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Abstract: The use of DNA sequence data in plant systematics has brought us closer than ever to formulating well-founded hypotheses about phylogenetic relationships, and phylogenetic research keeps on revealing that plant genera as traditionally circumscribed often are not monophyletic. Here, we assess the monophyly of all genera of vascular plants found in Germany. Using a survey of the phylogenetic literature, we discuss which classifications would be consistent with the phylogenetic relationships found and could be followed, provided monophyly is accepted as the primary criterion for circumscribing taxa. We indicate whether and which names are available when changes in generic assignment are made (but do not present a comprehensive review of the nomenclatural aspects of such names). Among the 840 genera examined, we identified c. 140 where data quality is sufficiently high to conclude that they are not monophyletic, and an additional c. 20 where monophyly is questionable but where data quality is not yet sufficient to reach convincing conclusions. While it is still fiercely debated how a phylogenetic tree should be translated into a classification, our results could serve as a guide to the likely consequences of systematic research for the taxonomy of the German flora and the floras of neighbouring countries.

Key words: classification, generic circumscription, German flora, monophyly, phylogeny

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Introduction

"All a taxonomist's decisions are subject to revision in time" (Davis & Heywood 1973), and indeed even the most cursory comparison of taxa at any rank through the history of plant systematics reveals that their circumscription has changed again and again. For example, as regards Rothmaler's "Exkursionsflora von Deutschland", used as basis for the present paper, well over 40 genera have been subject to changes in circumscription when comparing the 19th and 20th editions of the Grundband (Jäger 2012). Major reasons for changes in taxon circumscription, as described and discussed in great detail by e.g. Davis & Heywood (1973) and Stuessy (2009), include the discovery of new species, availability of new data (characters), new approaches in data analysis, and, often related to the preceding point, changes in concepts of classification. At any point in time an author suggesting change of taxon circumscription will have believed to provide something "better", where "better" had to be evaluated against the aim and purpose of the classification.

Post-Linnaean plant systematists (and indeed some systematists before Linnaeus) increasingly aimed at producing a "natural system" in which *a priori* selection of characters used for classification was replaced by the simultaneous evaluation of many characters (Davis & Heywood 1973; Stuessy 2009). With the publication of Darwin's (1859) "Origin of Species", introducing the concept of evolution, "natural" obtained a new meaning, and "natural" taxa were interpreted as groups of common ancestry. Although "Post-Darwinian systems have differed little in content, though they have differed in arrangement, from those of the later pre-Darwinian taxonomists" (Davis & Heywood 1973), "After Darwin, virtually all comprehensive systems of classification of plants were avowedly phylogenetic" (Stuessy 2009).

We are far from having DNA sequences of all species, and probably even farther from resolving all relationships among species and higher level lineages. However, most plant systematists (hopefully) will agree that the use of DNA sequence data in plant systematics has brought us closer than ever to formulating solid hypotheses about phylogenetic relationships, which could serve as basis for classification. Perhaps ironically, exactly how to translate a phylogenetic tree into a classification has resulted in fierce debates. Probably the majority of authors will argue that the branching pattern of a phylogenetic tree should be the primary criterion for classification and that only monophyletic taxa (consisting of ALL descendants of one common ancestor) should be accepted. Some nevertheless maintain that non-monophyletic taxa should also be accepted in order for classification to depict not only patterns of phylogenetic relationship, i.e. tree topology, but also degree of (phenotypic) divergence. (Most of these latter authors will describe the taxa they think of as paraphyletic; however, as is evident from Fig. 1, assessments of taxa as either paraphyletic or as polyphyletic based on tree topology alone are alternative ways to read a phylogenetic tree.) It is not our aim here to summarize or add to that discussion. For that, the reader is referred to a recent review by Schmidt-Lebuhn (2012), a proponent for recognizing only monophyletic taxa, and a response to that review by Stuessy & Hörandl (2014), opponents to that view. It is also not the aim of this paper to provide a general review of changes of genus concepts through time, which have been reviewed and discussed repeatedly (e.g. Humphreys & Linder 2009 and references therein).

Instead, our aims are: (1) Taking the generic circumscriptions of the 19th edition of the Grundband of Rothmaler (Jäger 2005) as starting point, to identify genera which are not or not unequivocally monophyletic. Such conclusions are based on a thorough survey of the phylogenetic literature. We make an effort to assess the quality of published phylogenies in terms of taxon sampling, DNA regions analysed and support for relationships identified. This sometimes results in the conclusion that a given genus may or may not be monophyletic, but that the data available are too preliminary for drawing taxo-

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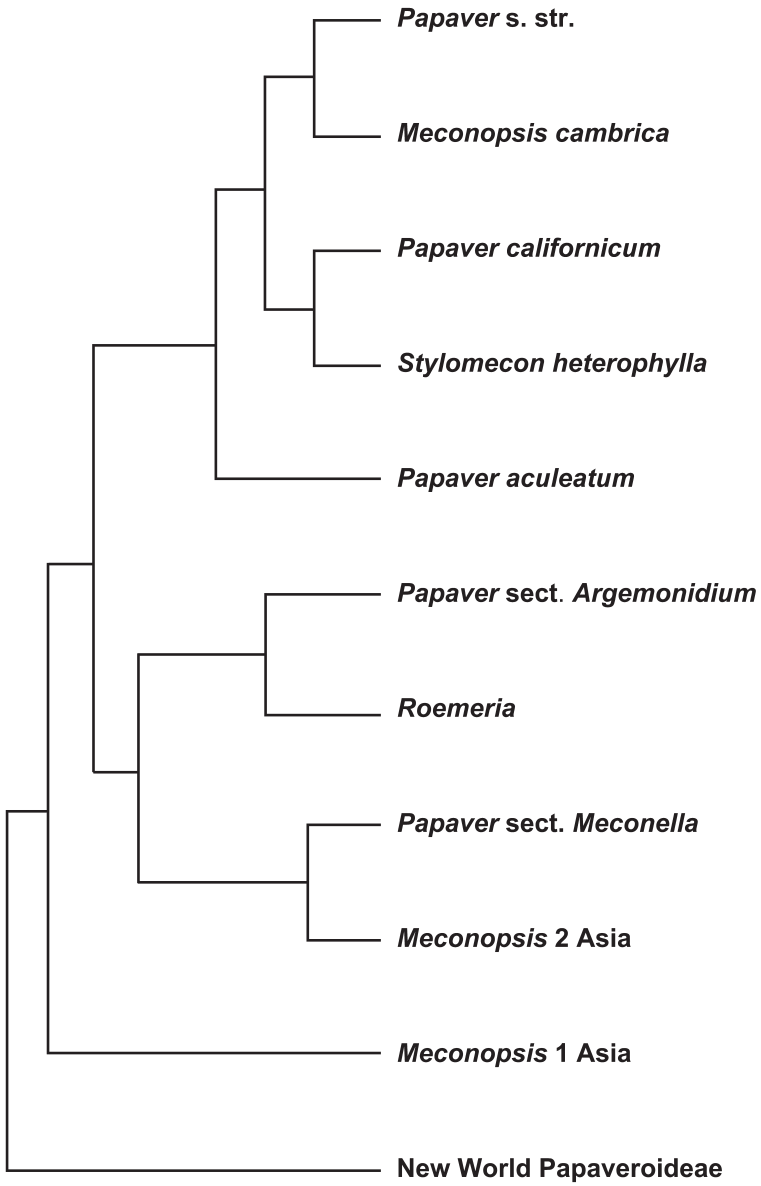

Fig. 1. Phylogenetic relationships among *Meconopsis*, *Papaver*, *Roemeria* and *Stylomecon* (simplified after Kadereit & al. 2011). Based on tree topology alone, *Papaver* can be interpreted either as paraphyletic (in relation to Asian *Meconopsis* 2, *Roemeria*, *Stylomecon* and *Meconopsis cambrica*) or as polyphyletic with *P.* sect. *Meconella*, *P.* sect. *Argemonidium*, *P. aculeatum*, *P. californicum* and *Papaver* s.str. as independent lineages. Interpretation of *Papaver* as both poly- and paraphyletic is also possible.

nomic conclusions. Genera not included in our compilation below either are monophyletic or have not been investigated in detail sufficient to draw conclusions on the matter. Some of the changes that we discuss have already been incorporated in the most recent, 20th edition of the Grundband of Rothmaler (Jäger 2011), and a proportion of those have been justified by Jäger (2012). We nevertheless base our discussion on the previous, 19th edition (Jäger 2005) in order to explain the phylogenetic basis for all of these recent changes. (2) We will discuss, with reference to discussions in the literature, which classifications would be consistent with the phylogenetic relationships found and could be followed provided monophyly is accepted as the primary criterion for circumscribing genera (and taxa in general). In general, these options are either to expand genera in order to include former satellites (based, as it turned out, on single or few autapomorphic characters), or to split genera into smaller generic entities. Recent trends with respect to these two strategies have been discussed by Humphreys & Linder (2009). Where easily available, we indicate whether and which names could be used when changes in generic assignment are made. We do not, however, present a comprehensive review of the nomenclatural aspects of such names.

It is our aim to convince the users of Floras, who want to name plant species for very different reasons and perhaps more often than not are rather reluctant to accept new names, that the name changes discussed here reflect the progress of systematic botany and should be considered just as the results of other branches of biology or of any other science are considered when based on solid evidence.

We follow family circumscriptions and the linear order of families as found in Jäger (2011) and will not discuss these further. For more information on angiosperm family circumscriptions the reader is referred to Stevens (2001 onwards) and APG III (2009).

As already indicated above, several changes of the generic circumscriptions used in the 19th edition of Rothmaler (Jäger 2005) have been made in the 20th edition of that work (Jäger 2011), and some of these changes have been discussed and justified by Jäger (2012). Similarly, some changes resulting from novel phylogenetic work have been implemented by Buttler & Hand (2008a, 2008b, 2011, 2013) and Hand & Buttler (2009, 2012, 2014) in their "Liste der Gefäßpflanzen Deutschlands". Work similar to that presented here has been presented for other European Floras (British Isles: Stace 2010; Italy: Banfi & al. 2005, 2011; Nordic countries: http://euphrasia.nu/checklista/ and http://www.slu.se/en/collaborative-centres-and-projects/dyntaxa/) and some Floras of other parts of the world have explicitly accepted only presumably monophyletic taxa (e.g. Baldwin & al. 2012, 2015).

In the end, it is left to the authors of Floras to decide which principles and strategies they follow when circumscribing genera (and other taxa). However, as pointed out at various times in history (for references see Humphreys

& Linder 2009), judgement should always be based on global and not regional knowledge. For example, it may appear shocking from a German perspective that *Anagallis* L. (incl. *Centunculus* L.), *Glaux* L. and *Trientalis* L. are all nested in a highly paraphyletic *Lysimachia* L. and should be included in the latter genus (Manns & Anderberg 2009; see below for details), but from a global perspective it is rather less so. Anderberg & al. (2007) pointed out similarities between, e.g. *Anagallis arvensis* L. and *Lysimachia nemorum* L., between *Trientalis* and the North American *Lysimachia* subg. *Seleucia* Bigelow and the South American *Lysimachia* subg. *Theopyxis* (Grisebach) J. D. Ray, and, while acknowledging their morphological distinctness, between *Glaux* and *Lysimachia mauritiana* Lam.

In the following, we describe and discuss the results of our literature survey. We looked at ALL genera contained in Jäger (2005) but present results only for genera that are not or not unequivocally monophyletic. The work presented here is work in progress. Any comment on what we have written is highly welcome and will help us in future updates of this paper.

Lycophytes and ferns

Lycopodiaceae (L.-B. Zhang)
Diphasiastrum was resolved as embedded within *Lycopodium* L. (Wikström & Kenrick 1997, 2001). Thus recognition of *Diphasiastrum* Holub as a separate genus would make *Lycopodium* paraphyletic, and Zhang & Iwatsuki (2013) suggested inclusion of *Diphasiastrum* in *Lycopodium*. However, this finding was based on plastid *rbcL* data and limited sampling only, and a final decision should await better sampling and use of additional DNA sequences.

Hymenophyllaceae (L.-B. Zhang)
A new classification of the family recognized only nine genera (Ebihara & al. 2006), and *Trichomanes speciosum* Willd. should now be known as *Vandenboschia speciosa* (Willd.) G. Kunkel. *Trichomanes* L. in a new circumscription is a mainly neotropical genus with a few species in continental Africa, Madagascar and the Indian Ocean (Ebihara & al. 2006) and was resolved as sister to *Vandenboschia* Copel. based on plastid *rbcL* data (Ebihara & al. 2007).

Aspleniaceae (L.-B. Zhang)
Plastid data resolved the family into two well-supported clades, *Asplenium* L. and *Hymenasplenium* Hayata (van den Heede & al. 2003; Schneider & al. 2004), which have different chromosome base numbers as well as distinct root characters (Murakami 1995; Schneider 1996). All other small segregate genera are nested within *Asplenium* (van den Heede & al. 2003; Schneider & al. 2004). Thus, synonymization of *Ceterach* Willd. and *Phyllitis* Hill with *Asplenium* is advocated (e.g. Smith & al. 2006; Lin & Vianne 2013). Consequently, *P. scolopendrium* (L.) Newman should be *A. scolopendrium* L. and *C. officinarum* Willd. should be *A. ceterach* L.

Thelypteridaceae (L.-B. Zhang)
Lastrea Bory was resolved as part of *Oreopteris* Holub based on plastid markers (He & Zhang 2012), and *L. limbosperma* (All.) Ching should now be known as *O. limbosperma* (All.) Holub.

Flowering plants

Hydrocharitaceae (J. W. Kadereit)
A phylogenetic analysis of the family based on nuclear, plastid and mitochondrial DNA sequences (Chen & al. 2012) provides some evidence that *Egeria* Planch. may not be monophyletic when *Elodea* Michx. is treated as a distinct genus. As only two of five species of *Elodea* were included in that study, and support in the relevant part of the tree is not entirely convincing, treatment of the two genera as separate is acceptable for the time being. If combined, as has been done in the past (for discussion see Les & al. 2006), *Elodea* would be the name to be used.

Zosteraceae (J. W. Kadereit)
The finding that *Heterozostera tasmanica* (M. Martens ex Asch.) Hartog is deeply nested in *Zostera* L. (Les & al. 1997; Les & al. 2002; Kato & al. 2003; Tanaka & al. 2003) opens the option to maintain *Zostera* including *Heterozostera* (Setch.) Hartog as one genus, or to divide this group into two or three genera. In both latter options *Z. marina* L. would remain in *Zostera* and *Z. noltii* Hornem. would have to be combined in *Nanozostera* Toml. & Posl. as *N. noltii* (Hornem.) Toml. & Posl. Subdivision into three genera has been advocated and justified with morphological distinctness in inflorescence and vegetative characters by Tomlinson & Posluzny (2001), and maintainance of *Zostera* as one genus has been recommended by Les & al. (2002).

Potamogetonaceae (J. W. Kadereit)
It has been shown that species of *Potamogeton* subg. *Coleogeton* (Rchb.) Raunk. constitute a monophyletic lineage which is well-supported sister to the remainder of *Potamogeton* L. (Lindqvist & al. 2006). As this lineage is morphologically well characterized, as well summarized by Preston (2005; but see also Wiegleb & Kaplan 1998), it could be separated at generic rank as *Stuckenia* Börner, as argued by Lindqvist & al. (2006) and other authors (Les & Haynes 1996; Holub 1997; Haynes & al. 1998; Kaplan 2008), or could be maintained within *Potamogeton* as argued by Wiegleb & Kaplan (1998). If treated as a distinct genus, *P. pectinatus* L. should be known as

S. pectinata (L.) Börner and *P. filiformis* Pers. as *S. filiformis* (Pers.) Börner.

Dioscoreaceae (J. W. Kadereit)
Tamus L. is clearly nested in *Dioscorea* L. (Caddick & al. 2002a, 2002b; Wilkin & al. 2005). In consequence, *T. communis* L. should be treated as *D. communis* (L.) Caddick & Wilkin. An alternative option, to split *Dioscorea* into many smaller genera, as suggested by Huber (1998), was discussed but rejected by Caddick & al. (2002b).

Liliaceae (J. W. Kadereit)
According to studies by Peterson & al. (2008; see also Peterson & al. 2004) and Zarrei & al. (2009), all based on a broad species sample and both nuclear and plastid sequences, a non-monophyletic *Lloydia* Rchb. is nested in *Gagea* Salisb. If *Lloydia* should be included in *Gagea*, as suggested by Peruzzi & al. (2008) and Zarrei & al. (2011), a name for *L. serotina* (L.) Rchb. in *Gagea* would be available (*G. serotina* (L.) Ker Gawl.).

Orchidaceae (M. Kropf)
Initiated by molecular phylogenetic studies by Pridgeon & al. (1997) and Bateman & al. (1997), European orchids, and especially the genus *Orchis* L. s.l., have become a prime example for recent rearrangements in generic delimitations (Stace 2010). Although subsequent phylogenetic studies (cf. Cozzolino & al. 1998, 2001; Aceto & al. 1999; Bateman 2001; Pridgeon & al. 2001; Bateman & al. 2003) generated support for (most of) these rearrangements (but almost exclusively based on ITS sequence variation only), most remained subject to fierce debates in the orchid community (cf. Wucherpfennig 1999, 2002, 2005; Bateman 2001, 2009, 2012a, 2012b; Buttler 2001; Devos & al. 2006; Kretzschmar & al. 2007; Tyteca & Klein 2008, 2009; Scopece & al. 2010; Paulus 2012; Tyteca & al. 2012). Possible and partially implemented rearrangements (cf. Jäger 2012) include either splitting of polyphyletic genera into smaller genera (e.g. *Orchis* s.l.), or inclusion of genera, either with several species (e.g. *Nigritella* Rich. in *Gymnadenia* R. Br.) or monospecific (e.g. *Aceras anthropophorum* (L.) R. Br. in *Orchis* s.str.), in (otherwise) paraphyletic genera in order to obtain monophyletic entities.

Phylogenetic studies placed the (previously) monospecific *Aceras anthropophorum* close to *Orchis italica* Poir. (Pridgeon & al. 1997; Bateman & al. 2003). This close relationship at the base of the *Orchis* s.str. group (see below) was not only supported by the original ITS sequence data, but also by seed ornamentation patterns (Gamarra & al. 2012), hybridization patterns (Klein 1989, 2004; Scopece & al. 2007), and the nuclear *OrcLFY*, *OrcPI*, *OrcP2* loci (Montieri & al. 2004; Cantone & al. 2009, 2011), although support by the mitochondrial *cox1* marker (Inda & al. 2010a) and chloroplast *rpl16* intron data (Inda & al. 2012) was ambiguous due to low resolution. Therefore, Bateman (2012a: 111–114) noted that the "most obviously problematic taxa are the readily recognized anthropomorphic species *Orchis* (*Aceras*) *anthropophora* (L.) All. and *O. italica* … shown as the two earliest-diverging species, making the anthropomorphic species paraphyletic relative to a monophyletic non-anthropomorphic group". Given the absence of a final solution to the question which taxon is indeed basally branching in *Orchis* s.str. (i.e. a sister group relationship between *A. anthropophorum* and *Orchis* s.str. is still possible; see Pridgeon & al. 1997; Bateman & al. 2003; see also Jacquemyn & al. 2011), and the still debated future treatment of *Orchis* s.str. in general (see below), one could also retain *A. anthropophorum* as the only species of *Aceras* and the only *Orchis*-like species without a spur. On the other hand, the inclusion of *Aceras* in *Orchis* s.str. is one of the most widely accepted changes of controversial generic circumscriptions in European orchids (see Bateman 2009: Tab. 1).

ITS phylogenies implied inclusion of *Coeloglossum viride* (L.) Hartm. in an otherwise paraphyletic *Dactylorhiza* Necker ex Nevski (as *Dactylorhiza viridis* (L.) R. M. Bateman & al.; see Bateman & al. 1997, 2003; Pillon & al. 2007). Further molecular markers, especially chalcone synthase variation (Inda & al. 2010b; see also Inda & al. 2010a, 2012), supported this inclusion because *C. viride* was found nested in *Dactylorhiza*. However, evidence against its inclusion exists, and a combined ITS and ETS phylogenetic tree resolved *C. viride* as sister to *Dactylorhiza* (Devos & al. 2006). The latter authors also compiled morphological characters differing between the two groups (Devos & al. 2006: Table 1; see also Wucherpfennig 1999). Most strikingly, *C. viride* has a nectariferous spur (van der Pijl & Dodson 1966), whereas *Dactylorhiza* has food-deceptive flowers. As *Coeloglossum* Hartm. is the earlier name, a proposal to conserve *Dactylorhiza* over *Coeloglossum* was needed (Cribb & Chase 2001).

As a consequence of studies uncovering the (morphological) heterogeneity and the phylogenetic intermingling of different infrageneric species groups of the closely related genera *Liparis* Rich. and *Malaxis* Sol. ex Sw., the monospecific *Hammarbya paludosa* (L.) Kuntze, certainly a close relative of these two genera (although not sampled in the respective studies; e.g. Cameron 2005), "has often been included in a broadly defined genus *Malaxis*" (Pridgeon & al. 2005: 464–465). There are a number of unique features characterizing *H. paludosa* (e.g. incumbent anthers (Szlachetko & Margońska 2002), vegetative reproduction by bulbils at the leaf margin), which, however, have been doubted to be sufficient for differentiation at the generic level given the high variation in *Malaxis* s.l. (Wucherpfennig 2005). Independently, and referring to recent (but still unpublished) phylogenetic analyses by G. A. Salazar, Pridgeon & al. (2005: 464–465) stated that *H. paludosa* "does not lie in the main *Malaxis* clade (Salazar, pers. comm.) but rather is sister to a large clade that includes both *Malaxis*

s.str. and *Liparis* s.str." Until comprehensive phylogenetic evidence on relationships among *Malaxis* and *Liparis* becomes available (see below), *H. paludosa* presently can be maintained in a monospecific genus.

The monospecific *Chamorchis alpina* (L.) Rich. and the dispecific *Traunsteinera* Rchb., represented by the widespread *T. globosa* (L.) Rchb. in Germany, form an independent, well-supported clade (Cozzolino & al. 2001; Bateman & al. 2003). This surprising result refutes the originally hypothesized sister group relationship between the latter taxon and *Orchis* s.str. (Pridgeon & al. 1997) and induced Pridgeon & al. (2005: 228) to state: "However, the two morphologically distinct genera are sufficiently similar in ITS sequences to be potentially viewed as congeneric". If treated as congeneric, *Chamorchis* represents the older genus name (cf. Alrich & Higgins 2011).

In (still unpublished) molecular phylogenetic analyses by Bateman and colleagues, *Neottia nidus-avis* (L.) Rich. is nested within a paraphyletic *Listera* R. Br. as sister to *L. ovata* (L.) R. Br. (illustrated by Pridgeon & al. 2005: 492). Already Chase & al. (2003) had considered *Listera* species as photosynthetic members of *Neottia* Guett. (without presenting the respective phylogenetic analysis, except for a "summary", i.e. Fig. 1 on p. 73) and suggested that the two genera should be combined (see also Tesitelová & al. 2015, where *Neottia* (n = 2) is nested within *Listera* (n = 3) based on ITS, 18S and *trnL*$^{(UAA)}$ intron data). A close relationship between the two genera has long been documented (e.g. Dressler 1990), and a combined generic treatment as *Neottia*, which is the older name, has already been published by Szlachetko (1995). In this treatment, however, *Neottia ovata* Bluff & Fingerh. is placed in *N.* subg. *Listera* (R. Br.) Szlach. The third species of a newly circumscribed *Neottia* native in Germany is *N. cordata* (L.) Rich. (*L. cordata* (L.) R. Br.).

Pridgeon & al. (1997) "took the controversial step of sinking the morphologically distinct *Nigritella* back into synonymy with *Gymnadenia* s.str., which would otherwise have been paraphyletic." (Pridgeon & al. 2001: 229). These authors stressed that "despite superficial differences in flower form and resupination, *Nigritella* shares several morphological characters with *Gymnadenia*: palmate-digitate tubers; two lateral, lobe-like stigmas; and two pollinia each with a caudicle…" (Pridgeon & al. 2001: 298). However, other authors, especially Wucherpfennig (1999, 2002), advocated maintaining *Nigritella* as a genus based on at least ten ("superficial") morphological characters, but also based on allozyme data (Hedrén & al. 2000). It was noted that a study of character evolution across *Orchidinae* clearly showed that *Nigritella* is a morphologically derived lineage (Wucherpfennig 2002) arguing for keeping the genus *Nigritella* even within a paraphyletic *Gymnadenia*. However, in a more recent molecular analysis of ITS and *rpl16* intron sequences, Pillon & al. (2006) documented a sister group relationship between their *Nigritella* (n = 2) and *Gymnadenia* (n = 5) samples. This illustrates that molecular phylogenetic relationships obtained obviously depend on taxon sampling, type of data analyses performed and outgroup selection (see Pillon & al. 2007). In consequence, *Nigritella* can still be recognized as a morphologically well-defined genus, until more comprehensive analyses are available.

Finally, species of *Orchis* s.l. were placed in at least three major and only distantly related groups based on ITS data (Bateman & al. 1997, 2003; Pridgeon & al. 1997). These three groups in principle correspond to hybridization patterns (Klein 1989, 2004; Scopece & al. 2007). As regards the first group, the formerly monospecific *Neotinea* Rchb. f. was expanded by Pridgeon & al. (1997) and Bateman & al. (1997) to encompass the "… small-flowered, essentially trilobed-lipped species of the *ustulata*-group that were formerly included in *Orchis* s.l. These could in theory have been treated as a genus separate from the more narrowly delimited original concept of *Neotinea*, given the relatively long molecular branch and distinct vegetative markings of *N. maculata*…" (Pridgeon & al. 2001: 228). Relevant for the German flora, the combinations *N. ustulata* (L.) R. M. Bateman & al. (*O. ustulata* L.) and *N. tridentata* (Scop.) R. M. Bateman & al. (*O. tridentata* Scop.) were provided (Bateman & al. 1997). However, the small flowers of *N. maculata* (Desf.) Stearn are different from the *ustulata*-group by producing nectar (Pridgeon & al. 2001; Duffy & al. 2009), and by being 100 % autogamous (Duffy & al. 2009), while the species of the deceptive *ustulata*-group depend on pollinator-mediated outcrossing. This would provide arguments for treating *N. maculata* as an independent genus. If this approach is taken, the names *Odontorchis ustulata* (L.) D. Tyteca & E. Klein and *Odontorchis tridentata* (L.) D. Tyteca & E. Klein are available (Tyteca & Klein 2008).

The second fairly well-supported clade encompasses all species of former *Orchis* that have $2n$ = 36 (or $2n$ = 32 in the case of *O. papilionacea* L.) chromosomes as well as *Anacamptis pyramidalis* (L.) Rich. (Pridgeon & al. 1997). Pridgeon & al. (2001: 255) stated that while "*A. pyramidalis* is distinctive… The other members of this newly circumscribed genus *Anacamptis* Rich. are difficult to distinguish morphologically from *Orchis* s.str., but their flowering stems bear cauline sheathing leaves." Members of *Anacamptis* in this new circumscription in the German flora are *A. coriophora* (L.) R. M. Bateman & al. (*O. coriophora* L.), *A. morio* (L.) R. M. Bateman & al. (*O. morio* L.) and *A. palustris* (Jacq.) R. M. Bateman & al. (*O. palustris* Jacq.).

The remaining *Orchis* s.l. taxa should then, following Pridgeon & al. (1997) and Bateman & al. (1997), be treated as *Orchis* s.str. comprising an anthropomorphic species group (with flowers shaped like "little men", i.e. sepals and petals forming a compact head and the labellum showing "arms" and "legs"; e.g. *O. militaris* L., the type of *Orchis*) plus *Aceras* R. Br. (see above) and a non-anthropomorphic group (e.g. *O. mascula* (L.) L.). However, suggestions have been put forward to split

Orchis s.l. further (Tyteca & Klein 2008, 2009), partly ignoring problems of paraphyly (criticized, e.g. by Scopece & al. 2010; Bateman 2012a). However, the two supported species groups within *Orchis* s.str. (Bateman & al. 2003) could be treated as *O.* subg. *Orchis* (i.e. *O. militaris*, *O. purpurea* Huds. and *O. simia* Lam.) and *O.* subg. *Masculae* H. Kretzschmar & al. (i.e. *O. mascula*, *O. pallens* L. and *O. spitzelii* Saut. ex W. D. J. Koch; Kretzschmar & al. 2007). Tyteca & al. (2012) compiled morphological and pollinator assemblage data for these two groups and concluded that all their information as well as molecular (Bateman & al. 2003) and seed micromorphology data (Gamarra & al. 2012) are in favour of a separation at the generic level, i.e. as *Orchis* and *Androrchis* D. Tyteca & E. Klein (Tyteca & al. 2012; see also Tyteca & Klein 2008 for respective names, i.e. *Androrchis mascula* (L.) D. Tyteca & E. Klein, *A. pallens* (L.) D. Tyteca & E. Klein and *A. spitzelii* (Saut. ex W. D. J. Koch) D. Tyteca & E. Klein).

Several orchid genera have been shown not to be monophyletic: *Liparis* and *Malaxis*, both comprising about 250 species (Mabberley 2008), are to some extent intermingled (Cameron 2005); *Platanthera* Rich. should include *Piperia* Rydb. (Bateman & al. 2003; already implemented there); and *Herminium* L. is phylogenetically intermingled with *Peristylus* Blume or *Habenaria* Willd. (Douzery & al. 1999; Bateman & al. 2003). However, irrespective of exact phylogenetic relationships, which are not yet completely resolved, the nomenclature of the species occurring in the German flora will not be influenced if their respective monophyletic clades are preserved at the generic level, as *Liparis loeselii* (L.) Rich., *Platanthera bifolia* (L.) Rich. and *Herminium monorchis* (L.) R. Br. are the types of the respective genus names (Alrich & Higgins 2011), and *Platanthera montana* (F. W. Schmidt) Rchb. f. (*P. chlorantha* Cust. ex Rchb.), the second native species of this genus, is definitely closely related to the type, *P. bifolia* (Bateman & al. 2003). However, *Malaxis monophyllos* (L.) Sw. might be affected by future changes: a BLAST search of recently published *matK* barcodes of this species (Kim & al. 2014; Xiang & al. 2014) revealed higher DNA sequence similarity to a group of *Liparis* species around the type, *L. loeselii*, than to the *Malaxis* species group around the type, *M. spicata* Sw. (cf. Cameron 2005). On the other hand, this critical point in the systematics of *Malaxideae* could alternatively be solved by choosing a wide genus concept. In this case, *Malaxis* would be an older name than *Liparis* (and *Hammarbya*; see above).

In summary, one major problem with respect to several recently suggested changes in generic circumscription in European orchids is that new molecular phylogenetic hypotheses often are based on only one molecular marker (i.e. ITS; Bateman & al. 2003). Other molecular markers often resulted in limited phylogenetic resolution given the probably young age of several European orchid lineages (cf. Inda & al. 2010a, 2010b, 2012). Although sometimes combined evidence of ITS plus cpDNA variation seems to improve results (e.g. Pillon & al. 2006), it does not in other cases, indicating the dominance of the ITS information (e.g. Inda & al. 2012). Moreover, it is striking that the overall taxon sampling, some 20 years after the first molecular phylogenetic publications, is still incomplete. Also, multiple samples of single taxa have rarely been included. In consequence, many molecular phylogenetic relationships have still not been solved satisfactorily, and some nomenclatural changes accordingly are premature, giving rise to frequent debate.

Amaryllidaceae (J. W. Kadereit)

Using a broad sample of *Galanthus* L. and *Leucojum* L., Lledó & al. (2004) reported that the former genus is deeply nested in the latter. In order to maintain these two genera, the authors recommend to recognize the additional genus *Acis* Salisb. for large parts of *Leucojum*. Generic allocation of *G. nivalis* L., *L. aestivum* L. and *L. vernum* L. would remain unaffected if this approach would be taken.

Cyperaceae (B. Gehrke)

Carex L. has been found to be paraphyletic and to include all other members of the *Cariceae*, i.e. *Cymophyllus* Mack., *Kobresia* Willd., *Schoenoxiphium* Nees and *Uncinia* Pers. (Roalson & al. 2001; Starr & al. 2004). The results of the molecular phylogenetic work are unambiguous. Retaining *Kobresia* would lead to the necessity of describing a myriad of morphologically indistinguishable smaller genera and would also mean that *Kobresia* would have to be either greatly extended to include many species of *Carex* subg. *Psyllophora* (Degl.) Peterm. (= *Primocarex* Kük.) or that *Kobresia* (and *Uncinia*) would have to be split into various smaller lineages. Combination of all names of *Cymophyllus*, *Kobresia*, *Schoenoxiphium* and *Uncinia* in *Carex* are currently underway (Global *Carex* Group 2015). The names *Carex myosuroides* Vill. for *Kobresia myosuroides* (Vill.) Fiori and *Carex simpliciuscula* Wahlenb. for *K. simpliciuscula* (Wahlenb.) Mack. should be used.

Eleogiton (L.) Link was recently discovered to be nested in *Isolepis* R. Br. (Muasya & al. 2001). *Isolepis* was thought to be characterized by having one or more pseudolateral spikelets and an erect culm, but the nodding culm of the single terminal spikelet, believed to characterize *Eleogiton*, is now known to have evolved from within *Isolepis* (Muasya & al. 2001). *Eleogiton fluitans* (L.) Link was therefore recently changed to *I. fluitans* (L.) R. Br.

Recent studies suggest that *Schoenoplectus mucronatus* (L.) Palla and *S. supinus* (L.) Palla are not part of *Schoenoplectus* (Rchb.) Palla, but belong to *Schoenoplectiella* Lye, a cosmopolitan group, which is most closely related to the African *Pseudoschoenus* (C. B. Clarke) Oteng-Yeb. (Shiels & al. 2014). *Schoenoplectiella* differs morphologically from *Schoenoplectus* by

having an unbranched inflorescence (Jung & Choi 2010), whereas *Schoenoplectus* has a pseudo-lateral branched inflorescence. Both genera have culm-like primary bracts opposed to the inflorescence with leafy bracts in *Scirpus* L. (Jung & Choi 2010). If recognition of *Schoenoplectiella* as suggested by Lye (2003) should be accepted, both *S. mucronatus* and *S. supinus* must be excluded from *Schoenoplectus* as *Schoenoplectiella mucronata* (L.) J. Jung & H. K. Choi and *Schoenoplectiella supina* (L.) Lye. However, final decisions must await a better understanding of relationships between *Pseudoschoenus* and *Schoenoplectiella*.

Poaceae (M. Röser)

A number of molecular phylogenetic studies employing nuclear and chloroplast DNA markers have shown that *Festuca* L. s.l. is a large paraphyletic group that encompasses *Lolium* L., *Micropyrum* (Gaudin) Link, *Vulpia* C. C. Gmelin and a number of further genera (Torrecilla & Catalán 2002; Catalán & al. 2004, 2007; Torrecilla & al. 2004; Inda & al. 2008). *Lolium* is nested within a more ancestral broad-leaved clade, whereas *Micropyrum* and *Vulpia* belong to the presumably more recently derived fine-leaved *Festuca* lineages. *Vulpia* additionally appears to be polyphyletic and encompasses separate diploid and tetraploid/hexaploid lineages, which are not sufficiently understood to date. Because of several uncertainties concerning limited sampling of intermediate taxa and missing representation of several *Festuca* groups, Catalán & al. (2007) argued for maintenance of *Lolium*, *Micropyrum* and *Vulpia*. This would require no name changes for taxa of the German flora. *Micropyrum* and *Vulpia* were included in *Festuca* by Soreng & al. (2015), but *Lolium* was kept separate and considered congeneric with *Schedonorus* P. Beauv. (syn. *F.* subg. *Schedonorus* (P. Beauv.) Peterm.), which was segregated from *Festuca*.

Polyploidy and hybridization play an important role in the evolution of *Sesleria* Scop. and allies. Preliminary data from Amplified Fragment Length Polymorphisms (AFLPs) and plastid DNA (*trnL-ndhF*) sequences support the recognition of *Oreochloa* Link as a separate genus (with only *O. disticha* (Wulfen) Link represented in the German flora) and underline that *Psilathera ovata* (Hoppe) Deyl diverges from the remainder of *Sesleria* (Lakušić 2013). Further study including a more comprehensive taxon sampling is needed to clarify whether the monospecific *Psilathera* Link (only *P. ovata* (Hoppe) Deyl in the German flora) can be maintained or should be merged with *Sesleria* as was done in Jäger (2011) and by Lazarević & al. (2015).

Delimitation of genera allied with *Helictotrichon* Besser ex Schult. & Schult. f. is a long-term matter of debate. Molecular phylogenetic studies using different chloroplast DNA and nuclear ITS sequences of a sufficiently broad sample of relevant taxa suggest to acknowledge three genera occurring in the German flora, namely *Avenula* (Dumort.) Dumort., *Helictochloa* Romero Zarco and *Helictotrichon* s.str. (Döring & al. 2007; Quintanar & al. 2007; Schneider & al. 2009; Röser & al. unpubl. data). *Avenula* is represented by *A. pubescens* (Huds.) Dumort., *Helictochloa* by *H. pratensis* (L.) Romero Zarco and *H. versicolor* (Vill.) Romero Zarco and *Helictotrichon* s.str. by *H. parlatorei* (Woods) Pilg. The description of the new genus *Helictochloa*, type designations and transfer of species to *Helictochloa* have been published by Romero Zarco (2011).

The distinctiveness of *Anthoxanthum* L. and *Hierochloe* R. Br. has repeatedly been questioned due to the occurrence of seemingly intermediate species in Africa and SE Asia. Following Schouten & Veldkamp (1985), the two genera have been merged by some authors (Wu & Phillips 2006; Allred & Barkworth 2007; Kellogg 2015; Soreng & al. 2015). The study by Pimentel & al. (2013), using AFLPs, chloroplast and nuclear DNA sequences, suggests that the intermediate taxa originated by ancient hybridization between the two genera. The question as to whether *Anthoxanthum* and *Hierochloe* should be kept separate or amalgamated in a single genus thus remains unanswered.

Ranunculaceae (E. Welk)

Traditionally *Aconitum* L., *Consolida* (DC.) Gray and *Delphinium* L. (and *Aconitella* Spach, see Soják 1969) were grouped in tribe *Delphinieae*. Molecular phylogenetic research revealed three *Delphinium* species (*D.* subg. *Staphisagria* J. Hill) to form the sister clade to all other *Delphinieae* (Jabbour & Renner 2011a; 2011b), and *Consolida* incl. *Aconitella* to be nested in *Delphinium* excl. *D.* subg. *Staphisagria*. The position of *D.* subg. *Staphisagria* is supported by biochemical, karyological and morphological characters. Furthermore, Wang & al. (2013) found a sister position of the Chinese *Aconitum gymnandrum* Maxim. to *Delphinium* (sensu Jabbour & Renner 2012). In order to arrive at monophyletic *Aconitum* and *Delphinium*, name changes are required. Of these, inclusion of *Consolida* (and *Aconitella*) into *Delphinium* (Jabbour & Renner 2012) is relevant for the German flora. In consequence, *C. ajacis* (L.) Schur, *C. hispanica* (Costa) Greuter & Burdet and *C. regalis* Gray should be listed as *D. ajacis* L., *D. hispanicum* Costa and *D. consolida* L., respectively.

Based on molecular phylogenetic analyses, Bittkau & Comes (2009) found *Garidella* L. to be clearly monophyletic while *Nigella* L., its sister group, was not well supported as monophyletic. This may imply future inclusion of *Garidella* in *Nigella*, which, however, would not affect naming of the German species of *Nigella*.

Combined analyses of DNA sequence data, biochemical data and morphology by Compton & al. (1998) suggested to include *Cimicifuga* Wernisch and *Souliea* Franch. in *Actaea* L. (also Compton & Culham 2002; Gao & al. 2008). However, it has also been argued to keep the genera separate based on the fleshy fruits of *Actaea* (e.g. Wang & al. 1997; Lee & Park 2004). *Ac-*

taea and *Cimicifuga* can also be distinguished using seed morphology and seed anatomical features (Ghimire & al. 2015). If *Cimicifuga* and *Souliea* should be included in *Actaea* based on phylogenetic relationships, German *Actaea* will not be affected because *Actaea* L. is the oldest genus name.

Hoot & al. (1994) suggested that *Hepatica* Mill., *Knowltonia* Salisb. and *Pulsatilla* Mill. should be included in *Anemone* L. s.l. (cf. Ehrendorfer & Samuel 2001; Schuettpelz & al. 2002). However, Pfosser & al. (2011) argued that these genera could also be retained because of unsuitable outgroup selection (*Clematis* L.) in Hoot & al. (1994) and Schuettpelz & al. (2002). Using *Ranunculus ficaria* L. as outgroup in their study, a position of *Clematis* within *Anemone* s.l. became probable. The sister-group relationship of species of *A.* subg. *Anemonidium* (Spach) Juz. (*A.* subsect. *Anemonidium* Spach, *A.* subsect. *Himalayicae* (Ulbr.) Tamura, *A.* subsect. *Keiskea* Tamura and *A.* subsect. *Omalocarpus* (DC.) Tamura) to *Hepatica* found in all studies renders *Anemone* paraphyletic in relation to the embedded *Hepatica* and *Pulsatilla*. Similar to combined karyological and molecular phylogenetic analyses by Mlinarec & al. (2012), Hoot & al. (2012) found, again with *Clematis* as outgroup, that *A.* subg. *Anemonidium* contains *Anemonastrum* Holub and *Hepatica*, while *Pulsatilla* is positioned within *A.* subg. *Anemone*. Accordingly, they suggested to incorporate *Hepatica* in *Anemone* as *A.* sect. *Hepatica* (Mill.) Spreng. or *A.* subg. *Hepatica* (Mill.) Peterm. For *Pulsatilla* they suggested inclusion in *Anemone* as *A.* sect. *Pulsatilloides* DC. or *A.* subg. *Pulsatilloides* (DC.) Juz. An alternative solution might be splitting *Anemone* into at least two genera corresponding to the $x = 7/8$ divergence seen in *Anemoninae*. At the moment, it seems best to wait for further analyses before combining the large number of taxa affected. However, from the results of all studies cited it seems inevitable for *Anemonastrum* Holub to be subsumed in *Anemone* again. The resulting combination is *Anemone narcissiflora* L.

Caltha L. has been divided into two sections: the monophyletic *C.* sect. *Psychrophila* (DC.) Bercht. & J. Presl in the S hemisphere and the paraphyletic *C.* sect. *Caltha* in the N hemisphere (Schuettpelz & Hoot 2004). Based on a broader sampling, Cheng & Xie (2014) showed that *Thacla* Spach (*Caltha natans* Pall.) diverged first in the genus, and that the other species fall into two monophyletic clades, i.e. *Caltha* s. str. and *Psychrophila*. Thus, it would be possible to raise *Psychrophila* to genus rank, but this would inevitably require *C. natans* to be raised to *Thacla*. Any decision here will not affect the name of *C. palustris* L.

A number of molecular phylogenetic studies revealed that *Ranunculus* L. in a wide sense is polyphyletic (Lehnebach & al. 2007; Hoot & al. 2008; Wang & al. 2009). Although the entire tribe *Ranunculeae* could be recognized as a very broadly circumscribed *Ranunculus*, this would result in a morphologically highly heterogeneous group. The morphological and geographical independence of *Ficaria* Huds. and *Ceratocephala* Moench is comparable to that of *Myosurus* L. It thus seems to be justified to follow Emadzade & al. (2010) who proposed to recognize *Ceratocephala*, *Ficaria* and *Myosurus* (plus several other small genera) as separate genera, but to include *Batrachium* (DC.) Gray and *Aphanostemma* A. St.-Hil., sometimes recognized as separate genera in the past, in a then monophyletic *Ranunculus*.

Berberidaceae (J. W. Kadereit)

Monophyletic *Berberis* L. with simple leaves clearly is nested in a paraphyletic grade of *Mahonia* Nutt. with compound leaves (Kim & al. 2004; Adhikari & al. 2015), a pattern of relationship already postulated by Ahrendt (1961). As the two genera are very similar to each other in many respects (for discussion see Adhikari & al. 2012), and the different lineages of *Mahonia* would be difficult to justify at generic rank, they probably are best treated as one genus, *Berberis*, as was done by these authors. *Mahonia aquifolium* (Pursh) Nutt. had originally been described as *B. aquifolium* Pursh.

Papaveraceae (J. W. Kadereit)

Papaver L. is part of a group of four genera distributed almost entirely in the Old World (Schwarzbach & Kadereit 1995). The other three genera are *Meconopsis* Vig., *Roemeria* Medik. and *Stylomecon* G. Taylor. Subdivision into these four genera is based largely on capsule morphology. Various analyses of these four genera (Kadereit & al. 1997; Carolan & al. 2006; Kadereit & al. 2011; Xiao 2013; Liu & al. 2014) revealed that patterns of relationship cut across traditional generic delimitations (see also Fig. 1). First, three subgroups of *Papaver*, i.e. (1) *Papaver* s.str. (all sections except *P.* sect. *Argemonidium* Spach, *P.* sect. *Californica* Kadereit, *P.* sect. *Horrida* Elkan and *P.* sect. *Meconella* Spach), (2) *P. californicum* A. Gray (*P.* sect. *Californica*) and (3) *P. aculeatum* Thunb. (*P.* sect. *Horrida*) form a clade together with *Meconopsis cambrica* (L.) Vig. and *Stylomecon heterophylla* (Benth.) G. Taylor. Second, *P.* sect. *Argemonidium* is most closely related to *Roemeria*. Third, *P.* sect. *Meconella* Spach is most closely related to one of three subgroups of *Meconopsis*. While this pattern of relationships allows several classifications, the following option has partly been followed (Kadereit & Baldwin 2011; Kadereit & al. 2011). A newly circumscribed *Papaver* should contain *Meconopsis cambrica*, *Papaver* s.str., *P. aculeatum*, *P. californicum* and *Stylomecon heterophylla*. Of the species found in Germany, *P. confine* Jord., *P. dubium* L., *P. lecoqii* Lamotte and *P. rhoeas* L. would remain in *Papaver*. *Meconopsis cambrica* was originally described as *P. cambricum* L., and the name *P. heterophyllum* (Benth.) Greene is available for *Stylomecon heterophylla*. *Papaver* sect. *Argemonidium*, represented by *P. argemone* and *P. hybridum* in the German flora, should be united with *Roemeria*, with which it shares sepal and pollen charac-

ters (Kadereit & al. 1997). The combination *R. argemone* (L.) C. Morales & al. is available for *P. argemone*.

Although *Papaver alpinum* L. as part of *P.* sect. *Meconella* should clearly be excluded from *Papaver*, the exact relationships of *P.* sect. *Meconella* to Himalayan *Meconopsis* are not sufficiently clear yet to suggest a formal name. However, it seems to be sister clade to a newly circumscribed *Meconopsis* (excl. *Cathcartia* Hook. f. and *M. cambrica*) and probably is best treated as a distinct genus.

Crassulaceae (J. T. Klein)

Sedum L. has repeatedly been shown to be highly polyphyletic (van Ham & al. 1994; van Ham & 't Hart 1998; Mort & al. 2001; Mayuzumi & Ohba 2004; Gontcharova & al. 2006; Carrillo-Reyes & al. 2009). In the most recent phylogenetic analysis of *Crassulaceae* based on combined nuclear ITS and chloroplast DNA (Klein & Kadereit in prep.), the 20 species of *Sedum* found in Germany fall into several lineages.

(1) *Sedum rosea* (L.) Scop. represents a lineage that is often accepted as the genus *Rhodiola* L., with c. 60 spp. mostly found in C and E Asia, in which *S. rosea* should be known as *R. rosea* L.

(2) *Sedum spurium* M. Bieb. represents a lineage that is often accepted as the genus *Phedimus* Raf., with c. 20 spp. mostly found in SW to E Asia, in which *S. spurium* should be known as *P. spurius* (M. Bieb.) 't Hart. *Phedimus* and *Rhodiola* are sister to each other and could be combined in one genus. However, among other morphological differences, *Phedimus* spp. have hermaphrodite flowers, whereas most *Rhodiola* spp. have unisexual flowers.

(3) *Sedum maximum* (L.) Hoffm., *S. telephium* L. and *S. vulgare* (Haw.) Link represent a lineage that is often accepted as the genus *Hylotelephium* H. Ohba, with c. 30 spp. distributed mainly in C and E Asia, and should be known as *H. maximum* (L.) Holub, *H. telephium* (L.) H. Ohba and *H. vulgare* (Haw.) Holub, respectively. *Hylotelephium* is closely related to the C to E Asian genera *Meterostachys* Nakai, *Orostachys* Fisch. (non-monophyletic, see below) and *Sinocrassula* A. Berger.

(4) *Sedum forsterianum* Sm., *S. ochroleucum* Chaix and *S. rupestre* L. represent a lineage that should be accepted as the genus *Petrosedum* Grulich, as was done, e.g., by Thiede & Eggli (2007). *Petrosedum* is closely related to a small group of SW Asian *Sedum* spp. that has not yet been excluded from *Sedum* (*S.* ser. *Nana* 't Hart & Alpinar).

The remaining species, including the type, *Sedum acre* L., fall into a large clade of the family that contains a large number of other genera (see below). If the species discussed above were to remain in a monophyletic *Sedum*, essentially two thirds of the family would have to be included in that genus. Accordingly, segregation of three of the above four genera, i.e. *Rhodiola*, *Phedimus* and *Petrosedum*, is likely to be stable irrespective of future name changes in other parts of the family. As regards *Hylotelephium*, future name changes are conceivable because relationships between this genus and *Meterostachys*, *Orostachys* and *Sinocrassula* are not yet fully resolved.

The large clade of the family containing the type consists of two subclades, known as the Leucosedum-clade and the Acre-clade (van Ham & 't Hart 1998), respectively.

The Leucosedum-clade, which also includes *Dudleya* Britton & Rose, *Mucizonia* A. Berger, *Pistorinia* DC., *Prometheum* (A. Berger) H. Ohba, *Rosularia* Stapf, *Telmissa* Fenzl and *Sedella* Britton & Rose, contains seven species of German *Sedum*, i.e. *S. album* L., *S. atratum* L., *S. cepaea* L., *S. dasyphyllum* L., *S. hispanicum* L., *S. rubens* L. and *S. villosum* L. These seven species are scattered across a number of subclades, which partly contain one or more of the genera listed above.

The remaining five species of German *Sedum*, i.e. *S. acre*, *S. alpestre* Vill., *S. annuum* L., *S. sexangulare* L. and *S. sarmentosum* Bunge fall into the Acre-clade, which also includes *Cremnophila* Rose, *Echeveria* DC., *Graptopetalum* Rose, *Lenophyllum* Rose, *Pachyphytum* Link, Klotsch & Otto, *Thompsonella* Britton & Rose and *Villadia* Rose. In this Acre-clade, *S. acre* is supported sister to all remaining taxa, and *S. alpestre*, *S. annuum*, *S. sarmentosum* and *S. sexangulare* again are scattered across a number of subclades.

In view of the relationships described above, several potential options exist for a monophyletic *Sedum*. (1) *Sedum* could be treated as monospecific with only its type, *S. acre*. Of course, species that have not been sampled yet may fall into this clade. (2) The entire Acre-clade could be treated as *Sedum*. This, however, would imply inclusion of *Cremnophila*, *Echeveria*, *Graptopetalum*, *Lenophyllum*, *Pachyphytum*, *Thompsonella* and *Villadia*. *Sedum* in such circumscription would contain c. 500 species. (3) The Acre-clade and the Leucosedum-clade (with c. 160 species) could be combined into *Sedum*, which would require additional inclusion of *Dudleya*, *Mucizonia*, *Pistorinia*, *Prometheum*, *Rosularia*, *Telmissa* and *Sedella*.

Whereas recognition of a monospecific *Sedum* (option 1) would require description of a large number of genera for former species of that genus, options 2 and 3 would require combination in one genus of morphologically very different genera that are geographically widely distributed. Of these three options, option 1 appears best to us, although the new genera that will have to be described partly may not be easy to differentiate morphologically or geographically. However, as *Sedum* has not yet been completely sampled, and many relationships within the Acre- and Leucosedum-clades are not supported, I recommend to retain all *Sedum* species of the Acre- and Leucosedum-clades in *Sedum* until relationships are understood better. However, such *Sedum* clearly is not monophyletic.

Saxifragaceae (J. W. Kadereit)
The non-monophyly of *Saxifraga* L., first shown by Soltis & al. (1993), has been confirmed in several studies (for discussion see Fernández Prieto & al. 2013; Tkach & al. 2015). In particular, a group of 70–90 species from North America and Eurasia is only very distantly related to the remainder of *Saxifraga* and has to be treated as the genus *Micranthes* Haw. The one species affected in the German flora is *Saxifraga stellaris* L., which should be treated as *M. stellaris* (L.) Galasso & al. Following Soltis (2007), the two genera are clearly distinct in pollen and ovule characters.

Linaceae (J. W. Kadereit)
A broadly sampled phylogeny of *Linum* L. and relatives by McDill & al. (2009) showed that the South American *Cliococca* Bab., the North American *Hesperolinon* (A. Gray) Small and *Sclerolinon* C. M. Rogers and the Eurasian *Radiola* Hill (with only *R. linoides* Roth) are nested within *Linum*. McDill & al. (2009) proposed to return these four genera to *Linum*, in which they have been classified before. *Radiola linoides* should then be *L. radiola* L.

Euphorbiaceae (J. W. Kadereit)
Following Webster (2014; see discussion of literature there), *Euphorbia* L. is best treated as one large genus with >2000 spp. as the four major clades recognized (Chamaesyce, Esula, Euphorbia and Rhizanthium), partly treated as subgenera (see, e.g., Bruyns & al. 2006; Zimmermann & al. 2010; Horn & al. 2012; Yang & al. 2012), cannot be defined morphologically. Accordingly, segregation of subclades, e.g. the Chamaesyce Clade (Webster 2014; *E.* subg. *Chamaesyce* Raf., e.g. Yang & al. 2012), at genus rank would result in a paraphyletic *Euphorbia*. In consequence, all species of *Euphorbia* growing in Germany should be retained in that genus.

Fabaceae (C. M. Ritz)
The circumscription of the genera *Cytisus* Desf. (40 spp.) and *Genista* L. (90 spp.) has been subject to long-standing discussions. The first published molecular phylogenies based on plastid (*rbcL*) and ITS data revealed two well-supported lineages, *Cytisus* and *Genista*, each containing numerous segregate taxa of uncertain position (Käss & Wink 1995, 1997). Reviewing the published phylogenies, Cristofolini and Troia (2006) proposed a new sectional classification of *Cytisus*. Since raising all monophyletic entities within *Cytisus* s.l. to generic rank would lead to an impracticably high number of small and often monospecific genera, the authors advocated inclusion of *Chamaecytisus* Link. (30 spp.), *Lembrotropis* Griseb. (monospecific) and *Sarothamnus* Wimm. (five spp.) in *Cytisus*. Molecular studies did indeed not separate *Chamaecytisus* from *Cytisus* s.str. (Käss & Wink 1995; Cubas & al. 2002; Pardo & al. 2004), and species with an intermediate morphology blur the boundaries between the two genera (Cristofolini & Conte 2002). *Lembotropis nigricans* (L.) Griseb. (*Cytisus nigricans* L.) is morphologically very distinct by its elongate racemes, calyx shape and naviculate hairs, but is phylogenetically nested within *Cytisus* (Käss & Wink 1995, 1997). *Sarothamnus scoparius* (L.) W. D. J. Koch (*C. scoparius* (L.) Link), which is widespread in Europe, is part of *C.* sect. *Spartiopsis* Dumort. with four more species distributed in the Iberian Peninsula (Cristofolini & Troia 2006).

Molecular phylogenies based on plastid and ITS markers support the monophyly of three subgenera of *Genista*, but the segregate genera *Genistella* Ortega (*Genista sagittalis* L. / *Genistella sagittalis* (L.) Gams) and *Ulex* L. (20 spp.; *U. europaeus* L. in Germany) are nested in the *Genista* clade (Pardo & al. 2004). However, a comprehensive revision of the complex is still missing.

The neophytic *Amorpha fruticosa* L. represents a poorly understood polyploid complex within the North American genus *Amorpha* L. (16 spp.). The monophyly of the genus is questionable: it is supported by plastid sequences, while phylogenies based on nuclear genes suggest its paraphyly because the clade also contains the North American shrubs *Errazurizia rotundata* (Wooton) Barneby and *Parryella filifolia* Torr. & A. Gray (McMahon & Hufford 2004, 2005; Straub & Doyle 2014). However, *Amorpha* is a Linnaean genus, and accordingly the name of the introduced *A. fruticosa* will remain unchanged if the above-named species are included in *Amorpha*.

Planted as ornamentals in Europe, *Wisteria* Nutt. contains four to seven deciduous lianas distributed in E Asia and North America. Phylogenetic reconstructions based on plastid and nuclear genes suggest the inclusion of the evergreen lianas *Afgekia* Craib and *Callerya* Endl. in *Wisteria* (Li & al. 2014). Since *Wisteria* is the oldest name, the names of the cultivated species in Germany will be not affected.

Coronilla L. (nine spp.) and *Securigera* DC. (13 spp.) each represent monophyletic entities in a highly supported clade that is sister to *Hippocrepis* L. according to an ITS-based phylogeny (Sokoloff & al. 2007). However, detailed analyses based on other genetic markers so far are missing. Based on present knowledge, two options, either adopting a large *Coronilla* s.l. including *Securigera* (Sokoloff 2003) or recognizing two genera (Lassen 1989), are equally possible. In the first case the name *C. varia* L. and in the second case *S. varia* (L.) Lassen should be used.

The most comprehensive study of *Anthyllis* L., based on plastid and nuclear markers, support its monophyly when *Hymenocarpus* Rchb. is included in *Anthyllis* and the Mediterranean genera *Dorycnopsis* Boiss. (two spp.) and the monospecific *Tripodion* Medik. are segregated (Degtjareva & al. 2012). Contradicting results were reported in an ITS-based phylogenetic study with a relatively small taxon sampling (Nanni & al. 2004). This study placed two annual species of *Anthyllis*, which were

clearly part of *Anthyllis* in the study by Degtjareva & al. (2012), together with *Tripodion* near *Lotus* L. However, this result is questionable because resolution and taxon sampling were much lower than in the study by Degtjareva & al. (2012). In any case, the name of the German *A. vulneraria* L. would not be affected. *Lotus* (190 spp.) in its traditional circumscription is polyphyletic and divided into an Old World clade and several New World lineages (Allan & Porter 2000; Allan & al. 2003). The latter have now been recognized as four genera (Arambarri & al. 2005). Studies focusing on the highly supported Old World clade revealed that the segregate genera *Tetragonolobus* Scop. (five spp.) and *Dorycnium* Mill. (ten spp.) should be returned to *Lotus* (Degtjareva & al. 2006; Degtjareva & al. 2008), a result already suggested by morphological studies (Polhill 1981). However, the phylogenies published so far rely on nuclear ribosomal DNA only. Since incongruencies between markers are a common phenomenon in *Fabaceae*, additional genetic data are required. When *Dorycnium* and *Tetragonolobus* are included in *Lotus*, the names *L. germanicus* (Gremli) Peruzzi (*D. germanicum* (Gremli) Rikli), *L. herbaceus* (Vill.) Jauzein (*D. herbaceum* Vill.), *L. hirsutus* L. (*D. hirsutum* (L.) Ser.) and *L. maritimus* L. (*T. maritimus* (L.) Roth) should be used.

All phylogenies based on plastid and nuclear markers published so far suggest a close relationship between *Calophaca* Fisch., *Caragana* L. and the monospecific Asian *Halimodendron* DC. (Sanderson & Wojciechowski 1996; Wojciechowski & al. 2000; Zhang & al. 2009; Duan & al. 2015). The morphologically distinct *Calophaca* and *Halimodendron* are probably nested within *Caragana*, but statistical support for this was low and more research is needed (Zhang & al. 2009). In any case, the name of the introduced *Caragana arborescens* Lam. will not be affected by any changes in generic circumscriptions because *Caragana* is the oldest genus name.

The monophyly of *Hedysarum* L., containing c. 180 spp. distributed in the N hemisphere, still remains questionable. Two N African species have been excluded from *Hedysarum* and recognized as *Greuteria* Amirahmadi & Kaz. Osaloo (Amirahmadi & al. 2014). According to plastid phylogenies, *Hedysarum* (including the monospecific genus *Sartoria* Boiss. from Turkey) is monophyletic (Amirahmadi & al. 2014; Duan & al. 2015). The close relationship of *Hedysarum* and *Sartoria* has also been corroborated by biochemical analyses (Arslan & Ertuğrul 2010). In contrast, trees based on ITS sequences separated *H.* sect. *Hedysarum* (containing the type, *H. alpinum* L.) from *H.* sect. *Multicaulia* (Boiss.) B. Fedtsch. and *H.* sect. *Stracheya* (Benth.) B. H. Choi. The latter two were sister to a clade comprising *Onobrychis* Mill. (Amirahmadi & al. 2014; Duan & al. 2015). Further studies including sequences of nuclear low-copy genes are needed to unravel the reasons for these incongruencies. If non-monophyly of *Hedysarum* should obtain further support, either all species of *Onobrychis* and some other smaller genera should be transferred to a very large *Hedysarum*, or *Hedysarum* should be split into several genera. In the latter case the name *H. hedysaroides* (L.) Schinz & Thell. would remain unchanged because this species is closely related to the type of the genus name.

Similar results were obtained for *Onobrychis* Mill. Plastid phylogenies supported *Onobrychis* as a monophyletic entity but ITS phylogenies failed to do so (Amirahmadi & al. 2014; Duan & al. 2015).

All published phylogenies revealed a close relationship between *Trigonella* L. (60 spp.) and *Melilotus* Mill. (20 spp.), which is supported by morphology (e.g. incised margin of stipules, notched apex of standard, smooth surface of seed coat). Most reconstructions based on either plastid, ITS or nuclear low-copy genes revealed *Trigonella* as paraphyletic in relation to *Melilotus* (Bena 2001; Steele & Wojciechowski 2003; Steele & al. 2010; Dangi & al. 2015). In contrast, a combined analysis of ITS and plastid data showed well-supported monophyly of both genera (Dangi & al. 2015). However, taxon sampling in both genera has not been sufficiently exhaustive to solve this problem. The so-called medicagoid species of *Trigonella* (23 spp.) distributed in the Mediterranean area share a complex explosive tripping mechanism of pollination with *Medicago* (Small & al. 1987). In support of this, nuclear ribosomal sequences corroborate the inclusion of these species in *Medicago* (Bena 2001).

A recent comprehensive study of tribe *Vicieae* based on plastid and ITS sequences revealed that neither *Vicia* L. (140 spp.) nor *Lathyrus* L. (160 spp.) are monophyletic in their current delimitation (Schaefer & al. 2012). Comparable results were also obtained by earlier studies based on *matK* sequences of a small number of species (Steele & Wojciechowski 2003; Wojciechowski & al. 2004). *Lathyrus* is paraphyletic in relation to two monophyletic groups: the Caucasian *Vavilovia* Fed. (two spp.) and *Pisum* L. (three spp.; Smykal & al. 2011; Schaefer & al. 2012). *Vicia* appears to be paraphyletic because annual species of *V.* sect. *Ervum* (L.) Taub. (e.g. *V. tetrasperma* (L.) Schreb.) and *V.* sect. *Ervilia* (Link.) W. Koch (including *V.* sect. *Ervoides* (Godr.) Kupicha and *Trigonellopsis* Rech. f. and *V. hirsuta* (L.) Gray) were sister to *Lathyrus* s.l. and the remaining species of *Vicia* including *Lens* Mill. (four spp.; Schaefer & al. 2012). Schaefer & al. (2012) recommended the inclusion of *Pisum* and *Vavilovia* in *Lathyrus. Vicia* could be then recognized as a monophyletic entity by including *Lens* and re-transferring *V. articulata* Hornem., *V. ervilia* (L.) Willd., *V. hirsuta* (L.) Gray, *V. parviflora* Cav., *V. sylvatica* L. and *V. tetrasperma* (L.) Schreber to either *Ervilia* Link or *Ervum* L.

Polygalaceae (J. W. Kadereit)

Several studies (Eriksen 1993; Persson 2001; Forest & al. 2007; Abbott 2011), of which the study by Abbott (2011), although not including full results, used a large sample and both nuclear and plastid sequences,

have shown that the large genus *Polygala* L. is highly polyphyletic. In consequence, several segregate genera of groups formerly included in *Polygala* have been proposed (for summary see Pastore 2012). Of the species of *Polygala* known in Germany, *P. chamaebuxus* L. should be removed from *Polygala*. According to Abbott (2011), this species is part of a lineage which should be called *Polygaloides* Haller and be treated as *P. chamaebuxus* (L.) O. Schwarz. Although not all other German species of the genus were sampled in any of the published phylogenies, their close relationship to each other has been documented (Lack 1995) and it seems safe to assume that they all will remain in *Polygala*.

Rosaceae (B. Gehrke)

Many genera of the *Potentilleae*, such as *Comarum* L., *Dasiphora* Raf., *Duchesnea* Sm. and even *Fragaria* L., have at some point been included in *Potentilla* L. (Mabberley 2002). However, recent molecular phylogenetic work clearly showed that *Fragariinae* and *Potentillinae* are distinct lineages. Based on molecular work authors tend to recognize *Potentillinae* as comprising only two genera. These are (1) *Potentilla* s.str. excluding *P. fruticosa* L., *P. palustris* (L.) Scop. and *P. rupestris* L. (see below) and including, amongst others, *Duchesnea indica* (Andrews) Teschem (as *P. indica* (Andrews) Th. Wolf), which is deeply nested in *Potentilla* s.str., and (2) *Argentina* Hill (Feng & al. 2015), a mostly Asian group, including *P. anserina* L. (as *A. anserina* (L.) Rydb.). The separation of *Argentina* s.l. and *Potentilla* s.str., which are sister lineages, is based on differences in the insertion of the styles, with *Potentilla* s.str. having subterminal styles, whereas *Argentina* has lateral ones (Dobes & Paule 2010; Sojak 2010; Feng & al. 2015). However, considering the relationship between these two genera, it would also be possible not to recognize *Argentina* as a separate genus and use the name *Potentilla* for all species of the *Potentillinae* (Eriksson & al. 2015).

The other monophyletic subtribe in the *Potentilleae*, the *Fragariinae*, has its highest species diversity in Asia and includes numerous smaller lineages as well as *Alchemilla* L., *Fragaria* and *Sibbaldia* L. Well nested in *Fragariinae* and more closely related to *Fragaria* than to *Alchemilla* or even *Potentilla* are *P. fruticosa* and *P. rupestris*. These should be treated as *Dasiphora fruticosa* (L.) Rydb., a monospecific genus, and *Drymocallis rupestris* (L.) Soják. *Drymocallis* Soják is a small genus confined to the N hemisphere. Alternatively, *Fragaria* could be extended to include *Dasiphora* and *Drymocallis*, amongst some other Asian groups, but the genus then would no longer be united by its characteristic fleshy receptacle. Leaving *D. fruticosa* and *D. rupestris* in *Potentilla* would necessitate including *Alchemilla*, *Fragaria* and *Sibbaldia* in *Potentilla* as well, which is obviously not desirable. Most authors therefore seem to prefer to recognize *Dasiphora* and *Drymocallis* as genera separate from *Fragaria.*

Alchemilla forms a clade with *Aphanes* L. and the mainly South American *Lachemilla* Rydb., easily recognizable by the lack of petals and the presence of only four calyx and epicalyx lobes (Notov & Kusnetzova 2004; Gehrke & al. 2008). Molecular phylogenetic work revealed the existence of a fourth, previously unknown clade with *Alchemilla* species from Africa (Gehrke & al. 2008). *Aphanes* is clearly nested among *Alchemilla*, *Lachemilla* and African *Alchemilla* (Gehrke & al. 2008). As there are no obvious morphological features to separate the African clade of *Alchemilla* from the European clade, and the entire clade is readily recognizable by floral morphology despite differences in life cycle, size and leaf morphology, I would like to recommend to include *Aphanes* in *Alchemilla* leading to reusing the names *Alchemilla arvensis* (L.) Scop. for *Aphanes arvensis* L. and *Alchemilla microcarpa* Boiss & Reut. for *Aphanes inexspectata* W. Lippert. Irrespective of this, *Alchemilla*, *Aphanes*, and *Lachemilla* in their traditional circumscriptions differ in habit and some details of floral morphology. Whereas *Alchemilla* and *Lachemilla* species are perennial and usually have four introrse stamens inserted at the outer side of the discus (*Alchemilla*) or 2(–4) extrorse stamens inserted at the inner side of the discus (*Lachemilla*), *Aphanes* species are annual or short-lived and have only a single extrorse stamen at the inner side of the discus.

Potentilla palustris is most closely related to *Alchemilla* as circumscribed above according to chloroplast data and to *Sibbaldia* using nuclear data. Unless included in either of these two genera, which is not desirable from a morphological point of view, it should be reinstated as *Comarum palustre* L. It seems that especially the Asian species of *Sibbaldia* require more work (Eriksson & al. 2015), but it is most likely that *S. procumbens* L. can retain its name.

Molecular phylogenetic work in combination with morphological character optimization has shown that *Rosaceae* contain only three major lineages (Potter & al. 2007): *Dryadoideae*, *Rosoideae* and *Spiraeoideae*. The last includes the formerly recognized *Amygdaloideae*, *Maloideae*, *Prunoideae* as well as *Pyrinae*. Evolution of derived fruit types (pome, drupe, achene) has been shown to be more complex than traditionally hypothesized (Morgan & al. 1994; Potter & al. 2002; Potter & al. 2007).

In the newly defined *Spiraeoideae*, the most prominent result of molecular phylogenetic work is the recognition that the species of *Sorbus* L. fall into two major clades. As part of the first major clade, *Sorbus* s.str., which is closely related to *Pyrus* L., should include only pinnate-leaved species (Campbell & al. 2007; Potter & al. 2007; Lo & Donoghue 2012). In this clade, *S. domestica* L. should be placed in the monospecific genus *Cormus* Spach according to Lo & Donoghue (2012) because this species is sister to a clade formed by *Sorbus* s.str. and *Micromeles* Decne. according to chloroplast data, with a weakly supported incongruent placement of *Mi-*

cromeles as sister to *Aria* (Pers.) Host (see below) according to nuclear ITS sequences. If this approach were taken, the only species remaining in *Sorbus* found in Germany would be the type, *S. aucuparia* L. Chloroplast and combined chloroplast and nuclear data suggest that *Sorbus* species with simple leaves are not closely related to *Sorbus* s.str., but are a subclade of the second major clade also including *Cydonia* Mill., *Malus* Mill. and others. In this subclade of simple-leaved *Sorbus* species, Lo & Donoghue (2012) suggested to recognize the monospecific genera *Aria* (with *S. aria* (L.) Crantz apparently as *A. nivea* Host), *Chamaemespilus* Medik. (with *S. chamaemespilus* (L.) Crantz as *C. alpina* (Mill.) K. R. Robertson & J. B. Phipps) and *Torminalis* Medik. (with *S. torminalis* (L.) Crantz as *T. clusii* (M. Roem.) K. R. Robertson & J. B. Phipps). However, *Chamaemespilus* and *Torminalis* form a well-supported clade together with *Aria* and could also be included in *Aria* (Li & al. 2012a; Lo & Donoghue 2012; Sennikov 2014). Lo & Donoghue (2012) pointed out that the former inclusion of *Aria* and satellite genera in *Sorbus* reflects the finding that numerous apomictic microspecies in Europe and W Asia are of apparent hybrid origin involving species of *Aria* (incl. *Torminalis*) and *Sorbus* s.str. (Aas & al. 1994; Nelson-Jones & al. 2002). Maintainance of *Sorbus* as one genus would require sinking *Cotoneaster* Medik., *Crataegus* L., *Malus* Mill. and many other genera in *Pyrus* L. (Sennikov 2014), which is evidently even less desirable.

Rhamnaceae (J. W. Kadereit)
Phylogenetic studies in *Rhamnaceae*, focusing on *Frangula* Mill. and *Rhamnus* L., suggested that *Frangula* and *Rhamnus* are distinct genera, and that *Rhamnus* is best divided into *Rhamnus* s.str., the Old World genus *Oreoherzogia* W. Vent and the New World genus *Ventia* Hauenschild (Hauenschild & al. 2016). Of the German species of *Rhamnus*, *R. pumila* Turra falls into *Oreoherzogia*, in which it should be known as *O. pumila* (Turra) W. Vent. Following Hauenschild & al. (2016), *Rhamnus* s.str. and *Oreoherzogia* can be distinguished by the number of lateral leaf vein pairs (3–5 in *Rhamnus*, 6–20 in *Oreoherzogia*) and by the position of a seed furrow (lateral-medial in *Rhamnus*, dorso-medial in *Oreoherzogia*).

Urticaceae (J. W. Kadereit)
Evidence has been presented that the generic circumscription of *Parietaria* L. in relation to *Gesnouinia* Gaudich. and *Soleirolia* Gaudich. may require modification (Wu & al. 2013). However, no sufficiently well-sampled phylogeny is available yet to tackle this problem.

Myricaceae (J. W. Kadereit)
Myrica L. has been found to be diphyletic by Huguet & al. (2005). Following these authors (for discussion of nomenclature see their paper), *M. gale* L. lectotypifies the genus name *Myrica*, and *M. pensylvanica* Mirb. should be treated as *Morella pensylvanica* (Mirb.) Kartesz.

Onagraceae (C. M. Ritz)
Heterogeneity of *Epilobium* L. in stamen characters had already been noticed by Linnaeus. Several sections are recognized in the genus, of which only *E.* sect. *Chamaenerion* Ség. and *E.* sect. *Epilobium* grow in Germany. While the former has alternate leaves, weakly zygomorphic flowers with only a very short hypanthium, almost entire petals, recurved stamens of almost equal length, a recurved style and pollen in monads (type: *E. angustifolium* L.), *E.* sect. *Epilobium* has opposite leaves, actinomorphic flowers with a distinct hypanthium, emarginate petals, erect stamens of different length, an erect style and pollen in tetrads (lectotype: *E. hirsutum* L.). All phylogenetic analyses of the family, partly using a broad taxon sampling and both nuclear and plastid sequences (Baum & al. 1994; Levin & al. 2003, 2004) invariably demonstrated that *E.* sect. *Chamaenerion* is sister to the remainder of the genus. Considering this pattern of relationship, it is both possible to treat *E.* sect. *Chamaenerion* at generic rank on account of its morphological distinctness, as was done in most North American Floras, or to include it in *Epilobium*. If treated as a distinct genus, this would affect classification of *E. angustifolium*, *E. dodonaei* Will. and *E. fleischeri* Hochst. The name *Chamaenerion* has long been discussed controversially. *Chamaenerion* Ség. instead of *Chamaenerion* Hill or *Chamerion* Raf. has to be used according to Sennikov (2011).

As shown in the well-sampled phylogeny of *Onagraceae* by Levin & al. (2004), *Oenothera* L. is only monophyletic when *Calylophus* Spach, *Gaura* L. and *Stenosiphon* Spach are included, as was done by Wagner & al. (2007).

Lythraceae (J. W. Kadereit)
A phylogenetic analysis of *Lythraceae* including several species of *Lythrum* L. and *Peplis portula* L. (Morris 2007) clearly showed that *Peplis* L. is deeply nested in *Lythrum* and should, as already done by Webb (1967), be treated as *L. portula* (L.) D. A. Webb.

Malvaceae (J. W. Kadereit)
A well-sampled phylogenetic analysis of *Alcea* L., *Althaea* L., *Lavatera* L. and *Malva* L. using nuclear and plastid sequences by Escobar García & al. (2009) revealed that, probably with the exception of *Alcea*, these genera are not monophyletic. This had been shown before for *Lavatera* and *Malva* by Ray (1995). The two species of *Althaea* found in Germany fall into two only distantly related clades, with *Althaea hirsuta* L. as representative of one clade more closely related to *Malva* / *Lavatera* and *Althaea officinalis* L. as representative of the second clade more closely related to *Alcea*. Species of *Malva* fall into three separate clades, of which the one containing *M. alcea* L. and *M. moschata* L. is more closely related to one of two clades of *Lavatera* that contains *L. thuringiaca* L. than to a second clade of *Malva* with *M. verticillata* L., *M. sylvestris* L. and *M. neglecta*

Wallr. As is evident, these patterns of relationship require taxonomic changes. Escobar García & al. (2009) did not present a new classification of this "Malva alliance", but both Banfi & al. (2005, 2011) and Stace (2010) suggested to recognize an enlarged *Malva* containing *Lavatera* and *Althaea hirsuta* and relatives.

Resedaceae (J. W. Kadereit)

A phylogenetic analysis of a broad sample of *Resedaceae* using nuclear and plastid sequences by Martín-Bravo & al. (2007) demonstrated that *Reseda* L. is paraphyletic in relation to the genera *Ochradenus*, *Oligomeris* and *Randonia*. This group of genera consists of two major lineages, and the four species of *Reseda* found in Germany fall into both. *Reseda alba* L. and *R. luteola* L. fall into two different subclades of the lineage that also contains *Oligomeris*, whereas *R. lutea* L. and *R. odorata* L. fall into two different subclades of the lineage that also contains *Ochradenus* and *Randonia*. Although the authors argued that *Ochradenus* and *Randonia* should be recognized at generic rank, they do not propose subdivision of *Reseda* into smaller genera. If this should eventually be proposed, the name *Reseda* would have to be applied to a clade containing *R. lutea*, the type of the genus name.

Brassicaceae (M. A. Koch)

Brassicaceae, currently recognized to contain 325 genera in 51 tribes (Al-Shehbaz 2012; Koch & al. 2012; Kiefer & al. 2014), show high levels of homoplasy in almost every morphological character used in the circumscription of tribes and genera in the past. Consequently, reliable systematic concepts often have to be obtained from molecular data, and many changes of tribal and generic circumscriptions have become necessary.

Based on molecular data, *Erophila* DC. is nested in *Draba* L. (Jordon-Thaden & al. 2010) and should be included in that genus, and *E. verna* (L.) Chevall. should be known as *D. verna* L. If recognized at species rank, *E. praecox* (Stev.) DC. and *E. spathulata* Lang should be *D. praecox* (Stev.) and *D. spathulata* (Lang) Sadler, respectively.

Several species of a formerly widely defined *Arabis* L. have to be transferred to other genera: *A. glabra* (L.) Bernh. has to be treated as *Turritis glabra* L., *A. pauciflora* Garcke as *Fourraea alpina* (L.) Greuter & Burdet and *A. turrita* L. as *Pseudoturritis turrita* (L.) Al-Shehbaz (Koch & al. 1999, 2000, 2001; Karl & Koch 2014). None of these three genera groups in tribe *Arabideae* any longer (Koch & al. 2007; Couvreur & al. 2010). Even after these changes, *Arabis* is still a paraphyletic taxon. Since *A. alpina* L. is the type of the genus name, all remaining *Arabis* species might be transferred to newly introduced genera in the future.

Cardaminopsis Hayek is the sister group of *Arabidopsis thaliana* (L.) Heynh. (Koch & Matschinger 2007; Hohmann & al. 2014), and it has been widely accepted to include *Cardaminopsis* in *Arabidopsis* Heinh. The German species of *Cardaminopsis* will be *A. arenosa* (L.) Lawalrée, *A. halleri* (L.) O'Kane & Al-Shehbaz and *A. lyrata* subsp. *petraea* (L.) O'Kane & Al-Shehbaz (Al-Shehbaz 2012; Kiefer & al. 2014).

A new classification of *Thlaspi* L. was proposed four decades ago (Meyer 1973, 1979), recognizing the genera *Microthlaspi* F. K. Mey., *Noccaea* Moench and *Thlaspi* for species of *Thlaspi* s.l. in the German flora. This concept has been confirmed by a series of molecular studies (e.g. Mummenhoff & al. 1997a, 1997b; Koch & Mummenhoff 2001). *Microthlaspi* and *Noccaea* do not group in tribe *Thlaspideae*, but are members of tribe *Coluteocarpeae* (Koch & German 2013). For the German flora, *T. caerulescens* J. Presl & C. Presl, *T. cepaeifolia* (Wulfen) Koch and *T. montanum* L. were transferred to *Noccaea* and should be recognized as *N. caerulescens* (J. Presl & C. Presl) F. K. Mey., *N. cepaeifolia* (Wulfen) Rchb. and *N. montana* (L.) F. K. Mey., respectively. *Thlaspi perfoliatum*, with its two morphologically slightly differentiated cytotypes (*T. erraticum* Jord. and *T. improperum* Jord.; Koch & Bernhardt 2004), has to be included in *Microthlaspi* as *M. perfoliatum* (L.) F. K. Mey. It has also been proposed to combine most genera of tribe *Coluteocarpeae* in a broadly defined *Noccaea* (Al-Shehbaz 2012). However, since comprehensive molecular analyses of the entire tribe with its more than 125 species (Koch & German 2013) are lacking, this concept should not be followed at the moment.

Considering the German flora, *Alyssum saxatile* L. has been shown to be member of a clade including various species of *Aurinia* Desv., which is sister to *Bornmuellera* Hausskn. and *Clypeola* L. (Cecchi & al. 2010; Resetnik & al. 2013). Consequently, *A. saxatile* is best treated as *Aurinia saxatilis* (L.) Desv. All other *Alyssum* species in Germany belong to a then monophyletic *Alyssum*.

Integration of *Dentaria* L. in *Cardamine* L. (Carlsen & al. 2009) and of *Coronopus* Mill. in *Lepidium* L. (Al-Shehbaz & al. 2002; Mummenhoff & al. 2008) is strongly supported and both are nested in the respective genera in molecular analyses. The four *Dentaria* species of the German flora should be known as *Cardamine bulbifera* (L.) Crantz, *C. enneaphyllos* (L.) Crantz, *C. heptaphyllos* (Vill.) O. E. Schulz and *C. pentaphyllos* (L.) Crantz. *Coronopus didymus* (L.) Sm. and *C. squamatus* (Forrsk.) Asch. are now best treated as *Lepidium didymum* L. and *L. coronopus* (L.) Al-Shehbaz, respectively.

Pritzelago Kuntze and *Hymenolobus* Nutt. of tribe *Erysimeae* are best included in *Hornungia* Bernh. These three genera form a well-supported clade (Mummenhoff & al. 2001; Kropf & al. 2003), and it has been demonstrated that there is no single character that reliably distinguishes the three genera (Al-Shehbaz & Appel 1997). Consequently, the following names should be used: *Hornungia alpina* (L.) O. Appel, *H. petraea* (L.) Rchb. and *H. procumbens* (L.) Hayek.

Maximum-likelihood trees derived from ITS1 and ITS2 sequences available from BrassiBase (Koch & al. 2012; Kiefer & al. 2014; http://brassibase.cos.uni-heidelberg.de/ clearly show that *Cheiranthus cheiri* L. is nested in *Erysimum* L., where it should be called *E. cheiri* (L.) Crantz. *Hirschfeldia* Moench of tribe *Brassiceae* consists of one species only: *H. incana* (L.) Lagr.-Fossat is most closely related to *Erucastrum* C. Presl. (including its type, *E. virgatum* C. Presl.; Arias & al. 2014). However, since *Erucastrum* as currently treated is a polyphyletic genus, and various other *Erucastrum* species might be transferred to different genera in future (Arias & Pires 2012), it seems best to keep *Hirschfeldia* separate until various phylogenetic hypotheses have been tested in more detail.

Santalaceae (J. W. Kadereit)
Thesium L. was found to be monophyletic only when the genera *Austroamericum* Hendrych and *Thesidium* Sonder are included (Moore & al. 2010). Discussing the options of either sinking these two genera into *Thesium* or maintaining them, requiring splitting of *Thesium* in its traditional circumscription into several smaller genera, Moore & al. (2010) preferred the former option for morphological reasons.

Polygonaceae (K. Wesche)
In *Rumex* L. two monophyletic subgenera can be distinguished: *R.* subg. *Acetosa* (Mill.) Rech. f. and *R.* subg. *Rumex*. This is the approach currently chosen in most C European floras, although it is possible (but not mandatory) to raise these subgenera to generic rank (Hejný & Slavik 1990). According to molecular analyses, *R.* subg. *Acetosa* includes the sometimes separately treated *R.* subg. *Acetosella* (Meisn.) Rech. f. (Schuster & al. 2015). This is supported by shared morphological characters, e.g. the presence of hastate leaves.

The taxonomy of *Polygonum* L. has posed particular challenges. The traditional broad concept had survived two centuries in spite of repeated criticism including calls to split the genus into up to nine sections, which commenced as early as 1856 (Meisner 1856). Based on morphological evidence, Haraldson (1978) reinforced these earlier proposals for splitting *Polygonum*, which have since been confirmed by studies of both plastid and nuclear DNA markers (Lamb Frye & Kron 2003; Galasso & al. 2009; Schuster & al. 2015). *Polygonum* s.l. clearly is polyphyletic and should be split into several genera, partly even belonging to different tribes. Some details, however, are still controversial, given that new molecular studies continue to differ from preceding ones, and no final conclusions have been reached. Accordingly, all inferences remain somewhat tentative.

Species of tribe *Polygoneae* have outer tepals with one primary vein and include a range of life forms. *Polygonum* s.str. is characterized by a distinct pollen morphology and by outer tepals that do not develop large appendages in fruit (Schuster & al. 2011a). In Germany it comprises few, mainly ruderal species (*P. aviculare* L. agg. – including *P. arenastrum* Boreau, *P. oxyspermum* Ledeb. and *P. raii* Bab., the latter sometimes treated as a subspecies of *P. oxyspermum*). In our context, these species are distinct by having essentially solitary or at the most approximate flowers in axillary glomerules and a silvery ochrea. Genetic studies support the monophyly of *Polygonum* L. s.str. (Schuster & al. 2015).

A clade related to *Polygonum* L. s.str. contains the genera *Reynoutria* Houtt. and *Fallopia* Adans. Their taxonomy is notorious for frequent changes and their treatment is inconsistent among C European Floras (Fischer & al. 2008; Jäger 2011; Tison & de Foucoult 2014). *Fallopia* in its traditional circumscription contains mostly lianas, while *Reynoutria* includes extremely tall herbs that are invasive in many regions. Both taxa share the presence of extrafloral nectaries and have wings on the floral bracts. Viable intergeneric hybrids are known, and polyploidy and extreme morphological variability add to the taxonomic difficulties. In consequence, *Reynoutria* has often been included in a broader *Fallopia* s.l., where it was treated as a section. Uncertainty about the treatment of the two genera pertains, although molecular approaches have used both chloroplast and nuclear markers for a very good taxonomic coverage. These studies support the monophyly of each of the two genera (Schuster & al. 2011b, 2015). The S hemisphere *Muehlenbeckia* Meisn., however, has been identified as closely related (Haraldson 1978), and recent molecular studies implied that it is indeed sister to *Fallopia* (Schuster & al. 2011b, 2015). This is in line with the fact that both *Fallopia* and *Muehlenbeckia* share a base chromosome number of 10 (11 in *Reynoutria*) and contain flavones (absent in *Reynoutria*). Including *Reynoutria* but not *Muehlenbeckia* in a broadly circumscribed *Fallopia* would thus result in a polyphyletic group. In view of this, keeping *Fallopia*, *Muehlenbeckia* and *Reynoutria* as separate genera currently is the best – but not necessarily final – solution.

The second large tribe relevant for relationships of *Polygonum* s.l. in Germany are the *Persicarieae*, which are monophyletic and morphologically distinct by the presence of three veins arising from the base of the tepals, of nectaries and of non-dilated stamen filaments (Lamb Frye & Kron 2003; Kim & Donoghue 2008; Sanchez & Kron 2008). The tribe includes *Aconogonon* (Meisn.) Rchb., *Bistorta* Mill. and *Persicaria* (L.) Mill. *Persicaria* is characterized by spicate or capitate panicles, a usually entire but often ciliate or pectinate ochrea, and has 4–8 stamens and 4 or 5 tepals. All recent treatments agree that it is monophyletic and should be excluded from tribe *Polygoneae* (Kim & Donoghue 2008; Fan & al. 2013). Thus, the following combinations should be used for the German species: *Persicaria amphibia* (L.) Delarbre, *P. hydropiper* (L.) Delarbre, *P. lapathifolia* (L.) Delarbre, *P. maculosa* Gray, *P. minor* (Huds.) Opiz, *P. mitis* (Schrank) Assenov and *P. pensylvanica* (L.) M. Gómez. Except

for *P. maculosa* (formerly *Polygonum persicaria* L.), epithets could be directly adopted from former names in *Polygonum*. Although the highly variable *P. amphibia* is a morphologically distinct taxon within *Persicaria* (Kim & Donoghue 2008), there is no need to raise it to genus level (Galasso & al. 2009).

Bistorta Mill. is morphologically distinct (with a rosette of basal leaves and usually only one terminal, spicate panicle), and both chloroplast and nuclear data imply that it is monophyletic within *Persicarieae* (Kim & Donoghue 2008; Fan & al. 2013). Molecular approaches, however, are not fully consistent with respect to its exact relationships to *Aconogonon* and *Koenigia* L. Nonetheless, most current Floras and also molecular studies (Galasso & al. 2009; Sanchez & al. 2011; Schuster & al. 2011a) accept its generic rank. The German species thus have to be named *B. officinalis* Delarbre and *B. vivipara* (L.) Delarbre (formerly *Polygonum bistorta* L. and *P. viviparum* L., respectively).

The taxonomy of *Aconogonon* is particularly complicated. Species in this group have been placed in *Persicaria*, *Polygonum* or *Rubrivena* M. Král (the last for *A. polystachyum* (Meisn.) Small as the only species of *Aconogonon* s.l. occurring in Germany). Recent molecular studies implied that *Aconogonon* species are distinct from *Bistorta* and *Persicaria*, but also revealed their close relationship with the mostly boreal and polar *Koenigia* (Galasso & al. 2009; Sanchez & al. 2009). *Aconogonon* and *Koenigia* have broadly similar pollen, and the two genera cannot easily be separated by morphological characters. Studies based on cpDNA have suggested that *Koenigia* in its traditional circumscription may be nested between *Aconogonon* and *Rubrivena* (Sanchez & al. 2011). The so-far most comprehensive study covering many taxa and employing both cpDNA and nuclear markers (Schuster & al. 2015) confirms this close relationship and finds one large clade that comprises all analysed species of *Aconogonon* and *Koenigia* (and *Rubrivena*). While most *Koenigia* species form a distinct group, some (but not all!) accessions of *K. delicatula* (Meisn.) H. Hara are sister group to a clade comprising other *Aconogonon* and *Koenigia* species (incl. *A. polystachyum*). This implies that *Koenigia* in its traditional sense is not monophyletic. Relationships of *Aconogonon* are even more puzzling, with a number of polyploid *Aconogonon* species being more closely related to *Koenigia* than to other members of the genus. Moreover, different accessions of some *Aconogonon* species appear on very different branches in the *Aconogonon* / *Koenigia* clade. Details of the evolution of this group clearly are not fully understood, and thus Schuster & al. (2015) advocate the fusion of all taxa in one large genus. They propose to unite them under the name *Koenigia*, which was chosen for priority reasons. These authors also draw the necessary taxonomic consequences and provide the new combination *K. polystachya* (Meisn.) T. M. Schust. & Reveal.

Though using a somewhat smaller species set, Fan & al. (2013) also presented a comprehensive molecular study, which confirmed the odd position of *K. delicatula* (plus one *Aconogonon* species). In their analysis, *A. polystachyum* is nested within other *Aconogonon* species, which jointly form the sister clade to the core *Koenigia* species. Fan & al. (2013) also discussed the possibility to adopt a broad concept of *Koenigia*. However, they acknowledged that merging the larger *Aconogonon* in the smaller *Koenigia* is somewhat impractical and also remarked on the apparently different chromosome base numbers in the two groups. They advocated keeping the two genera independent and placing the odd *K. delicatula* in a new monospecific genus, for which no valid name is available yet. This would also be supported by some of its morphological features that are transient to *Persicaria*. Splitting the whole complex into several, partly new genera indeed is an alternative solution to the problem implied by the tree of Schuster & al. (2015), but would presumably result in the formation of many small genera such as *Rubrivena*. Given that details of the evolution of *Acononogon* / *Koenigia* remain unclear, I opt for an intermediate position. The special position of *Aconogonon* and *Koenigia* in *Persicarieae* is undebated, but instead of drawing far-reaching taxonomic consequences, I rather acknowledge the level of uncertainty by keeping *Aconogonon* as a separate genus for the time being. In line with Fan & al. (2013), I regard evidence for a separate genus *Rubrivena* as questionable and maintain the established name *A. polystachyum* for the taxon occurring in C Europe.

Caryophyllaceae (M. S. Dillenberger)

Regarding generic delimitations in the *Caryophyllaceae*, Greenberg & Donoghue (2011) stated: “none of the eight largest genera (*Arenaria*, *Cerastium*, *Dianthus*, *Gypsophila*, *Minuartia*, *Paronychia*, *Silene*, *Stellaria*) appear to be strictly monophyletic”. For some genera taxonomic adjustments have already been made (e.g. Dillenberger & Kadereit 2014), but not for all. All taxonomic changes that were recently made for taxa in the German flora, or that need to be made in the future, are related to these eight genera.

There are several problems concerning the monophyly of *Cerastium* L. and *Stellaria* L. *Cerastium* is an almost cosmopolitan genus with about 100 species. *Stellaria* is cosmopolitan, too, and contains c. 120 species (Mabberley 2008). Both genera have emarginate to deeply lobed petals, but this character is shared with other genera, e.g. *Myosoton* Moench (Bittrich 1993). *Myosoton* is a monospecific genus, with *M. aquaticum* (L.) Moench as its only species. This species has recently (Jäger 2011; Seybold 2011) been treated as part of *Stellaria*, as *S. aquatica* L. This is congruent with the findings of Greenberg & Donoghue (2011), where *S. aquatica* is nested with good support in a clade of several *Stellaria* species, including *S. media* (L.) Vill. but not the

type of *Stellaria*, *S. holostea* L., and is closely related to *S. bungeana* Fenzl. Unfortunately, *Stellaria* does not become monophyletic by including *Myosoton*. With good support, *S. holostea* is sister to a clade containing the largest part of *Stellaria*, but also *Cerastium*, *Holosteum* L. and *Moenchia* Ehrh. Furthermore, *Cerastium* is not monophyletic since a well-supported clade of two species, *C. cerastoides* (L.) Britton and *C. dubium* (Bastard) Guépin, is sister to *Holosteum*. This position is poorly supported, but *Moenchia* is sister to the rest of *Cerastium* with good support, making it impossible to retain the two *Cerastium* species in *Cerastium* without including at least *Moenchia*. To amend these various violations of monophyly there are at least two possible solutions:

(1) The first solution is to merge *Cerastium*, *Holosteum*, *Moenchia* and *Stellaria* (including *Myosoton*) in one large genus with c. 230 species. Which name among those with equal priority (i.e. *Cerastium*, *Holosteum* and *Stellaria*) is correct for this genus needs further investigation. This genus combines most species with deeply lobed petals, but also some species with entire or emarginate petals.

(2) The second solution is to change generic circumscriptions and to describe new genera. On the basis of the phylogeny of Greenberg & Donoghue (2011), it is clear that *Stellaria* needs to be split into different genera. *Stellaria* retains only *S. holostea* and probably closely related species that were not included in the phylogeny of Greenberg & Donoghue (2011). The largest number of *Stellaria* species have to be transferred to a new genus. This new genus contains all former German *Stellaria* species except *S. holostea*. This genus is then sister to a clade containing *Cerastium*, *Holosteum* and *Moenchia*. *Moenchia* can be retained unmodified and is sister to *Cerastium*. *Cerastium* contains all German species with four or more styles. The two species with three styles that are sister to *Holosteum*, i.e. *C. cerastoides* and *C. dubium*, are best included in *Holosteum*, which also has three styles, or those two species (and maybe other *Cerastium* species from other regions with three styles) should be treated as a new genus. Both solutions require a large number of taxonomic changes and a decision between them cannot be easily made. However, changes in the circumscription of the above genera are inevitable.

In *Gypsophila* L. and relatives of interest (i.e. *Dianthus* L., *Petrorhagia* (Ser.) Link and *Vaccaria* Wolf.) two issues need to be discussed. The first is the treatment of *Vaccaria*. *Vaccaria* is a monospecific genus containing only *V. hispanica* (Mill.) Rauschert. This species is native to Eurasia, especially the Mediterranean region, but has become naturalized in large parts of the world (S Africa, Australia and North and South America). The phylogeny of Greenberg & Donoghue (2011) unambiguously placed *Vaccaria* within *Gypsophila*. It differs from *Gypsophila* mainly by its calyx wings. The position in the phylogeny allows two alternative solutions.

(1) *Vaccaria* remains a monospecific genus that is sister to the largest part of *Gypsophila*. Therefore at least *G. takhtadzhanii* Schischk. ex Ikonn. has to be excluded from *Gypsophila* because it is sister to *Vaccaria* and the rest of *Gypsophila*.

(2) *Vaccaria hispanica* is included in *Gypsophila* as *G. vaccaria* (L.) Sm.

I prefer the second solution for different reasons. *Vaccaria* is quite similar to *Gypsophila* and its inclusion in that genus will not require large changes in the circumscription of *Gypsophila*. The other point is that it is difficult to justify splitting *Gypsophila* into different genera only to retain *Vaccaria* as an independent genus. As Greenberg & Donoghue (2011) included only few of the 150 *Gypsophila* species in their phylogeny, I cannot foresee to what extent an independent *Vaccaria* would affect subdivision of *Gypsophila*.

The second issue concerns the paraphyly of *Petrorhagia* in relation to *Dianthus*, and the position of *Gypsophila muralis* L. and several other *Gypsophila* species from outside Germany as sister to *Dianthus* and *Petrorhagia* instead of being part of the rest of *Gypsophila*. *Petrorhagia* is a genus with 33 species distributed from the Canary Islands across the Mediterranean region to Kashmir (Mabberley 2008). Although the phylogeny of Greenberg & Donoghue (2011) contains only three species of *Petrorhagia*, it unambiguously shows that the genus is paraphyletic. Two solutions seem possible:

(1) *Dianthus*, *Petrorhagia* and *Gypsophila muralis* (and some more *Gypsophila* species from outside Germany) are included in a more broadly circumscribed *Dianthus*.

(2) *Petrorhagia* is split into at least two genera, and *G. muralis* is transferred into a new, probably monospecific genus. Regarding the other *Gypsophila* species in this group from outside Germany, this solution would require establishing additional small to monospecific genera for those *Gypsophila* species. *Dianthus*, *Petrorhagia* and the *Gypsophila* species of this clade show some morphological variation. It is difficult to decide whether this variation is sufficient to justify splitting *Petrorhagia* into different genera that can be distinguished from each other and from *Dianthus* and the small genera containing former *Gypsophila* species, or whether all species of this clade are sufficiently alike to be merged into one genus, i.e. *Dianthus*. Linnaeus (1753a) described the type of *Petrorhagia*, *P. saxifraga* (L.) Link, as *D. saxifragus* L., *P. prolifera* (L.) P. W. Ball & Heywood as *D. prolifer* L., but no name for *G. muralis* is available in *Dianthus*.

Minuartia L. (sensu McNeill 1962) comprises about 175 species that are distributed in the N hemisphere. It was delimited from most other genera of *Caryophyllaceae* by a combination of three styles and three capsule valves. Molecular phylogenies revealed that the genus consists of ten independent lineages (Fior & al. 2006; Harbaugh & al. 2010; Greenberg & Donoghue 2011; Dillenberger & Kadereit 2014), each of which is closest relative of another genus or group of genera. According to Dillenberger & Kadereit (2014) the genus is best divided into 11 genera instead of including other genera

in *Minuartia*. The ten lineages were divided into 11 genera because in one case there was no morphological or karyological character or combination of characters to define this clade as one genus. Therefore two subclades with more uniform morphologies were described as genera. Including other genera in *Minuartia* would have affected most genera of subfam. *Alsinoideae* or subfam. *Alsinoideae* and subfam. *Caryophylloideae*. In consequence, several species of *Minuartia* in the C European flora need to be treated as part of other genera. *Minuartia* species transferred to other genera are: *Cherleria sedoides* L. (*M. sedoides* (L.) Hiern), *Facchinia cherlerioides* (Sieber) Dillenb. & Kadereit (*M. cherlerioides* (Sieber) Bech.), present in the German flora only with *F. cherlerioides* subsp. *aretioides* (Port. ex J. Gay) Dillenb. & Kadereit, *F. rupestris* (Scop.) Dillenb. & Kadereit (*M. rupestris* (Scop.) Schinz & Thell.), *Sabulina austriaca* (Jacq.) Rchb. (*M. austriaca* (Jacq.) Hayek), *S. stricta* (Sw.) Rchb. (*M. stricta* (Sw.) Hiern), *S. tenuifolia* (L.) Rchb. (*M. hybrida* (Vill.) Schischk.), *S. verna* (L.) Rchb. (*M. verna* (L.) Hiern) and *S. viscosa* (Schreb.) Rchb. (*M. viscosa* (Schreb.) Schinz & Thell.). The only two species in Germany that remain in *Minuartia* are *M. rubra* (Scop.) McNeill and *M. setacea* (Thuill.) Hayek.

Silene L. contains c. 700 species that are restricted to the N hemisphere (Mabberley 2008). Although the genus is large, there exist only small problems with its monophyly. One point concerns *Lychnis* L., which contains c. 20 species distributed in N-temperate and arctic regions (Bittrich 1993). Its treatment as separate from *Silene* L. has repeatedly been regarded as doubtful (see Oxelman & Lidén 1995). *Lychnis* has usually five styles and five capsule teeth, whereas *Silene* has three or five styles and six or ten capsule teeth. Even the most recent phylogeny of the *Caryophyllaceae* could not unambiguously determine the position of *Lychnis* (Greenberg & Donoghue 2011). In that study *Silene* seems to be paraphyletic in relation to *Lychnis*. However, this position is not well supported, and a change of position is possible. For the moment, the species of *Lychnis* in the German flora, i.e. *L. coronaria* (L.) Desr. and *L. flos-cuculi* L., should be maintained, but future inclusion in *Silene*, as *S. coronaria* (L.) Clairv. and *S. flos-cuculi* (L.) Clairv., seems likely.

The second problem is related to *Cucubalus baccifer* L. Although *Silene* is not sufficiently well supported, the position of *C. baccifer* seems to be clearly within *Silene* (Greenberg & Donoghue 2011). Therefore it seems advisable to treat this species as *S. baccifera* (L.) Roth.

Several problems hinge on the acceptance of *Heliosperma* Rchb. and other smaller genera. When accepting *Heliosperma*, several smaller genera need to be recognized in order to keep *Silene* monophyletic. One of these genera is *Atocion* Adans. Based on a molecular phylogeny, Lidén & al. (2001) excluded five species, including *S. armeria* L. and *S. rupestris* L., from *Silene* and included them in *Atocion*. These results were verified with a large sample of *Silene* and related genera by Greenberg & Donoghue (2011) and should have taxonomic consequences. *Atocion* is sister to *Viscaria* Bernh. and the names for the two species are *A. armeria* (L.) Raf. and *A. rupestre* (L.) Oxelman. An inclusion of *Atocion* in *Silene* would also affect *Eudianthe* Rchb., *Heliosperma* and *Viscaria* and is therefore not desirable. *Atocion* is glabrous, has elliptic or oblanceolate leaves, a regular dichasium, and flowers with entire or emarginate petals and three stigmas (Lidén & al. 2001). *Silene* species with the same character combination of hairiness, inflorescence type and stigma number have lower leaves that are spathulate and petals that are usually lobed. Furthermore, these *Silene* species have anastomosing calyx veins, but *Atocion* has non-anastomosing veins (Lidén & al. 2001).

Irrespective of the inclusion of *Lychnis* in *Silene* or its separate treatment, *L. viscaria* L. is not part of either of these two genera. The species clearly belongs to a well-supported clade that is sister to *Atocion* (Greenberg & Donoghue 2011). The correct genus name for the species of this clade is *Viscaria* Bernh., and *L. viscaria* should be known as *V. vulgaris* Bernh. *Viscaria vulgaris* is the type of *Viscaria*.

Another problem is related to *Silene pusilla* Waldst. & Kit., which is nested in the well-supported *Heliosperma* (Rchb.) Rchb. The inclusion of *S. pusilla* in *Heliosperma* as *H. pusillum* (Waldst. & Kit.) Rchb. is justified and necessary.

Chenopodiaceae (G. Kadereit)

Chenopodium L. in its traditional wide circumscription, comprising c. 150 spp. worldwide, has been shown to be highly polyphyletic with *Chenopodium* lineages spread all over the phylogeny of subfam. *Chenopodioideae* (Kadereit & al. 2010; Fuentes-Bazán & al. 2012a, 2012b). According to Fuentes-Bazán & al. (2012a, 2012b), species of *Chenopodium* belong to six different genera: *Blitum* L., *Chenopodiastrum* S. Fuentes & al., *Chenopodium* L. s.str., *Dysphania* R. Br., *Lipandra* Moq. and *Oxybasis* Kar. & Kir. Although the sampling for the molecular analyses was far from complete, the polyphyly of *Chenopodium* seems well supported and future studies will reveal where unsampled species belong. Twenty of the 23 species of former *Chenopodium* occurring in the German flora were included in the molecular studies by Fuentes-Bazán & al. (2012a, 2012b), and these are distributed among all six genera. *Blitum* is represented by three species: *B. bonus-henricus* (L.) Rchb. (*C. bonus-henricus* L.), *B. capitatum* L. (*C. capitatum* (L.) Aschers.) and *B. virgatum* L. (*C. foliosum* Aschers.). *Chenopodiastrum* is represented by *Chenopodiastrum hybridum* (L.) S. Fuentes & al. (*Chenopodium hybridum* L.) and *Chenopodiastrum murale* (L.) S. Fuentes & al. (*Chenopodium murale* L.). Species with glandular hairs and an aromatic odour clearly need to be classified in *Dysphania*, which is only distantly related to core *Chenopodium*. In the German flora these are *D. ambrosioides* (L.) Mosyakin & Clemants (*C. ambrosioides* L.), *D. botrys* (L.) Mosyakin & Clemants

(*C. botrys* L.), *D. pumilio* (R. Br.) Mosyakin & Clemants (*C. pumilio* R. Br.) and *D. schraderiana* (Schult) Mosyakin & Clemants (*C. schraderianum* Schult). *Lipandra* is represented by *L. polysperma* (L.) S. Fuentes & al. (*C. polyspermum* L.) and *Oxybasis* by *O. chenopodioides* (L.) S. Fuentes & al. (*C. botryodes* Sm.), *O. glauca* (L.) S. Fuentes & al. (*C. glaucum* L.), *O. rubra* (L.) S. Fuentes & al. (*C. rubrum* L.) and *O. urbica* (L.) S. Fuentes & al. (*C. urbicum* L.). Of the remaining species present in the German flora, *Chenopodium album* L., *C. berlandieri* Moq., *C. ficifolium* Sm., *C. opulifolium* Schrader ex Koch & Ziz, *C. patericola* Rydb. and *C. vulvaria* L. belong to *Chenopodium* s.str. *Chenopodium hircinum* Schrader, *C. strictum* Roth and *C. suecicum* Murr have not yet been included in molecular analyses. *Chenopodium aristatum* L. (*Dysphania aristata* (L.) Mosyakin & Clemants) is a neophyte in the German flora and should be treated as *Teloxys aristata* (L.) Moq. This monospecific genus is closely related to *Cycloloma* Moq., *Dysphania* and *Suckleya* A. Gray (Kadereit & al. 2010; Fuentes-Bazán & al. 2012a).

Halimione Aellen is well-supported sister group of the large genus *Atriplex* L., from which it can be distinguished by unique seed and fruit characters (Kadereit & al. 2010). Inclusion of *Halimione* into *Atriplex* as proposed in Sukhorukov (2006) is possible, but not recommended by the present author (G. Kadereit).

Bassia All. and *Kochia* Roth were both found to be polyphyletic in molecular studies (Kadereit & Freitag 2011; Kadereit & al. 2014). Most species of *Kochia* including the two species present in Germany, *K. laniflora* (S. G. Gmelin) Borbás and *K. scoparia* (L.) Schrader, have been included in *Bassia*, and the remaining species were classified in two new genera, *Eokochia* Freitag & G. Kadereit and *Grubovia* Freitag & G. Kadereit. Other species of *Bassia* (*B. dasyphylla* Kuntze, *B. hirsuta* (L.) Kuntze and *B. sedoides* (Schrad.) Asch.) needed to be transferred to new genera (*Grubovia dasyphylla* (Fisch. & C. A. Mey.) Freitag & G. Kadereit, *Spirobassia hirsuta* (L.) Freitag & G. Kadereit and *Sedobassia sedoides* (Schrad.) Freitag & G. Kadereit) in order to define monophyletic genera in *Camphorosmeae* (Kadereit & Freitag 2011). Of these new genera only *Spirobassia* (*S. hirsuta*) occurs in Germany.

Salsola L. is a large and highly polyphyletic genus (Akhani & al. 2007). Unfortunately there is disagreement among experts concerning the typification of *Salsola*. Mosyakin & al. (2014) proposed a conserved type, *S. kali* L., while Akhani & al. (2014) argued in favour of the current type, *S. soda* L. If *S. soda* is accepted as type of *Salsola*, *S. kali* has to be included in *Kali* Mill., as *Kali soda* Moench (Akhani & al. 2007).

Nyctaginaceae (J. W. Kadereit)
As shown by Levin (2000), *Oxybaphus* Willd. is clearly part of *Mirabilis* L. where it should have the rank of section. Accordingly, *O. nyctagineus* (Michx.) Sweet should be treated as *M. nyctaginea* (Michx.) MacMill.

Hydrangeaceae (J. W. Kadereit)
Although *Philadelphus* L. appears to be paraphyletic in relation to the monospecific *Carpenteria* Torr. (Guo & al. 2013), classification of *P. coronarius* L. as a *Philadelphus* would not be affected as *P. coronarius* is the type of the genus name. *Philadelphus inodorus* L. falls into the same clade as *P. coronarius*.

Primulaceae (J. W. Kadereit)
Mast & al. (2001) demonstrated that *Cortusa* L. is deeply nested in *Primula* L. Accordingly, it should be treated as *P. matthioli* (L.) V. A. Richt.

As summarized by Manns & Anderberg (2009), several studies using either nuclear, plastid or both nuclear and plastid sequences have shown that a non-monophyletic *Anagallis* L. (incl. *Centunculus* L.), *Glaux* L. and *Trientalis* L. (as well as the non-C-European genera *Asterolinon* Hoffsgg. & Link and *Pelletiera* A. St. Hil.) are all nested in a highly paraphyletic *Lysimachia* L. Based on a careful consideration of morphological variation in this group of genera, and facing the choice between including all in *Lysimachia* or splitting *Lysimachia* in such a way that at least some of the above genera can be maintained, Manns & Anderberg (2009) argue: "It is, however, difficult to establish morphological characters to distinguish between different subgroups within *Lysimachia* and the morphological distinctiveness of these subgroups is not very high. Furthermore, the characters used to recognize *Lysimachia* are also present in *Anagallis* and to large extent also in *Asterolinon*, *Pelletiera* and *Trientalis*. Consequently, proposal of new genera for some *Lysimachia* (e.g. *L. nemorum* L. and *L. serpyllifolia* Schreb.), or transfer of *L. nemorum* and allied taxa to *Anagallis* would inevitably result in poorly diagnosed genera. Choosing among alternatives, we find it better to merge the smaller segregate genera with *Lysimachia*, rather than splitting *Lysimachia* further." Through earlier work and the work by Banfi & al. (2005) and Manns & Anderberg (2009) combinations are available for C European *Anagallis* (plus *Centunculus*), *Glaux* and *Trientalis* as species of *Lysimachia*. These would be *L. arvensis* (L.) U. Manns & Anderb. (*Anagallis arvensis* L.), *L. europaea* (L.) U. Manns & Anderb. (*Trientalis europaea* L.), *L. foemina* (Mill.) U. Manns & Anderb. (*A. foemina* Mill.), *L. maritima* (L.) Galasso & al. (*Glaux maritima* L.) and *L. tenella* L. (*A. tenella* (L.) L.).

Ericaceae (M. D. Pirie)
Three genera have been recently re-delimited to make them monophyletic. The first is *Kalmia* L., which becomes monophyletic only after inclusion of *Loiseleuria* Desv. (Gillespie & Kron 2013). Accordingly, *Loiseleuria procumbens* (L.) Desv. should be known as *Kalmia procumbens* (L.) Gift & al. ex Galasso & al.

The second is *Rhododendron* L., with c. 850 species, which should include *Ledum* L. based on morphological evidence by Kron & Judd (1990) and molecular evidence

by, e.g., Goetsch & al. (2005). In Germany, the native *L. palustre* L. should be known as *R. tomentosum* Harmaja and the introduced *L. groenlandicum* Oeder as *R. groenlandicum* (Oeder) Kron & Judd.

The third is *Monotropa* L., which is replaced by *Hypopitys* Hill. in Jäger (2011). Evidence from nuclear encoded markers suggests that the type of *Monotropa*, *M. uniflora* L., and that of *Hypopitys*, *H. monotropa* Crantz (*M. hypopitys* L.), are more closely related to other monotropoid genera than to each other (Bidartondo & Bruns 2001). Species delimitation within *Hypopitys* is controversial, but resolution of the precise number and delimitation of species (including *H. hypophegea* G. Don in Germany) across its broad geographic range seems unlikely to further affect generic boundaries.

Problems in generic delimitation remain in *Vaccinium* L. A number of different genera are apparently nested between its c. 450 species, with no evidence to suggest that the type, *V. uliginosum* L., is closely related to any of the other species of the German flora, and clear indication that *V. myrtillus* L. is more closely related to species elsewhere (Powell & Kron 2002). As the specialists are apparently not in favour of expanding the circumscription of *Vaccinium* it is likely that name changes will yet be required, but the current phylogenetic hypothesis is insufficiently resolved and sampled to offer a solution.

Rubiaceae (F. Ehrendorfer)

Since more than 20 years ago, DNA-analytical phylogenetic studies on the critical tribe *Rubieae* (*Rubiaceae*) have become available (e.g. Ehrendorfer & al. 1994; Manen & al. 1994; Natali & al. 1995, 1996; Soza & Olmstead 2010a, 2010b; and particularly Ehrendorfer & Barfuss 2014: Fig. 1 & 2, with clades and their reference numbers). These studies have made it increasingly clear that the traditional genera *Asperula* L. and *Galium* L., both well represented in the flora of Germany (Jäger 2005), are polyphyletic in their present circumscriptions. Monophyly was documented only for *Cruciata* Mill., *Rubia* L. and *Sherardia* L. In order to achieve monophyly for *Asperula* and *Galium*, one would have to lump all these genera (and several others except *Rubia*) into a giant *Galium* s.latiss. with about 900 species worldwide and a very complex infrageneric classification.

If a more narrow generic concept for C European *Rubieae* is preferred, *Asperula* would have to be restricted to its type, the annual *A. arvensis* L., and its perennial sister taxon *A. taurina* L. (clade V-B). The large *A.* sect. *Cynanchicae* (DC.) Boiss. (with *A. cynanchica* L. and *A. neilreichii* Beck), centred in the Mediterranean area, is more closely related to *Sherardia* (both in clade V-A) than to *Asperula* s.str. and might also deserve separate generic status. This also applies to *A. tinctoria* L., a member of the traditional *A.* sect. *Glabella* Griseb. (clade V-C) with a disjunct Eurasian distribution. Also into clade V-C falls *Galium* sect. *Aparinoides* (Jord.) Gren., a subclade of limnic habitats with a worldwide distribution, typified by *G. palustre* L., a well-known element of the European flora. The morphological distinctness and deviating chromosome base number $x = 12$ (otherwise mostly $x = 11$ in *Rubieae*) also suggest generic separation of this subclade.

It was no surprise to find two *Galium* species (*G. boreale* L. and *G. rotundifolium* L.) from *G.* sect. *Platygalium* (DC.) W. D. J. Koch in the same clade (V-D) as the generally recognized genera *Cruciata* and *Valantia* L.: they all are characterized by whorls of two leaves and only two additional leaf-like stipules. This and the relevant DNA data could justify the transfer of *G. boreale* and *G. rotundifolium* to a separate genus, corresponding to *G.* sect. *Platygalium* s.latiss. (also including the former European genus *Trichogalium* Fourr., the American genus *Relbunium* (Endl.) Benth. & Hook. and probably also the monotypic *Microphysa* Schrenk from C Asia) with a worldwide distribution and up to 230 other, clearly related former *Galium* and *Relbunium* species centred in E Asia and the Americas.

The majority of the remaining C European *Galium* species (24 in Germany; Jäger 2005) always have leaves and leaf-like stipules in whorls of more than four (and up to 12). They are clearly verified as members of a worldwide "monophylum" that corresponds to clade VI and the genus *Galium* s.str. with about 350 predominantly Old World species. The relationships of its species in Germany correspond quite well with the following more or less DNA-supported taxonomic sections: *G.* sect. *Aparine* W. D. J. Koch (*G. aparine* L. and *G. spurium* L.), *G.* sect. *Aspera* (DC.) W. D. J. Koch, syn.: *G.* sect. *Microgalium* Griseb. (*G. parisiense* L.), *G.* sect. *Galium* (*G. album* Mill., *G. aristatum* L., *G. glaucum* L., *G. intermedium* Schultes [*G. schultesii* Vest], *G. lucidum* All., *G. mollugo* L., *G.* ×*pomeranicum* Retz., *G. sylvaticum* L., *G. truniacum* (Ronn.) Ronn. and *G. verum* L.), *G.* sect. *Hylaea* (Griseb.) Ehrend. (*G. odoratum* (L.) Scop.), *G.* sect. *Kolgyda* Dumort. (*G. tricornutum* Dandy and *G. verrucosum* Huds.), *G.* sect. *Leptogalium* (*G. anisophyllon* Vill., *G. megalospermum* All., *G. noricum* Ehrend., *G. pumilum* Murray, *G. saxatile* L., *G. sterneri* Ehrend. and *G. valdepilosum* H. Braun) and *G.* sect. *Trachygalium* K. Schum. (*G. uliginosum* L.).

A more detailed presentation of our current knowledge concerning relationships within tribe *Rubieae* in C Europe can be found in Kästner & Ehrendorfer (in press). Before one can begin to execute the possible and DNA-supported taxonomic and nomenclatural changes within the *Rubieae* discussed above, further critical research appears obligatory.

Gentianaceae (J. W. Kadereit)

Several phylogenetic studies of *Gentianaceae–Swertiinae* (Chassot & al. 2001; von Hagen & Kadereit 2001, 2002) have shown that generic circumscriptions in this group require substantial revision. Thus, it is evident that *Gentianella ciliata* (L.) Borkh. and *G. tenella* (Rottb.) Börner are only distantly related to *Gentianella* s.str.,

and should be treated as *Gentianopsis ciliata* (L.) Ma and *Comastoma tenellum* (Rottb.) Toyok., respectively. Even after exclusion of these (and related) species, *Gentianella* is polyphyletic, as is *Swertia* L. If this eventually should result in the recognition of several smaller genera, the generic identity of the remaining German species of *Gentianella* would remain unaffected as they fall into the same clade as the type of the genus name, *G. campestris* (L.) Börner. As *S. perennis* L. is the type of *Swertia*, recognition of segregate genera will not affect the generic identity of *S. perennis*. For descriptions and discussion of genera see Struwe & al. (2002). Inclusion of *Comastoma* (Wettst.) Toyok. and *Lomatogonium* A. Braun in *Gentianella*, as suggested by Banfi & al. (2005), who in consequence provided a combination for *L. carinthiacum* (Wulfen) Rchb. in *Gentianella*, is not justified by the data available unless a much larger number of lineages, including several lineages of *Swertia*, are included in *Gentianella*.

Oleaceae (J. W. Kadereit)

As first suspected by Wallander & Albert (2000) on the basis of plastid sequences, a monophyletic *Ligustrum* L. was found deeply nested in a paraphyletic *Syringa* L. using nuclear sequences (Li & al. 2002). In consequence, inclusion of *Ligustrum* in *Syringa* may have to be considered once stronger evidence for such relationship is available. Interestingly, one species of *Ligustrum*, *L. sempervirens* (Franch.) Lingelsh., sometimes classified as a separate genus, is intermediate in fruit morphology between *Syringa* (capsules) and *Ligustrum* (berries or drupes) by having berries that become leathery and eventually dehisce.

Plantaginaceae (D. C. Albach)

A hundred years ago, *Veronica* L. included all *Scrophulariaceae* with a tetramerous flower and short corolla tube, two stamens and a flattened capsule. In that circumscription the genus included approximately 300 species. Subsequent authors treated more and more groups of distinct species as separate genera, such as *Hebe* Juss. mainly from Australasia, *Pseudolysimachion* Opiz from Eurasia (*V. longifolia* L. and *V. spicata* L. in the German flora) and *Veronicastrum* Farw. from E Asia and E North America. The first DNA-based phylogenetic analyses (e.g. Albach & Chase 2001; Wagstaff & al. 2002; Albach & al. 2004a) supported the separation of some genera (*Paederota* L. and *Veronicastrum*), but demonstrated that most genera split off in the 19th and 20th centuries are nested in a lineage that should be recognized as a monophyletic *Veronica*. These results caused a sometimes heated discussion on whether autapomorphies need to be considered as important as symplesiomorphies (e.g. Brummitt 2006). However, subsequent analyses added support to the molecular results and demonstrated that autapomorphies of these segregate genera are not as clear as sometimes believed, and that morphological transitions between *Veronica* and groups considered distinctive commonly exist. For example, such transitional species between *Pseudolysimachion* and *Veronica* occur in E Asia and Japan (Albach 2008). Thus, based on molecular and morphological arguments, these analyses suggest inclusion of these genera in *Veronica* rather than further splitting (Albach & al. 2004b; Garnock-Jones 2007). In C Europe, reintegration of Australasian *Hebe* and relatives and North American *Synthyris* Benth. will be of interest mainly to horticulturists, but reintegration of *Pseudolysimachion*, the species of *Veronica* with dense, spicate inflorescences, reverses a split adopted by many European Floras since the 1960s (Holub & Pouzar 1967). All European species of *Pseudolysimachion* were originally described as species of *Veronica*. Therefore, only taxonomic changes at the intraspecific level were necessary (Albach 2008).

Lamiaceae (M. S. Dillenberger)

Ballota L. contains c. 30 species that occur in Europe, the Mediterranean area, W Asia and, with one species, S Africa (Mabberley 2008). Several species of *Ballota* were included in a phylogenetic analysis of subfam. *Lamioideae* (Bendiksby & al. 2011b). This phylogeny unambiguously showed that *Ballota* is not monophyletic. The type of *Ballota*, *B. nigra* L. (the only species of the genus in Germany), is well-supported sister to *Marrubium* L., represented in the German flora by *M. peregrinum* L. and *M. vulgare* L. The other *Ballota* species are sister to this *B. nigra–Marrubium* clade. Only two other *Ballota* species, *B. frutescens* (L.) Woods and *B. integrifolia* Benth., form a separate clade that is sister to the former clade and a clade containing species of *Moluccella* L., *Otostegia* Benth. and *Sulaimania* Hedge & Rech. f. There are two solutions to obtain a monophyletic *Ballota*. The first is to merge all species of this clade (i.e. *Ballota*, *Marrubium*, *Moluccella*, *Otostegia* and *Sulaimania*) in one genus. The second solution is to exclude *B. frutescens* and *B. integrifolia* from *Ballota* and to combine the rest of *Ballota* including *B. nigra* and *Marrubium* in one genus. In order to avoid creation of one very large and heterogeneous genus, it seems reasonable to take the second approach. Since both genera were described by Linnaeus (1753b), it remains unclear at this point which genus name should be used. *Marrubium* contains 40 species (Mabberley 2008), so that a comparable number of new combinations would be needed when using either name.

The treatment and circumscription of *Clinopodium* L. is very different in different Floras of Germany (e.g. Jäger & Werner 2005; Jäger 2011; Seybold 2011). *Clinopodium* in its broad circumscription, including *Acinos* Mill., *Bancroftia* Billb., *Calamintha* Mill., New World *Micromeria* Benth. and *Satureja* L. contains c. 100 species and is almost cosmopolitan (Mabberley 2008). Seybold (2011) included *Acinos* and *Calamintha*, but not *Satureja*, in *Clinopodium*, and Jäger & Werner (2005) treated *Acinos*, *Calamintha*, *Clinopodium* and *Satureja* as separate

genera. A molecular phylogeny of subtribe *Menthinae* illustrates the whole dimension of the problem (Bräuchler & al. 2010). In this phylogeny, *Clinopodium* is highly polyphyletic and numerous genera are nested among different *Clinopodium* clades. The species of *Acinos* form a well-supported clade together with *Ziziphora* L., a genus of c. 20 species distributed from the Mediterranean area to C Asia, Afghanistan and Himalaya (Mabberley 2008). In this clade, *Acinos* and *Ziziphora* are not supported as monophyletic. *Calamintha* species are in a well-supported clade with the type and other species of *Clinopodium*. Another genus that causes problems with respect to the monophyly of *Clinopodium* is *Monarda* L., a small genus of c. 16 mostly North American species (Mabberley 2008) occurring in Germany with one introduced species, *M. didyma* L. (Jäger & Werner 2005). The large number of genera, species and clades makes several solutions possible. For the German species only two solutions need to be discussed. The first is to include all species of *Acinos*, *Calamintha*, *Clinopodium* and *Monarda* in one genus, together with the whole or parts of *Acanthomintha* (A. Gray) A. Gray, *Blephilia* Raf., *Bystropogon* L'Hér., *Conradina* A. Gray, *Cuminia* Colla, *Cunila* D. Royen ex L., *Cyclotrichium* Mandenova & Schengelia, *Dicerandra* Benth., *Glechon* Spreng., *Hedeoma* Pers., *Hesperozygis* Epling, *Hoehnea* Epling, *Killickia* Bräuchler & al., *Mentha* L., New World *Micromeria* Benth., *Minthostachys* (Benth.) Spach, *Monardella* Benth., *Obtegomeria* Doroszenko & P. D. Cantino, *Piloblephis* Raf., *Poliomintha* A. Gray, *Pycnanthemum* Michx., *Rhododon* Epling, *Stachydeoma* (Benth.) Small and *Ziziphora*. Alternatively, *Clinopodium* can be split into clades which could be treated as morphologically recognizable genera. In view of substantial morphological variation of the lineages concerned it is not meaningful to merge so many genera only to prevent *Clinopodium* from being split. Although it is not clear how exactly *Clinopodium* will be split in the future, the impact of this approach on German species can easily be seen. Since *Calamintha* is very closely related to the type of *Clinopodium*, and this relationship is well supported, there is no other solution than to transfer *Calamintha* to *Clinopodium*. The *Calamintha* species in Germany, *C. menthifolia* Host and *C. nepeta* (L.) Savi, will have to become known as *Clinopodium menthifolium* (Host) Stace and *Clinopodium nepeta* (L.) Kuntze. No species name in *Clinopodium* is available for the hybrid taxon *Calamintha* ×*foliosa* Opiz; at subspecies level *Clinopodium nepeta* nothosubsp. *subisidoratum* (Borbás) Govaerts has been used. It is not possible to treat the species of *Acinos* as part of *Clinopodium* without including in *Clinopodium* all genera listed above. Although the relationships between *Acinos* and *Ziziphora* are not fully resolved, it seems necessary to combine these two genera in one genus. *Ziziphora* has priority over *Acinos*, and the species of *Acinos* accordingly need new names in *Ziziphora*. These are not yet available. The only German *Clinopodium* species, *C. vulgare* L., is the type of the genus name and will therefore most likely not be affected by any changes of generic circumscriptions. The only genus of this group that seems to be unproblematic is *Satureja*. This genus, together with *Gontscharovia* Boriss., is part of a polytomy with the *Clinopodium*-clade (the numerous genera listed above) and a clade of Old World *Micromeria* (Bräuchler & al. 2010). Even if *Satureja* is paraphyletic in relation to *Gontscharovia*, *Satureja* has priority over *Gontscharovia* and no taxonomic changes will be necessary in the German flora.

A long-discussed problem is the correct placement and naming of species belonging to *Galeobdolon* Adans. / *Lamiastrum* Heist. ex Fabr. (Dandy 1967; Holub 1970; Rauschert 1974; Mennema 1989; Krawczyk & al. 2013). Choice of genus name is a nomenclatural problem, which will not be dicussed here. In recent Floras of or covering Germany, either both names were used: *Galeobdolon* (Jäger & Werner 2005; Jäger 2011) and *Lamiastrum* (Heywood & Richardson 1972; Seybold 2009), or the species of *Galeobdolon* / *Lamiastrum* were included in *Lamium* L. (Seybold 2011). Molecular phylogenies of subfam. *Lamioideae* (Bendiksby & al. 2011b) and of *Lamium* (including species of *Galeobdolon* / *Lamiastrum*; Bendiksby & al. 2011a) clearly showed that a well-supported clade of species of *Galeobdolon* / *Lamiastrum* is sister to a well-supported *Lamium*. Accordingly, both inclusion of *Galeodolon* / *Lamiastrum* in *Lamium* and treatment as two distinct genera would result in monophyletic genera. When included in *Lamium*, *G. argentatum* Smejkal, *G. flavidum* (F. Herm.) Holub, *G. luteum* Huds. and *G. montanum* (Pers.) Pers. ex Rchb. should be *L. argentatum* (Smejkal) Henker ex G. H. Loos, *L. flavidum* F. Herm., *L. galeobdolon* (L.) L. and *L. montanum* (Pers.) Hoffm. ex Kabath, respectively. The treatment of these four taxa at species level has been questioned. When treated as subspecies of *Lamium galeobdolon* (e.g. by Bendiksby & al. 2011a), the names to be used would be *L. galeobdolon* subsp. *argentatum* (Smejkal) J. Duvign., *L. galeobdolon* subsp. *flavidum* (F. Herm.) Á. Löve & D. Löve, *L. galeobdolon* subsp. *galeobdolon* and *L. galeobdolon* subsp. *montanum* (Pers.) Hayek, respectively.

Majorana Mill. and *Origanum* L. are two genera containing commonly used spices. *Origanum* is distributed in Eurasia and contains c. 38 species (Mabberley 2008). *Majorana hortensis* Moench was first described as *O. majorana* L. A phylogenetic analysis by Katsiotis & al. (2009) showed that *M. hortensis* is nested among other species of *Origanum*, so that recognition of *M. hortensis* would make *Origanum* paraphyletic. Therefore the inclusion of *M. hortensis* in *Origanum*, as *O. majorana*, is appropriate.

Salvia L. in its traditional circumscription is a large genus of 800–900 tropical to temperate species (Mabberley 2008). Recent molecular studies in the genus clearly showed that *Salvia* is highly polyphyletic (Walker & Sytsma 2007; Will & Claßen-Bockhoff 2014) and will have to be split into several genera (Will & Claßen-Bock-

hoff 2014; M. Will pers. comm.). The only alternative would be to include several smaller genera in *Salvia*, e.g. *Rosmarinus* L., which would inflate this large genus even more. The German flora is largely unaffected by these changes. According to the different phylogenies available, only one species of the German flora, *S. glutinosa* L., will have to be transferred to a new genus.

Stachys L. is a large genus of c. 450 species distributed in temperate and warm regions of the world, including tropical mountains but excluding Australasia (Mabberley 2008). Molecular phylogenies have shown that *Stachys* is highly polyphyletic, with many different genera nested among different *Stachys* clades (Bendiksby & al. 2011b; Salmaki & al. 2013). In Germany eight species and one hybrid taxon of *Stachys* can be found. These fall into four larger *Stachys* clades (Salmaki & al. 2013). Only *S. arvensis* L. and *S. palustris* L. fall into the clade containing the type of *Stachys*, *S. sylvatica* L. This clade also contains *Haplostachys* Hillebr., *Phyllostegia* Benth., *Stenogyne* Benth. and *Suzukia* Kudô. *Sideritis* L. is one of those genera nested among different *Stachys* clades (Bendiksby & al. 2011b; Salmaki & al. 2013). This genus of c. 140 N-temperate species of the Old World and Macaronesia (Mabberley 2008) occurs in Germany with only one species, *S. montana* L. Relationships among the genera listed above and several others are complicated and not fully resolved. At this point two solutions seem possible. One is to include all species of a clade called *Eurystachys* Salmaki & Bendiksby (including *Stachys* and *Sideritis*; Salmaki & al. 2013) in one genus. The other is to split *Stachys* into a large number of smaller genera. Both solutions are problematic. The first would result in a large genus that is morphologically heterogeneous and, according to Salmaki & al. (2013), c. 194 new combinations would have to be made. The second solution would allow maintaining morphologically distinct genera. However, it would require dividing *Stachys* into several genera that would be difficult to delimit (Salmaki & al. 2013). In this second approach a similarly high number of combinations would be necessary. The first solution would allow keeping all German species of *Stachys* in *Stachys*, which, however, would also have to include *Sideritis*. In the second solution, *Stachys alpina* L., *S. annua* L., *S. byzantina* K. Koch, *S. germanica* L. and *S. recta* L. most likely would need to be excluded from *Stachys*. The relationships of *Sideritis* are unresolved. It therefore remains unclear whether *Sideritis montana* would need a new name when opting for the second solution. A further difficulty of the second solution is a high level of incongruence between the nuclear and plastid data sets analysed (Salmaki & al. 2013). Future changes in this group are clearly necessary. They will affect large numbers of species on a global scale, but only few species of the German flora.

Orobanchaceae (D. C. Albach)
There has been some debate about the monophyly of *Orobanche* L., and some publications re-used the name *Phelipanche* Pomel, introduced for some morphologically deviant species more commonly treated as *O*. sect. *Trionychon* Wallr. (in Germany *O. arenaria* Borkh., *O. purpurea* Jacq. and *O. ramosa* L.; see lead 1 in the key to *Orobanche* in Jäger 2011). The group differs from the type section not only in flower morphology but also in seed ultrastructure (Plaza & al. 2004) and pollen morphology (Abu Sbaih & al. 1994). Whereas first cpDNA-based phylogenetic analyses suggested *O. ramosa* to be nested in the rest of *Orobanche* (Young & al. 1999; Manen & al. 2004), subsequent analyses using ITS (Schneeweiss & al. 2004) revealed a biphyletic *Orobanche* with *O.* sect. *Trionychon* and New World species of the genus forming a clade and *O*. sect. *Orobanche* sister to *Diphelypaea* Nicolson. More detailed analyses of cpDNA sequences demonstrated that the nested position of *O*. sect. *Trionychon* is due to horizontal gene transfer (Park & al. 2007). However, analyses of another nuclear marker (*PhyA*; Bennett & Mathews 2006) as well as cpDNA analyses removing introgressed sequences (Park & al. 2008) agree on phylogenetic relationships with *Orobanche* being monophyletic and *O*. sect. *Trionychon* and New World species being sister to *O*. sect. *Orobanche*. Thus, no taxonomic changes will be necessary.

Linderniaceae (D. C. Albach)
Only two species of *Linderniaceae* occur in Germany and are commonly still recognized under *Lindernia* L., one being the type of the genus name, *L. procumbens* (Krock.) Borbás. *Lindernia dubia* (L.) Pennell, though, has been demonstrated to be more closely related to *Micranthemum* Michx. than to *Lindernia* (Fischer & al. 2013). However, no generic realignment has been proposed so far. *Lindernia dubia* had been recognized as separate from *Lindernia* before under the names *Gratiola dubia* L. or *Ilysanthes riparia* Raf., but was included in *Lindernia* by Pennell (1935). *Ilysanthes* Raf. had been separated from *Lindernia* based on the reduction of the androecium to two stamens, which Pennell (1935) did not consider stable enough to merit generic rank. Fischer & al. (2013) seemed to favour inclusion of *Micranthemum* in *Lindernia*. However, since *Micranthemum* also has only two stamens and occurs sympatrically with *L. dubia* in North America, combining *L. dubia* in *Micranthemum* remains a possibility.

Convolvulaceae (J. W. Kadereit)
A monophyletic *Calystegia* R. Br. is clearly nested within *Convolvulus* L. (Stefanović & al. 2002; Carine & al. 2004; Williams & al. 2014) and should be classified in *Convolvulus* following Stefanović & al. (2002). Combinations are available for most German species of *Calystegia*, and *C. pulchra* Brummitt & Heywood should be *Convolvulus dubius* J. L. Gilbert, *C. sepium* (L.) R. Br. should be *Convolvulus sepium* L., *C. silvatica* (Kit.) Griseb. should be *Convolvulus silvaticus* Kit. and *C. soldanella* (L.) Roem. & Schult. should be *Convolvulus soldanella* L.

Solanaceae (J. W. Kadereit)

Lycopersicon Mill. is clearly nested in *Solanum* L. (Spooner & al. 1993) and should be treated in that genus. Accordingly, the tomato should be called *S. lycopersicum* L.

Whitson & Manos (2005) demonstrated that the two species of *Physalis* L. listed for Germany, *P. alkekengi* L. and *P. peruviana* L., fall into two distantly related clades of *Physalinae*. The authors argued: "To correct the paraphyly of *Physalis*, nomenclatural changes are required. Options include restricting the name *Physalis* to *P. alkekengi*, the type, and renaming the 75+ species of New World *Physalis*, or broadening the circumscription of *Physalis* by uniting the majority of the *Physalinae* into a single genus. However, the least taxonomically disruptive approach for dealing with this problem is to re-typify *Physalis* using a Linnaean species that is a member of the morphologically typical *Rydbergis* clade, such as *P. pubescens*. The atypical species could then be recognized as four small genera (for *P. carpenteri*, *P. alkekengi*, *P. microphysa*, and subgenus *Physalodendron*), which would produce a morphologically homogeneous *Physalis*. A proposal to re-typify *Physalis* is currently in progress." This proposal has been made by Whitson (2011), and conservation of *Physalis* L. with conserved type has been recommended (Applequist 2012). If accepted, *P. alkekengi* should be known as *Alkekengi officinarum* Moench.

Boraginaceae (M. Weigend)

Generic limits in the large family *Boraginaceae* (1500–1600 spp.) are highly problematic and numerous re-alignments of generic limits are required, but few of these problems concern the German flora. The genus *Omphalodes* Moench is represented only by two species in Germany: *O. scorpioides* (Haenke) Schrank and *O. verna* Moench. *Omphalodes scorpioides* has been shown to be more closely related to *Mertensia* Roth than to the typical representatives of *Omphalodes* (Weigend & al. 2013), and is now accommodated in the monospecific genus *Memoremea* A. Otero & al. as *Memoremea scorpioides* (Haenke) A. Otero & al. (Otero & al. 2014). This is clearly supported by molecular data, but also by gross differences in habit and its aberrant fruit morphology (circular wing of the nutlet forming a hollow ring, not a flat appendage). *Omphalodes* in the narrowest sense is restricted to those perennial, rhizomatous herbs which are closely related to *O. verna*, the type of the genus name. This group ranges from N Spain to N Iran. Other groups from Asia and the Americas previously assigned to *Omphalodes* either have already been segregated from the genus (Otero & al. 2014) or will likely be removed to other genera.

The genus *Buglossoides* Moench is also represented by only two species in Germany. *Buglossoides arvensis* (L.) I. M. Johnst., an annual weed with tiny white flowers and four triangular-ovate, verrucose nutlets and *B. purpurocaerulea* (L.) I. M. Johnst., a perennial herb with large, blue, hypocrateriform flowers and single, smooth, spherical nutlets. They represent the C European representatives of two highly natural and monophyletic species groups, which are retrieved as sister groups in molecular studies (Weigend & al. 2009; Cecchi & al. 2014). These species groups have recently been segregated into two different, easily distinguished genera (Cecchi & al. 2014): *Buglossoides* s.str., essentially comprising the two species *B. arvensis* and *B. incrassata* and largely restricted to the circum-Mediterranean region and Europe (and introduced as weeds elsewhere), and *Aegonychon* Gray with a total of three species, one narrow S Italian endemic and the widespread *A. purpurocaeruleum* (L.) Holub. in W Eurasia as sister to the morphologically barely distinguishable Japanese endemic *A. zollingeri* (A. DC.) Holub (Cecchi & al. 2014). The clear morphological differences between these two groups justify their separation into two well-defined genera, but phylogenetic data would equally permit a broader delimitation of *Buglossoides*, including *Aegonychon*.

The genera *Eritrichium* Schrad. ex Gaudin, *Hackelia* Opiz and *Lappula* Moench have a confused taxonomic history, but *Hackelia* was finally segregated from *Lappula* by Johnston (1923). The only C European species of *Hackelia* and *Lappula* and the types of those names, *H. deflexa* (Wahlenb.) Opiz and *L. squarrosa* (Retz.) Dumort., have recently often been treated as belonging to a single genus, i.e. *Lappula*. Recent molecular studies retrieved these two species in widely separate clades in tribe *Eritrichieae*, together with the bulk of the species currently assigned to the respective genera. There is therefore both morphological (Johnston 1923) and molecular (Weigend & al. 2013) evidence supporting the recognition of the two genera. The exact limits between *Eritrichium* and *Hackelia* and *Lappula* still require additional work, with several extra-European segregate genera apparently nested in them, and some species incorrectly placed. This, however, does not concern the German or European flora.

The delimitation of *Anchusa* L., characterized by radially symmetrical flowers, from *Lycopsis* L. with curved, slightly zygomorphic flowers, has been contentious in the past. Morphological differences are small but striking, and the segregate *Lycopsis* is currently not generally recognized. Hilger & al. (2004) advocated the subdivision of *Anchusa* into several smaller genera, including the separation of *Lycopsis*. However, their molecular data failed to retrieve the two species of *Lycopsis* as monophyletic, and there was no statistical support for *Anchusa* excluding *Lycopsis*. Generic limits in *Anchusa* s.l. clearly require more work, and it seems more sensible at this stage to recognize a single, more widely defined genus *Anchusa* until much better data are available.

Two other genera represented in Germany will likely be subject to re-definition in the near future, without affecting the taxonomy of German species: Both species of *Cynoglossum* L. were retrieved in the core-clade of *Cynoglossum* s.l. (Weigend & al. 2013) and certainly will remain part of a redefined *Cynoglossum*. However, *Cy-*

noglossum likely will have to include a whole range of W Eurasian segregate genera (Hilger & al. 2015). Similarly, *Heliotropium europaeum* L. is the type of *Heliotropium* L. and therefore will not be affected by name change, irrespective of how the limits of *Heliotropium*, with the large genus *Tournefortia* L. deeply nested in it (Luebert & al. 2011), will ultimately be redefined.

Apiaceae (K. Spalik)

Hacquetia DC. is nested within *Sanicula* L. (Valiejo-Roman & al. 2002; Calviño & Downie 2007) and should therefore be sunk into synonymy; for its only species, *H. epipactis* (Scop.) DC., the name *S. epipactis* (Scop.) E. H. L. Krause is available.

Apium L. s.l. is polyphyletic and among its European species only the type, *A. graveolens* L., is retained in the genus; the other true celeries are distributed throughout the S hemisphere (Spalik & al. 2010). For its other European members, the genus *Helosciadium* W. D. J. Koch has been reinstated (Hardway & al. 2004; Spalik & al. 2009; Ronse & al. 2010) including *H. inundatum* (L.) W. D. J. Koch (*A. inundatum* (L.) Rchb. f.), *H. nodiflorum* (L.) W. D. J. Koch (*A. nodiflorum* (L.) Lag.) and *H. repens* (Jacq.) W. D. J. Koch (*A. repens* (Jacq.) Lag.). The species of *Helosciadium* are hydrophytes or helophytes and are closely related to the morphologically and ecologically similar *Berula* W. D. J. Koch and *Sium* L., members of tribe *Oenantheae* (Spalik & al. 2014).

Carum L., the type of *Careae*, includes c. 30 species that in molecular analyses are located in several disparate clades interspersed with species of *Chamaesciadium* C. A. Mey., *Fuernrohria* K. Koch and *Grammosciadium* DC., with only few species closely related to the type of *Carum*, *C. carvi* L. (Zakharova & al. 2012). *Carum verticillatum* (L.) W. D. J. Koch is a very distant relative of its nominative congeners and, therefore, was placed in the reinstated monospecific genus *Trocdaris* Raf.; its proper name is *T. verticillata* (L.) Raf. (Zakharova & al. 2012). This species forms an isolated lineage in a clade of hydrophytic umbellifers constituting tribe *Oenantheae* (Spalik & al. 2014).

The genera *Angelica* L., *Cnidium* Cusson, *Libanotis* Haller ex Zinn, *Peucedanum* L., *Selinum* L., *Seseli* L. and *Trinia* Hoffm. are part of the taxonomically difficult tribe *Selineae* (Spalik & al. 2004; Downie & al. 2010). Many of its genera are polyphyletic while at the same time many monophyletic lineages have unnecessarily been split into small segregates. Numerous species have not yet been included in molecular phylogenetic studies, and the generic boundaries remain unclear. Phylogenetic relationships within this tribe were mostly examined using only nuclear ITS sequences that have some limitations. Moreover, the tribe originated relatively recently, c. 12 Mya, and underwent rapid radiation (Banasiak & al. 2013: Appendix S2). In effect, internal branches of the phylogenetic trees obtained from molecular data are short and often poorly supported, precluding unambiguous taxonomic inferences.

Seseli sensu amplo encompasses 100–120 species and is obviously polyphyletic: its species occur in tribes *Apieae*, *Pimpinelleae* and *Selineae* (Downie & al. 2010), and in *Selineae* they are placed in several clades (Spalik & al. 2004). *Seseli hippomarathrum* Jacq. together with three other congeners forms a clade that is not most closely related to *S. tortuosum* L., the type of the genus name; for this group, a restitution of *Hippomarathrum* G. Gaertn. & al. has been considered (Spalik & al. 2004). Depending on taxonomic sampling and the method of phylogenetic inference, this clade was placed sister to the *Seseli* clade (Spalik & al. 2004) or sister to *Peucedanum* s.l. (see Appendix S2 in Banasiak & al. 2013). Detailed molecular and morphological studies are necessary to elucidate the taxonomic status of this group. Upon restitution of *Hippomarathrum* the name *H. pelviforme* G. Gaertn. & al. would be available for *S. hippomarathrum. Seseli annuum* L. has not yet been included in molecular analyses; therefore, its phylogenetic affinities remain unknown.

Libanotis pyrenaica (L.) Bourgeau is closely related to *L. montana* Crantz, the type of *Libanotis*, and in *Flora iberica* (Aedo & Vargas 2003) the former was synonymized with the latter. In molecular analyses, the clade containing these two species is sister to a clade containing the type of *Seseli* (Spalik & al. 2004; Banasiak & al. 2013). If a broad definition of *Seseli* is adopted, e.g. based on the *Seseli* clade in Spalik & al. (2004), then *Libanotis* should be sunk into *Seseli* and the species is to be named *S. libanotis* (L.) W. D. J. Koch.

Ligusticum mutellinoides (Crantz) Vill. (*Pachypleurum mutellinoides* (Crantz) Holub) is also closely related to the *Libanotis–Seseli* clade in tribe *Selineae*, whereas the types of *Ligusticum* L. and *Pachypleurum* Ledeb. are placed in the *Acronema* clade, which deserves rank as a separate tribe (Downie & al. 2010; Banasiak & al. 2013). Depending on the delineation of *Libanotis* and *Seseli*, *Ligusticum mutellinoides* may be included in either of these two genera. Alternatively, *Neogaya* Meisn. may be reinstated. Its type is *N. simplex* (L.) Meisn., a taxonomic synonym of *L. mutellinoides*. In molecular phylogenetic trees, *Ligusticum mutellina* (L.) Crantz is placed in the *Conioselinum chinense* clade far from the type of *Ligusticum* and, therefore, should be excluded from the genus and placed in the reinstated *Mutellina* Wolf, as *M. purpurea* (Poir.) Reduron & al. (Valiejo-Roman & al. 2006).

Cnidium dubium (Schkuhr) Schmeil & Fitschen is not most closely related to the type of *Cnidium*, *C. monnieri* (L.) Spreng., and should therefore be recognized as *Kadenia dubia* (Schkuhr) Lavrova & V. N. Tikhom. (Valiejo-Roman & al. 2006).

Trinia is exceptional in *Apiaceae* due to its dioecious breeding system, and this feature seems to be synapomorphic for the genus. So far, only *T. hispida* Hoffm. has been included in molecular phylogenetic analyses and it was placed in the *Seseli* clade very close to the type of *Seseli* (Spalik & al. 2004). If this placement is confirmed

upon extended sampling of species and molecular markers, then either *Trinia* is to be included into the synonymy of *Seseli* or the latter is to be restricted to a clade of only a few closest relatives of its type.

Peucedanum sensu amplo includes c. 100–120 species worldwide and is a "dustbin" genus encompassing taxa that do not fit elsewhere. The European species have often been transferred to small segregate genera including *Cervaria* Wolf, *Dichoropetalum* Fenzl (= *Holandrea* Reduron & al.), *Imperatoria* L., *Oreoselinum* Mill., *Thysselinum* Adans. and *Xanthoselinum* Schur. Of these, however, only *Cervaria* and *Dichoropetalum* are unambiguously supported by molecular data because their types are distant relatives of *Peucedanum officinale* L., the type of the genus name. The remaining segregates form the *Peucedanum* s.l. clade that can be retained as one genus (Spalik & al. 2004). Therefore, the use of the names *Dichoropetalum carvifolia* (Vill.) Pimenov & Kljuykov (*P. carvifolia* Vill.) and *Cervaria rivini* Gaertn. (*P. cervaria* (L.) Lapeyr.) is advocated. If a very narrow definition of *Peucedanum* is adopted, the names *Imperatoria ostruthium* L. (*P. ostruthium* (L.) W. D. J. Koch), *Oreoselinum nigrum* Delarbre (*P. oreoselinum* (L.) Moench), *Thysselinum palustre* (L.) Hoffm. (*P. palustre* (L.) Moench) and *Xanthoselinum alsaticum* (L.) Schur (*P. alsaticum* L.) are available for the respective species of *Peucedanum*.

Molecular data have demonstrated that *Laserpitium* L. is polyphyletic (Weitzel & al. 2014; Lyskov & al. 2015), and this polyphyly is strongly supported by nrDNA and cpDNA markers (Banasiak & al. in press). Six closely related species including the type, *L. gallicum* L., as well as *L. latifolium* L. constitute *Laserpitium* s.str. *Laserpitium siler* L. forms an isolated lineage that is not closely related to the type and, therefore, the restitution of the monospecific *Siler* Crantz has been postulated; the respective name for *L. siler* is *S. montanum* Crantz. *Laserpitium prutenicum* L. is more closely related to *Daucus* L. than to *Laserpitium* s.str. and, together with its closest relative, *L. hispidum* M. Bieb., it deserves to be placed in a new genus, *Silphiodaucus* (Koso-Pol.) Spalik & al. (Banasiak & al. in press). The respective name for *L. prutenicum* would be *S. prutenicus* (L.) Spalik & al.

Dipsacaceae (J. W. Kadereit)
Virga Hill. with *V. pilosa* (L.) Hill and *V. strigosa* (Roem. & Schult.) Holub clearly groups in *Dipsacus* L. (Avino & al. 2009; Carlson & al. 2009) and these two species should be known as *Dipsacus pilosus* L. and *D. strigosus* Roem. & Schult., respectively.

Valerianaceae (J. W. Kadereit)
Neither *Valerianella* Mill. nor *Valeriana* L. are monophyletic according to Hidalgo & al. (2004) and Bell & Donoghue (2005). However, inclusion of *Fedia* Gaertn. emend. Moench in *Valerianella*, and both inclusion of *Plectritis* (Lindl.) DC. in *Valeriana* and exclusion of some species of *Valeriana* could make the two genera monophyletic.

Campanulaceae (N. Kilian)
The two German species of *Lobelia* L., *L. dortmanna* L. and *L. erinus* L., fall into two different clades of a highly paraphyletic *Lobelia* (Antonelli 2008). If this should result in splitting of *Lobelia*, an approach considered premature by Lammers (2011), *L. erinus* would belong to a different genus.

Wahlenbergia Roth has been shown to be polyphyletic (Haberle & al. 2009; Roquet & al. 2009; Prebble & al. 2012; Cupido & al. 2013). *Wahlenbergia hederacea* (L.) Rchb., the only species present in Germany, is not only misplaced in *Wahlenbergia* (typified by *W. elongata* (Willd.) Schrad., a synonym of the S African *W. capensis* (L.) A. DC.; Lammers 2007) but also in the otherwise monophyletic wahlenbergioid group of genera (Cupido & al. 2013). It appears instead to be a close relative of *Feeria* Buser and *Jasione* L. (Prebble & al. 2012; Cupido & al. 2013; Crowl & al. 2014; but not so in Mansion & al. 2012), but its systematic position still needs clarification.

A number of molecular phylogenetic studies of *Campanulaceae* (Eddie & al. 2003; Park & al. 2006; Roquet & al. 2008, 2009; Borsch & al. 2009; Haberle & al. 2009; Mansion & al. 2012; Crowl & al. 2014) have shown that *Campanula* L. in its present circumscription is not monophyletic, and that the species of this genus fall into at least four major clades, each containing other genera of the family. Referring, with a view on the German flora, to the analysis based on the most comprehensive sampling by Mansion & al. (2012), which also provides the best resolution so far, the three largest major clades are relevant. These are: (1) the *Campanula* s.str. clade (Park & al. 2006; Roquet & al. 2008, 2009; Borsch & al. 2009; Mansion & al. 2012), including the type of the genus name, *C. latifolia* L., and comprising clades 13–17 in Mansion & al. (2012), contains the majority of the *Campanula* species in Germany (*C. alliariifolia* Willd., *C. alpina* Jacq., *C. barbata* L., *C. bononiensis* L., *C. cervicaria* L., *C. glomerata* L., *C. latifolia*, *C. medium* L., *C. rapunculoides* L., *C. sibirica* L., *C. thyrsoides* L. and *C. trachelium* L., all nested in clade 17). The *Campanula* s.str. clade also includes the species of the S European *Trachelium* L., but the different analyses demonstrate that this genus does not constitute a natural group but is found dismembered in clades 13 and 16 in Mansion & al. (2012). (2) The Rapunculus clade (clades 5–12 in Mansion & al. 2012) includes all but one of the remaining species in Germany (*C. baumgartenii* Becker, *C. cochleariifolia* Lam., *C. rhomboidalis* L., *C. rotundifolia* L. [incl. *C. gentilis* Kovanda] and *C. scheuchzeri* Vill. in clade 12; *C. patula* L. and *C. rapunculus* L. in clade 9) and also contains (in clade 6) the genera *Adenophora* Fisch. and *Hanabusaya* Nakai. (3) The third major clade, which has low support, comprises the well-supported clades 2–4 in Mansion & al. (2012), in which several *Campanula* lineages (among

them the last German member *C. persicifolia* L. in clade 3) are mixed with *Asyneuma* Griseb. & Schenk, *Legousia* Durande and *Phyteuma* L. as well as with the American genera *Githopsis* Nutt., *Heterocodon* Nutt. and *Triodanis* Raf. Faced with different classificatory options, i.e. (1) treating all clades containing species of *Campanula* as one genus, (2) limiting *Campanula* to the *Campanula* s.str. clade, and (3) splitting *Campanula* into numerous small genera, an option briefly discussed by Park & al. (2006), Roquet & al. (2008) concluded: "We favor the first option in order to arrive at a generic delimitation that reflects the evolutionary history of *Campanula.* This approach is more consistent with previous taxonomic work, *Campanula* has always been very rich in number of species, and it does not seem to us reasonable to divide it ad nauseam. … However, a comprehensive study of the currently recognized genera that fall within *Campanula* should be conducted before changing their taxonomic status." If this approach would be taken, all species of *Adenophora*, *Legousia* and *Phyteuma* would have to be treated as *Campanula*.

Menyanthaceae (J. W. Kadereit)
Although *Nymphoides* Ség. was found to be non-monophyletic, with one species more closely related to one clade of a non-monophyletic *Villarsia* Vent. than to the remaining species of *Nymphoides* (Tippery & al. 2008), *N. peltata* (S. G. Gmel.) Kuntze will not change name even when combined with *Villarsia* because *Nymphoides* is the older name.

Asteraceae

Cardueae (A. Susanna & N. Garcia-Jacas)
Extensive molecular analyses in subtribe *Centaureinae* have demonstrated that *Centaurea* L., as defined in classic terms, was a polyphyletic assemblage (Susanna & al. 1995; Garcia-Jacas & al. 2001). As regards naming of the two main lineages, problems originated with an inadequate type of the genus name proposed by Britton & Brown (1913), a decision later ratified by Dittrich (1993): *C. centaurium* L. This species belongs to a group of some 20–25 taxa that are not closest relative of the largest part of the genus. Two alternate solutions were possible for achieving a natural delineation of the two genera that should be recognized: first, to keep the old type and limit the use of *Centaurea* to this group of species, which would imply renaming more than 200 species in a different genus; second, to conserve a new type belonging to the main group of the genus. This second, more conservative (in terms of botanical nomenclature) option finally prevailed: a new type, *C. paniculata* L., was proposed by Greuter & al. (2001) and is now the conserved type of *Centaurea* (Wiersema & al. 2015). The valid name for the genus comprising the smaller group of species is *Rhaponticoides* Vaill. This change, in Germany, affects only *C. ruthenica* Lam., which should be known as *R. ruthenica* (Lam.) M. V. Agab. & Greuter. As for the segregation of *C.* sect. *Cyanus* (Mill.) DC. as a separate genus (e.g. Greuter & al. 2001), molecular evidence, although inconclusive, points at a sister relationship of *C.* sect. *Cyanus* and *C.* sect. *Centaurea* (e.g. Garcia-Jacas & al. 2001). The latest proposal for a classification of the entire genus *Centaurea* (Hilpold & al. 2014) and the revisions of tribe *Cardueae* by Susanna and Garcia-Jacas (2007, 2009) do not accept *Cyanus* Mill. as generically different from *Centaurea*.

Cichorieae (N. Kilian)
Lapsana L., together with the equally epappose Mediterranean *Rhagadiolus* Juss., is nested in *Crepis* L., as has been shown in nuclear ribosomal (ITS) and chloroplast (*matK*) DNA marker phylogenies by Enke & Gemeinholzer (2008). To maintain *Lapsana*, which is monospecific after the well-supported segregation of the E Asian *Lapsanastrum* Pak & K. Bremer (Pak & Bremer 1995; Deng & al. 2014) and the dispecific *Rhagadiolus* as separate monophyletic genera, *Crepis* would have to be split into two morphologically ill-defined entities. This is definitely no practicable solution. If only monophyletic genera should be accepted, merging of both genera with *Crepis* would be the more appropriate solution, although breaking with a long tradition (no combination of *Lapsana* in *Crepis* has been published). The morphological circumscription of *Crepis* does not, however, preclude the inclusion of *Lapsana communis* L. (and of *Rhagadiolus*) if variation is extended to allow for the absence of a pappus. In other subtribes, parallel cases of epappose entities traditionally treated as separate genera are similarly found nested in regularly pappose genera (e.g. Deng & al. 2014).

The members of *Hypochaeris* L. cluster in two main clades according to the phylogenetic analyses of nuclear ribosomal (ITS) and several chloroplast DNA marker sequences by Samuel & al. (2003, 2006) and Enke & al. (2012). The results, however, are inconclusive as to whether the two clades actually form a sister group and thus to the monophyly of *Hypochaeris*. Based on these findings, Talavera & al. (2015a) opted for splitting the genus in the forthcoming treatment of *Flora iberica*, there recognizing the segregates *Achyrophorus* Adans. (in its narrow sense distributed in the Mediterranean region) and *Trommsdorffia* Bernh. (with *T. maculata* (L.) Bernh. [*H. maculata* L.] and *T. uniflora* (Vill.) Soják [*H. uniflora* Vill.] in the German flora), a solution that necessitates recognition of at least a fourth genus for the NW African-South American clade of *Hypochaeris* s.l.

Leontodon L. in its traditional circumscription is at least diphyletic (Samuel & al. 2006; Enke & al. 2012). *Leontodon* subg. *Leontodon* and *L.* subg. *Oporinia* (D. Don) Peterm., which both received strong support in molecular phylogenies, are nested in two different major clades of the subtribe. This finding from phylogenetic analyses

based on both nuclear ribosomal (ITS) and chloroplast (*matK*) DNA marker sequences necessitates the recognition of *L.* subg. *Oporinia* (including *L. autumnalis* L., *L. helveticus* Mérat and *L. montanus* Lam. in Germany) as a separate genus, *Scorzoneroides* Moench, with *S. autumnalis* (L.) Moench as type (Greuter & al. 2006) and *S. helvetica* (Mérat) Holub and *S. montana* (Lam.) Holub as additional species in the German flora. The authorship of *Scorzoneroides* should be attributed to Moench (Meth.: 549. 1794), because an earlier place of publication of that name and other genus names (in a German translation dated 1754–1756 of a pre-Linnaean work by Vaillant) is expected to be added to the list of suppressed works by the next International Botanical Congress (Applequist 2014: 1370). *Leontodon* s.str., moreover, is paraphyletic with respect to the small, chiefly Mediterranean genus *Hedypnois* Mill., not present in the flora of Germany (Enke & al. 2012). The nrITS phylogeny by Samuel & al. (2006) and Enke & al. (2012) also provide initial indication (without statistical support, and not supported by the *matK* phylogeny) that *L.* sect. *Thrincia* (Roth) Benth. (with only *L. saxatilis* Lam. [*Thrincia saxatilis* (Lam.) Holub & Moravec] in the German flora) forms a clade not sister to the remainder of *Leontodon* s.str. Based on these findings, Talavera & al. (2015b) revived the genus *Thrincia* Roth for this clade.

Picris L. is monophyletic after exclusion of the small Mediterranean-SW Asian genus *Helminthotheca* Zinn (Samuel & al. 2006; Enke & al. 2012). Its segregation has previously been concluded for morphological reasons by Lack (1975). The only species of the latter genus in Germany is *H. echioides* (L.) Holub (*Picris echioides* L.), which also provides the type of the genus name.

Scorzonera L. is polyphyletic in all current circumscriptions according to the initial molecular phylogenetic investigations in the subtribe by Mavrodiev & al. (2004) and Owen & al. (2006), using nuclear ribosomal (ITS and ETS) DNA markers and Amplified Fragment Length Polymorphisms (AFLP) variation, respectively. According to these analyses, the clade of *Scorzonera* s.str. (including the type of the name, *S. humilis* L., as well as *S. purpurea* L.) is sister to a clade comprising *Podospermum* DC. (of which the only member in the German flora, *P. laciniatum* (L.) DC. [*S. laciniata* L.], provides the type of that name). The other members of *Scorzonera* in its wider circumscription, as far as included in the analyses, are distributed over at least three further clades. Two of them, which form a clade sister to the clade comprising *Koelpinia* Pall. and the *Podospermum* and *Scorzonera* s.str. clades (Owen & al. 2006), each include one species in the German flora: *S. austriaca* L. and *S. hispanica* L. The third clade is the "*Lasiospora* clade" (including *S. hirsuta* L., the type of *Lasiospora* Cass.), which is sister to all other lineages of the subtribe but has no representatives in the German flora. Apart from the segregation of *Podospermum* DC. from *Scorzonera* s.str., which is supported as an option (but not a necessity), the current state of our knowledge of *Scorzonera* s.l. is still far too preliminary to draw taxonomic conclusions.

Sonchus L. has turned out to be paraphyletic with respect to various smaller Mediterranean-Macaronesian and Australian-New Zealand segregates as well as to the SE Pacific Ocean island endemics *Dendroseris* D. Don and *Thamnoseris* Phil. in a series of molecular phylogenetic analyses based on both nuclear ribosomal and chloroplast DNA markers (Kim & al. 2007 and references therein). The preferred and envisaged taxonomic solution is the broadening of the generic concept for *Sonchus* and (re)inclusion of all these genera (Mejías & Kim 2012). A splitting approach would inevitably dismember even the four German representatives of the genus, the congenerity of which has never been questioned.

The systematics of the *Lactuca* alliance, which is represented in the German flora by the genera *Cicerbita* Wallr., *Mycelis* Cass. and *Lactuca* L., has been in lively debate for more than 200 years. The first molecular phylogenetic analyses published (Koopman & al. 1998; Wang & al. 2013) explained the difficulties in arriving at a natural classification with frequent convergent evolution of morphological characters. Consequences for the generic classification of the species in Germany are to be expected, but phylogenetic reconstruction is still in progress and any reclassification would be premature at present.

Prenanthes L. has been redefined completely on the basis of molecular phylogenetics, now being understood as a probably monospecific genus, accommodating the chiefly European *P. purpurea* L. (Kilian & Gemeinholzer 2007; Kilian & al. 2009; Wang & al. 2013).

The placement of the C and SE European *Tolpis staticifolia* (All.) Sch. Bip., the only representative of *Tolpis* L. in the flora of Germany, is not settled yet. *Tolpis staticifolia* and the S and tropical African *T. capensis* (L.) Sch. Bip. (plus its close ally *T. mbalensis* G. V. Pope) have been excluded from that chiefly Mediterranean-Macaronesian genus based on palynological differences (Blackmore & Jarvis 1986) and on the results of a chloroplast *ndhF* sequence phylogeny by Park & al. (2001), which placed the two species as sister to *Taraxacum* F. H. Wigg. (*T. capensis*) and *Crepis* (*T. staticifolia*), respectively.

Recent molecular phylogenetic analyses of the *Hieracium* alliance using nuclear ribosomal, low-copy nuclear and chloroplast DNA markers (Fehrer & al. 2007, 2009; Krak & al. 2013) revealed conflicting topologies between the different gene trees in particular due to both reticulate evolution and incomplete lineage sorting during the rapid evolution of the alliance. Discussing the available evidence, the authors concluded that the nuclear ribosomal DNA gene trees provide the best approximation for the reconstruction of the species tree. Accordingly, *Hieracium* L. in the wide sense is polyphyletic. *Hieracium* subg. *Pilosella* (Hill.) Fr. is sister to the W Mediterranean

genus *Hispidella* Lam., both are sister to *H.* subg. *Hieracium* and the American *H.* subg. *Chionoracium* Sch. Bip. (= *Stenotheca* Monnier), the four taxa in turn are sister to the chiefly Mediterranean-Macaronesian genus *Andryala* L., and, finally, *H. intybaceum* All., which is restricted to the siliceous Alps, forms the sister group to all of them. The taxonomic consequences already widely drawn are the recognition as separate genera of *Hieracium* and *Pilosella* Hill (for taxonomy and new combinations needed see Bräutigam & Greuter 2007; for the authorship of *Pilosella* the above notes on *Scorzoneroides* also apply). The further consequence in order to arrive at monophyletic entities is the resurrection of the genus *Schlagintweitia* Griseb. to accommodate *H. intybaceum* (as *S. intybacea* (All.) Griseb.) and its few allies (Gottschlich & Greuter 2007; Greuter & Raab-Straube 2008).

Senecioneae (J. W. Kadereit)
Phylogenetic analyses of *Senecioneae* (Pelser & al. 2002, 2007, 2010) have shown that *Senecio* L. in its traditional circumscription is not monophyletic but rather both poly- and paraphyletic. As regards species in the German flora, it is evident that those species that lack outer involucral bracts, i.e. *S. congestus* (R. Br.) DC., *S. gaudinii* Gremli, *S. helenites* (L.) Schinz & Thell., *S. integrifolius* (L.) Clairv. and *S. rivularis* (Waldst. & Kit.) DC., need to be segregated as *Tephroseris* (Rchb.) Rchb., in which they are known as *T. palustris* (L.) Rchb. (for *S. congestus*), *T. tenuifolia* (Gaudin) Holub (for *S. gaudinii*), *T. helenites* (L.) B. Nord. (for *S. helenites*), *T. integrifolia* (L.) Holub (for *S. integrifolius*) and *T. crispa* (Jacq.) Rchb. (for *S. rivularis*). *Tephroseris* is only very distantly related to *Senecio* s.str. and even belongs to a different subtribe of *Senecioneae*.

Species related to *Senecio jacobaea* L. should be segregated as *Jacobaea* Mill., which again is only distantly related to *Senecio* s.str. These, besides *S. jacobaea* (*J. vulgaris* Gaertn.), include *S. abrotanifolius* L. (*J. abrotanifolia* (L.) Moench), *S. alpinus* (L.) Scop. (*J. alpina* (L.) Moench), *S. aquaticus* Hill (*J. aquatica* (Hill) G. Gaertn. & al.), *S. erraticus* Bertol. (*J. erratica* (Bertol.) Fourr.), *S. erucifolius* L. (*J. erucifolia* (L.) G. Gaertn. & al.), *S. incanus* subsp. *carniolicus* (Willd.) Braun-Blanq. (*J. incana* subsp. *carniolica* (Willd.) B. Nord.; for a recent account of the *S. carniolicus* aggregate see Flatscher & al. 2015), *S. paludosus* L. (*J. paludosa* (L.) G. Gaertn. & al.) and *S. subalpinus* Koch. (*J. subalpina* (W. D. J. Koch) Pelser & Veldkamp). Combinations in *Jacobaea* are available for all these species (Pelser & al. 2006).

Endocellion Turcz. ex Herder, containing two species in Asia, is clearly nested in *Petasites* Mill. (Steffen 2013) and should be treated as part of that genus. This does not affect the generic identity of the *Petasites* species in Germany.

Gnaphalieae (M. Galbany-Casals)
Phylogenetic analyses and morphological data show that *Filago* L. is not monophyletic, and that the species involved should now be placed in two separate genera not closely related to each other (Galbany-Casals & al. 2010; Andrés-Sánchez & al. 2011): *Logfia* Cass. includes *L. minima* (Sm.) Dumort. (*F. minima* (Sm.) Pers.) and *L. gallica* (L.) Coss. & Germ. (*F. gallica* L.), and *Filago* includes the rest of the species present in Germany. *Filago neglecta* (Soyer-Willemet) DC. has been claimed to be of hybrid origin between *L. gallica* and *Gnaphalium uliginosum* L. (Holub 1976; Jäger 2011), but this is currently considered highly doubtful (Andrés-Sánchez, pers. comm.). However, it is not clear yet if this rarely collected species belongs to *Filago* or *Logfia*.

Bombycilaena erecta (L.) Smoljan. has not been treated in Jäger (2005, 2011), but there exists at least one old record of this species from Germany (Andrés-Sánchez & al. 2014). The genus *Bombycilaena* (DC.) Smoljan. has been shown to be a lineage separate from *Micropus* L. and *Filago* in a molecular phylogeny and is currently considered to include only two species from the Old World (Galbany-Casals & al. 2010; Andrés-Sánchez & al. 2014).

Omalotheca Cass. (sensu Holub 1976) has often been considered a synonym of *Gnaphalium* L. (e.g. Anderberg 1991; Jäger 2005, 2011). However, a molecular phylogeny (Galbany-Casals & al. 2010) has shown that *Gnaphalium* s.l. is not monophyletic and that these two genera should be considered separate, given that *G. supinum* L. – the type of *Omalotheca* – is not closely related to *G. uliginosum* – the type of *Gnaphalium*. Additionally, Blöch & al. (2010) showed that *G. hoppeanum* W. D. J. Koch, *G. norvegium* Gunnerus and *G. sylvaticum* L., three species also present in Germany, form a clade with *G. supinum*. In conclusion, with regard to the German flora, *Gnaphalium* should be restricted to *G. uliginosum*, and the other four species named above should be considered to belong to *Omalotheca*, as *O. hoppeana* (W. D. J. Koch) Sch. Bip. & F. W. Schultz, *O. norvegica* (Gunnerus.) Sch. Bip. & F. W. Schultz, *O. supina* (L.) DC. and *O. sylvatica* (L.) Sch. Bip. & F. W. Schultz. Smissen & al. (2011) noted that *Gnaphalium* s.str. includes diploid species ($2n = 14$), whereas *Omalotheca* species are all polyploids, and that the latter genus is part of a large clade of ancient allopolyploid origin, together with, among others, genera such as *Antennaria* Gaertn, *Bombycilaena*, *Filago*, *Gamochaeta* Wedd., *Leontopodium* R. Br. ex Cass. and *Logfia* (Galbany-Casals & al. 2010).

Helichrysum Mill. is not monophyletic. Some Australasian species had already been transferred to other genera for morphological reasons (see Bayer 2001 and Ward & al. 2009 for a review) and later were shown not to be part of the main *Helichrysum* clade (Galbany-Casals & al. 2004; Ward & al. 2009; Smissen & al. 2011). This affects *H. bracteatum* (Vent.) Willd., an ornamental species (Jäger 2005), which should be known as *Xerochrysum bracteatum* (Vent.) Tzvelev (Bayer 2001). *Anaphalis* DC. and *Pseudognaphalium* Kirp., two genera of hypothesized allopolyploid origin, are embebbed in the main *Helichrysum* clade (Galbany-Casals & al. 2014).

The need for a generic re-circumscription of these three genera, plus others, was extensively discussed by Galbany-Casals & al. (2014), who recommended maintaining *Anaphalis*, *Helichrysum* and *Pseudognaphalium* as independent genera until more data are available. This affects two taxa present in Germany, *A. margaritacea* (L.) Benth. & Hook. f., an ornamental but naturalized (Jäger 2011) species native to Asia and North America, and *P. luteoalbum* (L.) Hilliard & B. L. Burtt. The latter species was treated as *Gnaphalium luteoalbum* L. in Jäger (2005). At present it remains unclear if this species should be included in *Helichrysum* or *Pseudognaphalium*, or if it should be treated as *Laphangium* Tzvelev as was done in Jäger (2011).

Astereae (C. Oberprieler)

The most comprehensive molecular phylogenetic analysis of tribe *Astereae* based on nrDNA ITS sequences was made by Brouillet & al. (2009). To a large extent, its results are supportive of the generic delimitation proposed by Greuter (2003) for the Euro+Med plantbase treatment of the tribe and of Nesom & Robinson's (2007) treatment of *Astereae* in Kubitzki's *The families and genera of vascular plants* (Kadereit & Jeffrey 2007).

In subtribe *Solidagininae*, results by Brouillet & al. (2009) confirm that *Solidago* L. is polyphyletic and that the naturalized *S. graminifolia* (L.) Salisb. should be transferred to *Euthamia* (Nutt.) Cass. as *E. graminifolia* (L.) Nutt. because it belongs to another lineage than the type of *Solidago* (i.e. *S. virgaurea* L.). While in subtribe *Bellidinae* the monophyly of both *Bellis* L. and *Bellium* L. was repeatedly found in molecular phylogenetic studies based on nrDNA ITS sequences (Fiz & al. 2002; Brouillet & al. 2009; Fiz-Palacios & Valcarcel 2011), phylogenetic analyses in subtribe *Asterinae* have led to extensive generic rearrangements due to the consistently demonstrated polyphyly of *Aster* L. in its classical circumscription. According to nrDNA ITS-based analyses by Brouillet & al. (2009), a more narrowly and more naturally circumscribed genus *Aster* in Germany would only comprise *A. alpinus* L. and *A. amellus* L., while *A. linosyris* (L.) Bernh. should be transferred to the Eurasian genus *Galatella* Cass. as *G. linosyris* (L.) Rchb. f., the halophilic *A. tripolium* L. to the genus *Tripolium* Nees as *T. pannonicum* (Jacq.) Dobrocz., and *A. bellidiastrum* (L.) Scop. not only to the separate and monospecific genus *Bellidiastrum* Scop. (as *B. michelii* Scop.) but also to another subtribe (*Bellidinae*). The last has also been confirmed by the phylogenetic analyses by Fiz & al. (2002) and Fiz-Palacios & Valcarcel (2011). Finally, molecular phylogenies based on nrDNA ITS alone (Brouillet & al. 2009) or on nrDNA ITS + ETS complemented by the intergenic spacer region *trnL-trnF* of the chloroplast genome (Li & al. 2012b) support the transfer of the naturalized "New World asters" (i.e. *A. laevis* L., *A. lanceolatus* Willd., *A. novae-angliae* L., *A. novi-belgii* L., *A. parviflorus* Nees, *A. salignus* Willd., *A. versicolor* Willd.) to the genus *Symphyotrichum* Nees (subtribe *Symphyotrichinae*). On the other hand, Li & al. (2012b) found no evidence for a close relationship between *Callistephus chinensis* (L.) Nees and any other genus of subtribe *Asterinae* and supported its independent generic status. Finally, in subtribe *Conyzinae*, it has been repeatedly demonstrated (Noyes 2000; Andrus & al. 2009; Brouillet & al. 2009) that neither *Conyza* Less. nor *Erigeron* L. as previously defined are monophyletic; a situation that is best accommodated by merging the two genera into *Erigeron,* as was already suggested by Greuter (2003). This requires the transfer of *C. bonariensis* (L.) Cronquist, *C. canadensis* (L.) Cronquist and *C. sumatrensis* (Retz.) E. Walker to this more broadly circumscribed genus (as *E. bonariensis* L., *E. canadensis* L., and *E. sumatrensis* Retz., respectively).

Anthemideae (C. Oberprieler)

In the S hemisphere subtribe *Cotulinae*, phylogenetic analyses by Himmelreich & al. (2012) based on sequence variation of nrDNA ITS and intergenic spacer regions (*psbA-trnH*, *trnC-petN*) of the chloroplast genome have shown that *Cotula* L. is non-monophyletic, even when the Mediterranean *C. cinerea* Delile is excluded as the independent and monospecific genus *Brocchia* Vis. (as *B. cinerea* (Delile) Vis.) following results by Oberprieler (2004a). Being the type of *Cotula*, sinking of *Leptinella* Cass. and *Soliva* Ruiz & Pav. into a broader, then monophyletic genus would not affect the name of *C. coronopifolia* L., naturalized in the N hemisphere. Of subtribe *Artemisiinae*, as circumscribed by Oberprieler & al. (2007a, 2009), only *Artemisia* L. and *Leucanthemella* Tzvelev are represented in our area. In the case of the former genus, there is a consistent tendency supported by many molecular phylogenetic studies of the last years (e.g. Vallès & al. 2003; Sanz & al. 2008; Pellicer & al. 2010, 2011; Garcia & al. 2011) for lumping the numerous small to large segregate genera (i.e. *Crossostephium* Less., *Filifolium* Kitam., *Mausolea* Poljakov, *Neopallasia* Poljakov, *Picrothamnus* Nutt., *Seriphidium* Fourr., *Sphaeromeria* Nutt. and *Turaniphytum* Poljakov) into a broadly defined and monophyletic *Artemisia.* On the other hand, studies focusing on phylogenetic relationships among the remainder of the *Artemisiinae* sensu Oberprieler & al. (2007a, 2009) in general and on the generic delimitation of *Ajania* Poljakov versus *Chrysanthemum* L. in particular, presented no consistent and well-supported evidence for the affiliation of *Leucanthemella* Tzvelev to any other genus of the subtribe (Masuda & al. 2009; Zhao & al. 2010). As a consequence, *Leucanthemella* with its sole European species *L. serotina* (L.) Tzvelev should be treated as an independent evolutionary unit at genus rank. After inclusion, motivated by molecular phylogenetic studies, of the Mediterranean monospecific *Otanthus* Hoffmanns. & Link and the equally monospecific Turkish endemic *Leuco-*

cyclus Boiss. in subtribe *Matricariinae* (Guo & al. 2004; Oberprieler 2004b; Ehrendorfer & Guo 2005), *Achillea* L. constitutes a monophyletic genus. Support from a comprehensive molecular phylogenetic analysis for the monophyly of the Eurasian and Mediterranean *Matricaria* L. with its presently accepted six species (Oberprieler & al. 2007b, 2009) is still missing. However, the transfer of the Aegean *M. macrotis* Rech. f. to *Anthemis* L. (as *A. macrotis* (Rech. f.) Oberpr. & Vogt) based on nrDNA sequence information (Oberprieler & Vogt 2006) and the repeatedly shown support for the generic independence of *Matricaria* (subtribe *Matricariinae*) from *Tripleurospermum* Sch. Bip. (subtribe *Anthemidinae*; e.g. Oberprieler 2004b, 2005; Oberprieler & al. 2007a) and from *Microcephala* Pobed. (subtribe *Handeliinae*; e.g. Oberprieler & al. 2007a; Sonboli & al. 2012) contributed strong evidence for the naturalness of *Matricaria* in its present circumscription. In subtribe *Anthemidinae* sensu Oberprieler & al. (2007a, 2009) with its species-rich core genera *Anthemis* L. and *Tanacetum* L., considerable efforts have been made to achieve a natural delimitation of genera based on molecular phylogenies. After Oberprieler (2001) had shown, with a limited taxon sample, that *Anthemis* in its traditional circumscription is paraphyletic, and that the species of *A.* sect. *Cota* (J. Gay) Rchb. f., distinct in their achene morphology, should be transferred to the independent genus *Cota* J. Gay ex Guss. (Greuter & al. 2003), Lo Presti & al. (2010) corroborated this finding based on a comprehensive species sampling (c. 75 % of the described species) and sequence information from both nuclear and plastid markers. With the exclusion of further four species from the Caucasus region (i.e. *A. calcarea* Sosn., *A. fruticulosa* M. Bieb., *A. marschalliana* Willd. and *A. trotzkiana* Bunge) from *Anthemis* and their accommodation in the newly described genus *Archanthemis* Lo Presti & Oberpr., and the above-mentioned inclusion of *Matricaria macrotis* (Oberprieler & Vogt 2006), three natural, morphologically distinct genera were established (Lo Presti & al. 2010; Sonboli & al. 2012). To reflect these phylogenetic findings, *Anthemis austriaca* Jacq. and *A. tinctoria* L., hitherto treated as *Anthemis* in Germany, should be transferred to *Cota*, as *C. austriaca* (Jacq.) Sch. Bip. and *C. tinctoria* (L.) J. Gay.

The natural circumscription of *Tanacetum* L. remains problematic even after considerable taxon and marker sampling. Based on nrDNA ITS and cpDNA *trnH-psbA* sequence information, Sonboli & al. (2012) could demonstrate that there is no support for a generic separation of the yellow-rayed or rayless species of *Tanacetum* from the white- and red-rayed species of *Pyrethrum* Zinn. On the other hand, even after exclusion of several enigmatic species from *Tanacetum* based on phylogenetic analyses (i.e. *T. annuum* L. and *T. microphyllum* DC. transferred to the newly established *Vogtia* Oberpr. & Sonboli [Sonboli & al. 2012]; *T. paradoxum* Bornm. transferred to *Artemisia* [Sonboli & al. 2011]; *T. semenovii* Herder transferred to *Richtera* Kar. & Kir. [Sonboli & Oberprieler 2012]) and the suggested inclusion in *Tanacetum* of many satellite genera (e.g. *Balsamita* Mill., *Gonospermum* Less., *Gymnocline* Cass., *Hemipappus* K. Koch, *Lugoa* DC., *Spathipappus* Tzvelev and *Xylanthemum* Tzvelev), support for a monophyletic *Tanacetum* remains weak and awaits phylogenetic reconstructions based on a broader sampling of molecular markers (Sonboli & al. 2012). For the time being, this argues for the presently used broad generic concept of *Tanacetum* in Germany.

After having been raised from sectional rank in *Tanacetum* to an independent genus by Heywood (1975), *Leucanthemopsis* (Giroux) Heywood was considered to be related to *Leucanthemum* Mill. by Bremer & Humphries (1993) until molecular phylogenetic studies revealed its even closer relationships with three monospecific genera endemic to the Iberian Peninsula, *Castrilanthemum* Vogt & Oberpr., *Hymenostemma* Willk. and *Prolongoa* Boiss. This resulted in its accommodation in the new subtribe *Leucanthemopsidinae* (Oberprieler & al. 2007a, 2009). More recently, a multilocus phylogenetic analysis of all species of the subtribe in a coalescent-based species-tree reconstruction clearly demonstrated the well-supported monophyly of *Leucanthemopsis* (Tomasello & al. 2015).

As already discussed by Vogt (1991) in his revision of *Leucanthemum* Mill. in the Iberian Peninsula, the genus in its traditional circumscription contained species that are only remotely related to its type, *L. vulgare* Lam. Accommodation of these divergent species in the independent genera *Mauranthemum* Vogt & Oberpr. and *Rhodanthemum* B. H. Wilcox & al. by Vogt & Oberprieler (1995) and Bremer & Humphries (1993), respectively, has led to a well-circumscribed and strongly supported monophyletic *Leucanthemum*, as was recently corroborated by a multi-locus phylogenetic analysis by Konowalik & al. (2015).

In subtribe *Santolininae* sensu Oberprieler & al. (2007a, 2009), genus delimitations were studied in molecular phylogenetic analyses by Oberprieler (2002). Based on nrDNA ITS and cpDNA *trnL-trnF* sequence variation, this study demonstrated the paraphyly of *Chamaemelum* Mill. relative to the monospecific *Cladanthus* Cass. Transfer of four W Mediterranean *Chamaemelum* species to *Cladanthus* led to two well-supported monophyletic sister genera, with the widely cultivated and sporadically naturalized *C. nobile* (L.) All. and the W Mediterranean *C. fuscatum* (Brot.) Vasc. as the only members of *Chamaemelum*.

Glebionis Cass. with the naturalized *G. segetum* (L.) Fourr. comprises only two species and is the type genus of the small subtribe *Glebionidinae* (Oberprieler & al. 2007a, 2009). Phylogenetic relationships within this subtribe were studied by Francisco-Ortega & al. (1997), who found little support for the monophyly of the subtribe and for the genus (sub *Chrysanthemum*) in

a maximum-parsimony analysis based on nrDNA ITS sequence variation. While more recent studies using model-based sequence analysis methods (maximum likelihood) gained strong support for the monophyly of the subtribe (Oberprieler 2005; Oberprieler & al. 2007a), relationships among the genera of *Glebionidinae*, i.e. the species-rich *Argyranthemum* Webb (24 spp.), *Glebionis* (two spp.), and the two monospecific genera *Heteranthemis* Schott and *Ismelia* Cass., remain unclear, especially after a recent study based on nrDNA ITS sequence variation by Imamura & al. (2015), who found *G. coronaria* (L.) Spach nested in a group of *Argyranthemum* species. If future studies should corroborate the non-monophyly of the four genera of *Glebionidinae*, and their merging would be necessary to arrive at a monophyletic genus, the oldest genus name for this entity would be *Heteranthemis* Schott. For the time being, however, retaining the four genera in their present circumscriptions appears preferable due to their morphological and geographical distinctness.

Inuleae (J. W. Kadereit)
Phylogenetic analyses of tribe *Inuleae* have shown that neither *Inula* L. nor *Pulicaria* Gaertn. are monophyletic (Anderberg & al. 2005; Englund & al. 2009), but this has not yet been translated into formal taxonomic changes, although possible taxonomic consequences were discussed by Englund & al. (2009). The species of *Inula* present in Germany fall into at least four different clades, of which *I. graveolens* (L.) Desf. is more closely related to *Pulicaria* and its relatives than to *Inula* and its relatives and has been treated as *Dittrichia* Greuter. Maintainance of this genus will depend on future treatment of the various lineages of *Pulicaria*. If, after exclusion of some lineages as suggested by Englund & al. (2009), a broad concept of *Pulicaria* is adopted, *Dittrichia* will have to be included in that genus. If, on the other hand, a narrow concept of *Pulicaria* is adopted, *Dittrichia* would remain an independent genus and the two species of *Pulicaria* present in Germany (*P. dysenterica* (L.) Bernh. and *P. vulgaris* Gaertn.) would remain in *Pulicaria*. Adoption of a broad concept of *Inula* would require inclusion of *Carpesium* L. and *Telekia* Baumg. Adoption of a narrow concept would require distribution of the German species in probably several genera, dependent on treatment, and only *I. helenium* L., as the type, would remain in *Inula*.

Helenieae (J. W. Kadereit)
Both *Bidens* L. and *Coreopsis* L. have been shown not to be monophyletic (Mort & al. 2008), but this has not yet been translated into taxonomic changes.

Heliantheae (J. W. Kadereit)
Both *Ambrosia* L. and *Iva* L. have been found not to be monophyletic (Miao & al. 1995). *Ambrosia* becomes monophyletic after inclusion of *Hymenoclea* Torr. & A. Gray, as proposed by Panero (2007), whereas parts of *Iva* are better accommodated in other genera. This affects the German *I. xanthiifolia* Nutt., which, according to Panero (2007), should be considered a species of *Euphrosyne* DC. and called *E. xanthiifolia* (Nutt.) A. Gray.

Madieae (J. W. Kadereit)
Although *Eriophyllum* Lag. does not appear to be monophyletic (Baldwin & al. 2002), *E. lanatum* (Push) Forbes, a naturalized ornamental in Germany, is part of the perennial clade, which also contains the type of the genus name. In consequence, no change of name will be necessary should the genus be split.

Conclusions

Among the 840 genera examined, we identified c. 140 where data quality is sufficiently high to conclude that they are not monophyletic, and an additional c. 20 where monophyly is questionable but where data quality is not yet sufficient to reach convincing conclusions. The resolution of these uncertainties will depend on the expansion of taxon and DNA sequence datasets, and on the interpretation of the results by taxonomic specialists. In many cases recognition of non-monophyly offers the options of either to expand genera in order to include former satellites or to split genera into smaller generic entities. As we do not know which of these options will be adopted in each case, we cannot say how the number of genera recognized in the German flora will be affected. General trends in global plant classification, e.g. towards larger genera based on molecular data (Humphreys & Linder 2009), may or may not be reflected in the consequences for the comparatively small and well-studied German flora. However, the summary presented here clearly indicates that considerable further change is inevitable provided monophyly is accepted as the primary criterion for circumscribing genera (and taxa in general). Although such developments may be met with some dismay by users of Floras, they reflect ongoing progress in our scientific understanding of plant diversity.

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