Effect of different dietary fiber on the expression rate of the inflammatory marker genes (TGFβ, TNFα and NFkB) in the gastrointestinal tract of weaning piglets

K. Schedle[1], M. Pfaffl[2], W. Windisch[1]

[1]University of Natural Resources and Applied Life Sciences, Vienna

[2]Technical University of Munich

University of Natural Resources and Applied Life Sciences, Vienna
Department of Food Science and Technology

Introduction

Feed components rich in dietary fiber are used restrictively in diets for growing pigs due to low concentration of energy and protein. In recent years, however, such components are discussed to exert also beneficial side effects through stimulation of microbial activity and fermentation in the large intestine. In the present study we investigated the effect of two insoluble fiber sources differing in microbial degradability on expression rate of the anti- and pro-inflammatory marker genes TGFβ and TNFα, as well as the transcription factor NFkB in the gastrointestinal tract of weaning piglets.

Materials und Methods

The study employed a total of 36 weanling piglets. Animals were distributed according to litter, sex and initial body weight (approx. 8.5 kg) among the 3 types of diet and were slaughtered after 37 experimental days. Two diets were modified by adding wheat bran or pollen from Chinese Masson pine (*pinus massoniana*), on base of equal amount of total dietary fiber.
1) Control: basal diet only (negativ control)
2) Addition of 3,00 % wheat bran (= + 15 g dietary fiber)
3) Addition of 2,55 % pine pollen (= + 15 g dietary fiber)
Animals were fed ad libitum a weaning diet (13.9 MJ ME/kg, 25% XP) during the first 9 days and then a starter diet (13.5 MJ ME/kg, 20% XP). Tissue samples of stomach, jejunum, ileum, colon, mesenterial lymph nodes and blood were collected and stored at -80 °C. Total RNA of samples was isolated using TriFast and the RNA quantity and quality were checked in the Bioanalyzer 2100 (Agilent Technolgies, Palo Alto, CA). q-PCR was carried out as two-step PCR. Relative quantification of cDNA (respectively, mRNA) was carried out with the Eppendorf realplex Cycler. The crossing points were acquired with the CT-method (Eppendorf Software, Hamburg, Germany) using the mean expression of two reference genes (histone H3 and beta-actin). Amplification PCR products underwent a melting curve analysis after the last cycle to specify the integrity of amplification and finally a cooling step was performed. Relative quantification was calculated by the delta-delta-Ct method, compared to untreated control group.

Results

Figure 1-3 presents expression rates compared to control group (x-fold). Significant differences to control level (=1) are expressed as * (p<0.05) and (*) (p<0.1)

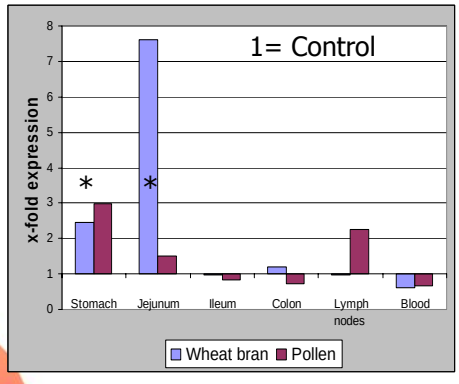

Figure 1: Gene expression von TGFβ

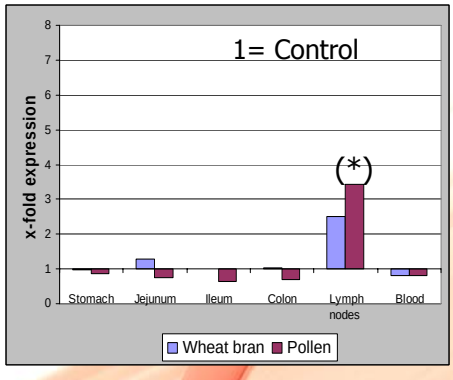

Figure 2: Gene expression von TNFα

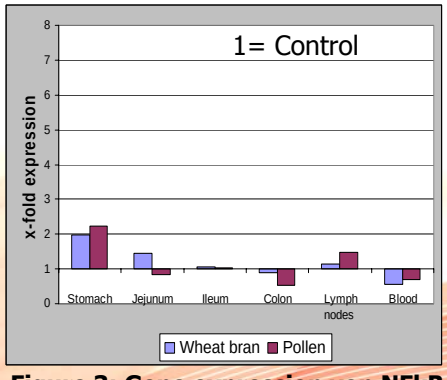

Figure 3: Gene expression von NFkB

Conclusion

- The results indicate the ability of fiber sources to affect the expression of inflammatory marker genes TGFβ and TNFα.
- The simultaneous up-regulation of both pro- and anti-inflammatory marker genes in mesenterial lymph nodes e.g. in case of the pine pollen group seem to reflect a general stimulation of activity of the immune system through additional dietary fiber intake. This hypothesis is supported by the absence of reaction of the pro-inflammatory marker gene TNFα, and NFkB, a transcription factor for TNFα in the small and large intestine.
- The stimulation of the gut immune system demonstrates beneficial effects of dietary insoluble fiber in diets with high nutrient density. The action of dietary fiber starts already in the front part of the gastrointestinal tract, and does not only refer just to stimulation of microbial activity in the hind gut.