Prednisolone's Effects On Serum Proteome In Dogs And Cats

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Prednisolone is commonly used in veterinary practice, but studies describing how it affects protein expression and their interactions are lacking. [1-3] The aim of this study is to investigate changes in serum proteomic profiles before and after prednisolone in healthy dogs and cats.

A randomised, double blinded, placebo-controlled crossover study was conducted using eight clinically healthy dogs and nine clinically healthy cats. Animals were administered a 15- day course of prednisolone or placebo with a tapering dosage, starting at 0.5mg kg^{-1} orally twice daily. After a washout period of four weeks, animals were switched to the other arm of the study. Serum samples were collected from each animal before and immediately after treatment in both phases of the study and were analysed using mass spectrometry-based proteomic techniques.

Substantial differences in proteomic profiles were found in dogs and cats before and after prednisolone, with effects persisting for up to four weeks after discontinuation of prednisolone. Several proteins were differentially abundant when comparing before and after prednisolone administration with fold change ≥|2| in both species. Lipid metabolism was upregulated in both species. Multiple protein pathways had opposite regulatory trends including synaptogenesis signalling pathway, complement cascade, coagulation cascade and acute phase response signalling. Changes in oxidative stress response were seen in cats, while increased expression of antioxidant pathways were detected in dogs immediately after prednisolone.

These differences in proteomic profiles may account for the differences in clinical signs and adverse effects to prednisolone seen between the two species in clinical practice.

References

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