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Publication date:
2012

Document Version
Early version, also known as pre-print

Abstract, Edinburgh 2012

Swine Leukocyte Antigen (SLA) class I allele typing of Danish swine herds and the identification of commonly expressed haplotypes using sequence specific low- and high resolution primers

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The genomic region (SLA) of the swine major histocompatibility complex (MHC), which bind and present endogenous peptides to circulating T cells of the immune system, is extremely polymorphic comprising high numbers of different alleles, many of which encode a distinct MHC class I molecule. Each SLA molecule is only able to bind a restricted number of peptides with specific biochemical characteristics matching important anchor positions in the peptide binding groove. Although the diversity of T cells is vast, the individual MHC make-up thus limits the range of potential T cell epitopes for any given individual. Therefore analyses of the prevalence of SLA alleles in a population are fundamental to employ pathogen-specific subunits or peptides in novel vaccines or immune diagnostics. In this study we present the use of low- and high-resolution PCR-based typing methods to identify individual and commonly expressed SLA class I alleles in Danish outbred swine. A total of 108 animals from eight different production herds were tested, and with low resolution sequence specific primer (SSP)-PCR typing the top five most commonly expressed SLA class I allele groups were found to be SLA-3*04XX, SLA-1*08XX, SLA-1*07XX, SLA-2*04XX, and SLA-1*04XX, respectively. Furthermore, customized high resolution primers were designed and used to identify specific alleles within the above mentioned allele groups and within the SLA-2*05XX group. In conclusion our studies suggest the most common haplotype in Danish pigs to be the Lr-4.0 expressing SLA-1*04XX, SLA-2*04XX and SLA-3*04XX.