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Molecular Typing of Paenibacillus larvae Isolates from Lithuanian Apiaries by using VNTR Allele Sizing Method

Paenibacillus larvae is a Gram-positive bacterium which is known as the causative agent of the American foulbrood (AFB), a highly contagious and fatal, widespread disease of honeybees. There are known four main bacteria genotypes classified as ERIC I - ERIC IV and recently detected ERIC V genotype. ERIC (enterobacterial repetitive intergenic consensus) genotypes differ in their virulence and prevalence in honeybee colonies. In this study we used 108 independent P. larvae isolates collected from different geographical regions of Lithuania in the last decade. Bacterial samples were investigated for genetic diversity using multiple locus variable number of tandem repeat analysis (MLVA). For MLVA five primers pairs representing different gene loci were used in multiplex PCR, and analysed by capillary electrophoresis (QIAxcel system). The aim of the study was by using MLVA method detect which ERIC genotypes are most common in Lithuania apiaries, identify and differentiate subtypes of defined genotype, and evaluate the ability of the QIAxcel Advanced System, using capillary gel electrophoresis, to be used as an automated improvement to the gel electrophoresis technology for sizing of P. larvae VNTR products. Molecular analysis data showed that 100 % of P. larvae bacterial isolates from Lithuania represent the ERIC I genotype, and capillary electrophoresis results did let us to differ P. larvae strains into 9 subtypes according to different length of VNTR.

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