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### Allotetraploid evolution in *Dactylorhiza* (Orchidaceae)

We have been studying species limits in the problematic genus *Dactylorhiza* using plastid microsatellites, low-copy nuclear gene sequences and ITS nuclear ribosomal spacer sequences. The limits of these taxa have been one of the most controversial among the European terrestrial orchids, and this affects how conservation priorities have been established. In western Europe, *D. fuchsii* and *D. maculata* are ecologically and morphologically easily distinguished, whereas in eastern Europe these two entities are difficult to distinguish on these bases. Allotetraploids that originated from crosses between these two taxa and members of the *D. incarnata* group are some of the most common and conspicuous orchids in Europe, and these too exhibit morphological and ecological differences. In addition to *D. incarnata* (almost always the maternal parent), one set of these was parented by an unknown diploid species, most likely found in southern Europe and similar to *D. foliosa* from Madeira and another set by a species similar to modern *D. fuchsii*. Furthermore, polyploidy formation took place in at least two phases (as deduced by gene conversion of ITS sequences). Although in many locations, these species coexist, the polyploids arose elsewhere, perhaps in southern Europe, and migrated along with the diploid progenitors to their current localities. Rather than conserving taxa, in *Dactylorhiza* it seems more appropriate to preserve the habitats where hybridization has been occurring, but knowing that few hybrids are currently being formed in northern Europe means that more attention must be focused on appropriate sites in southern Europe.