The Salivary Proteome in Dogs with Canine Parvovirosis

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Canine parvovirosis is a severe disease that causes up to 90% mortality in unvaccinated puppies. The most common clinical signs include acute severe vomiting and diarrhoea, fever, dehydration and lethargy; however, other organs and tissues can be affected. A correct diagnosis of canine parvovirosis in order to provide adequate treatment and to prevent death and virus spread is crucial. In this respect, proteomic investigation of non-invasive specimens such as saliva could provide novel biomarkers of the disease. Thus, the aim of the present study was to identify potential salivary biomarkers of diagnosis of canine parvovirosis.

Saliva samples from client-owned dogs were collected for diagnostic purposes and pooled into two groups: naturally infected dogs with severe clinical signs of parvovirosis (n=3) and control dogs (n=3). A Tandem Mass Tag (TMT) label proteomic approach was employed in order to identify proteins with different abundance between groups.

TMT allowed the identification of 225 peptides with different abundance between the groups, corresponding to 68 proteins. For these proteins, a functional characterization based on GO terms was done using the PANTHER database. A total of 50 genes were identified, corresponding with 46 total functions. Of these, 21 of the genes hits were related to binding, 20 to catalytic activity, 2 to antioxidant activity, 2 to structural molecule activity, and 1 was related to transporter activity.

The results of the present study suggest that canine parvovirosis causes alterations in the salivary proteome which could lead to the potential discovery of new non-invasive biomarkers for diagnosis and understanding of the pathophysiology of the disease.

DISCLOSURES
No disclosures to report.

SPEAKER INFORMATION
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