Duccio Cavalieri

duccio.cavalieri@fmach.it

Duccio Cavalieri (DC) started his career in 1995 applying molecular biology to ecological and evolutionary genomics of microorganisms in Florence in Mario Polsinelli's lab. After obtaining his PhD in Genetics from the University of Pavia in 1998 DC moved to Harvard as a postdoc with professor Daniel Hartl. In 2000 he applied for the first time DNA microarrays to study gene expression variation in wine strains of Saccharomyces cerevisiae. From 2001 to 2005 he was group leader and principal investigator of the Yeast comparative functional genomics unit at the Harvard Center for Systems Biology, where he pioneered the application of functional genomics to yeast population genetics.

His work on pathway analysis in 2002 was seminal to the development of bioinformatics for the interpretation of large "omics" datasets. In 2004 DC became group leader,researcher and "professore aggregato" at the Faculty of Pharmacy and Biotechnology of the University of Florence, in these years he applied genomics and bioinformatics to development of markers predictive of host microbe interaction, drug response, nutritional phenotypes and outcome of cancer therapies. Recently his interests are focused on the analysis of symbioses between humans, insects,plants and their microbiota, to study the boundaries between commensalism and pathogenicity in food borne microbes. Since

April 2012 as coordinator of the computational biology department at FEM, he has taken up a novel challenge, apply next generation sequencing and pathway and network analysis to study metagenomics, host microbe interaction at the systems level, genome evolution, and the effects of diet on human health and immune function. DC has been active in NUGO, DC-THERA, SYBARIS and other EU funded initiatives in nutrigenomics, metagenomics and immunogenomics. DC published 66 papers on JCR Journals (ISI-Web of Science), cited 2065 times. His H-index is currently equal to 22.

Recent publications

- De Filippo C., Ramazzotti M., Fontana P., Cavalieri D. Bioinformatic approaches for functional annotation and pathway inference in metagenomics data. Brief. in Bioinformatics Vol 6.N. 13. 1-15.

- Stefanini I, Dapporto L, Legras JL, Calabretta A, Di Paola M, De Filippo C, Viola R, Capretti P, Polsinelli M, Turillazzi S, Cavalieri D. Role of social wasps in Saccharomyces cerevisiae ecology and evolution. Proc Natl Acad Sci U S A. 2012 Aug 14;109(33):13398-403.
- Ramazzotti M, Berná L, Stefanini I, Cavalieri D. A computational pipeline to discover highly phylogenetically informative genes in sequenced genomes: application to Saccharomyces cerevisiae natural strains. Nucleic Acids Res. 2012 Jan 20.
- Rizzetto L, Cavalieri D. Friend or foe: using systems biology to elucidate interactions between fungi and their hosts. Trends Microbiol. 2011 Oct;19(10):509-15.
- De Filippo C., Cavalieri D., Di Paola M., Ramazzotti M., Poullet J.B., Massart S., Pieraccini, G., Collini S., and Lionetti P. “Impact of diet in shaping gut microbiota revealed by a comparative study in children from Europe and rural Africa”. Proc Natl Acad Sci U S A. 2010 Aug 17;107(33):14691-6.