Nuclear DNA contents, rDNAs, and karyotype evolution in subgenus *Vicia*: III. The heterogeneous section *Hypechusa*

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Received August 4, 2005; accepted September 29, 2005; published online July 17, 2006

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Summary. Nuclear DNA contents, automated karyotype analyses, and sequences of internal transcribed spacers from ribosomal genes have been determined in the species belonging to section *Hypechusa* of the subgenus *Vicia*. Karyomorphological results and phylogenetic data generated from the comparison of rDNA (genes coding for rRNA) sequences showed that sect. *Hypechusa* is not monophyletic; however, some monophyletic units are apparent (one including *Vicia galeata*, *V. hyrcanica*, *V. noeana*, and *V. tigridis*, another including *V. assyriaca*, *V. hybrida*, *V. melanops*, *V. mollis*, and *V. sericocarpa*), which partly correspond to morphology-based infrasectional groups. The relationships among these species and the species in sections *Faba*, *Narbonensis*, *Bithynicae*, and *Peregrinae* have been also investigated.

Keywords: *Vicia* species; Section *Hypechusa*; Karyotype; Nuclear DNA content; DNA sequence; Phylogeny.

Introduction

The genus *Vicia* L. is a member of the legume tribe Vicieae (Fabaceae). Ball (1968) divided the genus into four sections: *Vicia*, *Cracca* Gray, *Ervum* (L.) Gray, and *Faba* (Mill.) Gray; and Kupicha (1976) subsequently recognised two subgenera, *Vicilla* and *Vicia*, with 17 and 5 sections, respectively. Subgenus *Vicia* contains fewer species than *Vicilla* but includes the more agriculturally important species, such as faba bean (*Vicia faba* L.), narbon vetch (*V. narbonensis* L.), and common vetch (*V. sativa* L.). The faba bean is an important grain legume across the Northern temperate zone and at higher temperatures in some subtropical regions. It is unusual among pulse crops in

that no clear picture of its ancestry is yet available, and its close taxonomic relationships are imperfectly known (Khattab et al. 1988, Hanelt and Mettin 1989, Maxted et al. 1991, and references therein). Various studies suggested that the closest relatives of faba bean were to be found in sect. *Faba* sensu Kupicka (including, besides *V. faba*, *V. bithynica* and a group of species referred to as the Narbonensis complex); in particular, strong evidence was found to suggest that *V. narbonensis* and its closely related species are immediately related to *V. faba* (Ball 1968, Kupicha 1976). More recently, Maxted (1993) reexamined subgenus *Vicia* and proposed a new classification with nine sections: *Atossa* (Alef.) Asch. & Graebner, *Microcarinae* Maxted, *Hypechusa* (Alef.) Asch. & Graebner, *Peregrinae* Kupicha, *Wiggersia* (Alef.) Maxted, *Vicia*, *Narbonensis* (Radzhi) Maxted, *Bithynicae* (B. Fedtsch. ex Radzhi) Maxted, and *Faba* (Miller) Ledeb., where sections *Bithynicae* and *Faba* are monospecific units.

Various aspects of the classification proposed by Maxted (1993) have been recently confirmed (Fennell et al. 1998, Venora et al. 2000, Leht and Jaaska 2002, Frediani et al. 2005). Most notably, the remoteness of *V. faba* from *V. bithynica* and from the species of sect. *Narbonensis* has been proven by molecular methods. However, various issues remain obscure, including not only the position of *V. faba* but also the sectional membership of some species and the phylogenetic relationships among the sections.

Elucidating the taxonomic relationship between the crop and its wild relatives is important, especially in connection with the exploitation of the germplasm of wild relatives as a source of novel characteristics to be intro-

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