

MARIANGELA BONIZZONI

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Research Unique Identifier: ORCID ID 0000-0003-0568-8564
ERC field of expertise: LS2, LS8, LS9

ACADEMIC POSITIONS

- 03/2015-present ASSOCIATE PROFESSOR of ZOOLOGY, Dep. Biology and Biotechnology, University of Pavia, Italy
- 2011-2015 ASSISTANT PROJECT SCIENTIST, Program in Public Health, University of California at Irvine, USA
- 2007-2011 POSTDOCTORAL FELLOW, Program in Public Health (supervisor prof. Guiyun Yan) and Dep. Molecular Biology and Biochemistry (supervisor: Prof. Anthony A. James), University of California at Irvine, USA
- 2004-2006 POSTDOCTORAL FELLOW, Biology Department, University of Basilicata, Italy

EDUCATION

2004 Combined Italian-French PhD
Cellular Biology, University of Pavia, Italy
Genes, Genomes, Cellules, Universite' de Paris XI, France
1997 Master in Molecular Biology
Dep. Animal Biology, University of Pavia, Italy

RESEARCH FUNDING

2016-2021 ERC Consolidator NIRV_HOST_INT (M. Bonizzoni)
Population genomics of co-evolution between nonretroviral RNA viruses and their hosts
Role : PI

2009-2014 PSWRCE-U54-A165359 (A.A. James)
Mosquito innate immune response to arbovirus infection
Role: Co-investigator

2012-2015 NIH R21 AI098652-01 (M. Bonizzoni)
Transcriptomics and Population Genetics of Mosquito Resistance to Pyrethroids.
Role: PI

2008-2013 NIH R01 AI050243 (G.Yan)
Ecology of African Highland Malaria
Role: Co-investigator

2004-2006 FIRB (F. Pennacchio)
Insect functional genomics for the development innovative strategies for plant protection
Role: Co-investigator

2000-2004 IFAD (A.R.Malacrida)
African fruitfly initiative
Role: Co-investigator

2000-2001 Junior Scientists Projects (M. Bonizzoni)
Medfly sexual behavior: female remating frequency by microsatellite markers
Role: PI

2000 CITRUS RESEARCH BOARD 5510-141 (T. Chapman)
Determining the incidence of female medfly mating frequency in SIT programs
Role: Co-investigator

TEACHING EXPERIENCE

2015/2016 Zoology and Molecular Entomology
2014-2015 Applied Zoology
2014 Guest Lectures in Vector Biology, Human Parasitology
University of California at Irvine, USA

ORGANISER OF INTERNATIONAL SCIENTIFIC MEETINGS

2015 Organizer of the Symposium "Role of microbiota in vectors" to be presented at ICE 2016, XXV International Congress of Entomology Orlando Sept. 25-30, 2016
2013 Organizer and board member of the 1st International Workshop on *Aedes albopictus*, the Asian tiger mosquito (Pavia, Italy, March 21-22nd 2013)

COMMISSION OF TRUST

2015 *Ad hoc* reviewer for the Netherlands Organization for Scientific Research, VICI Scheme
2013-2014 NIH-NIAD review panel member for R13 and "International Collaborations in Infectious Diseases Research" U01 and U19 grants

PROFESSIONAL SERVICES

2014 Invited Associate Editor for PLoS Neglected Tropical Diseases
2012-current Associate Editor for BMC Genetics
2007-current Scientific Review for PNAS, Genetica, Diversity and Distributions, Journal of Insect Science, Journal of Applied Entomology, Journal of Medical Entomology, Molecular Ecology, Bulletin of Entomological Research, Infection Genetics and Evolution, Journal of Insect Physiology, BMC Genomics, PLoS Neglected Tropical Diseases, PLoS One and Heredity

CONTRIBUTION TO SCIENCE AND PUBLICATIONS

A well known idiom dictates that "prevention is better than cure". There are neither vaccines nor therapeutic treatments available for many arthropod-borne diseases. The only proven and consistent method of preventing transmission of the pathogens that cause these diseases is to act on the vectors by suppressing their contact to humans. My research agenda is guided by the above-mentioned idiom and aims at reducing the negative impact of insects on human health and economic development by studying innovative strategies of insect control. I started my career working on economically important pest species of the Tephritidae family, mainly species of the genera *Ceratitidis* and *Bactrocera*, later I included also vectors for human diseases. My specific contributions are listed below, following broadly a chronological order:

Contribution 1. Population genetic analyses and studies of invasion/diffusion processes. Population genetic approaches are informative in the analyses of the genetic plasticity of an organism, in assessing its demographic history, in studying its spread and the widespread of key features such as mutations associated with insecticide resistance. I characterized and applied molecular markers to understand the population genetic structure and the invasion/diffusion potentials of different economically- and public health-important insects.

Key citations:

- Bonizzoni et al. 2004. On the origins of medfly invasion and expansion in Australia. *Mol Ecol* 13: 3845-3855;
- Zhong et al., 2013. Genetic Analysis of Invasive *Aedes albopictus* Populations in Los Angeles County, California and Its Potential Public Health Impact. *PLoS One* 8: e6858.
- Chang et al., 2016. Landscape genetic structure and evolutionary genetics of insecticide resistance gene mutations in *Anopheles sinensis*. *Parasit Vectors*: 9:228.
- Xu et al., 2016. Multi-country survey revealed prevalent and novel F1534S mutation in voltage-gated sodium channel (VGSC) gene in *Aedes albopictus*. *PLoS Negl Trop Dis* 10: e0004696.

Contribution 2. Insect transposable elements (TE) and transgenesis. Studies of the role of TEs in shaping the insect genomes and to assess their use for the generation of transgenic insects. I contributed in the characterization of TE in different arthropods.

Key citations:

- Bonizzoni et al. 2007. Highly similar piggyBac transposase-like sequences in various *Bactrocera* (Diptera, Tephritidae) species. *Insect Molecular Biology* 16: 645-650.
- Amenya et al., 2010. Comparative Fitness Assessment of *Anopheles stephensi* Transgenic Lines Receptive to Site-Specific Integration. *Insect Mol Biol* 19: 263-269.

Contribution 3. Insect sexual behavior.

Strategies based on the “Insect Sterile Technique” (SIT) are being used in control of pest species, their success depends on female sexual behavior. I studied the mating behavior and reproductive physiology of the agricultural pest *Ceratitis capitata*.

Key citations:

- Bonizzoni et al., 2002. Microsatellite analysis reveals remating by wild Mediterranean fruit fly females, *Ceratitis capitata*. *Mol Ecol* 11: 1915-1921.
- Bonizzoni et al., 2006. Is polyandry a common event among wild populations of the pest *Ceratitis capitata*? *J Econ Entomol* 99: 1420-1429.
- Bertin et al., 2010. Sperm storage and use in polyandrous females of the globally invasive fruitfly, *Ceratitis capitata*. *J Insect Physiol* 56:1542-1551.

Contribution 4. Vector competence. The understanding of the interaction between vectors and pathogens is expected to unveil targets for control. I studied the effect of dengue virus infection in its main vector *Aedes aegypti* and I am studying the widespread and biological impact of integrations from nonretroviral RNA viruses into *Aede aegypti* and *Aedes albopictus*.

Key citations:

- Bonizzoni et al., 2012. Complex modulation of the *Aedes aegypti* transcriptome in response to dengue virus infection. *PLoS One* 7: e50512.
- Bonizzoni et al., 2013. The invasive mosquito species *Aedes albopictus*: current knowledge and future perspectives. *Trends Parasitol* 29: 460-468.

Contribution 5. Insecticide resistance in vectors. Insecticide resistance is recognized as one of the main obstacles in the malaria elimination/eradication agenda. I worked on insecticide resistance in malaria vectors.

Key citations:

- Bonizzoni et al., 2012. Comparative transcriptome analyses of deltamethrin-resistance and –susceptible *Anopheles gambiae* mosquitoes from Kenya by RNA-seq. *PLoS One* 7: e44607.
- Bonizzoni et al., 2015. RNA-seq analyses of changes in the *Anopheles gambiae* transcriptome associated with resistance to pyrethroids in Kenya: identification of candidate-resistance genes and candidate-resistance SNPs. *Parasit Vectors* 8:474

Contribution 6. Vector Genomics. I contributed in the analyses of the genome of dengue vectors.

Key citations:

- Bonizzoni et al., 2013. Probing functional polymorphisms in the dengue vector, *Aedes aegypti*. 14:739.
- Evans et al., 2015. A Multipurpose, High-Throughput Single-Nucleotide Polymorphism Chip for the Dengue and Yellow Fever Mosquito, *Aedes aegypti*. *G3* 5:711.
- Chen et al., 2015. Genome sequence of the Asian Tiger mosquito, *Aedes albopictus*, reveals insights into its biology, genetics, and evolution. *Proc Natl Acad Sci U S A* 112:E5907-15