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**PROGRAM,  
BOOK OF ABSTRACTS,  
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## The contribution of network and spatial analysis in understanding how diseases pressure and ergonomic requirements moulded evolution of insect societies

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Complex societies are formed by thousands to millions of individuals which incessantly interact in the sheltered shared nest space. Insect societies are thus complex systems which face every day with different evolutionary pressures, such as infectious disease and group coordination, working at the same time. Understanding how colony members interacts in space and time is thus of overwhelming interests to unravel how natural selection mould evolution of insect societies. Indeed, the last years saw an increasing attention towards the characterization of the networks of social connections and the use of space in social insects. In the present work we investigated the spatial positions and the contacts network of workers and queen in a honeybee society thanks to high resolution recordings of individual spatial behaviour and “network connections”. We quantified the exact spatial organization (the real space) and we delineated the structure of the interaction network (the abstract contact space) of each single worker of different age and the queen. Our results clearly show that the honeybee colonial network is highly compartmentalized both at the social (association network) and at the spatial (use of space on the comb) scale. Groups of different age workers, corresponding to different task-related groups, occupy different comb areas and show limited contact among them. Foragers, who usually may introduce the contagion to the colony are also the least connected individuals in the network and those that occupy the periphery of the social network. Young workers are the individuals more connected, and those that form the network core. The queen is completely embedded within young bees and sheltered by pathogens. Our data show that segregation in the interaction network corresponds also well with a segregation of honeybees in the real space on the comb. In addition, each category insists on a different part of the comb, clearly dependent on nest content and individual specific task. Foragers are clumped together on a small area near to the entrance of the hive, while young bees and queen avoid completely this region of the comb and alighted mainly on brood cells. The comb shows a characteristic well organized pattern of brood, pollen and honey and this configuration leads to a strong spatial division among older bees and both queen and younger bees influencing the dynamics between pathogens and their hosts. Opposite pressures exert by both pathogens and ergonomics requirements could have been contemporaneously at work in shaping the network design and spatial organization into the nest and the present study furnished empirical data that social organization and the pathogens could have been resolved in an evolutionary trade-off much more than previously thought.

## Characterization and phylogenetic analysis of the *Vitis vinifera* gibberellin oxidases

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Gibberellins (GAs) are phytohormones important to regulate several aspects of plant development, such as growth, flowering and fruit-set. GAs are used in viticulture to control berry size and bunch architecture, which are important traits that often determine the economic success of a grape variety. Despite the identification of 136 GA structures in nature, only a handful are biologically active. GA<sub>1</sub> and GA<sub>4</sub> are the most common bioactive GAs in grapevine and their pool is maintained through a combination of biosynthesis and deactivation activities, which involve a family of GA oxidases belonging to three distinct groups: GA 20-oxidase (GA20ox), GA 3-oxidase (GA3ox), and GA 2-oxidase (GA2ox). In this work we identified and characterized the family of grapevine GA oxidases, and identified six GA20ox, three GA3ox and eight GA2ox proteins, the latter further distinct into five C<sub>19</sub>-GA2ox and three C<sub>20</sub>-GA2ox proteins. Our phylogenetic analyses suggest a common origin of GA3ox and C<sub>19</sub>-GA2ox and challenge previous evolutionary models. The specific activity of the identified GA oxidases was confirmed in vitro by expression of the recombinant proteins, and in vivo by ectopic expression in the model species *Arabidopsis thaliana*. This work was supported by the Autonomous Province of Trento (Call 1 - Post doc 2009 - Incoming) awarded to Lisa Giacomelli.