of these fishes to recognize nematodes as self or non-self.

The results taken together suggested relevant immunity-related results providing a new perspective for future immunological studies in these species.

Session 2. Chairmen: L Ballarin, University of Padua, Padua, Italy; E Ottaviani, University of Modena and Reggio Emilia, Modena, Italy; M Cammarata, University of Palermo, Palermo, Italy

Evolution of the immune system

Lecture

Evolution of complement system

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The complement system is part of the immune system and in particular of the innate immunity. It is not adaptable and does not change over the course of an individual's lifetime. However, it can be recruited and brought into action by the adaptive immune system. The complement system is most famous for its role in immunity, orchestrating an exquisitely refined system for immune surveillance. At its core lies a cascade of proteolytic events that ultimately serve to recognize microbes, infected cells or debris and target them for elimination.

The human complement system is composed of more than 30 serum and cell surface components, and most of these components show a characteristic domain structure, enabling to trace the evolution of the genes based on their structures. Ongoing projects in both vertebrates and invertebrates revealed that most domains used by mammalian complement components are found in invertebrates. Unexpectedly, the complement system of an invertebrate shows a similar level of complexity and efficacy as that of mammals. Moreover complement components from different species demonstrated the capacity to cross-react.

Mounting evidence has shown that a number of proteins and proteolytic intermediaries in this cascade have, in themselves, other functions in the body, signalling through receptors to drive events that appear to be unrelated to immune surveillance. It seems, then, that the complement system not only functions as an immunological effector, but also has cell–cell signaling properties that are utilized by a number of non-immunological processes.

The scope of the complement system's function is indeed much greater than we might have imagined only a few years ago.

The protein pheromone family of the ciliate *Euplotes petzi*, the earliest branching species in the *Euplotes* phylogentic tree

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Self/non-self recognition in ciliates relies on signaling proteins (pheromones) synthesized in association with a genetic mating-type mechanism, that regulates the cell switching between the growth (mitotic) and sexual (mating) stages of the life cycle. In *Euplotes* species, these pheromones are freely released into the medium from where they can be purified in relative abundance. The knowledge of their molecular structures has so far been limited to four species, namely *E. raikovi*, *E. octocarinatus*, *E. nobilii* and *E. crassus*, that occupy varied positions in the *Euplotes* phylogenetic tree. Most research interest has now been focused on the pheromone family of *E. petzi* because of a major distinctive, phylogenetic trait of this species. Together with *E. sinicus*, *E. petzi* forms the earliest branching clade in *Euplotes* evolution.

Four structurally distinct *E. petzi* pheromones have so far been structurally characterized together with their coding genes. With respect to the other known *Euplotes* pheromones, they show smaller dimensions (only 32 amino acids vs. up to 108 in *E. octocarinatus*), a higher density of disulfide bonds (four), and a folding in which molecular districts with no regular structures equal in extension districts with regular structures represented by one extended and two single-turn alpha-helices. Considering that in the other *Euplotes* species pheromones have structures dominated by a bundle of three regular alpha-helices, the minimal dimensions and the relatively simple architecture of *E. petzi* pheromones thus indicates that the structural evolution of *Euplotes* pheromones involves a progressive increase of architectural complexity. And the finding that the *E. petzi* pheromone genes are practically half in dimensions the pheromone genes of the other *Euplotes* species reinforced this indication.

Autophagic cell death in the insect cell line IPLB-LdFB: evidence in absence of known mediators

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The larvae of holometabolous insects are privileged models for studying the programmed cell death (PCD). The IPLB-LdFB cell line has been derived from the larval fat body of the gypsy moth *Lymantria dispar*. IPLB-LdFB cells can undergo apoptosis after oxidative stress, but they also present autophagic cell death after a 2 h treatment with the F1-F0 ATP synthase inhibitor, oligomycin A. Autophagic cell death seems activated in IPLB-LdFB with an established program because the oligomycin A-treated cells can condition the culture medium making it lethal for untreated IPLB-LdFB cells.

Our observation demonstrated that conditioning time is critical for the lethality of the conditioned medium (CM), and that 1 h is enough to attribute lethal effects to the CM. In order to characterize