

Evolutionary History of the Genus *Capsella* (Brassicaceae) - *Capsella orientalis*, New for Mongolia

Barbara Neuffer^{1*}, Herbert Hurka², Nikolai Friesen², Dmitry A. German^{3,4} and
Andreas Franzke⁴

¹Department of Botany, University of Osnabrück, Barbarastr. 11, D-49076 Osnabrück, Germany,
fax: ++49 541 969 2845

²Botanical Garden of the University of Osnabrück, Albrechtstr. 29, D-49076 Osnabrück, 9 Germany

³South-Siberian Botanical Garden, Altai State University, Lenina Str. 61, 656049 Barnaul, Russia

⁴Heidelberg Botanic Garden, Centre for Organismal Studies (COS) Heidelberg, Heidelberg University, Im
Neuenheimer Feld 340, D-69120 Heidelberg, Germany

Abstract

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Corresponding:

neuffer@biologie.uni-
osnabrueck.de

To elucidate the evolutionary history of the genus *Capsella*, we included the hitherto poorly known species *C. orientalis* and *C. thracica* into our studies together with *C. grandiflora*, *C. rubella*, and *C. bursa-pastoris*. We sequenced the ITS, and four loci of noncoding cpDNA regions (trnL – F, rps16, trnH – psbA, trnQ – rps16). In common garden field experiments *C. orientalis* turned out as early flowering with a specific leaf type. The crossing ability of the species was tested in pollen germination experiments. *Capsella orientalis* (self-compatible, SC; 2n = 16) forms a clade (eastern lineage) with *C. bursa-pastoris* (SC; 2n = 32), which is a sister clade (western lineage) to *C. grandiflora* (self-incompatible, SI; 2n = 16) and *C. rubella* (SC; 2n = 16). *Capsella bursa-pastoris* is an autopolyploid species of multiple origin, whereas the Bulgarian endemic *C. thracica* (SC; 2n = 32) is allopolyploid and emerged from interspecific hybridisation between *C. bursa-pastoris* and *C. grandiflora*. The common ancestor of the two lineages was diploid and SI, and its distribution ranged from eastern Europe to central Asia, predominantly confined to steppe like habitats. Biogeographic dynamics during the Pleistocene caused geographic and genetic subdivisions within the common ancestor giving rise to the two extant lineages. *Capsella orientalis* is verified at several positions in western Mongolia.

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Introduction

Molecular systematic studies confirm that the genus *Capsella* belongs to the tribe, Camelinae (Al-Shehbaz *et al.*, 2006; Bailey *et al.*, 2006; German *et al.*, 2009; Warwick *et al.*, 2010). Scientific research is focusing its attention increasingly on *Capsella* addressing such key issues as speciation, adaptation, mating systems,

and evolutionary developmental biology of plant form (Hurka & Neuffer, 1997; Foxe *et al.*, 2009; Guo *et al.*, 2009; Paetsch *et al.*, 2010; Neuffer, 2011; Sicard *et al.*, 2011; Theißen, 2011). Additionally, sequencing of the *Capsella rubella* genome is currently being carried out by the Joint Genome Institute, United States Dept. of Energy.