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## Mapping and annotating of bactrian camel MHC gene by using the comparative genomic approach

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**Statement of the Problem:** MHC is a collective term for major histocompatibility complexes of all organisms. MHC not only controls allograft rejection, but more importantly, it is closely related to biological immune response, immune regulation and the production of certain pathological states. There are differences in the structure and name of MHC gene sequences in different mammalian species. Bactrian camels have long been known to be highly resistant animals. For the study of MHC, Bactrian camel is a practical biological model. However, the assembly and annotation levels of the Bactrian camel reference genome are imperfect and the MHC gene is not assembled and annotated in the Bactrian camel genome. The purpose of this study was to locate and annotate the Bactrian camel MHC gene sequence, which lays the foundation for further study of the Bactrian camel MHC gene.

**Methodology:** The human MHC gene with the best assembly level and the bovine MHC gene with the closest relationship with Bactrian camel were selected and compared with the reference genome of Bactrian camel. The MHC gene was mapped and annotated into the Bactrian camel using comparative genomics methods.

**Findings:** In this study, we found 24 MHC genes present in the Bactrian camel genome, including 1 class-I gene, 10 class-II genes, and 13 class-III genes. These genes were distributed on these three scaffolds with class-I and class-III genes distributed on NW\_011515227.1 (1.2M) and class-II genes distributed on NW\_011511766.1 (4.1M) and NW\_011514613.19 (15K). We mapped the Pseudo chromosome of Bactrian camel MHC and annotated the 24 MHC genes of Bactrian camel.

**Conclusion & Significance:** This study laid a theoretical foundation for further study of the Bactrian camel MHC gene and also provided a new idea for the localization and annotation of MHC genes in other species.