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EPIDEMIOLOGY AND GENETIC CHARACTERIZATION OF BORDER DISEASE VIRUS CIRCULATING IN SARDINIA

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Border Disease Virus (BDV), a pestivirus from the *Flaviviridae* family, is an important pathogen of sheep and goats responsible for significant losses in farms around the world. In spite of the relevance of this pathogen there are only a few epidemiological studies on BDV infection and, as a consequence, the economic impact on small ruminant productions is probably under-estimated. The aims of this study are i) to determine the distribution of BDV in small ruminant farms in Sardinia and genetically characterize circulating strains ii) analyze the relation between seroprevalence, Somatic Cells Count (SCC) and milk yield. ELISA was performed using “BVDV/MD/BDV p80 Protein Antibody Test Kit” (IDEXX) on serum of bulk tank milk (BTM) samples collected from 1291 Sardinian sheep flocks and 72 goat herds between spring 2014 and 2015. The number of sampled farms corresponded to 8.5% of all registered farms in Sardinia; sampling was performed according to the distribution of the farms in the Sardinian region. RNA was isolated using Qiaamp Viral RNA mini kit from the cellular fraction of each ELISA positive BTV sample and amplified by rt-PCR using complementary primers to a highly conserved region in the untranslated regions (UTRs) of the viral genome. The amplicons were sequenced for phylogenetic analysis. Geographic distribution of collected specimen, seroprevalence and virological positive samples were analyzed via GIS (ESRI ARCGIS 10.3) ELISA screening shows a seroprevalence of 8.3% among goat farms and 10.5% among ovine farms. These values are higher than 8% of prevalence average recorded in Europe but close to the 11% observed in Italy (1, 2, 3). In sheep flocks we highlight that the distribution of the seroprevalence, indicates above as 10.5% in average, is uneven between Sardinian provinces. Ten from the ELISA positive samples were found rt-PCR positive. The sequence analysis indicates that all the amplified samples match with BDV genomes and the phylogenetic analysis revealed that all the viruses clustered in the same

group classified as BDV-7, previously described in Italy from Lazio and Tuscany isolates (4). Despite what reported in the rest of Italy, where also BDV-1, BDV-3 and BDV-5 (5, 6) have been isolated, BDV-7 is the only group isolated in Sardinia so far. According to the first analysis, variations in SCC and milk yield appear to have no significant correlation with seroprevalence and virus positivity in the screened farms. This study represents a snapshot of current distribution of small ruminants Pestiviruses and a genetic characterization of BDV circulating strains in Sardinia. Further studies should be led in order to understand the origin, the evolutionary story and the epidemiology of BDV-7 in Sardinia. The role of BDV as an immunosuppressive agent, exacerbating the pathogenicity of co-infecting microorganisms, should also be considered.

1. Buonavoglia et al., 1994
2. Graham et al., 2001
3. Krametter-Froetscher et al., 2007b
4. Giammarioli et al, 2011
5. Rosamilia et al., 2014
6. Giammarioli et al., 2015