5th Congress

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V congress of the Italian Society for Evolutionary Biology. Trento, 28-31 August 2013 maritime pine seems to harbor large amounts of diversity for these genes due to a more stable demography; in addition, because of its more mesic distribution, higher environmental heterogeneity would have resulted in contrasted selective pressures that may have increased general levels of diversity at candidate genes. Using a wide range of neutrality tests, we found some of the candidate genes studied to evolve in non- neutral patterns. Interestingly, two of them showed statistical correlation with temperature variables, in particular with extremely high or low temperatures, and may constitute valuable tools for monitoring adaptive genetic diversity in these two Mediterranean pines. Our study shows that the use of complementary approaches can help capturing different aspects of the evolutionary processes that govern molecular variation at both intra- and inter-specific levels

## Evolutionary metagenomic analysis of the rumen microbial community of cattle

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Ruminants have evolved a mode of herbivory which utilises a multi-chambered digestive system to house a diverse community of anaerobic microbes capable of breaking down indigestible lignocellulosic material to readily absorbed volatile fatty acids. The microbial community consists of core and transitory species which fluctuate with changes in diet and even over the course of a single day. Some such as the methanogens often form stable associations with other rumen microbes to degrade complex organic compounds and supply their substrates. Metagenomic analysis of these communities have revealed that the genes for many of the core fermentative functions have been widely shared among the microbes, however the extent of variation of these genes and how it relates to their function is largely unknown. We undertook to assess the functional variation in the rumen microbial community through the metagenomic analysis of the rumen contents of 14 tube-sampled Holstein-Friesian cattle. After assembly and functional annotation of the metagenome we identified and annotated the SNPs that occurred and calculated an evolutionary rate for each gene from each taxonomic group. We found that the evolutionary variation calculated for individual taxonomic groups was highly replicable across animals. We also found that there were large differences in evolutionary rates for different microbial groups, suggesting that they may be subject to differential selective pressures. Finally, we identified genes which had differential evolutionary rates in different organisms, suggesting a link to the importance of the gene to organisms inhabiting different evolutionary niches and a mechanism of using an evolutionary approach to understanding the microbial ecosystem as a whole.

## How grapevine got pimples. The interkingdom horizontal transfer of an unusual symbiont

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Humans have established a long-lasting co-habitation with a variety of animals, plants and microbes. The human-gut microbe interaction has been recently explored, and cases have been reported of microbial host transfer from domesticated animals to humans. Much less is known regarding human-plant microbial transfers. Here we report a recently established symbiosis between the human-associated opportunistic pathogen *Propionibacterium acnes* and the highly domesticated grape *Vitis vinifera*. We detected *P. acnes* in many grape plants using pyrosequencing of 16S rDNA and fluorescent in-situ hybridization (FISH) which localized *P. acnes* in specific endosphere habitats (pith and bark). We also show that *recA* genes in uncultivable endophytic *P. acnes* of grape are pseudogenes, suggesting a recent obligate symbiosis which we tentative date as being not older than 7000 years ago, an age compatible with the domestication of grape by humans. Our results represent the first documented inter-kingdom horizontal host transfer of a human symbiont.