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Gene mapping of few selected putative behavioural genes from Apis mellifera using in silico approach

Social organisms such as mammals (mice, monkeys, and humans) and insects (honeybees, wasps, ants, and mites) depict a higher level of social interactions and therefore, these animals are widely used to study the biological mechanism of social behaviour. Among them, Apis mellifera is one of the eusocial insects that depicts different social behaviour such as mite-grooming, mating, aggressive, defensive, and foraging behaviour. To explore the role of these genes in the behavioural regulation, in the present study, few selected behavioural genes were mapped onto respective chromosomes of Apis mellifera. For this study, sequences of few selected behavioural genes associated with two main behavioural traits viz: (i) defensive and (ii) mite grooming were retrieved using BeeBase database.

The distance in centimorgan (cM) between few selected putative behavioural genes was calculated (scale used: 52 Kb = 1 cM) for mapping these genes onto respective chromosomes of Apis mellifera using MapInspect software. Chromosomal mapping has mapped few selected brain-related genes such as serotonin, atlastin, nexin, and ataxin variants onto chromosome 2, 3, 7 and 5, respectively. The close proximity of these genes on respective chromosomes exhibits linked association among them during regulation of defensive and mite grooming behaviour.

Keywords: Social behaviour, Apis mellifera, Behavioural genes, BeeBase, MapInspect, Centimorgan

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