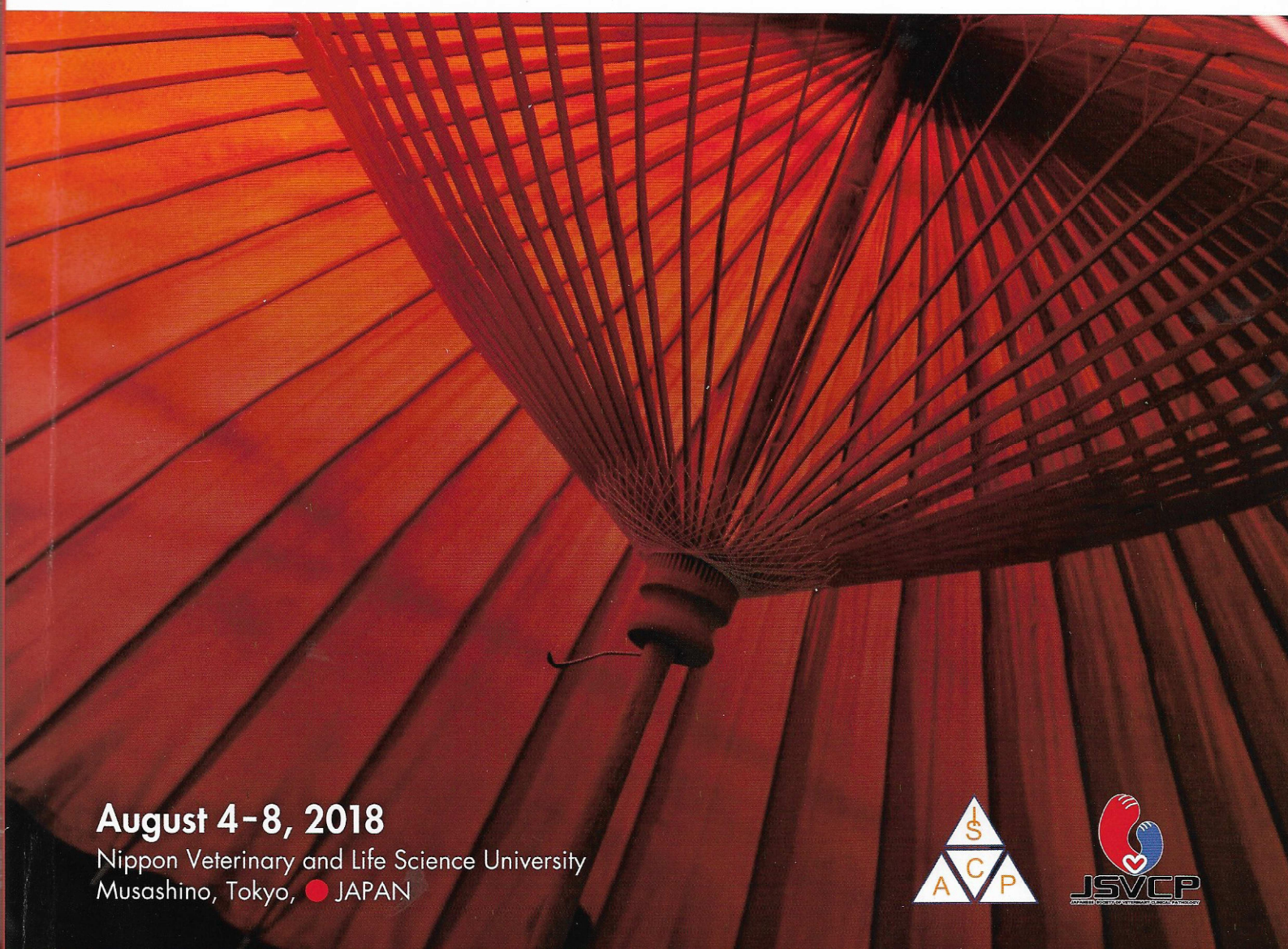




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IDENTIFICATION OF CHANGES IN SALIVARY PROTEOME IN CANINE OBESITY-RELATED METABOLIC DYSFUNCTION

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Background: In humans and some animal species, metabolic syndrome is related with physiopathological changes that can lead to increased risk for different diseases development and decreased lifespan. The main objective of this study was to compare the salivary proteomics of dog with and without canine obesity related metabolic dysfunction (ORMD) with the aim of identifying possible biomarkers of this syndrome in dogs.

Methods: Saliva samples from 12 overweight/obese dogs with and without ORMD, but otherwise healthy, was submitted to a proteomic analysis. Dogs were considered as having ORMD based on previously reported: (a) BCS 7-9/9; AND (b) any two of the following: 1) plasma triglycerides > 200 mg/dL; 2) plasma cholesterol > 300 mg/dL; 3) systemic blood pressure (SBP)> 160 mmHg; 4) fasting plasma glucose > 100 mg/dL, or previously diagnosed diabetes mellitus.

Results: Proteomic analysis revealed eight proteins that were differently expressed in their abundance between ORMD and non-ORMD groups: seven were decreased (Leukotriene A (4) hydrolase (F6Y290), Biliverdin reductase B (E2QVU9), Carbonic anhydrase 1(F1PBK6), GC vitamin D binding protein (F1P841) and 3 Uncharacterized proteins (J9P7B6, J9JHZ3, and F1Q3K7)) and one increased (uncharacterized protein F1Q0B9) in ORMD group dogs.

Conclusions: the data observed in present study suggest that canine ORMD is associated with changes in salivary proteome that could reflect altered metabolism in these dogs.