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## Improvement of the sequences and functional annotations of the eastern honeybee reference genome with the Nanopore long reads

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The eastern honeybee (Apis cerana) is a bee species of great importance used in beekeeping industry across Asian countries, with crucial ecological and economical value. Due to the short reads from second-generation sequencing, the current reference genome assembly version (ACSNU-2.0) of A. cerana still needs to be improved.. In this study, based on the obtained high-quality Nanopore long reads, the structures of the annotated genes in the A. cerana reference genome were optimized using bioinformatics, and the unannotated novel genes and transcripts were then identified and annotated, followed by prediction of SSR loci, complete ORFs and transcription factors (TFs). Here, 4648 annotated gene structures in the reference genome of A. cerana were optimized. In addition, 2148 new genes were identified, of which 818, 298, 587, 359 and 333 new genes were annotated to Nr, KOG, eggNOG, GO and KEGG databases, respectively. A total of 35432 new transcripts were identified, of which 30974, 21222, 29025, 19852 and 9214 new transcripts were annotated to the above five databases, respectively. Also, 22541 SSR loci were found, and the type with the highest distribution frequency was single base repeat (153.37/Mb). Totally, 58 TF families and 1611 members were predicted. Moreover, 28775 complete ORFs were predicted, of which the ORFs with coding length of 100-200 amino acids (38.99%) were the most. These results optimized the structure of the annotated genes on the reference genome of A. cerana, supplemented the unannotated novel genes, novel transcripts, SSR, complete ORF and TF on the reference genome, and improved the sequence and functional annotation of the reference genome of A. cerana. This work is believed to offer a valuable reference for relevant study on other species.