

Preliminary molecular phylogeny for Galerucinae sensu lato (Coleoptera: Chrysomelidae) based on rRNA gene for Large Subunit 28S with emphasis on Neotropical species

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Galerucinae sensu lato comprises genera from real galerucins and their sister group, the Flea Beetles (Alticinae), forming an important group, with relevance in economy due billion dollar damages in cultures, and also in evolution studies, containing species-model for coevolution, evolution of pharmacophagy and host choice. Galerucinae s.l. do not have a phylogenetic consensus for the systematic ranking of Galerucinae and Alticinae, neither for relationships between both groups and for their internal nodes, being the most important group in Insect systematics that do not have a phylogenetic resolution well accepted. The difficult of a resolution in Phylogeny of the Galerucinae s.l. is due to the high diversity and the broad distribution of species around the world. The aim of this work was create a molecular phylogeny for Galerucinae s.l. based on alignment of rRNA gene of a nuclear Large Subunit (28S), with sampling emphasis in Neotropical species, to provide a phylogenetic perspective of the Neotropical species and to increase their information available for posterior phylogenetic studies. For this, the D2 region of 28S rRNA gene of 8 species of Alticinae, and 2 external groups was amplified, sequenced and aligned with other 27 sequences provided by other studies and analyzed with Parsimony in PAUP*, with TBR heuristic algorithm, and 1000 replications. Bootstrap analysis was calculated with 1000 replications. The molecular phylogeny of 28S-D2 recovered the monophyly of Galerucinae s.l. and presented a situation where Galerucinae sensu stricto is monophyletic with a paraphyletic Flea Beetles clade. *Disonycha conjuncta* was placed within the Galerucinae s.s. clade and Luperini tribe (*Aulacophora indica*, *Diabrotica undecimpunctata*, *Phyllobrotica* sp. and *Monolepta nigrotibialis*) form a polyphyletic assemblage in this phylogeny as predicted by other previous analysis. *Wanderbiltiana festiva*, *Pleurasphaera deciprens*, *Omophoita communis*, *Omophoita personata* and *Alagoasa florigera* grouped with 60% of bootstrap values, supporting the *Oedionychina* tribal ranking inside the Flea Beetles. The paraphyly of Flea Beetles observed in analysis do not support the categorization of their assumption as tribe or subfamily. This analysis increases the number of species of Galerucinae s.l. includes in phylogenetic investigations and increases as well the number of characters available for posterior phylogenetic studies and other approaches. Financial Support: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - CAPES; CNPq-PQ Processo-308382/2011-0