endemic in Africa, the Middle and Near East, the Indian subcontinent and China. Understanding the molecular epidemiology and evolution of PPR virus (PPRV) can assist in the control of the transboundary spread of this economically important disease. We isolated PPRV from pathological and swab samples collected 42 years apart (1969 and 2011) in Benin, West Africa, and sequenced the full genome of two isolates (Benin/B1/1969 and Benin/10/2011). Phylogenetic analysis showed that all of the characterized isolates clustered within viral lineage II and that the 2011 isolates fell into two distinct subgroups. Comparison of the full genome sequences revealed a 95.3% identity at the nucleotide level, while at the protein level, the matrix protein was the most conserved between the two viruses with an identity of 99.7% and only one amino acid substitution over the 42-year sampling period. An analysis of specific amino acid residues of known or putative function did not identify any significant changes between the two viruses. A molecular clock analysis of complete PPRV genomes revealed that the lineage II viruses sampled here arose in the early 1960s and that these viruses have likely persisted in Benin since this time.

One-Step Multiplex RT-qPCR Assay for the detection of Peste des petits ruminants virus, Capripoxvirus, Pasteurella multocida and Mycoplasma capricolum subspecies (ssp.) capripneumoniae

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Respiratory infections, although showing common clinical symptoms like pneumonia, are caused by bacterial, viral or parasitic agents. These are often reported in sheep and goats populations and cause huge economic losses to the animal owners in developing countries. Detection of these diseases is routinely done using ELISA or microbiological methods which are being reinforced or replaced by molecular based detection methods including multiplex assays, where detection of different pathogens is carried out in a single reaction. In the present study, a one-step multiplex RT-qPCR assay was developed for simultaneous detection of Capripoxvirus (CaPV), Peste de petits ruminants virus (PPRV), Pasteurella multocida (PM) and Mycoplasma capricolum ssp. capripneumoniae (Mccp) in pathological samples collected from small ruminants with respiratory disease symptoms. The test performed efficiently without any cross-amplification. The multiplex PCR efficiency was 98.31%, 95.48%, 102.77% and 91.46% whereas the singleplex efficiency was 93.43%, 98.82%, 102.55% and 92.0% for CaPV, PPRV, PM and Mccp, respectively. The correlation coefficient was greater than 0.99 for all the targets in both multiplex and singleplex. Based on cycle threshold values, intra and inter assay variability, ranged between the limits of 2%–4%, except for lower concentrations of Mccp. The detection limits at 95% confidence interval (CI) were 12, 163, 13 and 23 copies/reaction for CaPV, PPRV, PM and Mccp, respectively. The multiplex assay was able to detect CaPVs from all genotypes, PPRV from the four lineages, PM and Mccp without amplifying the other subspecies of mycoplasmas. The discriminating power of the assay was proven by accurate detection of the targeted pathogen(s) by screening 58 viral and bacterial isolates representing all four targeted pathogens. Furthermore, by screening 81 pathological samples collected from small ruminants showing respiratory disease symptoms, CaPV was detected in 17 samples, PPRV in 45, and PM in six samples. In addition, three samples showed a co-infection of PPRV and PM. Overall, the one-step multiplex RT-qPCR assay developed will be a valuable tool for rapid detection of individual and co-infections of the targeted pathogens with high specificity and sensitivity.

Multilocus genotypic data reveal high genetic diversity and low population genetic structure of Iranian indigenous sheep

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Iranian livestock diversity is still largely unexplored, in spite of the interest in the populations historically reared in this country located near the Fertile Crescent, a major livestock domestication centre. In this investigation, the genetic diversity and differentiation of 10 Iranian indigenous fat-tailed sheep breeds were investigated using 18 microsatellite markers. Iranian breeds were found to host a high level of diversity. This conclusion is substantiated by the large number of alleles observed across loci (average 13.83, range 7–22) and by the high within-breed expected heterozygosity (average 0.75, range 0.72–0.76). Iranian sheep have a low level of genetic differentiation, as indicated by the analysis of molecular variance, which allocated a very small proportion (1.67%) of total variation to the between-population component, and by the small fixation index (FST = 0.02). Both Bayesian clustering and principal coordinates analysis revealed the absence of a detectable genetic structure. Also, no isolation by distance was observed through comparison of genetic and geographical distances. In spite of high within-breed variation, signatures of inbreeding were detected by the FIS indices, which were positive in all and statistically significant in three breeds. Possible factors