



Conference Abstract

High molecular diversity in the *Carabus variolosus/nodulosus* complex

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Abstract

Starting point of this study was the problem considering the status of *Carabus variolosus* and *C. nodulosus*: French and some German authors classified them as species, most German authors as subspecies and Casale as semispecies.

We performed analyses of mitochondrial genes (COI-5', COI-3', ND5) as well as nuclear ones (ITS2, wingless) and analysed the DNA sequences using Seqotron, CLUSTALX (editing and alignment), MEGA, DNAML, SplitsTree (phylogeny and network), 4SALE (compensatory base changes), and BEAST (coalescence).

We could study specimens from all regions except the western most part of the distribution area (Massif Central and French Jura, France).

The mitochondrial DNA data resulted in a geographic pattern of high diversity within both taxa indicating a series of glacial refuges. In addition, a considerably large area was found where introgressive hybridisation took place in the past - at least two times by *nodulosus* of different regions into *variolosus*.

The nuclear DNA data show a clear and constant difference between both taxa.

In consequence, this complex of forms may be characterised as semispecies from an evolutionary viewpoint but taxonomically as one species because of hybridisation and the lack of compensatory bases changes.

Keywords

Species status, introgressive hybridisation, multiple refuges

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