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## Serovar detector: a bioinformatic tool for serotyping *Actinobacillus pleuropneumoniae*

### Content

Serovar detector is a new bioinformatic tool for determining the serovar of *Actinobacillus pleuropneumoniae* using whole genome sequencing. The composition of capsular polysaccharide (*cps*) genes of isolates is compared to those of the serovar reference strains and the serovar is determined both by the number of common genes as well as the similarities between the homologous genes. A validation of the bioinformatic tool was performed using 732 genomes representing all described serovars. The isolates included had been characterized by conventional serotyping and PCR tests. Out of the 732 isolates included in the investigation, only 36 isolates (4.9%) could not be allocated into the 19 recognized serovars. The method could discriminate between most serovars, except for serovar 9 and 11. Phylogenetic analyses showed that although most serovars are genetically homogeneous, there is a degree of genetic variation that cannot be explained by the *cps* genes alone. This indicates that SNP-based phylogeny or wgMLST might be valuable supplements for assessing the variation of *A. pleuropneumoniae* in a given region. Serovar detector is a robust method for determining the serovar of isolates and a valuable tool for further characterization of the genetic heterogeneity within *A. pleuropneumoniae*.

### Keywords

*Actinobacillus pleuropneumoniae*; Serotyping

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### Professional Status of the submitter, who is also the speaker

Senior Scientist

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