

Quantifying livestock commingling in mapped areas of sustained *Brucella* spp. transmission in Kazakhstan

Thursday, July 18, 2024 11:40 AM (20 minutes)

Brucellosis is a global zoonosis caused by species of *Brucella* bacteria with high burden in underdeveloped countries. Kazakhstan, in Central Asia, reports high human/livestock burden, requiring high costs for animal testing and slaughter. *Brucella* spp. show high host affinity and vaccines are *Brucella* spp. specific. The risk of brucellosis transmission between commingling livestock and wildlife species is poorly understood, including in Kazakhstan. We first mapped patterns of *Brucella* spp. from phylogenetic studies to identify zones of mixed transmission in the country. Motion-triggered cameras were deployed on four farms within this overlap zone, and images were tagged with species/behavior observations to create kernel density estimates of species-specific diel grazing patterns and plots of commingling between sheep and other livestock species. We found overlaps in diel activity for most livestock (sheep, goats, cattle, horses). Livestock showed three grazing peaks: morning, afternoon, and evening. Wild roe deer, *Capreolus capreolus*, were crepuscular. High levels of direct commingling occurred between sheep and domestic cattle: 18.18% of the time sheep grazed, only cattle grazed with them; ~28% of the time sheep were grazing, cattle and other livestock also grazed. Sheep directly commingled with all livestock species. Sheep/cattle interactions are most likely for brucellosis transmission; molecular evidence suggests shared *Brucella* spp. in both species. Additionally, cattle indirectly commingled with roe deer on forested farms in the study area. These data will aid policy makers in the identification of effective and economically efficient intervention strategies to lessen the burden of brucellosis to Kazakhstan and other endemic disease foci.

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Session Classification: Poster Presentations

Track Classification: Global Health: Infectious Diseases