【Abstract】

Progress in the epidemics of Tibetan sheep and yaks in Qinghai Province in recent years.

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To summary what kinds of epidemics are happening on Tibetan sheep and yaks in Qinghai Province. Such as, the diarrhea of sheep and yaks caused by Escherichia coli and Salmonella; the diarrhea and deaths caused by multiple clostridial diseases; the infectious pleuropneumonia caused by Mycoplasma spp. in cattle and sheep; the prevention and treatment of foot rot disease and the purulent necrosis of internal organs caused by Fusobacterium necrophorum. The viral diarrhea caused by bovine viral diarrhea virus, rotaviruses and coronaviruses, bovine papillomavirus infections in yaks and cattle; infectious pustular dermatitis virus disease in sheep. Diagnosis and control of blood protozoan diseases in horses, cattle and sheep; the diarrhea caused by coccidia and nematodes in yaks; diagnosis and control of cestode and trematode diseases in yaks, cattle and sheep.

Optimization of single-tube nested PCR for the detection of Echinococcus spp.

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Echinococcosis is a serious zoonotic life-threatening parasitic disease caused by metacestodes of Echinococcus spp., and appropriate sensitive diagnosis and genotyping techniques are required to detect infections and study the genetic characterization of Echinococcus spp. isolates. In this study, a single-tube nested PCR (STNPCR) method was developed and evaluated for the detection of Echinococcus spp. DNA based on the COI gene. STNPCR was 100 times more sensitive than conventional PCR and showed the same sensitivity to common nested PCR (NPCR); the limit of detection of the developed STNPCR method was estimated to be 10 copies/ μL of the recombinant standard plasmids of Echinococcus spp. COI gene. The STNPCR method was suitable for epidemiological investigations and characteristic genetic studies of Echinococcus spp. tissue samples. The STNPCR method can effectively amplify low concentrations of genomic DNA from calcification samples and cyst residues infected with Echinococcus spp. Subsequently, the sequences of positive PCR products were obtained, which were useful for haplotype analysis, genetic diversity, and evolution studies of Echinococcus spp., and understanding of Echinococcus spp. dissemination and transmission among the hosts.