

Characterization of Ig $-/-$ chicken intestinal proteome

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Abstract

Besides high concentration of immunoglobulins (Ig) in blood, considerable amount of Ig is also secreted into the gut lumen where it binds intestinal bacteria and contributes to gut barrier function. In this study we examined impact of Ig absence on the proteome of gut tissue and on composition of intestinal microbial community. Conventional and Ig $-/-$ knockout chickens were used for comparison.

Using stable isotope dimethyl labeling and liquid chromatography-tandem mass spectrometry (LC-MS/MS) we have determined relative quantity of altogether 2366 proteins of the gut tissue. Using Gene Set Enrichment Analysis we have identified 17 protein categories as being significantly misregulated in Ig $-/-$ animals when compared to control group. Most downregulated protein categories were those involved in various metabolic processes including glycolysis, protein absorption and fatty acid metabolism indicating that epithelium of Ig $-/-$ animals may not handle food nutrients optimally.

Microbial composition of gut content was estimated using label-free LC-MS/MS and was found to be highly similar amongst experimental groups suggesting little potential of immunoglobulins to severely affect microbial composition. However, analysis of host proteins co-purified with intestinal bacteria revealed 35 proteins with different expression. High expression of five Ig-like proteins in control group was compensated in Ig $-/-$ animals by induction of two mucus forming proteins (Gga.56299 and MUC13) and LOC424523 (CLCA protein with probable relationship to mucus production). Moreover, SRCR-like and FGL1-like proteins, proteins recently described as capable of nonspecific microbial aggregation, were also expressed at higher level in Ig $-/-$.