/214/220/NA	4*x*
1087	0/NA/NA/NA	0/NA/NA/NA	168/NA/NA/NA	152/170/NA/NA	184/NA/NA/NA	163/167/NA/NA	218/220/NA/NA	2*x*
1088	159/162/NA/NA	0/NA/NA/NA	170/174/184/NA	152/156/160/NA	184/NA/NA/NA	0/NA/NA/NA	212/220/263/271	4*x*
1089	0/NA/NA/NA	0/NA/NA/NA	168/172/NA/NA	164/174/182/NA	184/NA/NA/NA	167/171/NA/NA	218/233/237/243	4*x*
1090	153/159/162/NA	114/NA/NA/NA	168/170/172/NA	154/168/NA/NA	184/NA/NA/NA	153/157/169/NA	209/241/247/NA	3*x*
1090A	149/163/183/NA	114/NA/NA/NA	168/170/NA/NA	0/NA/NA/NA	184/NA/NA/NA	157/169/NA/NA	203/209/235/NA	3*x*
1090B	149/163/183/NA	114/NA/NA/NA	168/NA/NA/NA	0/NA/NA/NA	184/NA/NA/NA	169/NA/NA/NA	203/209/235/NA	3*x*
1090C	149/163/183/NA	112/120/NA/NA	168/172/NA/NA	0/NA/NA/NA	184/NA/NA/NA	169/NA/NA/NA	203/209/235/NA	3*x*
1091	155/NA/NA/NA	114/NA/NA/NA	168/172/NA/NA	156/NA/NA/NA	184/NA/NA/NA	153/157/169/NA	235/NA/NA/NA	3*x*
1091A	155/NA/NA/NA	118/NA/NA/NA	168/NA/NA/NA	156/NA/NA/NA	184/NA/NA/NA	167/NA/NA/NA	235/237/NA/NA	2*x*
1091B	155/NA/NA/NA	0/NA/NA/NA	170/174/184/NA	156/NA/NA/NA	184/NA/NA/NA	0/NA/NA/NA	235/NA/NA/NA	3*x*
1091C	155/NA/NA/NA	114/120/NA/NA	170/NA/NA/NA	156/NA/NA/NA	184/NA/NA/NA	157/NA/NA/NA	235/NA/NA/NA	2*x*

ID	**CH01F02**	**CH03C02**	**CH04F06**	**CH04G04**	**CH05D44**	**CH05G07**	**CH05G11**	**ploidy**
1091D	155/NA/NA/NA	0/NA/NA/NA	168/172/NA/NA	156/NA/NA/NA	184/NA/NA/NA	165/167/169/NA	235/NA/NA/NA	3*x*
1091E	166/NA/NA/NA	114/NA/NA/NA	168/170/NA/NA	0/NA/NA/NA	184/NA/NA/NA	157/169/NA/NA	233/237/NA/NA	2*x*
1092	155/NA/NA/NA	0/NA/NA/NA	168/174/NA/NA	156/NA/NA/NA	184/NA/NA/NA	153/169/NA/NA	235/NA/NA/NA	2*x*
1093	155/NA/NA/NA	114/116/NA/NA	170/172/NA/NA	174/NA/NA/NA	184/NA/NA/NA	155/169/NA/NA	216/218/220/235	4*x*
1093s	174/NA/NA/NA	114/122/NA/NA	168/170/172/178	174/NA/NA/NA	184/NA/NA/NA	157/165/167/169	216/218/220/NA	4*x*
1093u	0/NA/NA/NA	116/NA/NA/NA	168/172/NA/NA	164/172/NA/NA	184/NA/NA/NA	153/169/NA/NA	216/218/220/NA	3*x*
1094	0/NA/NA/NA	108/NA/NA/NA	180/NA/NA/NA	162/168/NA/NA	184/NA/NA/NA	165/NA/NA/NA	218/224/NA/NA	2*x*
1095	157/NA/NA/NA	114/NA/NA/NA	168/NA/NA/NA	158/NA/NA/NA	184/NA/NA/NA	169/NA/NA/NA	224/226/NA/NA	2*x*
1096	0/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	152/164/NA/NA	184/NA/NA/NA	157/169/NA/NA	218/220/NA/NA	3*x*
1097	187/NA/NA/NA	114/NA/NA/NA	170/NA/NA/NA	168/NA/NA/NA	184/NA/NA/NA	157/171/NA/NA	218/220/NA/NA	2*x*
1098	181/NA/NA/NA	114/NA/NA/NA	168/172/174/NA	170/NA/NA/NA	184/NA/NA/NA	153/167/169/NA	218/NA/NA/NA	3*x*
1099	171/NA/NA/NA	114/NA/NA/NA	168/170/174/NA	164/170/NA/NA	184/NA/NA/NA	159/165/167/NA	218/220/224/NA	3*x*
1100	154/185/NA/NA	114/NA/NA/NA	168/170/NA/NA	159/170/NA/NA	184/NA/NA/NA	153/157/167/169	216/218/NA/NA	4*x*
1100A	0/NA/NA/NA	118/120/NA/NA	176/178/180/NA	170/NA/NA/NA	184/NA/NA/NA	0/NA/NA/NA	216/218/NA/NA	3*x*
1101	0/NA/NA/NA	108/NA/NA/NA	180/NA/NA/NA	164/NA/NA/NA	179/NA/NA/NA	161/165/NA/NA	220/NA/NA/NA	2*x*
1102	171/189/NA/NA	118/NA/NA/NA	168/172/NA/NA	166/168/NA/NA	184/NA/NA/NA	171/NA/NA/NA	218/220/NA/NA	2*x*
1103	177/NA/NA/NA	114/NA/NA/NA	168/NA/NA/NA	170/NA/NA/NA	184/NA/NA/NA	0/NA/NA/NA	218/220/NA/NA	2*x*
1104	185/NA/NA/NA	114/NA/NA/NA	172/174/NA/NA	168/170/NA/NA	184/NA/NA/NA	167/169/NA/NA	218/220/NA/NA	2*x*
1104A	149/159/165/NA	114/120/NA/NA	168/170/172/NA	158/162/NA/NA	184/NA/NA/NA	157/169/NA/NA	214/224/241/NA	3*x*
1105	175/NA/NA/NA	112/NA/NA/NA	168/172/NA/NA	162/170/NA/NA	184/NA/NA/NA	169/171/NA/NA	220/222/NA/NA	2*x*
1106	154/NA/NA/NA	114/NA/NA/NA	168/172/NA/NA	158/168/170/NA	184/NA/NA/NA	157/165/169/NA	214/222/NA/NA	3*x*
1107	0/NA/NA/NA	114/120/NA/NA	174/182/184/NA	170/NA/NA/NA	184/NA/NA/NA	0/NA/NA/NA	218/220/NA/NA	3*x*
1107A	0/NA/NA/NA	108/NA/NA/NA	180/NA/NA/NA	166/170/NA/NA	179/181/NA/NA	165/NA/NA/NA	218/220/NA/NA	2*x*
1108	0/NA/NA/NA	118/NA/NA/NA	172/176/NA/NA	163/170/NA/NA	184/NA/NA/NA	167/169/NA/NA	218/224/NA/NA	2*x*
1109	157/165/NA/NA	118/NA/NA/NA	166/172/NA/NA	158/162/NA/NA	184/NA/NA/NA	169/NA/NA/NA	224/NA/NA/NA	2*x*
1110	0/NA/NA/NA	114/NA/NA/NA	172/176/NA/NA	162/NA/NA/NA	0/NA/NA/NA	169/NA/NA/NA	228/237/NA/NA	2*x*
1111	157/NA/NA/NA	114/120/NA/NA	168/170/172/NA	158/NA/NA/NA	184/NA/NA/NA	157/169/NA/NA	226/NA/NA/NA	3*x*
1112	157/NA/NA/NA	114/116/NA/NA	172/174/NA/NA	162/168/NA/NA	184/NA/NA/NA	167/NA/NA/NA	224/228/NA/NA	2*x*
1113	0/NA/NA/NA	114/NA/NA/NA	172/NA/NA/NA	160/162/NA/NA	184/NA/NA/NA	157/NA/NA/NA	224/228/NA/NA	2*x*
1114	154/NA/NA/NA	114/NA/NA/NA	172/NA/NA/NA	160/166/170/NA	184/NA/NA/NA	167/169/NA/NA	214/218/228/NA	3*x*

ID	**CH01F02**	**CH03C02**	**CH04F06**	**CH04G04**	**CH05D44**	**CH05G07**	**CH05G11**	**ploidy**
1115	154/NA/NA/NA	108/NA/NA/NA	180/NA/NA/NA	160/166/170/NA	184/NA/NA/NA	161/165/NA/NA	214/218/228/NA	3*x*
1116	154/NA/NA/NA	0/NA/NA/NA	172/176/NA/NA	160/166/170/NA	184/NA/NA/NA	169/NA/NA/NA	214/218/228/NA	3*x*
1117	168/NA/NA/NA	116/NA/NA/NA	166/NA/NA/NA	160/162/NA/NA	184/NA/NA/NA	167/171/NA/NA	224/NA/NA/NA	2*x*
1118	0/NA/NA/NA	120/NA/NA/NA	168/NA/NA/NA	170/NA/NA/NA	184/NA/NA/NA	167/169/NA/NA	218/220/NA/NA	2*x*
1119	0/NA/NA/NA	114/NA/NA/NA	168/172/174/NA	164/170/NA/NA	184/NA/NA/NA	153/167/169/NA	218/220/NA/NA	3*x*
1120	0/NA/NA/NA	116/120/NA/NA	168/NA/NA/NA	164/168/NA/NA	184/NA/NA/NA	169/NA/NA/NA	216/218/220/NA	3*x*
1121	161/165/NA/NA	114/NA/NA/NA	170/172/NA/NA	156/NA/NA/NA	184/NA/NA/NA	157/NA/NA/NA	224/NA/NA/NA	2*x*
1122	0/NA/NA/NA	0/NA/NA/NA	168/174/NA/NA	170/NA/NA/NA	184/NA/NA/NA	155/167/171/NA	218/220/NA/NA	3*x*
1123	161/165/NA/NA	108/NA/NA/NA	180/NA/NA/NA	156/158/NA/NA	184/NA/NA/NA	165/NA/NA/NA	224/239/NA/NA	2*x*
1124	0/NA/NA/NA	114/NA/NA/NA	168/172/NA/NA	164/168/NA/NA	184/NA/NA/NA	169/NA/NA/NA	218/220/224/NA	3*x*
1125	165/NA/NA/NA	114/NA/NA/NA	170/NA/NA/NA	156/164/NA/NA	184/NA/NA/NA	157/NA/NA/NA	220/224/NA/NA	2*x*
1126	0/NA/NA/NA	114/116/NA/NA	170/NA/NA/NA	164/170/NA/NA	184/NA/NA/NA	157/NA/NA/NA	218/220/224/NA	3*x*
1127	0/NA/NA/NA	0/NA/NA/NA	168/174/NA/NA	164/170/NA/NA	184/NA/NA/NA	153/169/NA/NA	220/NA/NA/NA	2*x*
1128	161/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	158/164/166/170	184/NA/NA/NA	157/167/NA/NA	214/216/218/222	4*x*
1129	149/NA/NA/NA	114/NA/NA/NA	168/170/NA/NA	164/166/NA/NA	184/NA/NA/NA	153/157/165/169	214/218/243/NA	4*x*
1130	0/NA/NA/NA	118/NA/NA/NA	166/170/NA/NA	158/170/NA/NA	184/NA/NA/NA	169/NA/NA/NA	218/226/NA/NA	2*x*
1131	0/NA/NA/NA	108/NA/NA/NA	180/187/NA/NA	158/170/NA/NA	184/NA/NA/NA	165/NA/NA/NA	218/226/NA/NA	2*x*
1132	149/NA/NA/NA	114/NA/NA/NA	168/172/NA/NA	164/166/NA/NA	184/NA/NA/NA	167/169/NA/NA	214/218/243/NA	3*x*
1133	159/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	158/164/166/170	184/NA/NA/NA	157/NA/NA/NA	214/218/222/NA	4*x*
1134	149/NA/NA/NA	114/NA/NA/NA	168/172/NA/NA	164/166/NA/NA	184/NA/NA/NA	167/169/NA/NA	214/218/243/NA	3*x*
1135	157/NA/NA/NA	114/NA/NA/NA	168/172/174/NA	158/160/NA/NA	184/NA/NA/NA	153/167/169/NA	214/218/226/243	4*x*
1136	0/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	164/170/NA/NA	184/NA/NA/NA	153/157/169/NA	218/220/NA/NA	3*x*
1137	0/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	170/172/NA/NA	184/NA/NA/NA	157/167/NA/NA	216/220/NA/NA	2*x*
1138	0/NA/NA/NA	118/NA/NA/NA	168/174/NA/NA	164/170/NA/NA	184/NA/NA/NA	165/NA/NA/NA	218/220/NA/NA	2*x*
1139	0/NA/NA/NA	108/NA/NA/NA	180/NA/NA/NA	164/168/NA/NA	184/NA/NA/NA	161/165/NA/NA	218/220/NA/NA	2*x*
1140	154/NA/NA/NA	118/NA/NA/NA	170/172/NA/NA	160/170/NA/NA	184/NA/NA/NA	169/171/NA/NA	220/224/NA/NA	2*x*
1141	0/NA/NA/NA	114/NA/NA/NA	170/NA/NA/NA	158/168/NA/NA	179/NA/NA/NA	157/167/NA/NA	214/218/224/237	4*x*
1142	0/NA/NA/NA	114/116/NA/NA	172/NA/NA/NA	164/172/NA/NA	184/NA/NA/NA	157/NA/NA/NA	218/220/NA/NA	2*x*
1143	0/NA/NA/NA	116/120/NA/NA	168/170/174/NA	168/NA/NA/NA	184/NA/NA/NA	153/157/167/169	218/220/NA/NA	4*x*
1144	0/NA/NA/NA	114/120/NA/NA	168/NA/NA/NA	166/170/NA/NA	184/NA/NA/NA	171/NA/NA/NA	218/220/224/NA	3*x*

ID	CH01F02	CH03C02	CH04F06	CH04G04	CH05D44	CH05G07	CH05G11	ploidy
1145	165/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	162/166/170/NA	184/NA/NA/NA	157/167/171/NA	218/220/224/NA	3*x*
1146	149/159/165/NA	0/NA/NA/NA	174/NA/NA/NA	158/NA/NA/NA	184/NA/NA/NA	155/NA/NA/NA	214/224/241/NA	3*x*
1147	175/NA/NA/NA	108/116/NA/NA	168/174/180/NA	168/NA/NA/NA	184/NA/NA/NA	161/169/NA/NA	218/220/NA/NA	3*x*
1148	157/161/NA/NA	0/NA/NA/NA	172/176/NA/NA	158/162/NA/NA	184/NA/NA/NA	169/173/NA/NA	224/228/NA/NA	2*x*
1149	154/NA/NA/NA	114/NA/NA/NA	172/NA/NA/NA	156/160/NA/NA	184/NA/NA/NA	157/NA/NA/NA	224/NA/NA/NA	2*x*
1150	158/161/168/NA	0/NA/NA/NA	168/170/NA/NA	158/164/NA/NA	184/NA/NA/NA	169/171/NA/NA	214/220/224/NA	3*x*
1151	157/159/NA/NA	114/NA/NA/NA	168/NA/NA/NA	158/160/162/NA	184/NA/NA/NA	169/NA/NA/NA	214/224/241/NA	3*x*
1152	158/165/NA/NA	114/NA/NA/NA	172/NA/NA/NA	158/164/NA/NA	184/NA/NA/NA	157/171/NA/NA	214/218/220/224	4*x*
1153	149/154/159/NA	114/NA/NA/NA	168/NA/NA/NA	158/160/162/NA	184/NA/NA/NA	165/167/171/NA	214/216/226/NA	3*x*
1154	157/165/NA/NA	0/NA/NA/NA	174/178/182/NA	160/NA/NA/NA	184/NA/NA/NA	157/165/171/NA	222/224/NA/NA	3*x*
1155	157/165/NA/NA	116/NA/NA/NA	168/174/NA/NA	158/160/NA/NA	184/NA/NA/NA	169/NA/NA/NA	224/NA/NA/NA	2*x*
1156	167/NA/NA/NA	114/NA/NA/NA	168/172/NA/NA	160/NA/NA/NA	184/NA/NA/NA	157/167/169/NA	224/226/NA/NA	3*x*
1157	157/159/NA/NA	114/120/NA/NA	170/172/NA/NA	158/160/NA/NA	184/NA/NA/NA	157/NA/NA/NA	214/216/224/NA	3*x*
1158	157/NA/NA/NA	114/116/NA/NA	168/170/NA/NA	158/160/164/NA	184/NA/NA/NA	157/167/NA/NA	218/220/224/NA	3*x*
1159	157/NA/NA/NA	114/120/NA/NA	168/NA/NA/NA	158/160/164/NA	184/NA/NA/NA	167/169/NA/NA	218/220/224/NA	3*x*
1160	0/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	154/158/178/NA	184/NA/NA/NA	157/171/NA/NA	214/216/220/NA	3*x*
1161	157/NA/NA/NA	114/NA/NA/NA	166/168/170/NA	158/162/172/NA	184/NA/NA/NA	157/167/169/NA	214/224/235/NA	3*x*
1162	161/NA/NA/NA	114/NA/NA/NA	0/NA/NA/NA	160/162/NA/NA	184/NA/NA/NA	157/NA/NA/NA	214/216/224/226	4*x*
1163	157/NA/NA/NA	114/118/NA/NA	168/170/172/NA	158/162/172/NA	0/NA/NA/NA	157/171/NA/NA	214/224/235/NA	3*x*
1164	161/NA/NA/NA	114/120/NA/NA	168/176/NA/NA	154/158/178/NA	184/NA/NA/NA	157/169/NA/NA	214/216/220/NA	3*x*
1165	0/NA/NA/NA	114/NA/NA/NA	170/NA/NA/NA	159/164/NA/NA	184/NA/NA/NA	157/NA/NA/NA	214/216/218/NA	3*x*
1166	0/NA/NA/NA	108/NA/NA/NA	180/NA/NA/NA	159/NA/NA/NA	0/NA/NA/NA	165/NA/NA/NA	218/220/NA/NA	2*x*
1167	0/NA/NA/NA	114/116/NA/NA	168/NA/NA/NA	159/NA/NA/NA	0/NA/NA/NA	167/171/NA/NA	214/220/NA/NA	2*x*
1168	161/NA/NA/NA	116/NA/NA/NA	166/168/NA/NA	160/NA/NA/NA	0/NA/NA/NA	167/NA/NA/NA	212/216/226/NA	3*x*
1169	161/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	160/NA/NA/NA	0/NA/NA/NA	153/157/171/NA	212/216/226/NA	3*x*
1170	161/165/NA/NA	114/NA/NA/NA	166/168/170/NA	162/NA/NA/NA	184/NA/NA/NA	157/167/169/NA	214/216/224/NA	3*x*
1171	161/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	160/162/NA/NA	184/NA/NA/NA	153/157/169/NA	216/218/226/NA	3*x*
1172	161/NA/NA/NA	114/NA/NA/NA	168/172/NA/NA	160/162/NA/NA	184/NA/NA/NA	153/157/165/169	212/218/226/NA	4*x*
1173	149/159/165/NA	114/NA/NA/NA	168/172/NA/NA	158/162/NA/NA	184/NA/NA/NA	153/157/165/169	214/224/241/NA	4*x*
1174	161/NA/NA/NA	0/NA/NA/NA	172/NA/NA/NA	160/162/NA/NA	184/NA/NA/NA	167/NA/NA/NA	212/218/224/NA	3*x*

ID	**CH01F02**	**CH03C02**	**CH04F06**	**CH04G04**	**CH05D44**	**CH05G07**	**CH05G11**	**ploidy**
1175	149/159/165/NA	114/118/NA/NA	172/NA/NA/NA	158/162/NA/NA	184/NA/NA/NA	157/167/NA/NA	214/224/241/NA	3*x*
1176	161/NA/NA/NA	114/NA/NA/NA	172/NA/NA/NA	158/162/NA/NA	179/NA/NA/NA	167/169/NA/NA	214/224/241/NA	3*x*
1176A	154/165/NA/NA	114/NA/NA/NA	168/NA/NA/NA	158/NA/NA/NA	0/NA/NA/NA	167/169/NA/NA	216/224/NA/NA	2*x*
1177	159/165/NA/NA	114/NA/NA/NA	168/NA/NA/NA	158/NA/NA/NA	184/NA/NA/NA	165/167/171/NA	214/216/228/241	4*x*
1178	0/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	168/170/NA/NA	184/NA/NA/NA	153/157/169/NA	214/216/218/NA	3*x*
1179	159/NA/NA/NA	114/NA/NA/NA	168/172/NA/NA	158/160/162/NA	184/NA/NA/NA	153/157/169/NA	214/224/NA/NA	3*x*
1180	159/NA/NA/NA	0/NA/NA/NA	166/168/NA/NA	158/160/162/NA	184/NA/NA/NA	167/169/NA/NA	214/224/NA/NA	3*x*
1181	159/NA/NA/NA	114/116/NA/NA	168/NA/NA/NA	158/162/168/NA	184/NA/NA/NA	167/NA/NA/NA	214/216/220/NA	3*x*
1182	149/175/NA/NA	114/NA/NA/NA	168/172/NA/NA	158/168/NA/NA	184/NA/NA/NA	157/167/NA/NA	214/NA/NA/NA	2*x*
1183	157/NA/NA/NA	112/114/NA/NA	170/172/NA/NA	158/170/172/NA	184/NA/NA/NA	157/167/169/NA	214/218/224/NA	3*x*
1183A	158/161/168/NA	114/118/NA/NA	172/NA/NA/NA	158/164/NA/NA	184/NA/NA/NA	157/NA/NA/NA	214/216/220/224	4*x*
1183B	165/NA/NA/NA	118/NA/NA/NA	168/170/NA/NA	160/164/170/NA	184/NA/NA/NA	169/NA/NA/NA	218/220/224/NA	3*x*
1184	159/165/NA/NA	114/NA/NA/NA	170/172/NA/NA	158/162/NA/NA	184/NA/NA/NA	157/NA/NA/NA	214/224/228/NA	3*x*
1185	165/NA/NA/NA	118/NA/NA/NA	170/172/NA/NA	158/NA/NA/NA	184/NA/NA/NA	157/NA/NA/NA	214/216/224/NA	3*x*
1185A	154/165/NA/NA	114/NA/NA/NA	168/170/172/NA	158/160/NA/NA	184/NA/NA/NA	153/157/169/NA	216/224/NA/NA	3*x*
1186	158/165/NA/NA	114/NA/NA/NA	168/172/NA/NA	156/158/162/NA	184/NA/NA/NA	157/165/169/171	214/220/224/226	4*x*
1187	157/165/NA/NA	114/116/NA/NA	168/NA/NA/NA	156/162/NA/NA	184/NA/NA/NA	169/NA/NA/NA	214/224/NA/NA	2*x*
1187A	0/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	158/160/NA/NA	184/NA/NA/NA	157/NA/NA/NA	212/224/NA/NA	2*x*
1188	154/165/NA/NA	114/NA/NA/NA	168/172/NA/NA	156/160/NA/NA	184/NA/NA/NA	169/NA/NA/NA	214/216/224/NA	3*x*
1189	149/159/165/NA	116/NA/NA/NA	168/170/172/NA	158/162/NA/NA	184/NA/NA/NA	167/169/171/NA	214/216/224/241	4*x*
1190	149/159/165/NA	114/NA/NA/NA	168/172/NA/NA	158/162/NA/NA	184/NA/NA/NA	153/157/165/169	214/224/241/NA	4*x*
1191	149/159/165/NA	114/122/NA/NA	170/178/NA/NA	158/162/NA/NA	184/NA/NA/NA	157/167/169/NA	214/224/241/NA	3*x*
1192	149/159/165/NA	114/NA/NA/NA	0/NA/NA/NA	158/162/NA/NA	184/NA/NA/NA	171/NA/NA/NA	214/224/241/NA	3*x*
1193	157/165/NA/NA	114/NA/NA/NA	168/172/NA/NA	156/160/NA/NA	184/NA/NA/NA	157/165/169/171	216/226/228/NA	4*x*
1194	154/159/NA/NA	114/NA/NA/NA	168/170/172/NA	156/158/164/NA	184/NA/NA/NA	157/165/NA/NA	214/216/224/NA	3*x*
1195	157/165/NA/NA	114/NA/NA/NA	170/172/NA/NA	166/168/NA/NA	184/NA/NA/NA	157/NA/NA/NA	218/220/NA/NA	2*x*
1196	149/159/165/NA	114/NA/NA/NA	168/172/NA/NA	158/162/NA/NA	184/NA/NA/NA	153/159/169/NA	214/224/241/NA	3*x*
1196A	0/NA/NA/NA	116/NA/NA/NA	168/170/NA/NA	152/170/NA/NA	184/NA/NA/NA	169/171/NA/NA	220/222/NA/NA	2*x*
1197	154/NA/NA/NA	0/NA/NA/NA	168/174/NA/NA	158/168/170/NA	184/NA/NA/NA	0/NA/NA/NA	214/222/224/NA	3*x*
1198	149/159/165/NA	114/NA/NA/NA	170/NA/NA/NA	158/162/NA/NA	184/NA/NA/NA	157/167/171/NA	214/224/241/NA	3*x*

ID	CH01F02	CH03C02	CH04F06	CH04G04	CH05D44	CH05G07	CH05G11	ploidy
1198A	0/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	152/170/NA/NA	184/NA/NA/NA	157/169/NA/NA	218/220/NA/NA	3*x*
1199	0/NA/NA/NA	114/NA/NA/NA	168/170/NA/NA	166/174/NA/NA	184/NA/NA/NA	153/157/165/169	212/220/NA/NA	4*x*
1199p	155/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	156/NA/NA/NA	184/NA/NA/NA	157/NA/NA/NA	224/235/NA/NA	2*x*
1199c	0/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	170/NA/NA/NA	0/NA/NA/NA	157/NA/NA/NA	218/220/222/NA	3*x*
1200	0/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	174/NA/NA/NA	184/NA/NA/NA	153/157/171/NA	218/220/NA/NA	3*x*
1200p	155/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	0/NA/NA/NA	184/NA/NA/NA	157/171/NA/NA	216/224/235/NA	3*x*
1200c	0/NA/NA/NA	114/NA/NA/NA	168/170/NA/NA	174/NA/NA/NA	184/NA/NA/NA	153/157/165/169	218/220/NA/NA	4*x*
1201	155/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	168/NA/NA/NA	184/NA/NA/NA	157/NA/NA/NA	218/222/NA/NA	2*x*
1202	159/165/NA/NA	114/NA/NA/NA	168/170/172/NA	160/162/164/168	184/NA/NA/NA	153/157/169/NA	214/218/222/241	4*x*
1203	159/165/NA/NA	114/NA/NA/NA	168/170/172/NA	160/162/164/168	184/NA/NA/NA	153/157/169/NA	218/222/241/NA	4*x*
1204	149/159/NA/NA	114/NA/NA/NA	170/172/NA/NA	158/160/162/NA	0/NA/NA/NA	157/167/NA/NA	214/216/224/NA	3*x*
1205	149/159/165/NA	114/NA/NA/NA	168/170/172/NA	158/162/NA/NA	0/NA/NA/NA	153/157/169/NA	214/224/241/NA	3*x*
1206	149/159/165/NA	114/NA/NA/NA	170/NA/NA/NA	158/162/NA/NA	184/NA/NA/NA	157/NA/NA/NA	214/224/241/NA	3*x*
1207	159/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	158/160/NA/NA	184/NA/NA/NA	157/171/NA/NA	214/224/241/NA	3*x*
1208	149/159/165/NA	114/NA/NA/NA	168/170/NA/NA	158/162/NA/NA	184/NA/NA/NA	153/157/165/169	214/224/241/NA	4*x*
1209	154/159/NA/NA	114/NA/NA/NA	170/172/NA/NA	156/158/164/NA	184/NA/NA/NA	157/NA/NA/NA	214/216/224/NA	3*x*
1210	165/NA/NA/NA	116/NA/NA/NA	170/174/NA/NA	162/NA/NA/NA	184/NA/NA/NA	169/NA/NA/NA	214/216/224/228	4*x*
1211	0/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	164/166/NA/NA	184/NA/NA/NA	153/157/169/NA	216/218/NA/NA	3*x*
1212	157/170/NA/NA	114/NA/NA/NA	170/172/NA/NA	158/160/NA/NA	184/NA/NA/NA	157/171/NA/NA	216/224/NA/NA	2*x*
1213	0/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	158/170/NA/NA	184/NA/NA/NA	157/NA/NA/NA	214/216/218/224	4*x*
1214	154/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	164/170/NA/NA	184/NA/NA/NA	153/157/169/NA	214/218/220/NA	3*x*
1215	157/159/NA/NA	114/NA/NA/NA	170/172/NA/NA	158/160/168/NA	184/NA/NA/NA	157/NA/NA/NA	216/224/228/241	4*x*
1216	154/157/NA/NA	0/NA/NA/NA	168/176/NA/NA	158/160/NA/NA	184/NA/NA/NA	153/167/169/NA	214/226/228/NA	3*x*
1217	154/157/NA/NA	114/NA/NA/NA	168/170/172/NA	160/162/NA/NA	0/NA/NA/NA	153/157/169/NA	224/226/NA/NA	3*x*
1218	161/165/NA/NA	114/NA/NA/NA	172/NA/NA/NA	160/166/168/NA	184/NA/NA/NA	169/NA/NA/NA	214/220/224/NA	3*x*
1219	0/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	164/168/NA/NA	184/NA/NA/NA	153/157/169/NA	218/220/NA/NA	3*x*
1220	159/NA/NA/NA	116/NA/NA/NA	166/NA/NA/NA	160/162/168/NA	0/NA/NA/NA	167/171/NA/NA	218/224/241/NA	3*x*
1221	157/165/NA/NA	0/NA/NA/NA	170/NA/NA/NA	158/162/NA/NA	184/NA/NA/NA	157/NA/NA/NA	218/224/NA/NA	2*x*
1222	0/NA/NA/NA	114/NA/NA/NA	168/174/NA/NA	164/168/NA/NA	184/NA/NA/NA	167/169/NA/NA	218/220/222/NA	3*x*
1223	0/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	170/172/NA/NA	184/NA/NA/NA	157/171/NA/NA	214/218/220/224	4*x*

ID	CH01F02	CH03C02	CH04F06	CH04G04	CH05D44	CH05G07	CH05G11	ploidy
1224	0/NA/NA/NA	122/NA/NA/NA	168/NA/NA/NA	168/170/NA/NA	184/NA/NA/NA	153/161/169/171	218/222/NA/NA	4*x*
1225	0/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	158/164/NA/NA	178/184/NA/NA	153/157/169/NA	214/216/224/NA	3*x*
1226	157/NA/NA/NA	108/NA/NA/NA	180/NA/NA/NA	158/160/NA/NA	184/NA/NA/NA	157/165/NA/NA	216/224/NA/NA	2*x*
1227	157/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	156/162/NA/NA	184/NA/NA/NA	153/157/169/NA	216/224/NA/NA	3*x*
1228	157/NA/NA/NA	114/NA/NA/NA	168/172/NA/NA	158/160/NA/NA	184/NA/NA/NA	159/169/171/NA	216/224/228/NA	3*x*
1229	159/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	158/NA/NA/NA	184/NA/NA/NA	153/157/171/NA	212/214/224/241	4*x*
1230	154/NA/NA/NA	114/122/NA/NA	170/174/NA/NA	158/160/NA/NA	184/NA/NA/NA	157/167/169/173	214/224/NA/NA	4*x*
1231	0/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	160/166/NA/NA	184/NA/NA/NA	157/171/NA/NA	218/220/NA/NA	3*x*
1232	159/NA/NA/NA	114/NA/NA/NA	168/170/NA/NA	158/160/162/NA	0/NA/NA/NA	157/167/NA/NA	216/218/224/226	4*x*
1233	0/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	170/174/NA/NA	184/NA/NA/NA	153/157/167/169	218/220/NA/NA	4*x*
1234	159/NA/NA/NA	0/NA/NA/NA	170/174/NA/NA	158/160/162/NA	178/184/NA/NA	167/169/NA/NA	214/218/222/224	4*x*
1235	159/NA/NA/NA	114/NA/NA/NA	168/172/NA/NA	158/160/162/NA	184/NA/NA/NA	153/157/165/169	218/224/226/NA	4*x*
1236	0/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	168/170/NA/NA	184/NA/NA/NA	157/167/171/173	216/218/220/NA	4*x*
1237	159/NA/NA/NA	114/122/NA/NA	172/NA/NA/NA	162/NA/NA/NA	184/NA/NA/NA	169/171/NA/NA	224/228/NA/NA	2*x*
1238	157/NA/NA/NA	114/122/NA/NA	170/174/NA/NA	162/168/NA/NA	178/184/NA/NA	157/167/169/173	218/224/NA/NA	4*x*
1238A	157/NA/NA/NA	114/116/NA/NA	166/172/NA/NA	164/170/NA/NA	184/NA/NA/NA	167/169/NA/NA	218/220/224/NA	3*x*
1239	149/159/NA/NA	114/NA/NA/NA	168/170/172/NA	158/160/162/NA	184/NA/NA/NA	153/157/169/173	214/216/224/NA	4*x*
1240	157/159/NA/NA	114/122/NA/NA	170/172/178/NA	158/160/162/NA	184/NA/NA/NA	157/167/NA/NA	216/218/224/226	4*x*
1241	157/161/NA/NA	114/NA/NA/NA	168/170/172/NA	158/162/NA/NA	184/NA/NA/NA	153/157/169/NA	214/224/NA/NA	3*x*
1242	157/159/NA/NA	0/NA/NA/NA	172/NA/NA/NA	158/NA/NA/NA	184/NA/NA/NA	167/NA/NA/NA	214/224/243/NA	3*x*
1242A	0/NA/NA/NA	116/NA/NA/NA	168/172/NA/NA	162/168/NA/NA	184/NA/NA/NA	169/NA/NA/NA	216/218/220/NA	3*x*
1243	0/NA/NA/NA	114/118/NA/NA	170/172/NA/NA	152/164/NA/NA	184/NA/NA/NA	157/NA/NA/NA	218/220/224/NA	3*x*
1244	157/NA/NA/NA	114/NA/NA/NA	168/NA/NA/NA	162/164/166/NA	184/NA/NA/NA	169/NA/NA/NA	216/222/NA/NA	3*x*
1245	157/NA/NA/NA	114/NA/NA/NA	168/170/172/NA	162/164/166/NA	184/NA/NA/NA	153/157/171/NA	216/222/NA/NA	3*x*
1246	154/165/NA/NA	114/NA/NA/NA	170/172/NA/NA	158/160/NA/NA	184/NA/NA/NA	157/NA/NA/NA	224/NA/NA/NA	2*x*
1247	155/171/NA/NA	0/NA/NA/NA	166/170/NA/NA	166/170/NA/NA	178/184/NA/NA	167/NA/NA/NA	218/220/NA/NA	2*x*
1248	157/NA/NA/NA	114/NA/NA/NA	170/172/NA/NA	156/158/NA/NA	184/NA/NA/NA	157/NA/NA/NA	224/NA/NA/NA	2*x*
1249	181/NA/NA/NA	0/NA/NA/NA	172/176/NA/NA	170/172/NA/NA	184/NA/NA/NA	167/171/NA/NA	216/218/NA/NA	2*x*
1249A	0/NA/NA/NA	0/NA/NA/NA	168/176/NA/NA	154/166/NA/NA	184/NA/NA/NA	167/169/NA/NA	216/218/NA/NA	2*x*
1250	157/159/NA/NA	114/118/NA/NA	168/170/NA/NA	158/160/162/NA	184/NA/NA/NA	153/157/165/167	214/224/241/NA	4*x*

ID	CH01F02	CH03C02	CH04F06	CH04G04	CH05D44	CH05G07	CH05G11	ploidy
1250A	154/157/NA/NA	114/NA/NA/NA	170/NA/NA/NA	158/160/NA/NA	184/NA/NA/NA	157/167/NA/NA	224/226/NA/NA	2*x*
1251	157/NA/NA/NA	112/114/118/NA	168/170/NA/NA	145/164/170/NA	184/NA/NA/NA	157/167/169/NA	214/218/228/NA	3*x*
1252	157/NA/NA/NA	114/116/NA/NA	168/170/NA/NA	156/162/170/NA	184/NA/NA/NA	157/167/NA/NA	216/220/222/NA	3*x*
1253	149/157/159/NA	114/NA/NA/NA	168/172/NA/NA	158/162/NA/NA	184/NA/NA/NA	153/157/165/NA	214/235/241/NA	3*x*
1254	157/NA/NA/NA	114/116/NA/NA	168/170/NA/NA	156/162/170/NA	184/NA/NA/NA	157/167/NA/NA	212/214/216/228	4*x*
1255	157/NA/NA/NA	116/120/NA/NA	168/170/174/NA	158/160/NA/NA	184/NA/NA/NA	153/157/167/169	214/218/226/243	4*x*
1256	165/NA/NA/NA	114/120/NA/NA	170/172/NA/NA	158/162/NA/NA	184/NA/NA/NA	157/NA/NA/NA	216/224/NA/NA	2*x*

9.8 | Table S8 Assignment of individuals to morphological annotations at Region Lv. 1 and 2

Table S8 Assignment of individuals to morphological annotations at Region Lv. 1 and 2. Per individual the LOD score and the common logarithm of likelihood for each group is presented. The LOD score is the difference between the largest and the second largest common logarithms of the likelihoods for this individual in all regions.

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	*monogyna*	*subsphaerica*	*rhipidophylla*	*lindmanii*	*macrocarpa*	*laevigata*	*media*	Mispel	EUR	NAm	Annotated Region Lv. 2	Assigned Region Lv. 2	LOD	In	**Out**
1000A	monogyna	subsphaerica	0.260	-6.168	-5.908	-6.347	-10.914	-8.607	-10.052	-9.773	-9.266	-10.556	-12.214	In	In	1.943	-7.092	-9.036
1001	monogyna	monogyna	1.297	-6.799	-8.096	-10.457	-10.821	-10.867	-11.718	-11.882	-8.215	-13.918	-11.688	In	In	1.246	-7.893	-9.139
1002	monogyna	subsphaerica	0.038	-5.235	-5.197	-7.506	-10.277	-8.061	-8.597	-9.087	-7.283	-11.611	-9.348	In	In	1.881	-6.138	-8.019
1003	subsphaerica	rhipidophylla	0.143	-13.746	-9.615	-9.472	-15.333	-12.265	-12.341	-15.471	-16.088	-16.758	-16.936	In	In	4.254	-10.349	-14.603
1004A	subsphaerica	monogyna	0.526	-4.047	-4.574	-4.579	-9.131	-6.060	-7.631	-8.150	-6.282	-11.135	-7.974	In	In	1.455	-4.997	-6.453
1004	subsphaerica	subsphaerica	1.360	-12.475	-8.843	-10.871	-13.048	-11.003	-10.203	-11.959	-14.231	-13.326	-14.712	In	In	3.960	-9.632	-13.592
1005	subsphaerica	subsphaerica	0.714	-12.442	-10.885	-11.599	-17.689	-15.777	-15.133	-14.911	-16.411	-16.100	-18.970	In	In	4.126	-12.359	-16.484
1006	monogyna	monogyna	0.093	-5.564	-5.657	-6.334	-10.528	-7.762	-8.610	-10.245	-7.696	-11.531	-8.424	In	In	0.748	-6.382	-7.130
1007	laevigata	lindmanii	0.011	-11.679	-10.851	-10.230	-6.523	-7.964	-6.534	-8.529	-12.358	-12.451	-14.602	In	In	4.125	-8.091	-12.216
1008	macrocarpa	rhipidophylla	0.477	-10.213	-7.453	-6.842	-13.060	-7.319	-11.437	-11.994	-11.091	-13.945	-12.454	In	In	3.758	-7.447	-11.205
1009	laevigata	laevigata	4.448	-13.827	-12.219	-12.490	-12.164	-10.490	-6.042	-12.458	-14.592	-15.855	-15.381	In	In	4.585	-9.227	-13.812
1010	monogyna	monogyna	1.548	-4.361	-6.103	-6.238	-8.412	-8.649	-8.716	-8.533	-5.909	-11.169	-9.162	In	In	0.849	-6.265	-7.115
1011	laevigata	laevigata	2.046	-14.072	-12.620	-12.547	-12.355	-9.746	-7.700	-15.103	-16.684	-18.096	-17.714	In	In	6.063	-10.232	-16.295
1012	laevigata	laevigata	1.280	-10.314	-8.786	-7.888	-9.133	-6.011	-4.731	-8.029	-10.005	-12.935	-10.281	In	In	3.286	-6.485	-9.771
1013	macrocarpa	macrocarpa	2.171	-16.811	-15.157	-15.525	-17.704	-12.235	-14.406	-18.397	-19.853	-21.170	-21.638	In	In	6.727	-13.441	-20.168
1014	monogyna	monogyna	1.162	-8.340	-9.502	-10.770	-12.771	-11.330	-11.969	-11.516	-11.704	-12.773	-14.169	In	In	2.529	-9.032	-11.561
1015	subsphaerica	subsphaerica	2.257	-12.033	-9.259	-13.165	-14.886	-11.516	-12.969	-13.411	-14.866	-13.657	-14.727	In	In	2.899	-10.223	-13.122
1015A	laevigata	laevigata	2.810	-11.678	-10.934	-10.925	-11.240	-8.770	-5.625	-8.434	-11.913	-15.311	-10.412	In	In	2.484	-8.331	-10.815
1016	monogyna	monogyna	0.564	-5.160	-5.724	-7.652	-10.151	-6.996	-8.470	-7.526	-7.311	-11.484	-9.222	In	In	1.850	-6.019	-7.868
1017	monogyna	monogyna	2.393	-8.032	-10.426	-11.496	-14.652	-11.345	-11.939	-12.008	-12.205	-14.927	-13.534	In	In	2.347	-9.525	-11.872
1018	macrocarpa	rhipidophylla	1.317	-11.632	-8.463	-6.685	-11.180	-8.002	-10.116	-11.401	-12.057	-13.374	-13.516	In	In	4.191	-7.754	-11.945
1019	laevigata	laevigata	0.926	-11.704	-10.574	-9.592	-8.222	-7.627	-6.701	-9.648	-12.064	-12.906	-13.733	In	In	3.913	-8.123	-12.035
1020	monogyna	monogyna	0.394	-8.775	-11.539	-9.169	-13.033	-10.174	-11.411	-9.826	-11.065	-14.595	-12.427	In	In	2.630	-9.104	-11.734
1021	laevigata	laevigata	1.672	-9.954	-8.036	-8.375	-8.121	-5.845	-4.173	-8.208	-9.468	-12.381	-10.878	In	In	3.728	-6.275	-10.003
1022	laevigata	laevigata	1.107	-11.155	-9.449	-10.023	-7.050	-7.853	-5.943	-9.034	-12.233	-13.675	-12.954	In	In	3.893	-7.891	-11.784
1023	macrocarpa	macrocarpa	0.595	-16.704	-14.730	-16.343	-19.459	-14.135	-15.128	-19.96	-20.288	-20.518	-18.902	In	In	4.909	-13.836	-18.745
1024	macrocarpa	macrocarpa	0.767	-12.528	-10.769	-12.723	-15.828	-10.002	-11.735	-16.844	-17.926	-19.135	-19.513	In	In	8.062	-10.11	-18.173
1025	macrocarpa	macrocarpa	1.555	-14.405	-12.438	-13.376	-16.308	-10.883	-15.366	-14.704	-15.150	-17.413	-16.032	In	In	3.784	-11.109	-14.893
1026	monogyna	monogyna	3.412	-5.258	-8.741	-8.670	-11.579	-10.591	-11.868	-11.739	-11.041	-10.975	-12.815	In	In	3.011	-7.700	-10.711

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	*monogyna*	*subsphaerica*	*rhipidophylla*	*lindmanii*	*macrocarpa*	*laevigata*	*media*	Mispel	EUR	NAm	Annotated Region Lv. 2	Assigned Region Lv. 2	LOD	In	**Out**
1027	monogyna	rhipidophylla	0.708	-10.399	-12.322	-9.691	-16.261	-13.684	-13.366	-15.935	-16.598	-16.032	-16.119	In	In	3.657	-11.013	-14.670
1027A	laevigata	laevigata	1.395	-10.172	-7.720	-8.760	-7.193	-5.971	-4.576	-8.485	-9.681	-13.119	-10.717	In	In	3.870	-6.334	-10.204
1027B	macrocarpa	macrocarpa	1.361	-9.878	-8.377	-9.979	-8.970	-7.016	-9.448	-9.279	-11.458	-14.784	-12.269	In	In	3.828	-7.610	-11.438
1028	monogyna	monogyna	3.868	-7.068	-10.936	-11.736	-16.526	-12.702	-13.820	-13.321	-11.494	-13.043	-15.443	In	In	1.881	-9.889	-11.770
1029	monogyna	monogyna	3.799	-9.043	-12.842	-14.392	-16.186	-13.477	-16.759	-15.311	-15.171	-18.580	-15.852	In	In	2.415	-11.519	-13.934
1030	macrocarpa	macrocarpa	1.820	-11.148	-10.203	-10.900	-11.726	-8.383	-11.144	-12.827	-13.645	-11.049	-14.025	In	In	3.567	-9.021	-12.588
1031	monogyna	monogyna	0.141	-5.866	-6.006	-6.319	-10.483	-7.439	-8.861	-9.417	-7.960	-12.045	-9.877	In	In	2.102	-6.276	-8.378
1032	macrocarpa	monogyna	0.590	-8.415	-9.206	-9.005	-10.670	-9.652	-11.653	-12.404	-12.372	-11.345	-15.355	In	In	3.023	-8.660	-11.683
1033	macrocarpa	macrocarpa	1.463	-10.677	-9.586	-10.317	-10.040	-8.122	-10.519	-12.341	-12.390	-12.057	-11.201	In	In	2.818	-8.561	-11.379
1034	macrocarpa	macrocarpa	0.120	-12.444	-9.595	-8.628	-14.217	-8.507	-11.245	-14.628	-12.845	-15.492	-14.218	In	In	4.028	-8.964	-12.992
1035	subsphaerica	subsphaerica	0.160	-12.621	-9.594	-12.392	-15.038	-9.753	-12.216	-13.611	-13.513	-17.056	-14.815	In	In	3.886	-9.877	-13.763
1035A	laevigata	laevigata	2.195	-11.568	-8.957	-10.809	-9.960	-8.947	-6.015	-8.209	-11.523	-14.760	-11.373	In	In	2.135	-8.256	-10.391
1036	monogyna	subsphaerica	0.718	-10.036	-7.496	-10.044	-12.452	-8.215	-11.035	-13.114	-11.215	-15.809	-13.378	In	In	3.817	-8.387	-12.203
1037	monogyna	monogyna	1.778	-9.439	-11.217	-11.707	-14.263	-13.665	-14.884	-12.935	-16.557	-13.838	-17.411	In	In	2.824	-10.769	-13.593
1038	macrocarpa	subsphaerica	0.220	-10.959	-8.400	-9.626	-12.862	-8.620	-9.568	-10.809	-12.111	-14.701	-12.958	In	In	3.583	-8.158	-11.740
1038A	macrocarpa	laevigata	0.192	-9.748	-9.869	-8.591	-7.137	-6.438	-6.247	-8.783	-11.672	-11.266	-13.609	In	In	4.596	-7.073	-11.668
1038B	subsphaerica	subsphaerica	0.477	-9.630	-6.531	-8.147	-10.133	-7.008	-7.895	-10.199	-10.833	-11.966	-9.946	In	In	3.516	-6.653	-10.169
1039	macrocarpa	macrocarpa	0.345	-10.061	-7.966	-8.312	-12.493	-7.622	-9.654	-10.715	-10.771	-15.145	-11.082	In	In	2.619	-7.414	-10.034
1040	macrocarpa	macrocarpa	1.992	-13.773	-11.070	-12.247	-15.708	-9.078	-14.397	-14.976	-13.853	-17.362	-14.750	In	In	4.029	-10.099	-14.128
1041	laevigata	laevigata	0.621	-9.046	-6.979	-7.270	-5.127	-5.842	-4.506	-5.275	-9.964	-9.009	-10.008	In	In	3.342	-5.628	-8.970
1042	macrocarpa	macrocarpa	2.447	-15.466	-14.642	-14.129	-16.954	-11.682	-18.507	-18.643	-19.811	-17.834	-19.262	In	In	6.100	-12.523	-18.623
1043	laevigata	laevigata	1.415	-11.419	-11.277	-9.753	-9.895	-7.371	-5.956	-9.074	-11.070	-14.903	-12.729	In	In	3.555	-7.750	-11.305
1044	monogyna	monogyna	3.914	-9.070	-13.287	-14.160	-16.309	-14.572	-14.901	-12.985	-14.769	-15.390	-13.453	In	In	1.959	-10.961	-12.920
1045	monogyna	monogyna	5.973	-9.146	-15.987	-15.119	-15.709	-15.351	-16.592	-17.866	-16.357	-18.050	-17.909	In	In	4.355	-12.266	-16.621
1046	monogyna	monogyna	0.814	-7.659	-9.518	-10.297	-13.657	-10.357	-12.692	-11.921	-13.127	-8.473	-11.920	In	In	0.551	-8.889	-9.441
1047	monogyna	monogyna	2.386	-6.634	-9.020	-9.634	-13.495	-10.945	-11.815	-11.261	-10.917	-14.829	-12.566	In	In	2.317	-8.037	-10.354
1048	monogyna	monogyna	0.592	-3.977	-4.649	-4.569	-9.172	-6.349	-7.492	-7.982	-6.179	-10.506	-8.243	In	In	1.314	-5.047	-6.361
1049	monogyna	monogyna	0.970	-4.488	-5.459	-6.021	-9.968	-8.417	-8.816	-8.312	-5.993	-9.776	-9.450	In	In	0.601	-6.075	-6.676
1050	monogyna	monogyna	4.269	-8.288	-12.557	-13.295	-14.606	-13.961	-16.791	-15.786	-15.852	-15.172	-16.036	In	In	3.086	-11.354	-14.439
1050A	macrocarpa	macrocarpa	0.537	-14.166	-10.824	-11.294	-13.704	-10.287	-14.242	-14.070	-14.415	-16.224	-14.608	In	In	4.057	-10.189	-14.246
1050B	macrocarpa	rhipidophylla	0.320	-12.241	-12.465	-10.656	-15.522	-10.976	-11.544	-11.645	-13.686	-14.942	-15.014	In	In	1.978	-9.796	-11.775
1051	monogyna	monogyna	4.003	-8.296	-12.860	-12.300	-16.111	-14.151	-16.314	-16.149	-15.880	-15.972	-17.363	In	In	1.930	-11.132	-13.062
1052	monogyna	monogyna	1.787	-4.899	-6.687	-7.805	-9.276	-9.870	-9.956	-9.422	-9.841	-12.297	-11.682	In	In	1.985	-7.324	-9.308
1053	monogyna	monogyna	0.919	-4.872	-5.791	-7.317	-10.088	-6.666	-8.408	-8.898	-7.094	-11.421	-9.159	In	In	1.881	-5.949	-7.830
1054	monogyna	monogyna	0.558	-3.667	-4.569	-4.722	-8.920	-6.519	-7.239	-7.730	-4.225	-10.253	-7.991	In	In	0.639	-4.829	-5.469

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	*monogyna*	*subsphaerica*	*rhipidophylla*	*lindmanii*	*macrocarpa*	*laevigata*	*media*	Mispel	EUR	NAm	Annotated Region Lv. 2	Assigned Region Lv. 2	LOD	In	**Out**
1055	monogyna	Mispel	0.292	-7.836	-10.373	-8.272	-12.192	-8.819	-10.749	-11.532	-7.544	-14.485	-12.646	In	In	0.561	-8.287	-8.848
1056	monogyna	monogyna	1.507	-7.965	-9.472	-10.477	-14.661	-11.936	-14.201	-12.982	-13.106	-16.618	-14.873	In	In	1.937	-9.954	-11.891
1057	monogyna	monogyna	0.804	-5.727	-7.635	-6.530	-8.910	-8.198	-9.404	-9.901	-9.277	-9.086	-13.028	In	In	2.334	-6.743	-9.077
1058	macrocarpa	macrocarpa	2.383	-12.926	-12.763	-10.840	-12.829	-7.703	-10.086	-12.835	-12.780	-16.191	-14.932	In	In	3.682	-9.197	-12.878
1059	monogyna	subsphaerica	0.003	-5.465	-5.462	-6.540	-10.629	-8.616	-8.855	-9.857	-9.742	-9.284	-9.795	In	In	2.101	-6.545	-8.646
1060	monogyna	monogyna	2.976	-6.777	-9.754	-11.405	-13.770	-11.500	-12.218	-11.091	-12.463	-13.166	-13.949	In	In	3.096	-8.597	-11.693
1060A	monogyna	subsphaerica	0.180	-5.271	-5.091	-5.852	-9.447	-5.894	-7.767	-8.257	-6.366	-9.552	-8.119	In	In	1.673	-5.311	-6.984
1060B	monogyna	monogyna	0.767	-6.499	-8.065	-7.266	-12.101	-10.587	-11.155	-10.281	-10.801	-10.851	-11.878	In	In	1.629	-8.389	-10.018
1060C	monogyna	monogyna	1.118	-9.191	-12.198	-10.309	-15.785	-12.753	-13.785	-15.830	-15.576	-14.344	-17.415	In	In	2.384	-11.032	-13.415
1060D	Mispel	Mispel	6.657	-13.484	-11.565	-14.365	-14.280	-12.436	-14.025	-14.476	-4.908	-17.070	-12.530	**Out**	**Out**	5.625	-12.345	-6.720
1061	laevigata	laevigata	2.389	-10.757	-9.267	-8.833	-12.783	-8.422	-6.033	-9.528	-13.836	-11.669	-13.679	In	In	4.899	-7.777	-12.677
1062	laevigata	laevigata	4.788	-14.746	-13.505	-12.373	-15.777	-12.573	-7.585	-13.812	-15.514	-18.198	-16.418	In	In	3.292	-11.341	-14.632
1063	laevigata	laevigata	2.201	-9.622	-8.290	-8.803	-6.934	-6.853	-4.651	-7.199	-10.931	-11.313	-12.904	In	In	3.823	-6.667	-10.49
1064	laevigata	laevigata	1.857	-10.858	-7.914	-9.148	-7.834	-7.100	-5.244	-8.425	-12.397	-10.161	-13.546	In	In	3.207	-7.130	-10.337
1065	laevigata	laevigata	2.355	-10.423	-8.880	-9.328	-8.424	-7.128	-4.773	-8.969	-10.667	-13.737	-10.600	In	In	3.032	-7.158	-10.190
1066	laevigata	laevigata	2.363	-11.215	-10.215	-11.448	-12.203	-9.028	-6.665	-10.747	-12.442	-11.058	-13.912	In	In	2.802	-8.591	-11.393
1067	laevigata	media	0.009	-9.874	-8.871	-7.711	-10.452	-6.057	-5.356	-5.347	-10.315	-14.163	-11.002	In	In	3.834	-6.625	-10.459
1068	macrocarpa	macrocarpa	2.556	-17.441	-13.605	-14.513	-13.813	-11.049	-15.799	-16.117	-15.084	-17.326	-18.395	In	In	2.013	-12.459	-14.472
1069	subsphaerica	subsphaerica	0.431	-9.308	-7.649	-8.080	-10.324	-9.325	-10.448	-10.024	-11.226	-14.110	-12.104	In	In	3.597	-7.748	-11.344
1070	macrocarpa	macrocarpa	0.435	-14.088	-11.982	-12.147	-8.665	-8.231	-11.444	-12.704	-14.301	-16.677	-15.178	In	In	4.008	-9.959	-13.968
1071	subsphaerica	monogyna	1.092	-8.240	-9.332	-9.734	-14.634	-11.450	-11.930	-14.548	-14.362	-16.041	-16.139	In	In	5.056	-9.418	-14.474
1072	subsphaerica	monogyna	0.381	-7.722	-8.103	-11.413	-15.295	-12.252	-13.941	-14.275	-13.034	-14.423	-12.953	In	In	2.233	-9.803	-12.037
1073	laevigata	laevigata	1.568	-8.687	-6.746	-6.973	-6.918	-5.244	-3.675	-7.236	-9.027	-11.871	-10.016	In	In	3.175	-5.422	-8.597
1074	macrocarpa	macrocarpa	0.611	-14.868	-14.173	-11.118	-11.217	-8.778	-11.217	-9.390	-15.415	-17.428	-17.139	In	In	5.331	-10.382	-15.713
1075	macrocarpa	macrocarpa	3.969	-18.479	-18.322	-15.347	-19.213	-11.377	-15.980	-15.692	-19.129	-18.600	-20.295	In	In	5.413	-13.281	-18.694
1076	media	laevigata	0.918	-9.667	-9.031	-7.139	-10.331	-5.995	-4.964	-5.882	-9.996	-13.319	-9.883	In	In	3.576	-6.462	-10.037
1077	laevigata	laevigata	2.815	-12.146	-11.893	-10.304	-14.014	-9.874	-7.058	-12.303	-14.787	-14.743	-16.342	In	In	4.605	-9.166	-13.77
1078	laevigata	laevigata	3.462	-14.626	-12.808	-11.320	-15.290	-11.531	-7.858	-15.278	-17.922	-18.506	-18.963	In	In	7.001	-10.821	-17.822
1079	macrocarpa	macrocarpa	0.241	-15.295	-13.852	-11.353	-14.016	-9.500	-11.460	-9.740	-16.277	-16.942	-17.303	In	In	4.252	-10.670	-14.922
1080	monogyna	monogyna	0.748	-7.501	-8.993	-8.972	-11.029	-9.824	-11.333	-10.277	-8.249	-9.468	-12.663	In	**Out**	1.067	-8.497	-7.430
1081	macrocarpa	macrocarpa	0.347	-9.597	-7.851	-9.415	-10.965	-7.504	-8.893	-9.773	-10.315	-13.722	-9.371	In	In	2.992	-7.035	-10.027
1082	rhipidophylla	rhipidophylla	1.639	-13.134	-11.313	-9.674	-16.233	-14.167	-15.002	-15.190	-15.702	-13.233	-14.206	In	In	1.565	-11.826	-13.391
1082A	rhipidophylla	monogyna	0.904	-7.289	-9.087	-8.192	-10.141	-9.837	-10.546	-11.207	-11.664	-12.863	-14.891	In	In	2.639	-8.224	-10.863
1083	EUR	EUR	3.527	-7.462	-9.826	-7.673	-11.399	-9.714	-8.607	-7.364	-9.674	-3.837	-7.746	**Out**	**Out**	2.352	-7.877	-5.525
1083A	EUR	EUR	6.443	-13.183	-13.520	-12.628	-14.617	-13.697	-12.453	-11.896	-15.466	-5.452	-13.998	**Out**	**Out**	3.591	-12.557	-8.967

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	*monogyna*	*subsphaerica*	*rhipidophylla*	*lindmanii*	*macrocarpa*	*laevigata*	*media*	Mispel	EUR	NAm	Annotated Region Lv. 2	Assigned Region Lv. 2	LOD	In	**Out**
1083B	EUR	EUR	8.309	-15.101	-14.948	-13.553	-18.850	-14.439	-17.643	-17.567	-18.426	-5.244	-17.626	**Out**	**Out**	1.231	-13.808	-12.577
1084	NAm	NAm	11.151	-22.853	-22.980	-24.653	-23.538	-22.174	-24.173	-24.576	-23.777	-27.265	-11.023	**Out**	**Out**	6.889	-22.891	-16.002
1085	NAm	NAm	15.63	-26.563	-26.179	-27.033	-27.863	-26.676	-26.654	-27.108	-26.446	-28.537	-10.548	**Out**	**Out**	11.937	-26.595	-14.658
1086	monogyna	monogyna	3.471	-5.387	-8.858	-9.086	-12.567	-10.910	-11.388	-11.826	-9.574	-12.417	-13.895	In	In	2.219	-7.722	-9.941
1086A	rhipidophylla	rhipidophylla	3.319	-16.280	-15.681	-11.902	-19.214	-15.221	-17.331	-20.280	-20.532	-21.489	-21.485	In	In	5.947	-13.808	-19.754
1087	rhipidophylla	rhipidophylla	1.666	-8.287	-8.656	-6.621	-12.047	-11.479	-12.256	-12.368	-11.418	-12.023	-11.990	In	In	1.939	-8.197	-10.135
1088	NAm	NAm	9.464	-22.552	-19.909	-19.930	-22.602	-22.609	-22.136	-22.515	-20.145	-22.505	-10.444	**Out**	**Out**	6.707	-19.56	-12.853
1089	EUR	EUR	11.093	-16.419	-16.486	-16.711	-17.395	-16.537	-16.709	-16.949	-17.726	-5.326	-18.267	**Out**	**Out**	5.678	-16.503	-10.825
1090	NAm	NAm	9.315	-21.118	-18.824	-21.413	-22.244	-21.476	-20.890	-20.704	-20.666	-23.751	-9.509	**Out**	**Out**	7.225	-19.982	-12.757
1090A	NAm	NAm	9.990	-15.236	-14.940	-15.473	-16.573	-15.268	-15.004	-15.355	-14.795	-18.051	-4.804	**Out**	**Out**	8.346	-15.161	-6.815
1090B	NAm	NAm	10.541	-16.006	-15.691	-16.203	-15.678	-16.102	-16.111	-16.559	-16.413	-17.371	-5.137	**Out**	**Out**	8.226	-15.990	-7.764
1090C	NAm	NAm	8.581	-18.206	-19.571	-18.344	-19.553	-19.093	-19.640	-19.989	-19.913	-15.789	-7.208	**Out**	**Out**	9.586	-18.697	-9.111
1091	Mispel	Mispel	6.367	-14.102	-13.321	-15.139	-13.411	-15.300	-13.034	-14.819	-4.328	-17.455	-10.695	**Out**	**Out**	6.831	-13.460	-6.628
1091A	Mispel	Mispel	6.591	-13.510	-13.733	-13.832	-14.228	-12.977	-13.184	-16.086	-6.386	-15.316	-14.921	**Out**	**Out**	5.026	-12.674	-7.649
1091B	Mispel	Mispel	5.920	-16.366	-15.554	-15.436	-16.244	-17.343	-15.479	-17.466	-4.189	-17.439	-10.109	**Out**	**Out**	8.528	-14.906	-6.378
1091C	Mispel	Mispel	5.166	-13.122	-12.054	-13.283	-15.248	-12.775	-11.764	-15.476	-4.281	-17.214	-9.447	**Out**	**Out**	5.904	-11.879	-5.975
1091D	Mispel	Mispel	7.224	-14.297	-13.492	-15.033	-13.493	-15.412	-13.573	-15.148	-5.061	-16.382	-12.285	**Out**	**Out**	6.515	-13.658	-7.144
1091E	Mispel	Mispel	4.856	-12.163	-11.930	-12.341	-13.520	-12.397	-11.856	-12.151	-5.971	-10.827	-11.452	**Out**	**Out**	5.473	-12.135	-6.662
1092	Mispel	Mispel	4.337	-12.387	-11.770	-13.067	-11.895	-13.297	-11.753	-13.138	-4.308	-14.197	-8.645	**Out**	**Out**	6.148	-11.679	-5.531
1093	Mispel	Mispel	6.671	-13.447	-16.874	-18.671	-18.959	-18.359	-18.526	-18.060	-6.776	-18.230	-20.568	**Out**	**Out**	5.732	-15.554	-9.822
1093s	monogyna	monogyna	5.711	-11.267	-17.430	-17.701	-21.431	-18.365	-18.728	-21.345	-16.977	-20.530	-22.936	In	In	2.998	-15.199	-18.197
1093u	monogyna	monogyna	1.559	-6.788	-8.347	-10.521	-12.159	-10.338	-11.758	-10.474	-10.820	-13.636	-12.486	In	In	2.440	-8.662	-11.102
1094	monogyna	subsphaerica	0.752	-9.362	-8.523	-9.543	-13.922	-9.275	-11.928	-14.055	-13.489	-15.472	-15.547	In	In	4.871	-8.838	-13.709
1095	laevigata	laevigata	1.299	-9.070s	-7.411	-6.835	-7.367	-5.631	-4.332	-7.368	-9.932	-10.660	-7.850	In	In	2.742	-5.730	-8.472
1096	monogyna	monogyna	0.786	-5.086	-5.872	-6.602	-10.782	-9.092	-9.051	-9.360	-8.090	-11.969	-9.002	In	In	0.571	-6.733	-7.303
1097	monogyna	monogyna	3.135	-6.113	-9.248	-11.017	-14.874	-10.863	-11.356	-12.728	-11.383	-15.792	-12.106	In	In	2.121	-8.326	-10.447
1098	monogyna	monogyna	4.437	-6.850	-11.842	-11.287	-13.729	-14.491	-14.354	-13.060	-11.811	-14.936	-15.695	In	In	2.266	-10.353	-12.619
1099	monogyna	monogyna	2.775	-9.675	-12.450	-12.839	-18.578	-16.496	-16.044	-17.332	-16.396	-18.481	-16.828	In	In	4.139	-11.972	-16.111
1100	monogyna	monogyna	2.588	-9.857	-12.446	-15.453	-17.358	-15.683	-16.412	-14.449	-15.999	-19.375	-17.135	In	In	3.953	-12.208	-16.161
1100A	monogyna	monogyna	1.605	-9.046	-11.459	-10.651	-16.225	-13.140	-13.504	-14.708	-12.251	-16.133	-16.212	In	In	2.338	-10.835	-13.173
1101	monogyna	monogyna	2.074	-10.895	-13.892	-12.969	-18.684	-14.954	-18.789	-20.582	-18.774	-19.561	-18.422	In	In	5.086	-12.616	-17.702
1102	monogyna	monogyna	4.414	-10.111	-14.876	-14.524	-17.985	-15.358	-17.034	-19.189	-16.408	-16.810	-19.709	In	In	2.598	-12.903	-15.500
1103	monogyna	monogyna	3.479	-4.648	-8.128	-8.351	-10.896	-10.249	-11.121	-11.349	-8.558	-12.251	-10.838	In	In	2.038	-7.108	-9.146
1104	monogyna	monogyna	3.407	-6.803	-10.210	-10.662	-12.941	-12.472	-13.138	-12.835	-12.384	-13.915	-14.814	In	In	2.490	-9.286	-11.776
1104A	macrocarpa	macrocarpa	0.442	-13.438	-11.409	-11.454	-8.427	-7.985	-10.429	-13.387	-12.901	-15.662	-12.735	In	In	3.110	-9.402	-12.511

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	*monogyna*	*subsphaerica*	*rhipidophylla*	*lindmanii*	*macrocarpa*	*laevigata*	*media*	Mispel	EUR	NAm	Annotated Region Lv. 2	Assigned Region Lv. 2	LOD	In	**Out**
1105	monogyna	monogyna	1.356	-9.262	-10.618	-12.348	-17.123	-13.521	-15.671	-16.051	-15.078	-11.809	-15.485	In	In	1.609	-10.854	-12.462
1106	macrocarpa	subsphaerica	0.050	-11.290	-8.614	-8.664	-12.462	-9.644	-11.574	-11.493	-12.900	-15.293	-14.579	In	In	3.86	-8.905	-12.765
1107	rhipidophylla	rhipidophylla	1.123	-10.073	-12.049	-8.950	-15.926	-14.078	-14.394	-15.861	-11.529	-15.833	-14.194	In	In	1.392	-11.077	-12.470
1107A	subsphaerica	subsphaerica	0.749	-13.521	-12.300	-13.049	-19.595	-14.474	-18.594	-20.815	-16.234	-21.259	-21.259	In	In	2.568	-13.495	-16.063
1108	monogyna	monogyna	2.483	-8.530	-11.937	-11.013	-13.242	-11.603	-11.718	-13.318	-13.256	-14.459	-15.958	In	In	4.192	-9.306	-13.497
1109	laevigata	laevigata	0.512	-12.564	-11.177	-10.385	-7.229	-8.161	-6.717	-10.935	-13.707	-12.485	-14.519	In	In	4.059	-8.538	-12.597
1110	laevigata	laevigata	2.321	-9.689	-8.825	-10.227	-10.100	-8.789	-6.468	-10.002	-11.746	-12.661	-11.013	In	In	2.790	-8.095	-10.885
1111	laevigata	laevigata	2.959	-12.834	-11.682	-10.092	-14.184	-9.711	-6.753	-11.114	-12.951	-15.965	-12.179	In	In	2.597	-9.403	-12.000
1112	laevigata	laevigata	1.094	-11.437	-9.210	-10.128	-13.379	-9.826	-8.116	-11.153	-12.960	-13.286	-15.700	In	In	3.820	-8.851	-12.671
1113	laevigata	laevigata	0.856	-8.377	-6.736	-6.299	-6.251	-5.238	-3.970	-4.826	-8.177	-10.810	-9.440	In	In	2.857	-5.472	-8.328
1114	rhipidophylla	rhipidophylla	2.776	-11.827	-9.872	-7.096	-12.340	-10.155	-11.566	-10.310	-13.939	-14.343	-15.528	In	In	4.247	-8.924	-13.170
1115	rhipidophylla	rhipidophylla	4.802	-17.038	-16.862	-12.060	-23.033	-17.299	-20.062	-20.533	-23.020	-22.94	-23.019	In	In	7.533	-14.782	-22.315
1116	rhipidophylla	rhipidophylla	2.019	-12.268	-10.177	-8.158	-15.281	-11.636	-11.957	-12.961	-15.179	-15.268	-14.130	In	In	4.376	-9.669	-14.045
1117	laevigata	laevigata	0.242	-14.386	-10.962	-13.228	-13.007	-9.843	-9.601	-9.876	-16.036	-14.447	-18.285	In	In	5.315	-10.241	-15.555
1118	monogyna	monogyna	1.059	-5.015	-6.492	-6.074	-10.206	-8.215	-9.217	-10.245	-7.023	-8.248	-9.925	In	In	0.646	-6.424	-7.070
1119	monogyna	monogyna	1.352	-5.338	-7.210	-6.690	-9.359	-9.764	-9.984	-9.268	-9.270	-11.877	-11.325	In	In	1.518	-7.344	-8.861
1120	monogyna	monogyna	0.978	-7.314	-8.292	-9.977	-12.839	-10.641	-12.047	-13.591	-11.381	-13.105	-11.804	In	In	1.279	-9.041	-10.32
1121	laevigata	laevigata	2.235	-11.293	-9.261	-10.170	-9.741	-8.478	-5.725	-8.258	-7.960	-14.405	-10.089	In	In	1.290	-7.763	-9.053
1122	monogyna	monogyna	2.013	-6.470	-10.085	-9.898	-12.485	-12.404	-12.884	-12.806	-8.483	-12.200	-12.472	In	In	0.161	-8.921	-9.082
1123	laevigata	laevigata	2.241	-17.308	-15.330	-14.908	-18.030	-14.855	-12.613	-18.465	-19.893	-21.287	-19.736	In	In	5.411	-13.424	-18.835
1124	monogyna	monogyna	0.633	-5.115	-5.749	-7.273	-8.440	-7.575	-8.630	-9.005	-8.305	-9.905	-7.974	In	In	1.550	-6.072	-7.622
1125	macrocarpa	macrocarpa	0.261	-9.772	-7.070	-7.621	-10.831	-6.808	-9.293	-9.661	-9.532	-14.127	-10.966	In	In	2.137	-6.772	-8.909
1126	monogyna	monogyna	0.467	-6.230	-6.697	-7.354	-12.613	-8.340	-9.822	-10.059	-8.667	-13.424	-11.585	In	In	2.331	-6.953	-9.284
1127	monogyna	monogyna	1.239	-5.132	-6.529	-6.371	-8.939	-8.388	-9.261	-8.841	-7.905	-9.900	-8.205	In	In	0.896	-6.596	-7.492
1128	rhipidophylla	rhipidophylla	0.304	-12.417	-8.475	-8.170	-14.443	-10.573	-12.483	-10.896	-13.667	-16.814	-15.473	In	In	4.619	-9.367	-13.986
1129	rhipidophylla	rhipidophylla	2.972	-12.952	-11.153	-8.181	-14.497	-12.202	-15.227	-14.857	-14.578	-13.740	-15.691	In	In	2.348	-11.006	-13.354
1130	rhipidophylla	rhipidophylla	1.259	-9.664	-10.238	-7.016	-11.552	-8.275	-10.227	-9.351	-11.701	-11.428	-12.164	In	In	2.290	-7.587	-9.877
1131	rhipidophylla	rhipidophylla	4.213	-14.142	-14.026	-9.109	-16.346	-13.321	-16.131	-15.760	-16.502	-17.896	-17.971	In	In	5.052	-11.261	-16.313
1132	rhipidophylla	rhipidophylla	2.879	-11.069	-9.047	-6.168	-11.048	-10.115	-12.839	-12.673	-13.429	-9.462	-14.098	In	In	2.060	-8.953	-11.013
1133	rhipidophylla	rhipidophylla	0.445	-11.188	-8.131	-7.687	-13.158	-9.471	-12.877	-13.734	-12.691	-16.418	-14.085	In	In	4.034	-9.026	-13.060
1134	rhipidophylla	rhipidophylla	2.879	-11.069	-9.047	-6.168	-11.048	-10.115	-12.839	-12.673	-13.429	-9.462	-14.098	In	In	2.060	-8.953	-11.013
1135	rhipidophylla	rhipidophylla	1.318	-13.220	-12.350	-8.929	-11.172	-10.268	-10.247	-11.571	-14.322	-15.895	-14.524	In	In	3.739	-9.943	-13.683
1136	monogyna	monogyna	1.471	-4.477	-5.948	-5.994	-10.105	-8.518	-8.751	-8.565	-7.710	-11.613	-8.947	In	In	1.329	-6.317	-7.645
1137	monogyna	monogyna	0.579	-5.604	-6.183	-8.161	-10.474	-7.429	-8.938	-8.895	-8.029	-11.943	-9.825	In	In	2.057	-6.465	-8.522
1138	monogyna	monogyna	0.814	-6.529	-9.177	-7.343	-10.142	-9.332	-11.333	-12.867	-9.504	-12.704	-12.986	In	In	1.558	-8.057	-9.615

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	*monogyna*	*subsphaerica*	*rhipidophylla*	*lindmanii*	*macrocarpa*	*laevigata*	*media*	Mispel	EUR	NAm	Annotated Region Lv. 2	Assigned Region Lv. 2	LOD	In	**Out**
1139	monogyna	monogyna	0.759	-9.047	-11.194	-9.805	-17.424	-13.180	-15.547	-17.380	-16.358	-17.309	-17.384	In	In	5.439	-10.661	-16.101
1140	macrocarpa	rhipidophylla	0.103	-9.653	-10.576	-8.911	-14.711	-9.014	-10.517	-12.024	-11.743	-13.110	-15.074	In	In	2.999	-8.183	-11.182
1141	macrocarpa	macrocarpa	3.565	-13.371	-12.654	-14.419	-13.879	-9.089	-13.782	-14.913	-14.737	-18.521	-13.582	In	In	3.343	-10.816	-14.159
1142	monogyna	monogyna	0.703	-6.041	-6.744	-8.361	-10.944	-8.067	-9.636	-9.794	-8.663	-12.417	-12.426	In	In	2.566	-7.081	-9.647
1143	monogyna	monogyna	2.832	-8.114	-10.945	-12.211	-16.121	-13.749	-13.198	-14.385	-12.974	-16.162	-14.316	In	In	0.797	-10.992	-11.790
1144	monogyna	monogyna	0.994	-7.656	-8.649	-8.752	-13.545	-9.982	-11.458	-14.062	-11.447	-11.047	-11.930	In	In	1.068	-8.574	-9.642
1145	rhipidophylla	subsphaerica	0.581	-9.735	-7.883	-8.464	-13.590	-9.181	-10.683	-10.606	-11.959	-15.176	-13.836	In	In	3.995	-7.991	-11.985
1146	lindmanii	lindmanii	4.694	-16.082	-16.102	-14.923	-6.989	-11.683	-15.309	-16.976	-16.200	-17.930	-18.057	In	In	3.368	-12.316	-15.684
1147	monogyna	monogyna	4.078	-10.822	-14.900	-16.830	-23.180	-20.779	-20.465	-23.115	-22.351	-23.088	-21.731	In	In	6.161	-15.147	-21.308
1148	laevigata	laevigata	3.786	-13.334	-12.008	-12.39	-13.202	-10.574	-6.789	-13.641	-16.198	-15.386	-16.220	In	In	6.530	-9.483	-16.013
1149	laevigata	laevigata	1.708	-9.870	-8.712	-8.120	-8.979	-6.701	-4.993	-8.430	-10.471	-13.452	-9.910	In	In	2.582	-6.923	-9.505
1150	subsphaerica	macrocarpa	1.107	-13.065	-10.691	-12.363	-16.651	-9.584	-13.947	-14.547	-14.326	-12.890	-14.932	In	In	3.196	-9.924	-13.120
1151	subsphaerica	lindmanii	1.160	-12.208	-9.029	-10.249	-5.716	-6.876	-8.740	-10.952	-12.637	-13.596	-10.266	In	In	3.376	-8.112	-11.489
1152	rhipidophylla	macrocarpa	1.168	-12.883	-10.506	-9.908	-13.912	-8.740	-13.445	-14.182	-14.414	-16.053	-16.176	In	In	4.931	-9.380	-14.311
1153	macrocarpa	macrocarpa	2.049	-15.031	-14.267	-12.151	-13.974	-9.517	-12.572	-11.566	-16.165	-17.656	-16.202	In	In	4.564	-11.043	-15.606
1154	macrocarpa	macrocarpa	1.385	-17.731	-16.000	-14.588	-18.672	-13.202	-14.925	-16.348	-18.460	-19.925	-18.488	In	In	4.227	-13.242	-17.470
1155	laevigata	laevigata	1.739	-11.579	-10.049	-10.255	-9.328	-8.581	-6.841	-9.498	-11.954	-13.278	-11.512	In	In	3.156	-8.408	-11.563
1156	laevigata	laevigata	1.271	-13.283	-13.310	-12.517	-12.941	-11.397	-7.418	-8.690	-14.084	-15.990	-13.760	In	In	3.023	-9.642	-12.665
1157	macrocarpa	macrocarpa	1.021	-11.847	-9.667	-9.712	-11.998	-6.788	-7.809	-10.788	-11.479	-15.096	-10.854	In	In	3.139	-7.968	-11.107
1158	macrocarpa	subsphaerica	0.406	-9.510	-7.647	-8.097	-13.968	-8.053	-9.921	-11.268	-10.891	-14.422	-13.692	In	In	4.034	-7.357	-11.392
1159	macrocarpa	rhipidophylla	0.064	-10.212	-8.895	-8.446	-12.867	-8.510	-10.502	-13.515	-12.348	-13.145	-12.812	In	In	3.548	-8.026	-11.574
1160	subsphaerica	subsphaerica	2.856	-11.233	-7.724	-11.372	-14.604	-10.580	-11.852	-12.531	-12.118	-15.161	-13.822	In	In	2.401	-9.523	-11.924
1161	macrocarpa	macrocarpa	1.102	-13.699	-10.888	-12.243	-12.477	-9.786	-11.696	-12.778	-15.126	-15.718	-16.141	In	In	2.532	-10.269	-12.801
1162	macrocarpa	media	2.556	-12.383	-10.049	-9.915	-10.357	-8.007	-7.785	-5.229	-11.996	-14.910	-12.919	In	In	4.011	-8.184	-12.195
1163	macrocarpa	macrocarpa	2.164	-13.038	-12.419	-12.807	-13.608	-9.508	-11.672	-15.472	-13.545	-16.346	-16.255	In	In	2.560	-10.306	-12.866
1164	subsphaerica	subsphaerica	3.666	-15.580	-10.685	-14.351	-18.752	-15.076	-14.872	-16.845	-17.643	-20.454	-17.221	In	In	4.492	-12.650	-17.142
1165	subsphaerica	subsphaerica	0.973	-7.635	-6.662	-9.174	-11.839	-8.550	-10.444	-9.826	-9.972	-14.077	-10.868	In	In	2.733	-7.620	-10.353
1166	subsphaerica	monogyna	0.185	-8.793	-8.978	-10.549	-14.947	-11.779	-13.946	-16.167	-14.160	-16.611	-16.611	In	In	4.752	-9.955	-14.707
1167	subsphaerica	subsphaerica	0.811	-7.927	-7.116	-9.750	-13.288	-9.836	-10.922	-10.846	-11.615	-11.052	-13.270	In	In	2.628	-8.182	-10.811
1168	media	media	5.911	-15.685	-14.134	-13.158	-15.757	-13.744	-12.950	-7.039	-18.261	-16.273	-18.688	In	In	3.634	-12.348	-15.982
1169	media	media	4.080	-13.471	-12.662	-11.768	-15.486	-11.462	-9.897	-5.817	-14.220	-17.368	-14.433	In	In	2.769	-10.354	-13.123
1170	media	media	2.508	-12.647	-9.759	-11.540	-11.340	-9.565	-8.665	-6.157	-14.800	-15.100	-15.826	In	In	3.358	-9.198	-12.556
1171	media	media	4.345	-11.648	-10.379	-9.701	-11.211	-9.335	-9.186	-4.841	-12.090	-15.176	-12.510	In	In	3.500	-8.462	-11.963
1172	media	media	5.515	-13.853	-12.571	-11.340	-11.381	-12.172	-11.571	-5.825	-14.635	-16.931	-16.316	In	In	3.976	-10.662	-14.638
1173	lindmanii	lindmanii	3.602	-13.767	-11.798	-11.798	-4.201	-7.803	-10.736	-11.869	-13.656	-15.782	-15.337	In	In	4.332	-9.546	-13.878

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	*monogyna*	*subsphaerica*	*rhipidophylla*	*lindmanii*	*macrocarpa*	*laevigata*	*media*	Mispel	EUR	NAm	Annotated Region Lv. 2	Assigned Region Lv. 2	LOD	In	**Out**
1174	media	media	3.812	-11.573	-9.564	-9.502	-9.359	-9.293	-9.628	-5.482	-13.508	-12.102	-15.016	In	In	4.009	-8.466	-12.474
1175	lindmanii	lindmanii	2.459	-13.999	-12.948	-11.190	-5.205	-7.664	-10.994	-13.525	-14.393	-16.100	-17.565	In	In	5.259	-9.583	-14.842
1176	lindmanii	lindmanii	2.092	-14.139	-10.951	-12.578	-6.700	-8.792	-11.481	-11.217	-15.979	-16.246	-16.076	In	In	5.180	-9.860	-15.040
1176A	laevigata	laevigata	0.563	-9.673	-8.050	-8.171	-8.618	-6.196	-5.633	-6.319	-10.557	-11.301	-10.845	In	In	3.045	-6.564	-9.609
1177	macrocarpa	macrocarpa	2.312	-15.396	-12.704	-12.993	-12.078	-9.767	-12.799	-15.438	-16.716	-17.918	-16.041	In	In	4.174	-11.280	-15.455
1178	monogyna	subsphaerica	0.061	-6.175	-6.115	-7.563	-10.612	-8.376	-9.258	-7.857	-9.034	-12.119	-9.454	In	In	1.339	-6.823	-8.161
1179	lindmanii	lindmanii	1.499	-10.435	-8.188	-8.525	-4.644	-6.142	-7.021	-7.972	-11.031	-13.369	-10.804	In	In	3.533	-7.005	-10.538
1180	lindmanii	lindmanii	1.422	-11.483	-8.463	-8.692	-5.166	-6.588	-7.776	-8.194	-13.415	-10.617	-13.709	In	In	3.768	-7.528	-11.296
1181	subsphaerica	subsphaerica	0.755	-11.303	-8.086	-10.416	-12.406	-8.841	-12.189	-13.21	-13.913	-13.748	-14.943	In	In	3.950	-8.953	-12.902
1182	subsphaerica	subsphaerica	0.752	-12.544	-9.523	-10.549	-10.781	-10.275	-10.892	-12.113	-13.170	-13.987	-13.285	In	In	3.662	-9.031	-12.693
1183	macrocarpa	macrocarpa	0.436	-11.708	-10.685	-10.519	-15.565	-10.083	-12.494	-13.146	-14.533	-16.148	-14.068	In	In	3.115	-9.179	-12.294
1183A	macrocarpa	macrocarpa	3.132	-15.804	-14.517	-14.147	-15.616	-11.014	-16.155	-18.182	-16.566	-18.732	-19.509	In	In	5.268	-12.026	-17.294
1183B	macrocarpa	rhipidophylla	0.775	-10.409	-10.225	-9.065	-13.053	-9.839	-11.961	-13.113	-12.426	-14.663	-12.726	In	In	3.449	-8.730	-12.180
1184	macrocarpa	macrocarpa	0.812	-11.681	-8.902	-9.053	-8.669	-6.242	-7.054	-9.427	-11.001	-14.143	-12.363	In	In	4.166	-7.347	-11.513
1185	macrocarpa	macrocarpa	1.237	-11.720	-10.459	-9.356	-10.750	-7.032	-8.269	-10.353	-12.069	-15.160	-13.900	In	In	4.004	-8.009	-12.094
1185A	media	laevigata	0.345	-11.245	-9.898	-9.828	-11.301	-7.490	-6.051	-6.396	-11.131	-14.524	-10.792	In	In	3.289	-7.796	-11.085
1186	macrocarpa	macrocarpa	2.229	-14.784	-12.698	-12.150	-15.468	-9.921	-12.525	-14.974	-15.210	-17.059	-16.444	In	In	3.678	-10.745	-14.423
1187	laevigata	laevigata	1.162	-11.885	-8.566	-10.117	-10.464	-8.527	-7.364	-11.370	-12.404	-13.642	-12.735	In	In	2.413	-8.435	-10.848
1187A	laevigata	laevigata	0.048	-7.642	-6.815	-6.476	-8.005	-5.682	-4.879	-4.927	-7.671	-10.993	-7.557	In	In	0.955	-5.674	-6.629
1188	laevigata	laevigata	1.197	-12.277	-10.126	-10.321	-12.350	-8.805	-7.608	-9.720	-12.761	-13.815	-9.587	In	In	1.535	-8.751	-10.286
1189	macrocarpa	macrocarpa	2.810	-14.297	-12.019	-13.328	-13.418	-9.209	-12.520	-12.443	-15.561	-14.869	-17.397	In	In	4.409	-10.547	-14.956
1190	macrocarpa	lindmanii	3.602	-13.767	-11.798	-11.798	-4.201	-7.803	-10.736	-11.869	-13.656	-15.782	-15.337	In	In	4.332	-9.546	-13.878
1191	macrocarpa	macrocarpa	0.819	-15.310	-13.093	-12.863	-10.039	-9.220	-12.188	-16.098	-18.045	-18.599	-19.066	In	In	6.686	-11.002	-17.688
1192	macrocarpa	lindmanii	0.818	-12.567	-10.205	-10.988	-5.985	-6.803	-10.194	-12.504	-13.027	-12.111	-13.892	In	In	3.759	-8.582	-12.342
1193	laevigata	laevigata	3.255	-15.763	-14.113	-13.086	-15.702	-12.264	-9.009	-13.001	-16.054	-17.904	-14.851	In	In	1.975	-11.672	-13.648
1194	macrocarpa	macrocarpa	1.877	-12.623	-10.161	-10.376	-14.016	-8.284	-11.192	-11.865	-12.369	-15.610	-14.237	In	In	3.059	-9.035	-12.093
1195	subsphaerica	subsphaerica	0.794	-7.796	-6.983	-7.778	-11.598	-8.308	-9.183	-11.550	-9.746	-14.073	-11.811	In	In	2.299	-7.259	-9.558
1196	rhipidophylla	lindmanii	2.750	-14.563	-13.748	-12.157	-7.748	-10.498	-11.680	-14.645	-16.113	-16.610	-16.284	In	In	5.231	-10.644	-15.875
1196A	subsphaerica	subsphaerica	0.444	-7.472	-7.028	-8.819	-15.201	-10.799	-11.347	-11.003	-10.252	-12.086	-13.468	In	In	0.347	-8.667	-9.014
1197	macrocarpa	subsphaerica	0.123	-9.527	-7.790	-7.913	-11.264	-8.186	-10.238	-10.084	-11.613	-10.979	-11.251	In	In	3.598	-7.403	-11.001
1198	macrocarpa	macrocarpa	0.769	-13.789	-11.214	-11.709	-8.139	-7.370	-10.925	-12.357	-13.991	-16.848	-14.855	In	In	4.357	-9.401	-13.758
1198A	subsphaerica	monogyna	0.796	-4.870	-5.665	-6.534	-10.700	-9.010	-8.969	-9.278	-8.008	-11.887	-8.921	In	In	0.288	-6.658	-6.946
1199	monogyna	monogyna	1.936	-9.329	-12.126	-11.265	-14.067	-13.082	-13.554	-13.184	-12.905	-13.173	-13.031	In	**Out**	2.170	-11.133	-8.963
1199p	Mispel	Mispel	6.008	-10.881	-9.571	-11.173	-11.375	-10.164	-9.575	-11.871	-3.564	-14.394	-10.079	**Out**	**Out**	4.041	-9.577	-5.536
1199c	Mispel	monogyna	0.464	-5.220	-5.975	-6.525	-10.707	-8.202	-9.169	-9.706	-5.684	-12.361	-10.114	**Out**	In	0.999	-6.599	-7.598

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	*monogyna*	*subsphaerica*	*rhipidophylla*	*lindmanii*	*macrocarpa*	*laevigata*	*media*	Mispel	EUR	NAm	Annotated Region Lv. 2	Assigned Region Lv. 2	LOD	In	**Out**
1200	monogyna	Mispel	0.150	-6.150	-8.936	-9.148	-12.899	-9.794	-10.173	-10.266	-6.000	-11.252	-12.117	In	**Out**	0.902	-8.049	-7.147
1200p	Mispel	Mispel	3.397	-8.528	-8.283	-10.193	-12.140	-8.739	-9.400	-10.132	-4.885	-12.277	-10.904	**Out**	**Out**	2.517	-8.723	-6.206
1200c	Mispel	Mispel	0.406	-6.982	-10.151	-10.613	-12.596	-11.459	-12.083	-11.713	-6.576	-12.581	-12.648	**Out**	**Out**	1.385	-9.541	-8.156
1201	subsphaerica	subsphaerica	0.257	-6.934	-6.644	-9.338	-12.642	-9.760	-10.165	-11.453	-6.901	-13.976	-10.258	In	**Out**	1.065	-8.201	-7.136
1202	subsphaerica	subsphaerica	0.186	-13.665	-9.473	-11.197	-13.003	-9.658	-13.243	-13.554	-13.48	-16.625	-13.820	In	In	3.808	-9.756	-13.563
1203	subsphaerica	subsphaerica	0.663	-13.564	-9.333	-11.285	-12.903	-9.996	-13.142	-13.453	-13.379	-16.525	-13.719	In	In	3.688	-9.663	-13.351
1204	macrocarpa	macrocarpa	2.241	-11.378	-9.116	-8.846	-8.316	-5.884	-8.413	-8.126	-11.523	-14.622	-11.655	In	In	3.455	-7.427	-10.882
1205	macrocarpa	lindmanii	1.326	-12.953	-10.740	-11.192	-6.200	-7.525	-10.214	-11.237	-12.498	-15.275	-12.919	In	In	3.557	-8.938	-12.495
1206	macrocarpa	lindmanii	0.146	-13.217	-10.572	-10.965	-6.515	-6.661	-10.404	-12.228	-12.512	-16.229	-13.408	In	In	4.131	-8.793	-12.924
1207	macrocarpa	macrocarpa	1.552	-11.164	-8.753	-9.505	-8.006	-6.454	-8.440	-10.649	-11.649	-14.357	-11.359	In	In	2.900	-7.664	-10.564
1208	macrocarpa	lindmanii	1.653	-13.769	-11.667	-12.080	-5.985	-7.638	-10.895	-12.080	-13.278	-16.563	-14.492	In	In	3.958	-9.569	-13.527
1209	macrocarpa	macrocarpa	2.074	-12.057	-9.476	-9.660	-13.770	-7.403	-10.284	-11.288	-11.801	-15.331	-13.163	In	In	3.225	-8.320	-11.545
1210	media	media	2.003	-14.969	-12.628	-13.942	-16.248	-12.480	-12.297	-10.294	-16.279	-18.405	-16.181	In	In	3.377	-12.055	-15.432
1211	monogyna	monogyna	0.646	-5.890	-6.536	-6.573	-10.756	-8.542	-9.402	-7.764	-8.570	-10.295	-9.598	In	In	1.046	-6.984	-8.030
1212	laevigata	laevigata	2.536	-11.684	-10.665	-11.166	-13.336	-9.298	-6.762	-9.587	-11.752	-15.238	-12.734	In	In	1.345	-8.791	-10.136
1213	subsphaerica	macrocarpa	0.609	-8.358	-6.865	-7.088	-10.541	-6.256	-8.925	-8.363	-8.506	-12.233	-10.175	In	In	2.647	-6.238	-8.885
1214	monogyna	rhipidophylla	0.233	-7.358	-7.894	-7.125	-13.039	-9.756	-10.261	-9.999	-11.461	-14.547	-11.882	In	In	2.955	-7.847	-10.802
1215	laevigata	macrocarpa	1.253	-13.726	-10.745	-11.876	-13.866	-8.374	-9.627	-14.003	-12.960	-16.687	-13.023	In	In	4.201	-9.282	-13.484
1216	laevigata	laevigata	1.894	-13.807	-12.560	-9.989	-13.405	-10.273	-8.095	-11.338	-15.704	-16.595	-15.608	In	In	5.251	-9.866	-15.117
1217	laevigata	laevigata	1.481	-12.140	-10.898	-10.529	-11.750	-8.267	-5.693	-7.174	-11.897	-15.062	-12.318	In	In	3.515	-8.270	-11.785
1218	macrocarpa	subsphaerica	0.017	-12.523	-9.878	-10.251	-11.305	-9.895	-11.708	-10.98	-13.822	-15.021	-13.509	In	In	3.702	-9.242	-12.944
1219	monogyna	monogyna	1.235	-4.816	-6.052	-7.255	-10.378	-8.467	-9.024	-8.838	-7.983	-11.885	-9.220	In	In	1.362	-6.589	-7.951
1220	macrocarpa	macrocarpa	0.766	-15.678	-11.803	-13.571	-15.72	-11.037	-14.997	-14.884	-17.960	-15.973	-19.088	In	In	5.349	-11.546	-16.895
1221	macrocarpa	macrocarpa	0.971	-8.677	-6.546	-7.221	-8.009	-5.176	-6.148	-7.821	-8.788	-11.079	-10.057	In	In	3.672	-5.593	-9.265
1222	monogyna	monogyna	0.621	-6.096	-6.717	-7.852	-9.925	-9.309	-10.464	-10.174	-9.805	-10.882	-11.263	In	In	1.513	-7.644	-9.157
1223	monogyna	monogyna	1.004	-6.952	-7.955	-10.063	-12.918	-9.183	-10.289	-11.124	-10.423	-13.193	-11.800	In	In	2.637	-7.753	-10.39
1224	monogyna	monogyna	2.966	-9.832	-13.122	-12.798	-17.611	-16.008	-17.297	-18.418	-18.154	-17.946	-17.827	In	In	4.481	-12.643	-17.124
1225	macrocarpa	macrocarpa	0.928	-10.101	-8.335	-10.240	-13.014	-7.407	-10.643	-10.125	-11.449	-13.938	-11.870	In	In	3.382	-7.904	-11.286
1226	macrocarpa	macrocarpa	0.345	-12.327	-10.138	-9.875	-13.847	-9.153	-9.499	-13.222	-15.322	-17.413	-16.182	In	In	5.840	-9.424	-15.264
1227	laevigata	laevigata	2.233	-10.749	-8.273	-10.363	-12.712	-8.396	-6.040	-9.712	-11.103	-14.495	-11.820	In	In	2.094	-7.962	-10.056
1228	laevigata	laevigata	3.221	-12.921	-12.141	-10.341	-12.409	-10.736	-7.120	-11.511	-14.900	-15.785	-13.995	In	In	4.984	-9.400	-14.384
1229	macrocarpa	macrocarpa	2.117	-13.140	-11.275	-11.856	-12.657	-8.859	-10.976	-13.167	-13.838	-17.020	-15.019	In	In	3.124	-9.853	-12.976
1230	laevigata	laevigata	1.114	-14.155	-15.129	-13.390	-15.033	-10.590	-9.476	-14.095	-17.914	-18.892	-17.173	In	In	6.405	-11.256	-17.661
1231	monogyna	monogyna	0.004	-6.721	-6.889	-6.725	-11.898	-8.025	-9.158	-9.890	-8.511	-12.035	-10.662	In	In	0.932	-6.751	-7.683
1232	macrocarpa	macrocarpa	1.206	-10.656	-9.416	-9.355	-9.167	-6.571	-9.561	-7.777	-11.725	-14.778	-12.164	In	In	4.146	-7.523	-11.67

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	*monogyna*	*subsphaerica*	*rhipidophylla*	*lindmanii*	*macrocarpa*	*laevigata*	*media*	Mispel	EUR	NAm	Annotated Region Lv. 2	Assigned Region Lv. 2	LOD	In	**Out**
1233	monogyna	monogyna	1.072	-5.322	-8.694	-7.914	-11.395	-10.264	-10.254	-9.718	-6.395	-13.100	-11.707	In	**Out**	0.131	-7.963	-7.831
1234	macrocarpa	macrocarpa	1.391	-13.091	-10.450	-12.462	-13.082	-9.059	-13.489	-13.407	-15.821	-16.163	-16.568	In	In	5.082	-10.096	-15.179
1235	macrocarpa	lindmanii	0.223	-11.446	-10.552	-9.812	-7.698	-7.921	-10.233	-8.379	-12.493	-14.790	-13.900	In	In	4.187	-8.353	-12.540
1236	monogyna	monogyna	2.707	-6.444	-9.152	-11.169	-13.899	-10.902	-10.860	-12.637	-11.900	-14.174	-12.780	In	In	2.668	-8.719	-11.387
1237	laevigata	laevigata	1.125	-11.235	-9.469	-10.035	-11.180	-8.528	-7.403	-10.385	-14.329	-12.475	-14.948	In	In	4.072	-8.339	-12.411
1238	monogyna	macrocarpa	0.052	-13.675	-14.166	-17.176	-21.919	-13.622	-14.849	-20.018	-20.344	-21.585	-20.726	In	In	7.647	-12.602	-20.248
1238A	subsphaerica	subsphaerica	0.254	-9.290	-8.284	-8.538	-13.087	-10.976	-10.976	-11.505	-13.869	-13.242	-16.738	In	In	3.993	-8.696	-12.689
1239	macrocarpa	macrocarpa	1.162	-13.137	-12.463	-12.540	-11.334	-8.243	-9.405	-11.189	-14.584	-16.233	-13.673	In	In	4.655	-9.372	-14.027
1240	macrocarpa	macrocarpa	1.812	-13.675	-12.476	-11.576	-13.426	-8.836	-10.648	-12.436	-16.857	-17.815	-17.599	In	In	7.172	-9.707	-16.879
1241	laevigata	laevigata	1.358	-11.226	-8.538	-9.439	-7.340	-7.181	-5.823	-8.702	-10.945	-13.642	-11.365	In	In	3.703	-7.280	-10.983
1242	macrocarpa	macrocarpa	1.250	-12.403	-9.809	-8.745	-8.585	-7.335	-9.895	-11.674	-13.406	-11.866	-13.659	In	In	3.854	-8.320	-12.173
1242A	subsphaerica	subsphaerica	0.276	-6.730	-6.454	-9.132	-11.300	-8.880	-9.525	-9.804	-9.693	-11.338	-10.777	In	In	1.866	-7.475	-9.340
1243	monogyna	monogyna	1.053	-7.075	-8.864	-8.128	-11.871	-9.224	-10.200	-12.158	-9.397	-13.488	-12.690	In	In	1.703	-7.747	-9.450
1244	macrocarpa	subsphaerica	1.839	-10.347	-7.537	-9.376	-12.516	-9.726	-11.540	-13.674	-12.740	-12.635	-11.804	In	In	3.035	-9.014	-12.048
1245	subsphaerica	subsphaerica	1.831	-10.899	-8.519	-10.350	-15.951	-10.435	-11.828	-13.659	-12.844	-14.513	-14.981	In	In	3.214	-9.646	-12.859
1246	laevigata	laevigata	1.359	-10.444	-9.003	-8.377	-8.952	-6.115	-4.755	-6.667	-9.891	-13.564	-10.127	In	In	3.464	-6.700	-10.165
1247	subsphaerica	subsphaerica	0.881	-11.944	-11.062	-13.764	-18.738	-14.627	-17.622	-16.918	-18.229	-16.870	-20.095	In	In	2.977	-13.135	-16.112
1248	laevigata	laevigata	1.877	-9.433	-7.208	-7.798	-9.391	-5.977	-4.100	-9.182	-9.208	-12.880	-8.859	In	In	2.121	-6.195	-8.316
1249	monogyna	monogyna	3.100	-7.642	-10.742	-13.018	-16.636	-12.945	-13.541	-13.905	-15.119	-14.194	-16.596	In	In	4.853	-9.898	-14.751
1249A	subsphaerica	subsphaerica	2.505	-8.813	-6.308	-9.508	-11.934	-10.443	-10.270	-10.173	-11.421	-11.705	-13.205	In	In	1.183	-8.084	-9.267
1250	macrocarpa	lindmanii	0.053	-13.855	-12.548	-11.996	-7.846	-7.899	-10.144	-12.905	-13.804	-16.913	-15.731	In	In	4.681	-9.657	-14.338
1250A	laevigata	laevigata	1.141	-11.269	-9.994	-8.193	-10.952	-6.519	-5.378	-7.857	-11.334	-14.747	-11.344	In	In	4.005	-7.190	-11.195
1251	rhipidophylla	rhipidophylla	2.466	-15.800	-12.759	-10.293	-18.773	-14.485	-15.874	-16.529	-17.752	-19.226	-18.496	In	In	3.170	-12.395	-15.565
1252	rhipidophylla	subsphaerica	2.404	-11.087	-7.824	-10.228	-15.729	-10.601	-11.683	-13.029	-12.214	-16.183	-15.453	In	In	2.772	-9.299	-12.071
1253	lindmanii	lindmanii	3.131	-14.244	-13.105	-12.818	-6.226	-9.356	-12.487	-12.638	-13.991	-16.089	-14.171	In	In	1.620	-10.93	-12.551
1254	subsphaerica	subsphaerica	1.040	-14.001	-10.300	-11.340	-17.317	-12.314	-12.321	-12.123	-14.638	-17.680	-16.811	In	In	3.344	-10.759	-14.103
1255	rhipidophylla	rhipidophylla	1.208	-15.377	-14.939	-11.504	-16.960	-12.712	-12.993	-15.468	-16.427	-18.965	-17.585	In	In	3.647	-12.350	-15.998
1256	laevigata	laevigata	0.359	-10.391	-8.049	-8.613	-10.633	-6.601	-6.242	-8.311	-9.912	-13.183	-11.330	In	In	3.090	-7.116	-10.206

9.9 | Table S9 Assignment of individuals to genetic annotations

Table S9 Assignment of individuals to genetic annotations. Per individual the LOD score and the common logarithm of likelihood for each group is presented. The LOD score is the difference between the largest and the second largest common logarithms of the likelihoods for this individual.

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	2	2.3	3	4	4.6	5	5.5	6	6.6	7	7.7	1	Mispel	EUR	NAm
1000A	2	2	0.302	-5.941	-6.451	-8.727	-12.037	-7.516	-10.199	-9.898	-7.068	-6.244	-10.656	-9.402	-7.505	-9.262	-10.489	-12.160
1001	2	2	1.807	-6.395	-8.694	-10.979	-10.824	-12.048	-9.921	-11.784	-10.404	-10.338	-11.608	-12.658	-10.210	-8.203	-13.923	-11.696
1002	2	2	0.936	-4.946	-5.881	-8.588	-7.737	-9.547	-8.756	-9.037	-7.236	-7.391	-8.458	-9.734	-7.065	-7.270	-11.596	-9.336
1003	4.6	4.6	4.197	-15.845	-14.319	-13.028	-17.356	-8.191	-15.834	-14.568	-13.669	-12.388	-13.003	-14.431	-13.911	-16.129	-16.801	-16.976
1004A	2	2	0.403	-3.738	-5.572	-5.832	-6.639	-7.514	-7.484	-7.908	-4.942	-4.717	-7.430	-8.891	-4.140	-6.278	-11.137	-7.972
1004	4.6	4.6	2.659	-13.155	-12.761	-13.512	-14.607	-7.671	-12.349	-10.333	-11.483	-10.332	-10.33	-10.935	-12.040	-14.289	-13.378	-14.763
1005	3	3	4.248	-13.857	-12.441	-8.095	-18.259	-12.343	-17.112	-15.888	-15.654	-14.818	-15.546	-15.396	-15.488	-16.370	-16.090	-18.982
1006	2.3	2.3	0.142	-5.584	-5.442	-9.802	-7.594	-6.139	-9.412	-8.775	-7.515	-5.774	-8.959	-10.687	-9.995	-7.702	-11.486	-8.418
1007	7	7	0.124	-11.733	-11.825	-11.858	-14.441	-9.374	-8.489	-7.010	-8.599	-9.223	-6.886	-9.306	-12.712	-12.364	-12.408	-14.564
1008	6	6	2.809	-10.438	-11.250	-10.894	-10.684	-12.094	-11.535	-11.790	-5.495	-9.500	-11.281	-13.006	-8.303	-11.180	-14.060	-12.545
1009	7	7	4.107	-14.546	-15.208	-14.892	-15.127	-10.395	-11.115	-10.481	-11.093	-10.959	-6.288	-11.319	-11.667	-14.673	-15.921	-15.439
1010	2	2	0.844	-4.174	-5.784	-7.781	-9.129	-8.834	-8.674	-9.464	-7.605	-6.822	-8.486	-9.546	-5.018	-5.910	-11.169	-9.172
1011	7	7	1.908	-14.371	-13.781	-13.533	-14.877	-11.480	-9.840	-11.692	-12.214	-11.238	-7.932	-10.485	-15.498	-16.529	-17.921	-17.532
1012	7	7	0.798	-10.529	-10.505	-10.092	-9.639	-7.518	-7.243	-6.274	-6.725	-8.161	-4.749	-5.547	-9.370	-9.913	-12.833	-10.179
1013	7.7	7.7	4.393	-17.086	-14.162	-13.774	-21.400	-15.108	-15.027	-14.467	-16.417	-19.088	-16.333	-9.381	-20.672	-19.663	-21.003	-21.479
1014	2.3	2.3	2.700	-9.591	-6.891	-10.838	-12.014	-11.579	-12.187	-11.431	-10.759	-10.151	-12.547	-11.863	-10.513	-11.679	-12.711	-14.107
1015	4.6	4.6	2.962	-12.441	-12.016	-15.825	-15.723	-9.053	-13.905	-13.384	-12.922	-12.721	-12.226	-13.612	-13.597	-14.99	-13.782	-14.748
1015A	7	7	3.484	-12.121	-12.232	-13.939	-13.897	-9.232	-9.847	-8.921	-9.554	-8.693	-5.210	-8.768	-10.102	-11.846	-15.234	-10.374
1016	2	2	0.646	-5.145	-5.791	-8.426	-7.344	-6.577	-8.657	-8.502	-7.169	-7.514	-7.621	-8.019	-7.131	-7.325	-11.497	-9.238
1017	2	2	2.379	-8.221	-11.968	-13.284	-11.826	-13.245	-11.712	-12.403	-10.599	-11.376	-11.702	-13.368	-11.515	-12.165	-14.879	-13.475
1018	6.6	6.6	0.054	-12.263	-12.587	-10.640	-11.050	-8.007	-11.635	-10.374	-7.277	-7.223	-9.317	-11.553	-9.302	-12.152	-13.475	-13.633
1019	5.5	5.5	1.834	-11.910	-11.771	-11.416	-13.632	-9.149	-7.890	-5.862	-9.528	-7.696	-7.718	-10.878	-12.751	-12.112	-12.923	-13.768
1020	2.3	2.3	1.306	-11.672	-7.384	-8.690	-12.199	-11.765	-11.383	-11.072	-10.195	-11.607	-9.887	-10.416	-11.386	-11.029	-14.576	-12.393
1021	7	7	1.509	-9.981	-10.620	-10.947	-10.564	-7.257	-6.162	-5.863	-6.037	-5.924	-4.355	-7.063	-8.157	-9.396	-12.291	-10.804
1022	5.5	7	0.994	-11.784	-12.883	-13.670	-14.989	-8.086	-8.040	-7.465	-8.418	-7.600	-6.472	-8.138	-10.914	-12.303	-13.727	-13.012
1023	4.6	4.6	6.932	-18.898	-18.545	-16.888	-17.956	-9.243	-21.189	-17.511	-16.175	-16.852	-18.587	-19.097	-18.929	-20.430	-20.719	-19.019
1024	6.6	6.6	3.620	-14.401	-14.140	-12.228	-17.082	-13.383	-13.635	-13.664	-11.769	-7.810	-11.430	-13.899	-15.519	-17.724	-18.926	-19.311
1025	6	6	4.328	-14.586	-16.414	-16.427	-18.289	-15.031	-15.237	-14.683	-8.620	-13.326	-15.271	-16.081	-12.948	-15.103	-17.372	-15.972
1026	2	2	2.095	-4.820	-6.916	-9.323	-11.355	-11.282	-12.097	-11.272	-9.840	-8.753	-12.130	-11.850	-8.643	-11.198	-11.128	-12.982

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	2	2.3	3	4	4.6	5	5.5	6	6.6	7	7.7	1	Mispel	EUR	NAm
1027	2.3	3	1.160	-13.778	-8.464	-7.304	-13.355	-13.880	-15.443	-14.712	-15.542	-14.380	-13.452	-16.301	-15.826	-16.562	-15.997	-16.080
1027A	7	7	1.318	-10.178	-10.768	-10.958	-10.728	-7.345	-6.589	-6.075	-5.905	-7.687	-4.587	-6.851	-9.747	-9.666	-13.095	-10.702
1027B	5.5	5.5	1.014	-10.683	-11.973	-13.843	-13.538	-11.205	-7.861	-6.846	-7.949	-9.527	-8.605	-11.151	-10.746	-11.521	-14.841	-12.283
1028	2	2	0.162	-7.021	-7.183	-12.296	-12.472	-12.408	-13.810	-13.151	-12.716	-11.333	-13.506	-12.745	-11.988	-11.533	-13.092	-15.502
1029	2	2	3.118	-8.794	-11.911	-15.482	-16.865	-13.563	-17.072	-15.462	-13.098	-15.083	-16.071	-16.328	-13.178	-15.445	-18.900	-16.116
1030	5.5	5.5	3.111	-11.972	-11.593	-14.047	-14.957	-11.995	-9.829	-6.717	-10.998	-10.262	-11.209	-12.843	-14.991	-13.664	-11.057	-14.030
1031	2	6	0.073	-5.729	-7.436	-8.930	-9.654	-7.928	-8.839	-9.335	-5.656	-5.903	-8.584	-10.309	-6.357	-7.942	-12.032	-9.848
1032	2	6.6	0.607	-8.086	-9.410	-8.751	-13.889	-12.168	-11.313	-10.47	-10.038	-7.479	-13.155	-11.927	-11.365	-12.342	-11.308	-15.333
1033	5.5	5.5	3.438	-11.478	-11.347	-11.842	-13.013	-11.634	-9.758	-6.320	-10.183	-9.809	-10.789	-12.552	-13.291	-12.410	-12.067	-11.205
1034	6	6	0.157	-12.899	-13.320	-13.403	-14.414	-8.520	-12.810	-12.119	-7.689	-7.847	-11.331	-14.462	-13.108	-12.906	-15.544	-14.257
1035	6	6	2.374	-12.887	-13.112	-16.621	-15.709	-12.402	-12.865	-11.233	-8.859	-11.604	-12.577	-15.169	-13.372	-13.486	-17.012	-14.758
1035A	7	7	1.236	-11.571	-11.784	-12.406	-13.539	-7.256	-8.712	-8.393	-9.435	-8.933	-6.021	-10.357	-10.421	-11.421	-14.640	-11.357
1036	6	6	2.458	-10.865	-11.150	-14.354	-13.632	-12.476	-10.924	-9.391	-6.933	-9.519	-11.586	-14.320	-12.644	-11.284	-15.897	-13.406
1037	3	3	1.730	-8.798	-14.895	-7.068	-15.388	-14.444	-14.956	-13.202	-14.845	-13.092	-15.855	-13.064	-12.813	-16.500	-13.794	-17.354
1038	6	4.6	0.171	-11.647	-13.032	-13.472	-15.257	-7.505	-12.351	-9.472	-7.928	-7.676	-10.222	-10.156	-10.091	-12.185	-14.767	-13.021
1038A	7	5.5	0.547	-10.688	-9.223	-8.792	-13.652	-7.973	-7.425	-5.870	-7.747	-6.561	-6.417	-9.910	-10.752	-11.734	-11.331	-13.700
1038B	6	6.6	0.195	-10.323	-10.538	-10.814	-11.033	-6.637	-10.932	-7.441	-6.266	-6.070	-8.716	-8.985	-7.768	-10.909	-12.045	-10.02
1039	6	6	0.018	-10.547	-11.434	-11.901	-11.806	-7.380	-11.182	-10.100	-6.753	-6.771	-8.228	-10.672	-8.791	-10.810	-15.215	-11.123
1040	6	6	4.706	-13.829	-14.605	-14.231	-14.932	-14.358	-13.890	-13.249	-7.098	-11.813	-13.923	-15.835	-11.803	-13.739	-17.302	-14.639
1041	7	7	0.938	-9.341	-9.498	-8.964	-7.776	-6.258	-6.524	-5.364	-6.120	-7.543	-4.426	-5.985	-8.346	-10.080	-9.116	-10.105
1042	6	6	3.389	-16.072	-17.056	-15.362	-19.169	-15.088	-18.486	-15.324	-11.531	-14.920	-17.820	-18.447	-16.471	-19.704	-17.763	-19.120
1043	7	7	1.741	-11.533	-11.989	-11.736	-12.167	-9.593	-8.203	-7.613	-7.734	-9.446	-5.872	-9.560	-11.954	-11.079	-14.884	-12.694
1044	3	3	1.810	-9.790	-12.911	-7.980	-14.618	-14.073	-15.101	-14.909	-14.896	-14.786	-14.323	-13.499	-14.914	-14.744	-15.366	-13.427
1045	2	2	0.056	-9.069	-14.448	-9.125	-16.079	-17.162	-16.474	-14.924	-15.258	-14.643	-16.952	-18.406	-16.672	-16.307	-18.047	-17.928
1046	2	2.3	0.286	-7.916	-7.630	-13.844	-11.792	-8.824	-12.514	-11.847	-11.285	-9.844	-12.026	-11.722	-13.582	-13.230	-8.478	-11.922
1047	2	2	3.379	-6.207	-9.586	-10.193	-12.498	-11.741	-12.157	-12.082	-10.647	-10.814	-10.763	-12.017	-10.655	-11.087	-14.997	-12.738
1048	2	2	0.078	-3.705	-5.589	-5.986	-6.640	-7.638	-7.659	-7.940	-5.016	-4.783	-7.361	-8.637	-3.783	-6.173	-10.499	-8.240
1049	2	2	0.549	-4.323	-4.871	-5.661	-8.395	-7.294	-9.424	-8.461	-7.482	-5.889	-9.645	-8.803	-6.132	-5.993	-9.793	-9.466
1050	2	2	3.046	-8.050	-11.096	-13.585	-16.974	-12.65	-16.874	-15.075	-13.549	-13.872	-16.081	-15.938	-12.976	-15.893	-15.239	-16.076
1050A	6	6	4.257	-14.378	-15.495	-14.894	-16.146	-15.306	-14.103	-14.621	-7.943	-12.676	-13.984	-15.279	-12.201	-14.441	-16.262	-14.634
1050B	7.7	7.7	2.190	-13.632	-12.997	-13.047	-15.605	-12.295	-12.605	-13.006	-11.859	-12.258	-10.160	-7.970	-14.477	-13.704	-14.951	-15.013
1051	2	2	2.597	-8.195	-10.792	-11.852	-15.809	-13.016	-16.273	-15.930	-14.331	-13.014	-16.276	-16.469	-14.748	-15.813	-15.908	-17.291
1052	2	2	1.678	-4.703	-6.381	-10.857	-10.400	-9.574	-9.809	-10.432	-8.524	-7.577	-9.604	-10.894	-7.801	-9.842	-12.304	-11.678
1053	2	2	1.795	-4.643	-6.438	-8.393	-7.541	-8.095	-8.560	-8.841	-7.040	-7.195	-8.262	-9.538	-6.870	-7.075	-11.400	-9.141
1054	2	2	0.531	-3.510	-4.451	-5.483	-6.401	-6.931	-7.419	-7.701	-5.732	-4.867	-7.121	-8.397	-4.041	-4.225	-10.259	-8.000

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	2	2.3	3	4	4.6	5	5.5	6	6.6	7	7.7	1	Mispel	EUR	NAm
1055	2	Mispel	0.375	-7.928	-7.950	-8.327	-10.435	-10.699	-10.379	-10.158	-8.870	-9.426	-10.207	-12.141	-11.025	-7.553	-14.513	-12.633
1056	2	2	1.478	-8.076	-10.384	-10.890	-15.396	-9.554	-14.731	-12.513	-11.015	-10.541	-14.678	-15.150	-10.715	-13.177	-16.751	-14.915
1057	2	2	0.054	-5.645	-5.699	-7.732	-11.480	-7.527	-9.469	-8.859	-7.655	-6.123	-8.852	-9.821	-9.200	-9.290	-9.061	-13.036
1058	5	5	0.341	-12.886	-13.254	-12.944	-13.744	-11.978	-7.578	-7.919	-9.882	-11.258	-9.824	-12.269	-12.801	-12.597	-15.998	-14.719
1059	2.3	2.3	1.473	-7.017	-4.544	-6.698	-7.023	-6.017	-10.751	-10.296	-7.980	-7.071	-8.505	-9.418	-8.834	-9.719	-9.259	-9.784
1060	2	2	0.517	-6.681	-7.199	-11.903	-15.286	-9.859	-13.429	-11.603	-10.687	-10.083	-12.696	-11.500	-12.224	-12.609	-13.318	-14.131
1060A	2	6	0.332	-5.140	-6.402	-7.518	-6.518	-8.008	-7.919	-7.905	-4.766	-5.097	-7.621	-8.897	-6.613	-6.350	-9.546	-8.101
1060B	2	1	1.209	-6.403	-8.432	-9.558	-12.331	-10.346	-10.770	-11.766	-8.600	-8.582	-10.105	-11.313	-5.194	-10.766	-10.851	-11.846
1060C	2	2.3	0.067	-9.569	-8.205	-8.272	-14.511	-14.123	-13.827	-14.825	-14.323	-12.634	-13.497	-14.082	-14.168	-15.502	-14.286	-17.332
1060D	Mispel	Mispel	7.527	-12.639	-13.171	-14.487	-14.590	-14.857	-13.111	-12.435	-13.763	-14.297	-13.871	-15.208	-13.928	-4.907	-17.089	-12.538
1061	7	7	0.627	-13.184	-9.406	-9.919	-10.917	-7.024	-9.819	-8.497	-9.925	-9.173	-6.397	-10.925	-12.113	-13.877	-11.705	-13.701
1062	7	7	2.539	-15.637	-16.849	-16.933	-16.797	-10.610	-12.754	-12.505	-12.798	-12.576	-8.071	-13.107	-14.479	-15.709	-18.382	-16.583
1063	7	7	0.772	-9.777	-9.621	-10.450	-12.354	-7.203	-7.143	-5.679	-7.407	-6.307	-4.907	-7.437	-8.279	-10.839	-11.214	-12.808
1064	5.5	5.5	0.314	-10.992	-12.172	-11.822	-11.920	-8.427	-6.890	-6.09	-8.767	-6.404	-7.124	-6.841	-9.859	-12.375	-10.152	-13.511
1065	7	7	2.455	-11.092	-12.428	-13.017	-12.071	-7.902	-7.317	-7.602	-7.353	-7.878	-4.861	-7.830	-8.071	-10.735	-13.790	-10.655
1066	7	5.5	0.175	-11.548	-11.190	-13.266	-12.186	-8.914	-9.752	-7.170	-10.579	-10.014	-7.345	-10.175	-14.122	-12.405	-11.023	-13.860
1067	7	7	1.427	-10.888	-8.825	-9.328	-11.059	-7.788	-8.805	-6.127	-7.172	-7.665	-4.701	-8.115	-9.149	-10.345	-14.198	-11.033
1068	5.5	5.5	3.638	-15.435	-17.366	-16.988	-18.503	-13.671	-12.514	-8.876	-16.105	-16.079	-15.659	-15.023	-14.599	-14.897	-17.037	-18.115
1069	6.6	6.6	1.460	-9.559	-10.344	-12.196	-13.540	-10.334	-10.879	-10.814	-8.390	-6.929	-10.225	-12.204	-10.242	-11.342	-14.216	-12.219
1070	5	5	2.255	-13.901	-14.604	-15.290	-16.743	-12.590	-5.967	-8.222	-11.070	-12.614	-12.243	-13.406	-16.191	-14.106	-16.464	-14.972
1071	2	2.3	0.409	-8.443	-8.034	-9.128	-12.413	-11.886	-12.464	-14.131	-12.624	-9.945	-11.57	-13.209	-12.717	-14.254	-15.923	-16.021
1072	2	2	0.785	-7.553	-8.338	-10.603	-14.470	-12.821	-14.350	-13.849	-10.840	-11.852	-14.503	-15.375	-11.865	-13.364	-14.811	-13.270
1073	7	7	1.664	-9.188	-9.905	-9.617	-10.062	-5.457	-5.684	-5.430	-5.562	-5.643	-3.766	-5.968	-6.145	-9.038	-11.857	-10.008
1074	5.5	5.5	2.307	-14.700	-15.350	-15.418	-16.874	-13.240	-10.444	-7.874	-11.819	-13.591	-10.180	-11.309	-13.776	-15.280	-17.285	-17.026
1075	5.5	5.5	6.706	-18.514	-18.219	-16.477	-20.812	-15.562	-15.534	-8.828	-17.553	-17.080	-15.645	-16.828	-19.340	-18.891	-18.359	-20.055
1076	7	7	1.802	-10.651	-9.142	-9.118	-10.855	-7.670	-8.738	-6.163	-6.876	-7.820	-4.361	-7.073	-8.587	-10.035	-13.355	-9.916
1077	7	7	1.236	-14.533	-10.811	-11.425	-11.641	-8.920	-11.072	-9.905	-11.367	-10.440	-7.684	-13.744	-14.738	-14.827	-14.744	-16.326
1078	7	7	2.057	-15.464	-14.899	-13.736	-16.651	-10.558	-12.734	-12.279	-13.571	-10.197	-8.140	-13.473	-16.159	-17.919	-18.495	-18.960
1079	5.5	5.5	2.867	-14.922	-15.710	-13.222	-17.424	-13.381	-11.002	-8.135	-13.573	-13.018	-12.187	-11.236	-13.226	-16.041	-16.741	-17.056
1080	2.3	2.3	0.775	-8.567	-7.446	-8.528	-12.693	-10.500	-11.450	-10.831	-10.313	-9.763	-10.337	-10.246	-9.854	-8.221	-9.536	-12.724
1081	6	6	1.561	-9.805	-11.169	-12.563	-12.688	-9.325	-9.450	-8.605	-6.764	-8.941	-8.325	-9.567	-8.966	-10.205	-13.605	-9.348
1082	4	4	4.303	-13.221	-12.557	-9.816	-5.513	-15.536	-15.242	-14.252	-14.161	-13.000	-14.363	-14.765	-15.160	-15.536	-13.185	-14.148
1082A	2	2	1.019	-6.705	-9.177	-9.267	-13.364	-11.609	-10.840	-9.909	-9.577	-7.724	-12.017	-12.331	-9.850	-11.606	-12.798	-14.807
1083	EUR	EUR	2.300	-8.071	-7.406	-6.137	-11.278	-8.802	-9.779	-10.243	-10.075	-9.861	-8.391	-8.401	-11.278	-9.680	-3.836	-7.733
1083A	EUR	EUR	5.085	-13.354	-13.630	-10.538	-16.233	-13.683	-13.699	-12.390	-16.525	-13.281	-13.625	-12.401	-14.664	-15.438	-5.453	-13.963

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	2	2.3	3	4	4.6	5	5.5	6	6.6	7	7.7	1	Mispel	EUR	NAm
1083B	EUR	EUR	8.318	-15.197	-15.167	-17.289	-15.750	-13.563	-17.804	-17.364	-15.087	-14.796	-17.667	-17.394	-16.965	-18.434	-5.245	-17.536
1084	NAm	NAm	10.96	-23.099	-25.039	-25.955	-24.187	-22.192	-24.174	-23.299	-21.987	-24.376	-24.023	-25.960	-24.085	-23.813	-27.326	-11.027
1085	NAm	NAm	15.73	-26.435	-26.602	-27.231	-26.723	-27.022	-26.610	-26.639	-26.279	-26.460	-26.803	-27.656	-26.469	-26.326	-28.431	-10.549
1086	2	2	1.176	-5.070	-6.246	-10.785	-10.343	-11.188	-11.721	-11.478	-10.639	-9.220	-11.730	-12.519	-9.805	-9.734	-12.578	-14.057
1086A	3	3	5.516	-17.435	-16.807	-11.291	-19.392	-17.728	-17.272	-17.990	-19.116	-17.058	-17.001	-19.393	-17.517	-20.552	-21.517	-21.479
1087	2	2	2.627	-5.991	-10.187	-8.618	-10.517	-12.583	-12.021	-12.180	-11.123	-10.712	-12.253	-12.310	-11.044	-11.427	-12.033	-12.000
1088	NAm	NAm	9.648	-22.519	-22.462	-20.328	-22.461	-22.594	-22.467	-22.568	-22.534	-22.627	-21.853	-22.462	-22.461	-20.092	-22.461	-10.444
1089	EUR	EUR	10.552	-16.439	-15.878	-18.782	-17.738	-17.087	-16.359	-16.053	-16.830	-16.287	-16.894	-16.704	-17.736	-17.691	-5.3260	-18.240
1090	NAm	NAm	10.588	-20.884	-22.131	-23.453	-22.661	-21.850	-20.784	-21.704	-20.745	-21.446	-20.477	-21.870	-20.096	-20.503	-23.578	-9.508
1090A	NAm	NAm	9.925	-15.102	-15.734	-16.625	-14.885	-15.554	-15.018	-15.702	-14.853	-15.300	-14.816	-16.420	-14.741	-14.729	-17.986	-4.804
1090B	NAm	NAm	10.654	-15.916	-15.793	-16.719	-15.798	-16.693	-15.936	-16.010	-15.910	-15.893	-16.272	-16.511	-16.298	-16.353	-17.310	-5.138
1090C	NAm	NAm	8.516	-18.365	-17.807	-20.092	-19.494	-18.193	-20.019	-19.533	-19.776	-19.633	-20.008	-20.074	-19.680	-19.901	-15.725	-7.209
1091	Mispel	Mispel	6.518	-15.303	-14.406	-16.608	-16.927	-14.915	-14.192	-15.934	-14.618	-15.742	-13.108	-15.979	-14.699	-4.328	-17.602	-10.847
1091A	Mispel	Mispel	6.177	-14.413	-12.568	-13.085	-16.951	-13.435	-14.553	-14.178	-14.162	-13.929	-13.564	-15.950	-16.336	-6.391	-15.403	-15.031
1091B	Mispel	Mispel	6.072	-17.631	-15.644	-14.063	-17.584	-16.165	-16.687	-17.672	-17.139	-17.647	-15.805	-17.589	-17.584	-4.189	-17.584	-10.261
1091C	Mispel	Mispel	5.243	-14.070	-12.419	-13.861	-13.096	-12.731	-12.942	-13.699	-13.805	-13.534	-12.165	-16.233	-15.329	-4.281	-17.280	-9.524
1091D	Mispel	Mispel	7.362	-15.490	-13.482	-14.471	-16.774	-13.979	-14.604	-15.814	-15.408	-16.900	-13.833	-15.436	-15.054	-5.060	-16.524	-12.422
1091E	Mispel	Mispel	4.917	-12.168	-12.740	-13.547	-11.777	-12.468	-12.174	-12.809	-12.138	-12.366	-11.875	-13.136	-11.580	-5.970	-10.887	-11.531
1092	Mispel	Mispel	4.414	-13.332	-12.543	-13.853	-16.106	-12.277	-12.658	-14.014	-12.818	-13.246	-12.316	-13.167	-14.531	-4.307	-14.269	-8.721
1093	Mispel	Mispel	7.420	-15.184	-14.196	-17.150	-20.648	-18.890	-17.839	-18.907	-18.397	-18.891	-19.150	-17.440	-18.181	-6.776	-18.474	-20.758
1093s	2.3	2.3	5.035	-14.418	-9.382	-15.246	-17.948	-19.326	-18.743	-20.191	-19.086	-17.826	-17.849	-17.301	-19.401	-16.411	-19.948	-22.300
1093u	2	2	1.940	-6.616	-8.556	-11.682	-11.965	-10.662	-11.761	-11.038	-10.182	-10.097	-12.256	-11.471	-11.146	-10.787	-13.641	-12.490
1094	2.3	2.3	0.155	-9.666	-7.391	-8.687	-15.436	-8.587	-14.007	-12.570	-11.640	-12.452	-13.693	-7.545	-13.593	-13.438	-15.436	-15.511
1095	7	7	0.205	-9.735	-9.179	-8.772	-8.379	-6.211	-7.553	-5.608	-6.479	-7.292	-4.490	-4.695	-7.905	-9.936	-10.647	-7.843
1096	2	2	2.477	-4.601	-7.932	-7.078	-7.889	-9.859	-9.373	-9.819	-7.972	-8.003	-8.945	-10.545	-7.243	-8.052	-11.934	-8.969
1097	2	2	2.897	-5.961	-8.858	-9.766	-10.708	-11.260	-11.809	-11.896	-9.783	-9.828	-11.963	-13.442	-11.958	-11.274	-15.671	-12.004
1098	2	2	2.255	-6.660	-8.915	-12.672	-16.885	-12.839	-14.808	-15.004	-13.821	-12.380	-14.095	-13.423	-11.671	-12.056	-15.172	-15.950
1099	2	2	3.870	-9.321	-13.191	-13.473	-19.312	-17.119	-15.885	-18.048	-15.562	-14.769	-16.530	-18.086	-15.204	-16.735	-18.821	-17.167
1100	2.3	2.3	2.712	-11.515	-8.803	-16.697	-15.861	-16.145	-15.846	-16.414	-15.063	-15.398	-15.095	-15.616	-14.219	-15.791	-19.176	-16.922
1100A	2.3	2.3	0.066	-10.667	-7.290	-7.356	-14.244	-10.335	-15.038	-13.414	-15.093	-12.530	-14.528	-14.363	-12.996	-12.160	-16.066	-16.145
1101	2	2	1.047	-10.812	-11.939	-11.860	-18.799	-14.524	-20.540	-18.499	-16.547	-18.191	-20.540	-15.823	-17.334	-18.705	-19.550	-18.347
1102	2.3	2.3	4.199	-13.200	-9.001	-16.955	-16.880	-16.563	-16.793	-16.517	-14.761	-13.280	-17.673	-18.361	-18.083	-16.535	-16.958	-19.866
1103	2.3	2.3	2.510	-7.020	-4.509	-8.706	-9.599	-10.402	-10.858	-11.286	-9.783	-8.492	-11.042	-11.309	-8.064	-8.539	-12.231	-10.828
1104	2	2	0.285	-6.725	-7.010	-11.695	-14.358	-11.256	-13.451	-12.783	-10.981	-9.678	-13.262	-13.101	-12.386	-12.134	-13.657	-14.557
1104A	5	5	1.393	-13.328	-13.631	-14.324	-12.151	-12.489	-5.933	-7.326	-11.649	-12.412	-11.361	-14.097	-14.045	-12.708	-15.440	-12.542

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	2	2.3	3	4	4.6	5	5.5	6	6.6	7	7.7	1	Mispel	EUR	NAm
1105	2.3	2.3	0.563	-9.457	-8.894	-16.787	-15.289	-10.874	-15.982	-15.995	-13.747	-12.596	-16.019	-16.286	-17.060	-15.187	-11.836	-15.499
1106	6	6	0.766	-12.751	-11.205	-13.080	-14.728	-8.992	-12.848	-12.710	-8.226	-9.873	-11.141	-13.477	-10.698	-13.024	-15.403	-14.687
1107	3	3	2.421	-10.036	-10.316	-7.616	-12.519	-13.521	-14.845	-14.199	-14.790	-12.212	-14.695	-15.820	-12.568	-11.518	-15.816	-14.192
1107A	2	3	0.129	-11.810	-11.776	-11.647	-19.812	-15.283	-19.688	-17.827	-17.861	-17.640	-20.443	-14.378	-16.914	-16.198	-21.171	-21.171
1108	3	3	3.214	-12.175	-10.605	-6.982	-13.844	-10.196	-13.469	-12.243	-12.714	-11.675	-10.948	-13.658	-13.119	-13.247	-14.472	-15.964
1109	5.5	5.5	1.219	-12.258	-13.466	-10.806	-14.917	-10.299	-7.694	-6.345	-10.272	-7.563	-9.095	-9.118	-12.495	-13.591	-12.413	-14.420
1110	4.6	4.6	2.680	-11.253	-8.900	-9.653	-9.776	-6.093	-10.395	-10.029	-10.865	-10.582	-8.774	-11.032	-11.609	-11.728	-12.638	-10.995
1111	7	7	2.143	-13.650	-13.608	-12.667	-11.533	-10.403	-11.900	-9.434	-12.078	-11.456	-6.836	-8.978	-12.419	-13.030	-16.022	-12.247
1112	6	4.6	0.086	-11.914	-11.452	-12.277	-16.709	-7.377	-11.947	-8.589	-9.052	-7.463	-10.429	-10.585	-12.634	-12.967	-13.245	-15.670
1113	7	7	0.636	-8.377	-8.169	-8.468	-8.536	-5.987	-5.134	-4.631	-5.568	-5.074	-3.995	-7.517	-8.096	-8.182	-10.812	-9.452
1114	6.6	6.6	0.808	-13.455	-10.768	-9.121	-15.340	-8.684	-13.321	-10.806	-9.825	-7.876	-10.644	-14.059	-10.941	-14.087	-14.491	-15.698
1115	3	3	2.343	-18.810	-13.865	-11.522	-23.141	-15.002	-23.137	-21.379	-19.915	-17.952	-20.675	-18.327	-21.288	-23.220	-23.141	-23.220
1116	4.6	3	0.207	-15.275	-10.318	-8.484	-13.045	-8.692	-15.604	-13.183	-12.019	-9.836	-11.530	-15.262	-13.464	-15.320	-15.409	-14.270
1117	6.6	6.6	0.798	-14.133	-14.501	-14.282	-18.220	-12.560	-11.351	-9.552	-11.744	-8.754	-12.613	-11.461	-15.865	-16.050	-14.456	-18.296
1118	2	2	0.308	-4.981	-5.289	-5.732	-8.706	-7.585	-9.518	-8.135	-9.382	-6.438	-9.544	-10.666	-7.258	-7.026	-8.259	-9.928
1119	2	2	1.616	-5.095	-7.839	-8.786	-11.520	-9.683	-10.164	-10.326	-8.114	-7.245	-10.147	-9.876	-6.711	-9.255	-11.861	-11.306
1120	2	2	0.325	-7.276	-7.601	-10.252	-10.556	-10.833	-12.559	-10.623	-10.098	-8.915	-13.096	-13.370	-12.441	-11.349	-13.069	-11.767
1121	7	7	1.728	-11.298	-11.937	-12.793	-11.881	-8.744	-9.967	-8.904	-7.581	-9.830	-5.854	-9.418	-10.542	-7.951	-14.381	-10.078
1122	2	2	2.145	-6.340	-8.736	-9.318	-12.647	-11.627	-11.112	-12.997	-11.714	-10.033	-13.214	-12.586	-10.764	-8.485	-12.221	-12.494
1123	4.6	4.6	0.288	-17.361	-15.488	-15.398	-21.255	-12.047	-19.826	-18.965	-16.973	-20.294	-17.292	-12.335	-20.593	-19.848	-21.255	-19.689
1124	2	2	0.607	-5.048	-6.333	-8.719	-8.857	-8.676	-8.911	-8.444	-5.655	-5.907	-8.882	-9.263	-7.421	-8.267	-9.869	-7.935
1125	6	6	0.673	-9.703	-10.379	-11.339	-11.002	-9.041	-9.290	-8.516	-5.738	-6.410	-9.143	-11.053	-9.803	-9.548	-14.142	-10.976
1126	2	2	0.362	-5.922	-7.849	-8.660	-11.307	-9.451	-9.858	-9.832	-6.889	-6.646	-10.101	-10.854	-6.284	-8.654	-13.419	-11.539
1127	2	2	1.371	-4.849	-7.329	-7.946	-9.980	-8.692	-9.358	-9.153	-7.087	-6.220	-9.582	-8.782	-6.976	-7.898	-9.885	-8.198
1128	6	6	2.157	-13.160	-13.398	-13.710	-14.011	-10.699	-13.763	-12.796	-8.348	-10.505	-11.593	-14.879	-11.061	-13.921	-17.089	-15.736
1129	1	1	6.797	-12.926	-14.745	-13.335	-16.836	-12.020	-13.627	-14.355	-13.429	-15.090	-14.878	-14.261	-5.223	-14.691	-13.879	-15.749
1130	3	3	2.463	-10.384	-10.063	-5.937	-12.671	-9.480	-10.407	-8.770	-10.294	-8.400	-10.743	-9.529	-9.932	-11.693	-11.475	-12.174
1131	3	3	4.036	-15.167	-12.757	-7.332	-17.842	-12.840	-16.413	-16.418	-15.116	-16.593	-15.915	-11.367	-16.112	-16.435	-17.843	-17.918
1132	1	1	5.313	-11.118	-11.961	-9.643	-14.546	-9.396	-11.996	-10.695	-11.533	-11.302	-12.931	-11.833	-4.083	-13.480	-9.539	-14.105
1133	6	6	2.391	-12.408	-12.846	-13.482	-14.254	-11.986	-11.552	-11.893	-7.446	-9.837	-12.220	-14.942	-10.931	-12.755	-16.518	-14.125
1134	1	1	5.313	-11.118	-11.961	-9.643	-14.546	-9.396	-11.996	-10.695	-11.533	-11.302	-12.931	-11.833	-4.083	-13.480	-9.539	-14.105
1135	7.7	7.7	1.754	-13.993	-15.142	-16.129	-17.204	-9.333	-12.417	-10.502	-11.780	-11.41	-10.330	-7.579	-13.245	-14.440	-16.022	-14.635
1136	2	2	0.046	-4.160	-7.024	-8.111	-9.313	-9.189	-8.800	-9.683	-6.751	-6.609	-8.493	-9.886	-4.206	-7.697	-11.594	-8.939
1137	2	2	0.889	-5.513	-6.402	-9.052	-8.694	-7.429	-9.171	-8.173	-7.796	-7.883	-8.751	-10.050	-7.473	-8.040	-11.933	-9.829
1138	2	2	0.456	-6.273	-7.597	-6.729	-13.213	-10.387	-10.603	-10.853	-8.862	-8.674	-11.962	-10.964	-10.356	-9.500	-12.736	-13.017

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	2	2.3	3	4	4.6	5	5.5	6	6.6	7	7.7	1	Mispel	EUR	NAm
1139	2	2.3	0.606	-8.976	-8.371	-9.344	-15.888	-13.136	-17.301	-17.153	-14.326	-14.359	-17.328	-12.551	-15.879	-16.295	-17.248	-17.323
1140	6.6	6.6	1.748	-10.96	-9.139	-10.449	-13.189	-9.996	-11.997	-9.403	-9.525	-7.391	-10.687	-13.868	-11.999	-11.792	-13.173	-15.123
1141	4.6	4.6	2.114	-13.971	-15.866	-16.099	-17.325	-8.659	-14.604	-12.157	-10.773	-14.027	-14.618	-16.718	-14.992	-14.896	-18.759	-13.606
1142	2	2	1.415	-5.726	-7.141	-9.622	-9.839	-9.098	-10.103	-9.792	-8.176	-8.141	-10.116	-10.075	-8.033	-8.643	-12.358	-12.367
1143	2	2	1.165	-8.141	-9.306	-13.115	-16.051	-11.637	-14.500	-13.386	-13.269	-11.662	-14.795	-15.466	-14.178	-12.935	-16.146	-14.340
1144	2	2.3	0.531	-7.878	-6.970	-10.603	-10.425	-11.264	-11.128	-10.473	-11.152	-7.501	-12.223	-12.581	-10.783	-11.464	-11.039	-11.966
1145	6.6	6.6	1.902	-10.011	-10.271	-12.339	-14.294	-9.844	-11.126	-10.571	-8.782	-6.880	-10.534	-13.142	-11.966	-12.073	-15.278	-13.936
1146	5	5	3.494	-15.943	-17.823	-16.637	-17.828	-16.423	-8.385	-11.879	-14.586	-16.631	-16.202	-15.696	-18.202	-16.040	-17.819	-17.970
1147	2.3	2.3	1.144	-11.067	-9.924	-15.195	-21.709	-15.413	-23.091	-22.976	-21.199	-20.994	-23.105	-17.783	-21.651	-22.330	-23.073	-21.745
1148	7	7	2.645	-14.928	-14.326	-13.296	-14.065	-10.073	-11.379	-11.427	-12.273	-11.399	-7.428	-12.314	-16.110	-16.163	-15.337	-16.185
1149	7	7	1.729	-10.674	-9.638	-10.782	-11.212	-7.737	-9.021	-8.071	-6.604	-6.554	-4.825	-10.252	-8.487	-10.510	-13.488	-9.958
1150	6	6	3.703	-13.239	-13.404	-14.520	-13.224	-13.571	-13.818	-12.733	-7.883	-11.586	-14.131	-14.713	-12.431	-14.210	-12.783	-14.812
1151	5	5	0.644	-12.091	-11.968	-12.616	-11.973	-11.552	-5.998	-6.642	-8.146	-10.685	-9.534	-9.605	-12.473	-12.529	-13.486	-10.242
1152	6	6	3.990	-13.133	-13.624	-14.893	-14.211	-14.760	-13.086	-13.105	-7.566	-11.556	-13.323	-15.103	-11.696	-14.449	-16.106	-16.251
1153	5.5	5.5	1.149	-14.937	-13.933	-15.616	-16.273	-12.988	-10.635	-9.486	-13.116	-15.033	-11.795	-10.960	-16.530	-15.975	-17.450	-15.993
1154	4.6	4.6	2.583	-18.117	-16.562	-15.864	-19.776	-11.671	-16.740	-16.535	-15.389	-15.490	-14.771	-14.253	-19.776	-18.344	-19.776	-18.369
1155	7	7.7	0.600	-11.550	-11.990	-11.362	-14.730	-7.840	-8.669	-7.622	-8.785	-7.605	-8.286	-7.006	-13.618	-11.866	-13.195	-11.424
1156	7	7	3.947	-13.912	-13.118	-14.063	-15.438	-11.974	-13.534	-10.922	-13.016	-13.353	-6.577	-10.525	-13.197	-14.215	-16.113	-13.912
1157	5.5	5.5	1.060	-11.896	-11.989	-12.241	-11.596	-10.24	-7.471	-6.412	-8.723	-9.839	-7.627	-9.527	-12.212	-11.363	-14.980	-10.827
1158	6	6.6	0.557	-9.948	-10.505	-11.459	-14.021	-8.581	-11.749	-10.790	-7.280	-6.723	-10.330	-10.618	-8.637	-10.935	-14.432	-13.700
1159	6.6	6.6	2.083	-10.832	-10.696	-11.370	-12.471	-9.510	-12.420	-10.276	-9.651	-7.427	-10.935	-12.276	-11.248	-12.397	-13.174	-12.856
1160	4	4	5.409	-11.234	-11.641	-13.292	-4.859	-12.997	-11.750	-11.001	-10.268	-10.985	-11.778	-13.445	-11.689	-12.128	-15.170	-13.828
1161	5	5	1.806	-13.953	-15.453	-14.182	-16.541	-11.133	-9.327	-12.553	-13.660	-11.655	-13.020	-12.583	-11.151	-15.158	-15.780	-16.161
1162	7	7	1.007	-12.775	-12.011	-12.465	-10.768	-10.013	-10.917	-7.555	-8.864	-11.435	-6.548	-9.020	-12.852	-12.227	-15.176	-13.154
1163	5	5	2.025	-13.637	-13.915	-15.895	-14.552	-10.988	-8.963	-12.965	-12.491	-11.704	-11.889	-14.331	-14.626	-13.617	-16.393	-16.301
1164	4	4	10.067	-17.309	-15.151	-16.062	-4.838	-15.246	-18.551	-15.369	-16.217	-17.035	-14.905	-18.957	-17.982	-17.836	-20.629	-17.414
1165	2	2	0.603	-7.458	-8.061	-10.138	-9.100	-10.060	-10.042	-9.986	-8.192	-9.231	-9.702	-10.631	-9.138	-9.953	-14.104	-10.852
1166	2.3	2.3	2.553	-8.788	-6.234	-9.063	-15.210	-12.172	-15.087	-15.416	-14.125	-15.074	-15.842	-9.777	-14.538	-14.103	-16.569	-16.569
1167	2.3	2.3	1.038	-7.794	-6.756	-11.875	-11.278	-10.694	-10.994	-9.954	-9.555	-9.300	-11.494	-10.647	-10.440	-11.604	-10.996	-13.203
1168	7.7	7.7	2.456	-16.367	-14.779	-12.294	-18.335	-13.574	-16.678	-13.095	-16.096	-14.983	-13.152	-9.838	-17.791	-18.397	-16.454	-18.913
1169	7	7	1.545	-14.443	-13.109	-13.860	-14.448	-11.951	-13.531	-12.423	-12.349	-14.022	-7.950	-9.495	-15.255	-14.361	-17.496	-14.590
1170	5.5	5.5	1.874	-12.664	-13.423	-12.625	-16.187	-11.437	-10.030	-7.904	-10.963	-10.939	-9.777	-9.904	-11.123	-14.804	-15.141	-15.819
1171	7	7	1.597	-12.638	-11.695	-12.928	-12.351	-10.302	-11.002	-9.413	-9.494	-11.827	-7.148	-8.746	-11.849	-12.256	-15.331	-12.676
1172	7	7	1.343	-14.864	-13.560	-14.628	-14.426	-12.533	-12.811	-12.479	-12.636	-15.202	-8.928	-10.271	-14.229	-14.882	-17.169	-16.544
1173	5	5	3.523	-13.491	-14.462	-16.027	-15.276	-13.664	-4.679	-8.202	-10.652	-14.189	-11.327	-12.290	-12.857	-13.509	-15.621	-15.171

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	2	2.3	3	4	4.6	5	5.5	6	6.6	7	7.7	1	Mispel	EUR	NAm
1174	7	7	0.657	-12.221	-10.926	-10.769	-12.374	-9.308	-11.285	-8.603	-10.256	-10.979	-7.946	-9.001	-12.977	-13.690	-12.278	-15.243
1175	5	5	1.650	-13.726	-13.995	-14.173	-16.573	-13.341	-5.572	-7.222	-10.705	-12.276	-11.525	-14.259	-14.738	-14.204	-15.882	-17.378
1176	5.5	5.5	1.232	-14.539	-16.104	-15.896	-15.708	-11.158	-10.766	-8.382	-9.614	-14.427	-12.017	-14.208	-15.225	-16.236	-16.526	-16.296
1176A	7	7	0.216	-9.867	-9.801	-9.706	-10.677	-7.593	-6.630	-5.817	-6.931	-6.967	-5.601	-6.147	-8.894	-10.504	-11.226	-10.770
1177	5	5	2.057	-15.404	-14.867	-17.536	-16.017	-15.062	-8.202	-10.259	-12.022	-16.699	-13.253	-12.913	-16.738	-16.707	-17.904	-16.007
1178	2	2	0.911	-6.186	-7.471	-10.369	-9.237	-7.680	-9.326	-9.503	-7.196	-7.365	-8.632	-9.070	-7.097	-9.044	-12.119	-9.464
1179	5	5	0.775	-10.974	-12.077	-13.053	-12.704	-9.340	-5.182	-5.957	-6.672	-8.871	-6.579	-9.275	-9.137	-11.051	-13.379	-10.817
1180	5	5.5	0.994	-11.768	-12.802	-10.271	-14.197	-9.698	-6.114	-5.121	-8.969	-8.518	-8.998	-8.772	-9.856	-13.422	-10.637	-13.710
1181	6	5.5	0.240	-11.921	-11.345	-12.264	-12.891	-11.805	-11.943	-8.375	-8.616	-10.06	-13.624	-12.855	-12.307	-13.939	-13.731	-14.947
1182	4.6	4.6	0.913	-12.648	-13.181	-13.103	-12.507	-8.646	-10.893	-10.596	-9.559	-10.784	-11.656	-12.724	-10.458	-13.081	-13.870	-13.182
1183	4.6	4.6	3.539	-12.866	-13.404	-14.495	-16.185	-7.410	-14.534	-12.677	-11.647	-11.339	-11.865	-13.292	-10.948	-14.640	-16.244	-14.146
1183A	6	6	4.875	-15.998	-16.285	-16.524	-18.068	-17.722	-15.861	-14.365	-9.166	-14.041	-15.951	-18.743	-15.428	-16.528	-18.709	-19.501
1183B	6.6	6.6	1.911	-11.215	-11.388	-10.705	-14.058	-11.135	-12.227	-10.843	-9.740	-7.829	-12.342	-14.651	-13.283	-12.520	-14.806	-12.867
1184	5	5	0.780	-11.584	-12.137	-11.928	-12.111	-9.199	-5.205	-5.985	-6.720	-8.943	-7.079	-10.668	-11.299	-10.941	-14.092	-12.305
1185	5.5	5.5	0.623	-11.990	-12.614	-11.533	-13.083	-9.680	-7.733	-7.110	-7.903	-8.854	-8.189	-11.219	-12.141	-12.186	-15.338	-14.059
1185A	7	7	1.640	-11.359	-12.368	-13.503	-13.592	-9.649	-8.206	-7.250	-8.096	-8.384	-5.610	-8.032	-10.545	-11.130	-14.509	-10.784
1186	6	6	2.654	-14.852	-14.877	-16.827	-16.569	-14.096	-14.27	-14.031	-10.049	-15.409	-12.704	-15.496	-15.844	-15.253	-17.089	-16.464
1187	6	6.6	0.064	-11.744	-11.587	-12.391	-13.049	-7.854	-9.467	-9.461	-7.937	-7.790	-8.779	-9.165	-10.687	-12.317	-13.507	-12.600
1187A	7	7	1.182	-7.917	-8.069	-7.806	-8.494	-6.208	-5.315	-6.823	-6.549	-7.038	-4.132	-5.478	-7.832	-7.674	-10.993	-7.555
1188	7	7	1.032	-12.358	-12.355	-12.885	-12.788	-9.476	-10.632	-9.157	-8.837	-8.826	-7.794	-11.010	-11.367	-12.744	-13.800	-9.584
1189	5	5	0.357	-14.123	-14.539	-16.218	-17.290	-12.876	-7.366	-7.723	-12.231	-13.605	-13.696	-14.090	-16.864	-15.413	-14.781	-17.306
1190	5	5	3.523	-13.491	-14.462	-16.027	-15.276	-13.664	-4.679	-8.202	-10.652	-14.189	-11.327	-12.290	-12.857	-13.509	-15.621	-15.171
1191	5	5	3.029	-15.310	-14.835	-14.372	-16.446	-14.548	-7.592	-10.62	-13.835	-13.244	-12.503	-15.201	-17.055	-17.756	-18.290	-18.766
1192	5	5	2.109	-12.493	-11.848	-13.870	-12.952	-12.471	-4.433	-6.542	-9.751	-11.195	-11.327	-10.928	-13.546	-12.839	-11.912	-13.730
1193	7	7	2.750	-15.641	-15.893	-16.729	-17.358	-11.551	-14.412	-12.754	-13.357	-14.554	-8.801	-14.397	-16.632	-16.042	-17.878	-14.841
1194	6	6	2.146	-12.604	-12.903	-13.646	-14.609	-11.254	-9.946	-10.284	-7.801	-12.119	-10.528	-11.745	-11.403	-12.284	-15.525	-14.151
1195	6.6	6.6	0.607	-7.670	-7.953	-10.965	-10.114	-8.944	-9.766	-10.075	-6.749	-6.142	-9.347	-10.041	-9.442	-9.647	-13.972	-11.713
1196	5	5	4.139	-14.278	-16.070	-16.680	-16.106	-15.403	-6.092	-10.232	-12.996	-14.94	-12.208	-14.798	-15.497	-15.894	-16.384	-16.066
1196A	2	2	2.167	-7.057	-9.224	-10.474	-11.824	-10.861	-11.625	-11.388	-9.739	-9.376	-12.072	-11.740	-13.066	-10.258	-12.077	-13.446
1197	6.6	6.6	0.559	-11.162	-9.649	-10.350	-12.886	-7.157	-11.669	-10.685	-7.101	-6.542	-10.290	-11.383	-11.034	-11.731	-11.096	-11.368
1198	5	5	2.412	-13.530	-14.004	-15.200	-15.416	-12.407	-5.130	-7.542	-10.467	-12.345	-11.308	-13.454	-14.584	-13.798	-16.664	-14.650
1198A	2	2	1.983	-4.461	-7.893	-6.445	-7.850	-9.820	-9.334	-9.780	-7.933	-7.964	-8.905	-10.505	-7.204	-8.013	-11.895	-8.930
1199	2	2.3	0.021	-9.699	-9.678	-11.992	-15.013	-14.09	-12.671	-14.506	-13.131	-14.861	-13.054	-14.054	-12.742	-12.868	-13.167	-12.974
1199p	Mispel	Mispel	6.102	-11.749	-10.552	-11.919	-11.954	-10.793	-10.094	-12.075	-10.319	-11.383	-9.665	-12.591	-11.292	-3.563	-14.453	-10.151
1199c	Mispel	2	0.605	-5.077	-5.849	-8.874	-9.987	-8.995	-9.154	-9.580	-6.765	-6.396	-8.886	-10.638	-7.349	-5.682	-12.365	-10.102

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	2	2.3	3	4	4.6	5	5.5	6	6.6	7	7.7	1	Mispel	EUR	NAm
1200	2	Mispel	0.236	-6.236	-6.878	-9.537	-11.060	-11.427	-9.817	-10.752	-9.001	-9.214	-9.893	-9.340	-9.746	-6.000	-11.244	-12.067
1200p	Mispel	Mispel	3.280	-9.782	-8.200	-11.001	-9.654	-10.697	-8.165	-10.356	-9.655	-9.959	-9.493	-10.848	-10.558	-4.885	-12.421	-11.046
1200c	Mispel	Mispel	0.426	-7.005	-7.616	-10.955	-12.152	-12.612	-11.193	-13.021	-10.636	-11.775	-11.577	-10.389	-9.766	-6.579	-12.586	-12.585
1201	2.3	2.3	0.640	-7.875	-6.241	-11.482	-11.517	-9.138	-11.176	-11.178	-7.947	-8.597	-10.879	-12.155	-10.855	-6.882	-14.016	-10.318
1202	6	6	3.010	-13.768	-14.803	-16.530	-15.731	-13.987	-11.545	-12.666	-8.535	-12.627	-12.726	-14.733	-13.046	-13.393	-16.543	-13.733
1203	6	6	2.728	-13.668	-14.702	-16.429	-15.630	-13.887	-11.445	-12.566	-8.717	-12.526	-12.626	-14.632	-12.946	-13.293	-16.443	-13.632
1204	5	5	0.039	-11.304	-11.916	-11.807	-13.532	-9.111	-5.421	-5.460	-8.232	-8.816	-7.867	-9.757	-9.867	-11.413	-14.516	-11.660
1205	5	5	2.734	-12.720	-14.010	-14.874	-14.544	-12.456	-4.897	-7.631	-9.790	-12.135	-10.578	-12.296	-11.978	-12.305	-15.063	-12.726
1206	5	5	2.570	-12.946	-13.452	-13.729	-13.435	-12.477	-4.659	-7.230	-9.272	-11.699	-10.708	-12.890	-13.047	-12.321	-16.076	-13.220
1207	5	5	1.593	-11.723	-12.085	-13.724	-11.595	-11.319	-5.368	-6.960	-7.717	-10.935	-8.665	-10.485	-12.499	-11.656	-14.362	-11.352
1208	5	5	3.889	-13.478	-14.596	-15.900	-15.276	-13.292	-4.627	-8.516	-10.646	-14.224	-11.408	-12.726	-13.005	-13.131	-16.404	-14.326
1209	6	6	2.248	-12.086	-12.582	-13.146	-12.888	-10.907	-9.489	-8.913	-6.665	-9.994	-9.648	-11.946	-11.020	-11.718	-15.265	-13.082
1210	5.5	5.5	1.273	-15.378	-15.202	-14.657	-18.840	-11.396	-13.559	-10.123	-12.964	-11.723	-13.590	-16.581	-19.141	-16.447	-18.651	-16.412
1211	2	1	1.356	-5.910	-7.500	-8.639	-9.490	-9.021	-9.434	-9.853	-6.763	-7.151	-8.399	-8.813	-4.553	-8.538	-10.293	-9.572
1212	7	7	2.305	-11.729	-11.958	-13.321	-12.191	-10.522	-9.246	-9.034	-9.788	-9.907	-6.729	-9.779	-12.342	-11.694	-15.155	-12.654
1213	1	6	0.801	-8.818	-9.378	-8.624	-10.042	-7.963	-8.852	-8.458	-6.016	-6.955	-7.968	-9.539	-6.817	-8.543	-12.307	-10.218
1214	1	1	2.966	-8.196	-9.318	-9.825	-12.059	-10.956	-11.827	-11.305	-8.126	-8.080	-9.743	-12.857	-5.113	-11.568	-14.643	-11.987
1215	5.5	5.5	0.297	-13.618	-14.25	-15.168	-14.379	-13.170	-10.004	-8.534	-8.832	-12.312	-12.043	-13.848	-13.391	-12.880	-16.643	-12.990
1216	7	7	0.941	-15.279	-13.711	-12.930	-14.012	-8.898	-13.556	-10.508	-12.310	-12.743	-7.956	-11.197	-13.601	-15.685	-16.566	-15.576
1217	7	7	2.738	-12.256	-12.777	-13.944	-14.079	-9.343	-10.527	-7.884	-9.383	-9.530	-5.146	-7.960	-10.264	-11.841	-14.996	-12.261
1218	6	6	1.135	-13.063	-12.019	-13.651	-14.103	-11.700	-13.571	-10.304	-8.656	-9.791	-11.855	-12.576	-12.094	-13.871	-15.070	-13.578
1219	2	2	1.521	-4.568	-7.056	-9.960	-9.562	-9.327	-9.049	-9.932	-6.089	-6.978	-8.742	-10.134	-6.939	-7.945	-11.842	-9.187
1220	5.5	5.5	3.109	-15.991	-15.802	-16.194	-19.740	-14.901	-14.242	-10.095	-13.708	-13.204	-17.676	-15.582	-18.988	-18.016	-16.013	-19.174
1221	7	6.6	0.095	-8.628	-9.083	-8.966	-9.756	-6.272	-6.069	-5.980	-5.383	-5.210	-5.305	-6.210	-8.645	-8.712	-11.006	-9.983
1222	2	2	0.913	-5.966	-7.177	-10.492	-13.173	-9.319	-10.575	-10.360	-6.879	-6.951	-10.773	-10.405	-11.111	-9.766	-10.828	-11.208
1223	2	2	1.141	-6.954	-8.095	-12.363	-10.513	-9.846	-10.041	-10.697	-8.676	-9.144	-10.163	-11.839	-9.873	-10.429	-13.214	-11.809
1224	2	2	0.174	-10.020	-10.194	-16.574	-16.564	-15.972	-16.631	-16.759	-14.865	-13.179	-17.059	-18.443	-18.679	-18.173	-17.954	-17.834
1225	6.6	6	0.855	-11.429	-12.661	-10.877	-13.527	-10.702	-9.969	-10.460	-6.821	-7.676	-10.166	-11.499	-8.381	-11.289	-13.775	-11.709
1226	7.7	7.7	2.667	-12.821	-11.289	-11.047	-17.352	-8.633	-12.550	-11.962	-12.412	-13.138	-11.035	-5.966	-13.995	-15.277	-17.353	-16.116
1227	7	7	1.861	-11.384	-12.393	-14.042	-13.618	-8.327	-10.339	-9.530	-7.942	-8.066	-6.081	-9.696	-9.188	-11.156	-14.534	-11.867
1228	7	7	2.598	-13.389	-15.112	-14.923	-15.148	-10.649	-9.928	-10.221	-11.242	-10.662	-7.330	-11.433	-13.157	-14.936	-15.823	-14.026
1229	5	5	3.738	-13.991	-15.152	-15.918	-15.469	-14.244	-7.061	-10.988	-10.799	-14.051	-10.841	-12.943	-14.277	-13.910	-17.097	-15.046
1230	7	7	1.184	-15.917	-15.481	-14.676	-17.348	-13.645	-11.607	-12.210	-12.779	-10.434	-9.250	-15.945	-16.006	-18.012	-18.998	-17.268
1231	2.3	6.6	0.179	-7.008	-6.383	-8.847	-7.889	-8.831	-9.048	-9.919	-7.422	-6.203	-9.092	-10.447	-8.736	-8.492	-12.020	-10.646
1232	7	5.5	0.021	-11.820	-11.444	-11.828	-13.559	-10.112	-7.959	-7.116	-8.250	-10.561	-7.137	-9.007	-11.717	-11.788	-14.862	-12.206

Individual	Annotated Region Lv. 1	Assigned Region Lv. 1	LOD	2	2.3	3	4	4.6	5	5.5	6	6.6	7	7.7	1	Mispel	EUR	NAm
1233	2	2	1.123	-5.273	-6.773	-9.055	-10.901	-11.127	-10.217	-10.950	-9.202	-9.270	-9.877	-11.547	-7.901	-6.396	-13.098	-11.694
1234	6	6	0.125	-15.045	-15.434	-12.813	-18.109	-11.822	-12.386	-10.906	-9.499	-9.624	-13.381	-14.524	-16.632	-15.739	-16.089	-16.463
1235	7	7	0.816	-12.543	-12.745	-13.993	-14.329	-11.563	-8.388	-8.713	-9.324	-12.917	-7.572	-9.000	-11.909	-12.561	-14.849	-13.919
1236	2	2	1.670	-6.653	-8.599	-12.407	-11.231	-11.831	-10.861	-12.948	-11.060	-8.323	-10.686	-13.725	-11.138	-11.884	-14.171	-12.767
1237	5.5	5.5	0.643	-11.866	-10.865	-12.531	-10.754	-10.922	-7.850	-7.035	-9.404	-8.980	-7.679	-12.845	-14.705	-14.179	-12.330	-14.831
1238	6.6	6.6	5.039	-16.158	-17.135	-16.393	-19.813	-15.746	-18.293	-16.664	-14.426	-9.388	-14.478	-19.019	-19.210	-20.212	-21.464	-20.596
1238A	1	1	0.730	-9.275	-11.702	-10.124	-16.659	-10.868	-13.343	-10.540	-10.918	-7.484	-13.221	-10.807	-6.754	-13.892	-13.249	-16.726
1239	5	5	2.103	-13.313	-15.114	-15.531	-15.357	-12.810	-6.623	-8.726	-11.770	-10.962	-8.945	-12.584	-13.210	-14.509	-16.169	-13.663
1240	7	7	1.688	-14.258	-12.793	-12.585	-15.516	-13.060	-10.886	-10.587	-12.134	-11.958	-8.392	-10.081	-16.377	-16.676	-17.642	-17.466
1241	7	7	0.989	-11.265	-12.568	-13.187	-13.148	-8.162	-6.889	-7.225	-6.772	-9.537	-5.783	-7.814	-9.243	-10.989	-13.667	-11.409
1242	5.5	5.5	1.345	-12.435	-12.120	-11.447	-13.117	-9.478	-9.109	-6.384	-9.664	-11.512	-9.948	-7.729	-9.585	-13.309	-11.760	-13.687
1242A	2	2.3	0.608	-6.916	-6.308	-8.811	-9.355	-8.786	-10.930	-8.092	-7.743	-7.182	-11.358	-10.615	-10.235	-9.687	-11.367	-10.806
1243	2	2	1.974	-6.666	-9.707	-8.678	-11.990	-11.65	-10.177	-10.232	-8.812	-8.640	-10.091	-12.820	-10.659	-9.358	-13.442	-12.631
1244	6.6	6.6	0.542	-11.131	-10.360	-12.887	-12.996	-10.034	-12.997	-12.168	-8.150	-7.608	-11.831	-12.123	-12.114	-12.783	-12.675	-11.822
1245	6	6	0.006	-11.665	-12.029	-15.213	-15.451	-10.978	-13.086	-13.453	-8.697	-8.703	-11.676	-12.921	-13.122	-12.879	-14.534	-14.981
1246	7	7	1.432	-10.417	-11.056	-11.282	-11.000	-8.058	-6.526	-6.147	-6.614	-6.550	-4.715	-7.132	-9.660	-9.832	-13.499	-10.061
1247	3	3	1.760	-14.102	-12.559	-9.242	-18.787	-17.154	-17.735	-16.597	-15.635	-11.001	-19.125	-17.340	-13.565	-18.267	-16.943	-20.146
1248	7	7	1.075	-9.808	-10.447	-11.303	-10.391	-6.155	-8.022	-7.719	-5.492	-5.945	-4.417	-8.418	-7.859	-9.223	-12.890	-8.857
1249	2.3	2.3	1.262	-8.889	-7.627	-13.406	-12.965	-10.643	-15.337	-14.589	-14.711	-14.074	-13.219	-13.779	-15.459	-15.266	-14.348	-16.738
1249A	3	4	0.166	-10.335	-8.061	-5.777	-5.611	-8.740	-12.119	-11.032	-11.039	-10.568	-9.727	-10.375	-10.312	-11.400	-11.688	-13.180
1250	5	5	2.257	-13.635	-14.527	-15.896	-16.284	-13.420	-6.542	-8.799	-10.070	-13.912	-10.530	-12.207	-14.750	-13.727	-16.811	-15.666
1250A	7	7	1.655	-11.352	-11.357	-10.787	-12.908	-7.496	-9.010	-6.714	-7.799	-8.346	-4.888	-6.543	-9.758	-11.244	-14.649	-11.242
1251	4.6	4.6	4.416	-16.367	-16.511	-16.870	-18.869	-10.055	-17.612	-16.284	-15.156	-14.471	-15.156	-17.169	-15.906	-17.817	-19.280	-18.548
1252	6.6	6.6	0.862	-11.543	-11.430	-14.619	-15.789	-9.481	-13.518	-12.836	-8.985	-8.123	-12.098	-12.387	-11.476	-12.287	-16.201	-15.468
1253	5	5	4.934	-13.920	-14.726	-16.152	-15.578	-14.007	-6.386	-11.320	-12.528	-14.412	-11.966	-12.469	-13.429	-13.780	-15.856	-14.163
1254	4.6	4.6	2.298	-14.659	-14.992	-14.261	-17.283	-8.984	-13.931	-14.374	-12.410	-11.282	-12.209	-14.177	-12.975	-14.782	-17.811	-16.939
1255	4.6	4.6	1.248	-16.156	-17.312	-17.634	-20.388	-10.568	-15.577	-12.504	-15.504	-13.832	-13.666	-11.816	-17.057	-16.546	-19.099	-17.716
1256	5.5	5.5	0.811	-10.652	-10.565	-11.281	-10.416	-8.346	-7.037	-5.753	-8.157	-7.117	-6.564	-9.620	-11.541	-9.958	-13.189	-11.371

9.10 | Table S10 Sum of squares of the AMOVA by model and data set

Table S10 Sum of squares of the AMOVA by model and data set.

	genetic group	#Haplotypes	both *n* IAM	*n* = 302 SMM	*n* = 278 SMM	morphological classification	#Haplotypes	both *n* IAM	*n* = 302 SMM	*n* = 278 SMM
lv. 2	In	795	2171.50	223478.36		In	795	2186.98	228682.90	
	Out	70	177.29	33349.40		Out	70	177.29	33349.40	
Sum of squares within each region lv. 1	2	192	475.09	47616.75	45688.75	*monogyna*	222	580.88	60164.28	57919.34
	2.3	47	127.71	13946.91	13658.16					
	3	29	84.32	10230.82	10156.03	*subsphaerica*	95	254.86	23902.07	23840.58
	4	8	17.11	2204.31	2216.09	*rhipidophylla*	69	163.51	17507.32	17511.19
	4.6	42	113.93	11669.87	11601.70					
	5	92	217.77	21792.29	21806.50	*lindmanii*	22	52.60	5667.72	5678.81
	5.5	65	162.48	13356.31	13377.36					
	6	102	263.19	18874.40	18967.44	*macrocarpa*	231	607.91	52778.11	52883.73
	6.6	43	105.25	7777.43	7821.86					
	7	139	343.39	37205.71	30237.93	*laevigata*	128	308.24	34178.47	27027.40
	7.7	16	39.91	3201.26	3132.51					
	1	20	37.17	4927.97	4861.27	*media*	28	69.16	5871.46	5741.59
	Mispel	35	78.46	10832.71		Mispel	35	78.46	10832.71	
	EUR	11	21.39	2295.68		EUR	11	21.39	2295.68	
	NAm	24	57.43	16612.66		NAm	24	57.43	16612.66	
Sum of squares within each population	2_2	62	165.15	14786.61	14876.11	*monogyna*_2	74	198.33	17162.48	17299.43
	2_3	90	216.92	21037.27	20495.09	*monogyna*_3	96	237.73	23965.31	23297.83
	2_4	40	71.46	7277.71	5972.74	*monogyna*_4	52	122.04	13903.93	12447.40
	2.3_2	24	68.89	6717.99	6681.36					
	2.3_3	15	34.22	4072.98	3948.96					
	2.3_4	8	14.67	1888.34	1820.10					
	3_2	10	28.26	3416.09	3447.08	*subsphaerica*_2	20	61.59	6111.00	12474.04
	3_3	15	39.36	4633.85	4546.33	*subsphaerica*_3	51	131.96	12546.85	6104.88
	3_4	4	6.04	656.06	656.68	*subsphaerica*_4	24	48.48	4910.64	4940.63
	4_2	2	1.00	52.26	52.26	*rhipidophylla*_2	8	18.17	2240.05	2254.31
	4_3	6	10.83	1543.34	1550.67	*rhipidophylla*_3	33	78.80	8427.31	8400.14
	4.6_2	6	16.36	1960.79	1968.05	*rhipidophylla*_4	28	59.27	6454.85	6477.71
	4.6_3	24	62.76	5666.42	5668.85					
	4.6_4	12	26.73	3296.29	3231.52					
	5_3	60	146.19	14502.49	14516.30	*lindmanii*_3	18	43.20	4632.06	4642.63
	5_4	32	63.89	6996.96	6996.96	*lindmanii*_4	4	6.04	830.40	830.40
	5.5_2	10	17.21	1078.17	1085.46					
	5.5_3	39	98.83	8083.40	8113.62					
	5.5_4	16	34.24	3413.00	3397.45					
	6_2	6	11.60	723.69	725.69	*macrocarpa*_2	10	24.68	1729.30	31694.89
	6_3	48	122.98	8151.88	8194.47	*macrocarpa*_3	141	375.92	31569.20	18809.83
	6_4	48	118.10	9275.24	9320.70	*macrocarpa*_4	80	198.31	18836.54	1736.72
	6.6_2	6	12.73	832.96	836.69					
	6.6_3	33	77.15	5863.62	5895.97					
	6.6_4	4	5.95	340.93	341.55					
	7_2	56	124.93	8071.80	8026.46	*laevigata*_2	70	163.38	11282.81	11261.97
	7_3	51	125.18	16792.50	12529.30	*laevigata*_3	42	98.27	14596.95	10066.31
	7_4	32	70.84	9195.69	7106.43	*laevigata*_4	16	31.19	5431.85	3975.47
	7.7_2	2	1.50	66.22	66.22					
	7.7_3	6	13.70	1104.03	1055.16					
	7.7_4	8	12.18	1416.51	1416.51	*media*_2	2	1.50	6.21	6.22
	1_3	12	20.06	2334.35	2345.35	*media*_3	18	42.59	3675.62	3554.15
	1_4	8	13.03	2057.08	2000.39	*media*_4	8	13.92	1269.43	1276.07
	8_2	12	24.78	2738.43		*germanica*_2	12	24.78	2738.43	
	8_3	12	20.42	2571.46		*germanica*_3	12	20.42	2571.46	
	9_3	3	1.76	24.60		*+Crataegomespilus*_3	3	1.76	24.60	
	9_4	8	11.35	1265.17		*+Crataegomespilus*_4	8	11.35	1265.17	
	10_2	4	5.93	293.18		*azarolus*_2	4	5.93	293.18	
	11_3	3	3.73	64.72		*caucasica*_3	3	3.73	64.72	
	12_4	4	4.63	576.80		*wattiana*_4	4	4.63	576.80	
	13_3	3	4.73	1156.72		*arnoldiana*_3	3	4.73	1156.72	
	14_4	4	5.59	2460.67		*intricata*_4	4	5.59	2460.67	
	15_4	8	19.35	6422.19		*punctata*_4	8	19.35	6422.19	
	16_3	9	11.88	3779.04		*succulenta*_3	9	11.88	3779.04	

10 | Insurance policy

I declare that I have completed this dissertation single-handedly without the unauthorized help of a second party and only with the assistance acknowledged therein. I have appropriately acknowledged and cited all text passages that are derived verbatim from or are based on the content of published work of others, and all information relating to verbal communications. I consent to the use of an anti-plagiarism software to check my thesis. I have abided by the principles of good scientific conduct laid down in the charter of the Justus Liebig University Giessen „Satzung der Justus-Liebig-Universität Gießen zur Sicherung guter wissenschaftlicher Praxis“ in carrying out the investigations described in the dissertation.

Gießen, 30.06.2022

André Fichtner