
口頭発表 | 2. 育種・遺伝

育種・遺伝2

Chairperson: Masaaki TANIGUCHI, Akira Ishikawa(Graduate School of Bioagricultural Sciences, Nagoya University), Shinji Sasazaki, Norihide Yokoi, Tomokazu Fukuda(Iwate University), Youko Aida

Fri. Sep 16, 2022 1:30 PM - 4:40 PM Zoom会場2 (オンライン)

II-16-19~II-16-22 : 谷口 雅章

II-16-23~II-16-25 : 石川 明

II-16-26~II-16-28 : 笹崎 晋史

II-16-29~II-16-31 : 横井 伯英

II-16-32~II-16-34 : 福田 智一

II-16-35~II-16-37 : 間 陽子

3:10 PM - 3:20 PM

[II-16-29] Comparison of BLV infectivity between bovine leukemia virus susceptible and resistant cattle

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Bovine leukemia virus (BLV) infects cattle worldwide and induces severe economic losses. The major transmission route is via infected blood. Polymorphisms of bovine lymphocyte antigen (*BoLA*)-*DRB3* alleles are related to susceptibility to BLV proviral load (PVL). However, whether differential *BoLA-DRB3* alleles affect BLV infectivity is still unclear. Here, we evaluated BLV infectivity in susceptible and resistant cattle in a three-year follow-up investigation. The *BoLA-DRB3* alleles, PVLs, and infectivity were analyzed. Among tested 179 cattle, the rates of susceptible and resistant alleles were 22 % and 16%, respectively. The mean PVL of resistant cattle was significantly lower than those of susceptible and neutral cattle. Susceptible cattle showed stronger BLV infectivity than both resistant and neutral cattle. BLV-infected resistant cattle were found to be at a low risk of BLV transmission owing to weak BLV infection and low PVL. Our results show that the *BoLA-DRB3* allele directly or indirectly associates with BLV infectivity. The breed selection based on resistant *BoLA-DRB3* allele is an effective strategy for reducing and controlling BLV infection.