

Molecular characterization of bovine major histocompatibility complex (MHC) class I & II genes

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Characterizing bovine major histocompatibility complex (MHC) genes is critical to understanding T-cell mediated immune responses to antigens derived from high impact viral pathogens such as the structural proteins of foot and mouth disease virus (FMDV). In contrast to humans and mice, the diversity of the bovine leukocyte antigen (BoLA) locus is poorly defined, compromising progress in vaccine development for virus infections of cattle. We have characterized the MHC diversity of purebred Holstein dairy cattle from a single herd using polymerase chain reaction with sequence-specific primers (PCR-SSP), for the class I MHC alleles from 66 cattle. We found alleles *N*01302*, *N*02301*, *N*00801*, and *N*01901* were each present in 24-41% of animals. PCR restriction fragment length polymorphism (PCR-RFLP) was used to determine the alleles of the MHC class II gene, *BoLA-DRB3*, of 50 animals from the same herd. We identified 13 different *DRB3* alleles of which four, **1001*, **1501*, **1101*, and **0101*, were each expressed in 18-20% of animals. These alleles correspond to reported *DRB3* PCR-RFLP types 3, 16, 22 and 24, respectively. This approach facilitates rapid identification of MHC class I and II alleles in cattle and will provide the foundation for analyzing the T-cell response of cattle to bovine pathogens, as well as strengthen our understanding of MHC functional diversity of Holstein cattle.

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