



**Figure S2. Whole-genome duplication evidence by gene duplication patterns.** Clock-calibrated phylogenetic tree from 215 genes detected within duplicated blocks and with exactly two copies in the genomes of *Pmeg* and *Ppal* but only one copy in the rest of the species. The presence of the duplicated genes still within the duplicated blocks strongly suggest that they were duplicated in the WGD, thus the timing of their divergence is good estimate for the WGD event. (B) Percentage of genes estimated to have been duplicated at the WGD event (approximately  $K_s < 0.5$ ). Percentage of gene families represented at the WGD event overall (C) and divided by duplication pattern (D). Average number of genes per gene family duplicated at the WGD event and separated by duplication patterns.