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The feed-a-gene project

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The Feed-a-Gene project aims to better adapt different components of monogastric livestock production systems (i.e. pigs, poultry and rabbits) to improve the overall efficiency and to reduce the environmental impact. This involves the development of new and alternative feed resources and feed technologies, the identification and selection of robust animals that are better adapted to fluctuating conditions, and the development of feeding techniques that allow optimizing the potential of the feed and the animal. The project started on March 1st 2015 for a 5 year period and has been awarded a grant from the European Commission (Grant agreement no: 633531) under the EU Framework Programme for Research and Innovation Horizon 2020. The project will: (1) Develop new and alternative feeds and feed technologies to make better use of local feed resources, green biomass and by-products of the food and biofuel industry; (2) Develop methods for the real-time characterization of the nutritional value of feeds to better use and adapt diets to animal requirements; (3) Develop new traits of feed efficiency and robustness allowing identification of individual variability to select animals that are more adapted to changes in feed and environmental conditions; (4) Develop biological models of livestock functioning to better understand and predict nutrient and energy utilization of animals along their productive trajectory; (5) Develop new management systems for precision feeding and precision farming combining data and knowledge from the feed, the animal, and the environment using innovative monitoring systems, feeders, and decision support tools; (6) Evaluate the overall sustainability of new management systems developed by the project; (7) Demonstrate the innovative technologies developed by the project in collaboration with partners from the feed industry, breeding companies, equipment manufacturers, and farmers' organizations to promote the practical implementation of project results; (8) Disseminate new technologies that will increase animal production efficiency, whilst maintaining product quality and animal welfare and enhance EU food security to relevant stakeholders. For more information about the project and registration at the stakeholder platform: www.feed-a-gene.eu.

Session 24

Theatre 2

Effect of feeding regime and presence of antibiotics in diet on rabbit's microbial gut composition

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Simultaneous *Bacteria* and *Archaea* detection by 16S rDNA-based MiSeq sequencing was performed to assess rabbit gut microbiota composition subjected to different factors: feeding regime (*ad libitum* (aL) vs restricted (R)), presence/absence of antibiotics in the diet, and the global environmental conditions defined by the farm. Caecum samples from 66-days-old rabbits (236 fed aL and 215 fed under R) were collected from two different farms (375 farm A and 94 farm B). 24 samples from farm B came from animals fed with the same standard feed but without antibiotics. Average daily gain (ADG) was recorded individually and its association with microbiome composition was studied. Globally, a total of 4,613 OTUs without singletons were clustered from 15,296,317 filtered contigs with a QIIME pipeline. Taxonomic assignment, based on Greengenes database *gg_13_5_otus*, revealed that intestinal microbiota was dominated by *Firmicutes* (79.2%), *Tenericutes* (6.6%), and *Bacteroidetes* (5.4%) phyla, *Archaea* domain was present at low percentage (1.5%). PCoA based on weighted Unifrac distance matrix showed that farm exerted a more relevant effect than feeding regime or the presence/absence of antibiotics. Nevertheless, 3 OTUs belonging to *Clostridiales* order (*Firmicutes*) and *Methanobacteriaceae* family (*Euryarchaeota*) were overrepresented in samples from animals fed aL relative to those under R. Moreover, 57 OTUs were differentially represented in animals receiving diet with or without antibiotics. On the other hand, significant associations with ADG were found for 45 OTUs. This was negative for 13 families and 5 phyla, and positive for 3 families and 2 phyla. OTU richness was positively associated to ADG. Our results point to the fact that bacterial taxa abundance might explain an important percentage of ADG variability since the content in half of the detected phyla is associated to ADG. This study is part of the Feed-a-Gene project and received funding from the European Union's H2020 program under grant agreement n° 633531.