CHICKEN IMAGE

Chicken-IMAGE

Database

Blast

INFORMATIONS

Pathogen diseases are a major cause of death in flocks, with many diseases causing prolonged and severe suffering before death. Progress in diagnosis, treatment and cure of the various types of diseases require advances in both basic knowledge of the processes involved and the development of specific applications. Microarray analysis of gene expression in chickens is a fundamental method of scientific investigation that will be used in many areas of research whose ultimate aims are the improvement of the welfare of commercial poultry and the improvement of the quality of life of the European consumer by reduction of the risks and costs by the food-borne pathogens that are associated with chicken meat. The chicken- image project has made a substantial contribution to these goals by providing a tool for fundamental investigations whose applications are very wide.

In this project we have developped an array of chicken cDNAs expressed in tissues involved in significant functions in regulation and effector functions of both innate and adaptive arms of the immune system, and we have optimised procedures for application of this array in hybridisation analyses of mRNA populations to the study of immune responses and disease resistance in chickens. This was accomplished by construction of normalised cDNA libraries from sources involved in active immune responses, identification of expressed genes by EST sequencing from these libraries, and construction of arrays with these sequences.

Four cDNA libraries using the “SMART cDNA library kit (CLONTECH)” have been constructed and normalised: -1-Eimeria tenella-infected caecal tonsil; -2- Marek’s disease virus-infected spleen; -3- PHA-activated splenocytes; -4- LPS-activated macrophage cell line HD11 (mixture of different time intervals).

The chicken cDNA libraries prepared in this project were deliberately and carefully made by pooling mRNA isolated from tissues samples collected over sources chosen to represent as many as possible of the relevant cell types, stages and states of immune system activation.

The resources developed in the form of DNA arrays were used to measure the expression levels of the identified genes in active immune responses in infected or vaccinated animals. Three infection models -i- infection by Infectious Bursal disease virus (IBDV).-ii- infection by Marek’s Disease virus (MDV).-iii- infection by Eimeria tenella have been selected on the basis of their importance both to animal welfare and productivity of the poultry industry and because they represent different facets of pathology and immune response. In each case two well-characterised protocols for controlled infection are established and information regarding the nature and time-course of pathology is available. The three different infections selected for study include both acute and chronic infections and both systemic and mucosal immune tissues. They involve innate, B and T cell arms of the immune response. In each case there is known to be very significant immunological activity, and pronounced differences in genetic resistance. The material harvested from these experiments provided a very comprehensive platform from which we were able to determine the capabilities of the microarray gene expression analysis.