Journal of Biotechnology 256S (2017) S17–S43

Contents lists available at ScienceDirect

Journal of Biotechnology

journal homepage: www.elsevier.com/locate/jbiotec

Abstracts of European Biotechnology Congress 2017 held in Dubrovnik, Croatia during 25–27 May 2017

Oral Presentation

Animal Biotechnology

Identification and molecular characterization of lumpy skin disease virus from cattle in North Cyprus

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Lumpy skin disease (LSD) is a disease of the domestic ruminants; characterized with fever and typical skin nodules. Lumpy skin disease virus (LSDV) belongs to genus Capripoxvirus. In 2014, the disease was appeared for the first time in the North Cyprus. In this study, PCR based virus identification and phylogenetic analysis were performed from cattles. Blood and testicular, skin tissue from bull and heifer were processed, respectively. After identifying the capripoxvirus nucleic acid, the PCR assay was performed using the specific primer pairs. Then the amplicons were purified and sequenced. For the phylogenetic tree, the sequenced amplicons of ORF 117 gene and ITRs region were aligned with other capripoxvirus sequences. Phylogenetic analysis revealed LSD viruses detected in animals in TRNC were close related to those either vaccine strains or local strains of the geography. Concerns on spreading of LSDV may have likely been for many reasons; like actual political situation in the middle and near East. Also, migration of the thousands of refugees and unvaccinated domestic ruminants from infected may cause more outbreaks in the future. This is the first report of the molecular based virus identification and phylogenetic analysis from 2 cattle diagnosed as LSD in TRNC.

http://dx.doi.org/10.1016/j.jbiotec.2017.06.607

Estimation of genetic parameters and genetic trend of Holstein cattle population in Turkey

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In this study, records of milk and fertility yield of Holstein Friesian dairy cattle reared in Turkey were evaluated. Data were taken from the Turkish Central Union of Cattle Breeders. Total of 194,408 lactation records obtained from some regions of Turkey were determined. The 305-day milk yield (305-DMY), lactation length (LL) and dry period (DP) as milk production traits and the calving interval (CI) as the reproductive traits were used. The effects and relations of year of birth, lactation number, calving month, location and calving age factors that were thought to be effect to 305-DMY, LL, DP and CI were evaluated. Heritability and repeatability of these traits were calculated by using MTDFREML. The heritability of 305 DMY, LL, DP and CI were estimated as 0.22; 0.01; 0.01 and <0.01 and repeatability of these were 0.22; 0.01; 0.02 and 0.01 respectively. Genetic trend was, also, estimated 7.44 kg/year. As a result, the estimated variance components, genetic parameters and breeding values could be used as selection criteria and to increase the success of the selection in breeding studies for Holstein cattle population in Turkey.

Acknowledgments

This work was supported by the Ahi Evran University Scientific Research Projects Coordination Unit. Project Number: ZRT.E2.17.03.

http://dx.doi.org/10.1016/j.jbiotec.2017.06.608

0168-1656/