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Identification and analysis of SNP and InDel loci in Nosema ceranae

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N. ceranae is a single-cell fungal pathogen that exclusively infects honeybee midgut's epithelial cell, widely infecting bee colonies throughout the world. The objective of this study is to perform identification and analysis of single nucleotide polymorphism (SNP) and insertion and deletion (InDel) loci in N. ceranae using the obtained high-quality transcriptome data from clean spores of N. ceranae, aiming to enrich the information of SNP and InDel loci in N. ceranae and provide a basis for developing novel molecular markers. SNP and InDel loci in N. ceranae were detected using GATK software. SnpEff software was used to predict genomic regions occurred with mutation sites and affection caused by mutation. Genes containing SNP or InDel loci were respectively aligned to GO and KEGG databases to gain corresponding function and pathway annotation. A total of 28 195 SNP loci were identified in N. ceranae, and the numbers of conversion and transversion were 21 403 and 6 792. These SNP loci had 12 mutation types, among them the most abundant one was C/T. SNP loci distributed in CDS region were the most. Additionally, the largest mutation type of codons of SNP loci was synonymous mutation. Moreover, genes containing SNP loci can be annotated to 43 GO terms such as metabolic process and cellular process, and 85 KEGG pathways such as metabolic pathway and ribosome. In N. ceranae, 2 831 InDel loci were identified, and those distributed in intergenic region were the most, while those distributed in CDS region was the least. The most abundant mutation type of codons was frameshift mutation. Genes containing Indel loci could be annotated to 38 GO terms including cellular process, cell and binding, and 73 KEGG pathways including metabolic pathways and biosynthesis of secondary metabolites. There are plenty of SNP and InDel loci in N. ceranae; the main mutation type of SNP loci is conversion. The genomic distribution rule of functional elements and mutation type of SNP loci are obviously different from those of InDel loci. Genes containing SNP and InDel loci have potential relationship with adaptation of N. ceranae to intracellular environment and pathogen proliferation process.