

In the EADGENE joint research programme several specific host (e.g. cow, pig)-pathogen relationships get special attention. In Newsletter four the functional genomics of host pathogen interactions in common were discussed by Mari Smits. Functional genomics is the analysis of the function of genes of an animal. One of the goals of the joint research groups is to identify the genes of the pathogens that are involved in host-pathogen interactions, in this Newsletter Salmonella will be discussed by Anne-Marie Rebel.

Host Pathogen Interactions Salmonella

Upon an infection, Salmonella can induce various pathological changes and clinical signs of disease in animal hosts. The molecular aspects of the host response upon a salmonella infection are, however, relatively unknown. Many different factors determine the type, the specificity and efficiency of such a host response. Examples of these factors are: genetic background of the individual host; breed; age; health status; salmonella strain and subtypes; environmental factors; etc. In the joint salmonella research project we will compare the host (e.g. chicken, pig, cattle) responses at the molecular level in different models of salmonella infections. From this we will extract the common response parameters of a salmonella-induced host response. Initially, we will concentrate on host responses within one animal species (chicken, pig and cattle) and later on we will also compare the responses of different animal species, for example pigs vs. chicken. We will perform this by generating a list of genes that are up- or down-regulated upon an infection with salmonella in each animal model operative in the participating institutes. We will exchange information on gene sequences (order of bases in a gene which determines which protein a gene will produce), in order to evaluate the behaviour of genes, found to be up- or down-regulated in one infection model, in all the other infection models. This will identify genes that are common “response genes” for different kind of infection models and response genes that are specific for a particular model.

Another subject is the identification of the cell types that execute the host response. Here we will evaluate whether the expression pattern of the common response genes is linked to specific cell subsets. This research will identify molecular pathways that form potential targets for improvement of (salmonella) resistance