

Postmating isolation and evolutionary relationships among Fejervarya species from Lesser Sunda, Indonesia and other Asian countries revealed by crossing experiments and mtDNA Cytb gene sequences

Mahmudul Hasan¹, Nia Kurniawan², Aris Soewondo², Wilmientje Nalley³, Masafumi Matsui⁴, Takeshi Igawa⁵, and Masayuki Sumida⁵

¹Bangamata Sheikh Fojilatunnesa Mujib Science and Technology University

²Brawijawa University

³University of Nusa Cendana

⁴Kyoto University

⁵Hiroshima University

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Abstract

In order to interpret the degree of postmating isolation and the evolutionary relationships among Fejervarya species from Indonesia (Lesser Sunda), Bangladesh, China, and Japan, crossing experiments and molecular phylogenetic analyses were carried out using frogs of Fejervarya species from these countries. The crossing experiments revealed that the reciprocal hybrids among F. iskandari, F. verruculosa, and F. sp. Large type, and those between F. multistriata and F. kawamurai were viable through metamorphosis, but those between F. iskandari group and F. limnocharis group were completely or partially inviable at the tadpole stage, and those between Southeast -Asian and South-Asian Fejervarya groups were completely inviable at the embryonic stage. The matured reciprocal hybrids between F. iskandari and F. verruculosa from Indonesia, Lesser Sunda showed some degree of abnormality in spermatogenesis. The phylogenetic analyses using mtDNA Cytb gene sequences demonstrated that F. iskandari formed a sister clade with F. verruculosa from Lesser Sunda, Indonesia with 8.1% sequence divergence. Fejervarya multistriata from China made a clade with Thailand, Malaysia and Indonesian (topotype) populations of F. limnocharis which showed sister relationships to F. kawamurai from Japan with 8.9% sequence divergence of Cytb gene. Fejervarya sp. small type from Bangladesh formed a clade with the other South-Asian members of Fejervarya group and made a sister clade with Southeast-Asian Fejervarya group having 23.1% sequence divergence of Cytb gene. This study showed that the degree of postmating isolation reflects the molecular phylogenetic relationships, and that the two species, F. iskandari and F. verruculosa from Indonesia (Lesser Sunda) are reproductively isolated by abnormal spermatogenesis, and genetically deviated.

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