Association of bovine leukocyte antigen *DRB3*007:01* and **009:02* to host resistance to *Candidatus Mycoplasma haemobos* infection in Kedah-Kelantan x Brahman cattle

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Abstract

The bovine leukocyte antigen (BoLA) gene is a significant genetic part of the immune system and has been used as a disease marker in cattle. The 16SrRNA gene of *Candidatus Mycoplasma haemobos* was detected in 37 out of 85 (43.5%) Kedah-Kelantan x Brahman (KKB) cattle and allelic association of the *BoLA-DRB3* gene to *C. M. haemobos* infection was evaluated. The association between an allele and *T. orientalis* were evaluated by Fisher's exact and Cochran Mantel Haenszel (CMH) test. The odds ratios (OR) and their 95% confidence intervals for susceptibility or resistance were calculated for *each* allele. The amplification of the *BoLA-DRB3* gene produced clear single bands of 281 bp by the single-step PCR analysis. Sequencing of the PCR amplicons yielded 279 - 320 nucleotides. The PCR-sequence based typing of *BoLA-DRB3.2* gene from KKB cattle revealed that the gene is highly polymorphic. Ten novel alleles were detected (*BoLA-DRB3*012:04, *015:08, *015:09, *015:11, *015:12, *017:05, *017:07, *024:33, *107:04, *168:01)*, and these alleles shared about 90.7-95.8% and 85-92% nucleotide and amino acid identities respectively, with the *BoLA-DRB3*016:01* cDNA clone NR-1. Five alleles were detected in the *C. Mycoplasma haemobos* infected cattle namely: *DRB3*012:01, *015:01, *007:01, *018:01, *009:02.* The alleles with the highest frequencies were *DRB3*009:02* (50%) and **007:01* (34.2%) in the *C. Mycoplasma haemobos* positive cattle and *DRB3*018:01* (41.2%) and **015:01* (35.3%) in the *C. Mycoplasma haemobos* negative cattle. The associated alleles of *C. Mycoplasma haemobos* infection resistance was *DRB3*007:01* (OR = 0.161; P_{CMH} = 0.020) and **009:02* (OR = 0.084; P_{CMH} = 0.000). No susceptibility alleles were detected following the Bonferroni correction of *p*-value, $p > 0.0125$. Therefore, we presented *BoLA-DRB3.2* alleles associated with resistance to *C. M. haemobos* infection and suggests that during breeding, genetic selection of resistant animals could be a natural strategy for tick-borne disease control, particularly when there is no available global vaccine for the prevention and control of this infections.

***Keywords*:** bovine leukocyte antigen; alleles; *Candidatus Mycoplasma haemobos*; Kedah-Kelantan x Brahman cattle; PCR-Sequence based typing.