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Partial Scholarship Award Winner

Whole genome analysis (WGA) of five pea aphids biotypes for the identification and classification of SNPs

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Abstract

Leguminous plants are the rich source of dietary proteins that account for 27% of the world primary crop production. Their high vulnerability to the pathogens resulted in the annual loss of ~2.0 - 2.1 million tonnes of crops. Among the various pests, pea aphids represent the highly specialized and most devastating pathogens of the leguminous plants. During the evolution, they evolved themselves in such a manner that showed reduced performance when grown in the alternative host plant. In order to understand their host preference, genome level scan is required. Therefore, in this study, we used the genome-wide SNP scan of five pea aphid biotypes of >70 GB raw sequencing reads. We used the pea aphid genome as a reference having size of ~450 MB. Using quality filtering, BWA alignment, and GATK tool, we identified more than 1.5 million bi-allelic and around 1500 multi-allelic nuclear SNPs with a Ts/Tv ratio of 1.42. A high rate of mutation was observed in *T. pratense* biotype as compared to the *M. Sativa*. Their functional classification revealed approximately 26K - 30K missense and ~400 nonsense variation in their nuclear genome. Furthermore, the genome-wide scan revealed that an average of 5.42% of the identified SNPs located in the exon regions while a major portion ~80% were present in the intron region of the genome. This is the first report of genome-wide SNPs analysis on different pea aphid biotypes which in future could be used for host-pathogen interaction, and diversity analysis. Our future goal is the analysis of more biotypes and development of a unique resource of SNP's present biologically important class of genes playing role in immunity, olfactory response, etc.

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