



Figure S1. Maximum-likelihood phylogeny of *Epicephala* moths based on 582 base pairs of the mitochondrial COI gene. The nine Japanese species are highlighted in color. Asterisks on branches represent nodal support based on bootstrap analysis (*, >70; **, >90; ***, >95). Highland Taiwan population of *Epicephala obovatella* is genetically divergent from populations in Japan and lowland Taiwan (>4% pairwise sequence difference), but they are hardly distinguishable morphologically and thus are considered the same species.