

Molecular phylogeny of European *Saga*: comparison with chromosomal data

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Abstract

The six European *Saga* species (Orthoptera Tettigoniidae) were mitochondrially analyzed for the COI gene. Results were compared with available karyological data, the two analyses producing complementary and congruent conclusions. European *Saga* species appear to be monophyletic, and probably derived from Asiatic species by a Robertsonian translocation. *Saga natoliae* Serville separated first from their common trunk, followed by *Saga hellenica* Kaltenbach and *Saga rhodiensis* Salfi. The three other species share several gene mutations and two chromosomal changes. The parthenogenetic *Saga pedo* (Pallas) from France and Balkans on the one hand and *Saga campbelli* Uvarov and *Saga rammei* Kaltenbach on the other hand represent two sister clades. Their proximity is in agreement with the possible origin of the pentaploid karyotype of *S. pedo*, by addition of haploid genomes from species close to *S. campbelli* and *S. rammei*, as proposed earlier. Molecular level of divergence indicates that the separation of French and Balkans lineages of *S. pedo* occurred between 420,000 and 650,000 years ago.

Key words: Tettigoniidae, European *Saga*, genetics, cytogenetics, phylogeny.

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