11.15 - Gammaherpesvirus latency impacts the host immune response and induces protection against asthma development.

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The immune system is continuously shaped by environmental antigens. However, the effect of the infection history is ignored in most animal models. Gammaherpesviruses are highly prevalent pathogens that establish lifelong latency in their host. While these viruses persist in lymphoid tissues, little is known about how they imprint the host immune response. In humans, although the Epstein-Barr virus (EBV) and the Kaposi's Sarcoma-associated Herpesvirus (KSHV) are associated with several malignancies, most of their infections remain asymptomatic. Studying how EBV and KSHV imprint the human immune response is difficult because they have no well-established *in vivo* infection model. Related animal gammaherpesviruses allow us to tackle the same fundamental questions in a more accessible form. In this study, we used Murid herpesvirus 4 (MuHV-4), a natural pathogen of rodents, to investigate the impact of gammaherpesvirus infection on subsequent allergic asthma development. Using a murine model of house dust mite (HDM)-induced allergic asthma, we compared the sensitization of mice mock infected or infected by MuHV-4 by: (i) broncho-alveolar lavage analysis, (ii) lung histology, (iii) determination of serum total level of IgE and (iv) restimulation of bronchial lymph node cells. These experiments showed that previous infection by MuHV-4 is associated with protection against HDM-induced airway allergy. As epidemiological studies suggest that similar phenomenon could happen with human gammaherpesviruses, these results could have important implications for researches on asthma development. Moreover, these results reinforce the view that lifelong persistence of herpesviruses is a symbiotic relationship that could be beneficial to the host in some circumstances.

11.30 - Study of the microbial flora of freshwater and seawater fish filets in different packaging conditions by metagenomic analysis targeted on the 16S ribosomal DNA.

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Metagenomics has appeared as a powerful tool to study bacterial composition of various environmental samples. This work describes the application of this technique to study the bacterial population of two fresh fish filets. The two fish species are from freshwater (pangasius) and seawater (haddock), respectively. Samples where directly analyzed the day of receipt. Others samples were analyzed at the end their shelf life after storage at 4°C (1/3 of their shelf life) and 8°C (2/3 of their shelf life). For these samples, packagings were made in plastic wrap for atmospheric air condition and in trays under modified atmosphere. Classical microbiological and 16S rDNA metagenomic analysis were carried out on all these samples. The composition and evolution of microbial populations of fish filet stored under different packaging conditions and temperatures of storage were investigated with identification of bacteria species. A total of 40 different species were identified for both fish types. Gram-negative bacteria are always predominated among the initial flora and at the end of the shelf life in all the trials. At the beginning of storage, the predominant Gram-negative microflora consisted of *Moraxellaceae* (*Acinetobacter* spp, *Psychrobacter* spp.), *Pseudomonadaceae* (*Pseudomonas* spp), and *Shewanella* spp and the Gram-positive flora was identified as *Lactobacillaceae* (*Carnobacterium* spp), *Brochothrix thermosphacta* and *Planococcus donghaensis* (only for pangasius). For the pangasius, *Planococcus donghaensis* is only present before the fish is packed and its dominant presence could provide an indication of the freshness of the fish. The metagenomic analysis is a useful tool to identify and to measure the relative proportions of bacterial species in fish filet samples.