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Development of ELISA and real time PCR for the diagnosis of strangles in horses

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Abstract

Strangles caused by *Streptococcus equi* (Se) is the most prevalent contagious bacterial disease of horses world-wide. Prevention and control are highly dependent on knowledge of the infection status of individual horses. PCR and ELISA that target the sequence encoding M-like protein (SeM) and antibody to this protein are widely used for diagnosis of strangles. However, interpretation of results may be complicated by variations in *sem* sequence, and by the presence in horse sera of *S. zooepidemicus* (Sz) specific antibodies that cross react with SeM.

Comparative genomic analysis of isolates of Se, and Sz was used to select Se specific sequences for design primers and probes, or for producing peptides for ELISA. Real-time PCR assays targeting the 5´ terminus of *seM* gene, 3´ terminus of *Seq4* prophage and *eqbE* gene of Se showed high sensitivity and specificity for differentiation of Se and Sz isolates and for detection of Se in specimens from horses. Two of 8 peptides (SeM-N and Se75.3-N) demonstrated strong specific reaction only with sera from horses infected with Se. Other peptides demonstrated reactivity with some sera from horses with Sz pneumonia/lymphadenitis suggesting cross reactivity with Sz or another unknown organism.

Substitution of full-length SeM by the N-terminal peptides of SeM and Se75.3 substantially increased the specificity of ELISA for antibody to Se. Multiplex real-time PCR provided more confident detection of Se in clinical samples.

Biography

Sergey C. Artiushin is an assistant professor of bacteriology at University of Kentucky. Dr. Artiushin earned his Ph.D. in microbiology from Moscow State University, Russia.