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**Respiratory infection by different genus and subgenus of coronaviruses in newborn alpaca (Vicugna pacos) from a rural community in the southern Peruvian highland**

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**Introduction:** Infectious diseases, particularly respiratory and diarrheal infections, are major causes of neonatal death in South American camelids (SAC). Coronavirus (CoV) infections in alpacas can cause serious enteric and respiratory problems. Furthermore, combined with other viral, bacterial, and parasitic infections can still aggravate the clinical picture. The main goal of this study was to detect and identify the CoV genus and subgenus associated with a severe respiratory outbreak that caused 100% mortality in newborn alpacas from a rural community located in the southern highlands of Peru in 2012. **Methods:** For this, samples of frozen lung lavage (n=32) were analyzed, one for each dead animal; these samples came from animals from 1 to 6 weeks of age from the rural community of Silly located in the district of Marangani, province of Canchis, department of Cuzco. The viral RNA was extracted to be subjected to RT-PCR and nested PCR using specific primers to amplify a conserved region of the gene that encodes the RNA depending on the viral RNA polymerase (RdRp) of all CoV genus reported. In the nested PCR for CoVs, specific primers for betacoronavirus (BetaCoV) were used. BetaCoV-positive samples were analyzed by nested PCR to identify the Embecovirus subgenus. **Results:** show that 30 (93.8%) samples were positive for CoVs. BetaCoV was identified in 26 (86.67%), of which 17 (56.7%) belonged to the Embecovirus subgenus, and 9 (30%) could not identify the subgenus. The genus of CoV has not been identified in 4 (13.3%) samples (Table 1, figure 1). Our data show a high frequency of infection by CoVs in newborn alpacas that died in the respiratory outbreak. **Conclusions:** This virus shows a wide genetic variety since we can observe more than one genus of CoV circulating in these animals, with betacoronaviruses being the predominant genus. Strains identified as betacoronavirus have more than one circulating subgenus in this rural community. Our work expands the molecular epidemiology of CoVs in alpacas raised in Peruvian rural communities and aims to develop animal sanitary programs to prevent and control clinical episodes and provide a vision of prevention in public health due to the zoonotic potential of this virus.

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