

学 位 論 文 要 約

Dissertation Abstract

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論 文 名: The molecular phylogenetic study of the subgenus *Sophophora* and its related
(Dissertation Title) taxa inferred from 53 nuclear gene loci, with descriptions of two new species,
Drosophila longicrura and *D. setiscutellata*.

The subgenus *Sophophora* is one of the largest group in the genus *Drosophila*, and includes the important model organisms, *D. melanogaster* and *D. pseudoobscura*. This subgenus has been studied for long time in the fields of evolutionary biology with the model organisms, and should continue to be an important group of the fields. Although the monophyly of *Sophophora* was suggested by traditional phylogenetic studies, recent molecular studies suggested that the subgenus was paraphyletic in respect to the genus *Lordiphosa* and *Hirtodrosophila duncani*. In addition, the two undescribed species, *D. longicrura* and *D. setiscutellata* of which morphology was quite different from the members of *Sophophora* had been suggested that these species belonged to the subgenus *Sophophora*. In the present study, the phylogenetic relationships of the subgenus *Sophophora* and its related taxa were determined by the construction of molecular phylogenetic trees.

In order to amplify the nucleotide sequences of gene loci, 53 primer pairs for

Sophophora and its related taxa were used based on data of the whole genome sequenced species. The phylogenetic trees were constructed by Bayesian and Maximum likelihood (ML) analysis inferred from the combined data set of obtained sequences. The analysis included a total of 55 ingroup species and five outgroup species. The ingroup species consisted of 47 species of *Sophophora*, followed by five species of *Lordiphosa*, one species of *Hirtodrosophila*, and two species of the undescribed species. In addition, the taxonomic descriptions of *D. longicrura* and *D. setiscutellata* were carried out.

The phylogenetic tree constructed by Bayesian analysis showed the highest posterior probabilities on all nodes. Most of the bootstrap values of the tree constructed by ML analysis were 100%, but seven branches showed less than 100%. The topology of the phylogenetic trees was identical between two analyses. The paraphyly of *Sophophora* with respect to *Lordiphosa* was well supported by higher node support values. The genus *Lordiphosa* formed the sister clade between the Neotropical *saltans-* *willistoni* clade. *Hirtodrosophila duncani* was placed at basal branch of the subgenus *Sophophora* contrary to results of the previous studies. The monophyletic clade formed by *D. longicrura* and *D. setiscutellata* was clearly included in *Sophophora*, and recognized as the new species group. This new group was defined and established as the *longicrura* species group. The known species groups of *Sophophora* formed the monophyletic clade in each. Within the species group, the *melanogaster* group got the new species subgroups by division of the *suzukii* subgroup. The four species of the *suzukii* subgroup, *D. lucipennis*, *D. nyinyii*, *D. unipectinata*, and *D. oshimai* were divided into two groups. The former two species were placed close to the *elegans* and *rhopaloa* subgroups, and the latter two species formed the new species subgroup named as the *unipectinata* subgroup. The ungrouped species, *D. majtoi* was closely related to the *ananassae* species subgroup, and recognized as the member of the new

subgroup, the *majtoi* subgroup.

The present study indicated that the subgenus *Sophophora* included the genus *Lordiphosa*, *H. duncani*, and the *longicrura* species group. The morphology of these taxa might be incompatible with traditional diagnostic characters of the subgenus *Sophophora*. Thus, the present study suggests that the taxonomic revision of morphological characters of *Sophophora* should be needed based on the molecular data.