



The role of gene duplication in the evolution of the fire ant social chromosome

Author(s): Fontana Silvia, Fontana Silvia , Ni-Chen Chang , John Wang

Institution(s): Biodiversity Research Center, Academia Sinica, Taipei, Taiwan; Department of Life Science, National Taiwan Normal University, Taipei, Taiwan ; Biodiversity Research Center, Academia Sinica, Taipei, Taiwan ; Biodiversity Research Center, Academia Sinica, Taipei, Taiwan ; Biodiversity Research Center, Academia Sinica, Taipei, Taiwan; Department of Life Science, National Taiwan Normal University, Taipei, Taiwan

The fire ant *Solenopsis invicta* shows two distinct social forms (monogyne and polygyne colonies, with one and multiple queens, respectively) under genetic control of a ~12.5 Mb supergene. The supergene includes ~600 genes linked together by a big inversion, which prevents recombination between the two variants, 'Social B' (SB) and 'Social b' (Sb). In this study we characterized genetic duplications on the non-recombining social supergene. We found 475 genes with differences in copy number (>1.5-fold) between SB and Sb, of which 430 (90.5%) are in greater copy number in Sb. The duplicated genes in the Sb allele are approximately evenly partitioned between transposable elements (TEs, n=241, 56%) and normal genes (n=189, 44%). While TE accumulation was expected, since repetitive elements tend to accumulate on non-recombining chromosomes, finding many normal genes duplicated in the Sb supergene was surprising. We characterized both duplicated TE and normal genes. No bias was found towards DNA transposons or retrotransposons ($P=0.66$). Only the *BEL* LTR retrotransposon family was disproportionately duplicated in the supergene ($P<0.01$). We found no clear correlation between TE duplication and expression, suggesting that TEs were duplicated at different times during the evolution of the supergene, with some of them being already silenced. Normal genes duplicated in Sb encompass various functions: putative enzymes responsible for cuticular hydrocarbons (CHCs) and juvenile hormone synthesis, transcription factors, histones, and kinases. We identified candidate duplications potentially responsible for different CHC profiles in SB and Sb queens. These duplicated genes may be important for queen recognition and the maintenance of the colony social form.