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Published in:
Next generation animal models

Publication date:
2012

Document version
Early version, also known as pre-print

Citation for published version (APA):
Seim-Wikse, T., Jörundsson, E., Nødtved, A., Grotmol, T., Bjørnvad, C. R., Kristensen, A. T., & Skancke, E. (2012). Significant breed predisposition of canine gastric carcinoma. In *Next generation animal models: translating discoveries to proof of concept* (pp. 32)

Proceedings 6th International SHARE Symposium

14th of November 2012

University of Copenhagen, Frederiksberg Campus,
Thorvaldsensvej 40, 1870 Frederiksberg C

"Next Generation Animal Models"

Translating discoveries to proof of concept



Lundbeck



Significant breed predisposition of canine gastric carcinoma

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Introduction: A breed predisposition for gastric carcinoma in dogs has been suspected. Results of previous studies are however inconsistent and mainly based on case series. Prognosis of gastric carcinoma is poor, and early diagnosis is necessary if treatment is to be attempted. Better knowledge of breeds at risk may facilitate early detection of gastric carcinoma in at risk breeds.

The hypothesis of the present study was that a breed predisposition exists for canine gastric carcinoma.

Materials and methods: The Norwegian Canine Cancer Register (NCCR) was used for retrospective calculation of proportional morbidity ratio (PMR) by breed for the period 1998 to 2009. Histologically verified canine tumours ($n=19,715$) in the NCCR were studied. PMR was calculated by dividing the number of gastric carcinomas in a breed (a_1) with all tumours in the breed (n_1), over the number of gastric carcinomas in all other breeds (a_0) divided by all other tumours in the other breeds in the database (n_0) = $(a_1/n_1)/(a_0/n_0)$. The 95% confidence interval for the PMR was computed on a logarithmic scale. Breeds for which the 95% confidence interval did not include the value 1 were considered to have a significant increased (or decreased) risk of gastric carcinoma.

Results: Thirty-one cases of gastric carcinomas representing 16 breeds were identified. A breed predisposition was identified. Tervuren (PMR=56.1), Bouvier des Flandres (PMR=36.5), Groenendael (PMR=34.5), Collie (PMR=26.1), Standard poodle (PMR=7.6) and Norwegian elkhound (PMR=6.1) had a significantly increased risk of gastric carcinoma.

Conclusion: A breed predisposition to gastric cancer was identified in the study, namely Tervuren, Bouvier des Flandres, Groenendael, collie, standard poodle, and Norwegian elkhound were found to have a significantly increased risk of gastric carcinoma according to the proportional morbidity ratios (PMRs). The breed predisposition observed in the current study indicates a genetic susceptibility to gastric carcinoma.

In breeds at risk of developing gastric carcinoma, gastritis symptoms should prompt earlier and more aggressive investigation to rule out gastric cancer, allowing early appropriate therapy if diagnosed.

Gut microbiome and associations with Overweight and Obesity in cats

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Introduction: The gut microbiota of mice and humans is altered in obese individuals. Whether there is a changed microbiota in response to an obesogenic diet or the microbiota directly contributes to weight gain is currently discussed. Obesity is prevalent in the cat population but gut microbiome changes associated with obesity have not been studied. Considering the carnivorous nature of cats such a change would probably be unrelated to a diet high in fat and carbohydrates. The aim of this study was to compare the gut microbiome of overweight and obese cats with that of lean cats.

Materials and methods: We included 77 shelter cats in the study. Individual faecal samples were obtained by rectal swab, and when available a paired litter box sample. Included cats had been at the shelter for three or more consecutive days and all cats received Royal Canin dry food and Sheba wet food. Body condition was assessed with a 9 point body condition score (BCS) system. DNA was extracted and the 16S rRNA gene was amplified. The amplified samples were analyzed with the Fluidigm Access Array 48.48, through 19 primers specific for different taxonomical bacterial groups and one archaea specific primer. For the statistical analysis Wilcoxon signed-rank test, PCA, ANOVA and t-test were used.

Results: BCS was found to be a significant ($p < 0.05$) explanatory factor for differences in the gut microbiota. The difference was not significant when data for each taxonomical group was analyzed individually. Overweight and obese cats had median lower counts than lean cats for the Bacteroidetes and Firmicutes groups and higher median counts for the Bacilli and Clostridium cluster IV groups. Rectal swab samples obtained more bacteria than the litter box samples ($p < 0.0001$).

Conclusion: Overweight and obese cats had a significantly different gut microbiome when compared to lean cats. This difference, however, could not clearly be linked to any of the analyzed bacterial groups. Moreover, we found a difference in the amount and the diversity of bacteria obtained by rectal swab and the litter box samples. Our results indicate that overweight and obese individuals may have a deviant gut microbiome compared to lean, which is not related to a diet high in fat and carbohydrates. Furthermore rectal swab samples seem to be a useful, alternative method to litter box samples.