

Supporting Information

Hasselmann et al. 10.1073/pnas.1005617107

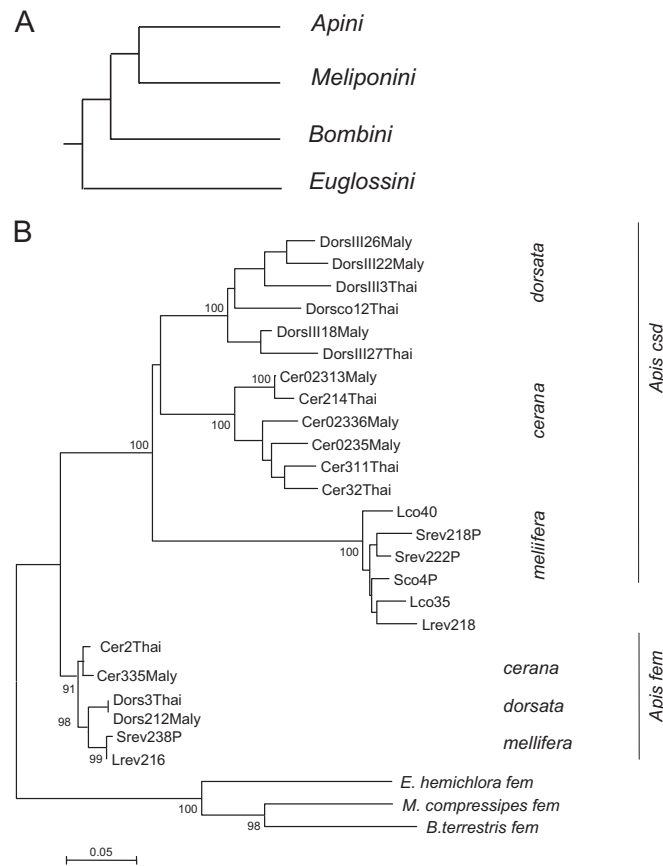


Fig. S1. Phylogenetic and gene tree of *csd* and *fem* of corbiculate bees. (A) Phylogeny of the four major groups of corbiculate bees (redrawn after ref. 1). (B) Genealogy of *csd* and *fem* protein sequences using the minimum evolution method. Numbers denote bootstrap values > 80%.

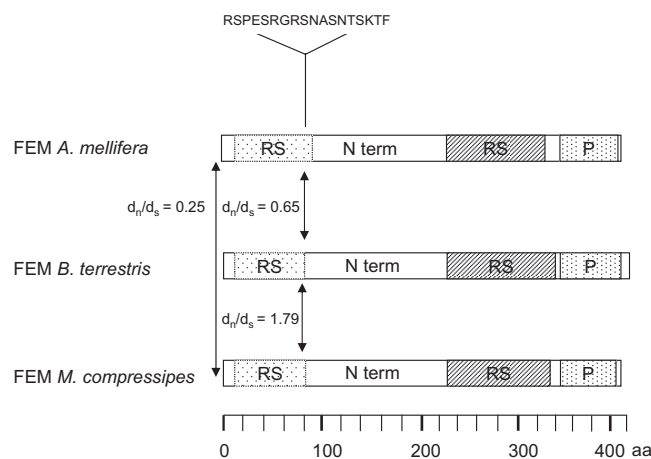


Fig. S2. Putative region of strong purifying selection in Fem of *Apis*. Shown are Fem proteins of *Apis* (represented here by *A. mellifera*) and non-*Apis* species (*M. compressipes* and *B. terrestris*) with domains (RS and P) and the N-term region. Using a sliding window (window length, 30 bp; step size, 10 bp), d_n/d_s ratios were calculated for each window between *A. mellifera*/*M. compressipes*, *A. mellifera*/*B. terrestris*, and *B. terrestris*/*M. compressipes*. One region comprising 18 amino acids was detected that showed the lowest d_n/d_s between *Apis* and non-*Apis* but the highest d_n/d_s for the non-*Apis* comparison, indicative of strong purifying selection in *Apis*.

1. Grimaldi D, Engel MS (2005) *Evolution of the Insects* (Cambridge Univ Press, Cambridge, UK).

