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Screening weight related genes of velvet antlers by gene ontology and pathway analysis of whole genome in Formosan Sambar deer (*Rusa unicolor swinhoei*)

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The velvet antler is an organ that has important biological significance in deer, and its growth is a complicated biological metabolism process. The growth of antlers is correlated with the seasonal variation of serum androgens. Moreover, seasonal levels of testosterone in plasma are well established, steroid concentration have been determined in the tissues of growing antlers. However, the molecular mechanism underlying the process remains elusive. Previous research suggests that genetics factors play essential roles in the weight of velvet antlers. In this study, we screen weight related genes of velvet antlers by Gene Ontology (GO) and pathway analysis of whole genome in Formosan Sambar Deer (*Rusa unicolor swinhoei*). The investigation and sampling is conducted in five deer fields, blood and antler tissue of 7-year-old Formosan Sambar Deer (*Rusa unicolor swinhoei*) were collected from March to May. Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analysis identifies the major signaling pathways involved. The results showed that 10, 7, 13 and 8 genes have been respectively screened in steroid biosynthesis, steroid hormone biosynthesis, terpenoid backbone biosynthesis and primary bile acid biosynthesis pathways. However, there is no gene screened in steroid degradation and brassinosteroid biosynthesis pathways. Collectively, we screened genes related to the velvet antler weight in Formosan Sambar Deer by gene ontology and pathway analysis of whole genome and identified 38 genes related to the velvet antler weight. We hope that the results will contribute to further mechanistic studies of velvet antler development and compare the differences in every age-group of deer's.

Biography

Tzu Chao has completed her graduate degree from Tunghai University at the Department of Animal Science and Biotechnology and has obtained her Master's degree in Animal Biotechnology and is interested in genome of livestock.

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