

学 位 論 文 要 旨	
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題 目	Systematic study on the family Stathmopodidae (Lepidoptera) (ニセマイコガ科の分類学的研究 (鱗翅目))
<p>The family Stathmopodidae contains more than 390 species belonging to 39 genera (Terada and Sakamaki, 2013), and 43 species belonging to nine genera have been recorded in Japan, containing 13 unidentified species. I have hitherto reported 13 new species and one species as new to Japanese fauna (Terada <i>et al.</i>, 2011; Terada, 2012, 2013a, c, 2014). However, many Japanese species of the group have been left unrecorded because there have been a few studies on the group in Japan. In this thesis, I newly found 18 species and four genera, among which 12 species and one genus are new to science, and seven species and three genera are new to the Japanese fauna, containing five unidentified species. In addition, I described four new species and reported two species new to Japanese fauna that had been treated as unidentified species in Oku (2003a), Sugisima (2003) and Sawamura <i>et al.</i> (2009). Besides, I treated five known unidentified species in Oku (2003a, b) as junior synonym. Therefore, I elucidated that the family Stathmopodidae from Japan contain 57 species belonging to 13 genera.</p> <p>I tried to elucidate the phylogenetic relationships among species belonging to the family Stathmopodidae by molecular phylogenetic analysis of DNA sequence. I used the concatenated data consisting of <i>COI</i> (1098 bp) sequence from the mitochondrial genome, and <i>EF-1<math>\alpha</math></i> (506 bp) and <i>CAD</i> (772 bp) sequences from the nuclear genome. The materials consisted of 25 stathmopodid species belonging to seven genera as well as two outgroups, whose feeding habits had been clarified. The Maximum likelihood (ML) tree was reconstructed with 700 trials of Likelihood ratchet (Vos, 2003) method. The ML tree indicated the holophyly of genera <i>Calicotis</i>, <i>Cuprina</i> and <i>Pachyrhabda</i>, respectively, but the genus <i>Stathmopoda</i> might be polyphyletic group. However, the clades of later two genera will be unvaluable. Besides, the fern-spore-feeding habit might developed only once in their common ancestor, and the spinning behavior of “nests of peculiar structures” by larvae of fern-spore-feeding stathmopodid moths (Sugisima, 2003) developed independently at least twice in the family Stathmopodidae. In addition, it was supposed that the predator, <i>S. melanochra</i>, derived from gall feeders, and an opportunistic predation in gall feeders (Sugiura and Yamazaki, 2004) might be one of factors in diversifying carnivore taxon. However, the clade consisting predator and the gall feeders, which closely related to predator, are unvaluable. Further study is necessary to decide the preadaptation for the predatory trait in the family Stathmopodidae.</p>	