

# Mariangela Bonizzoni

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ERC field of expertise: LS2, LS8, LS9

SSD: Bio05/B1

## ACADEMIC POSITIONS

03/2015 to present ASSOCIATE PROFESSOR of ZOOLOGY, Dep. Biology and Biotechnology, University of Pavia  
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  
Dept. Animal Biology, University of Pavia

## RESEARCH FUNDING

2017-2021 MIUR-FARE Project R1623HZA5 "Viral integrations in the genome of the arboviral vector *Aedes albopictus*: exploring the role of the piRNA pathway"  
Role: PI  
2017-2020 Human Science Frontier Program RGP0007/2017 (M. Bonizzoni, R. van Rij, J. Souza-Neto)  
Exploring the concept of adaptive immunity to viruses in mosquitoes  
Role: PI  
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  
 2000-2001 Junior Scientists Projects (M. Bonizzoni)  
 Medfly sexual behaviour: 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

### ORGANIZATION OF SCIENTIFIC EVENTS

2017 Organizer and board member of the 3rd International Workshop on *Aedes albopictus*, the Asian tiger mosquito (Pavia, Italy, April 10-12, 2017)  
 2016 Organizer of the Symposium "Role of microbiota in vectors", 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 21-22, 2013)

### COMMISSION OF TRUST

2017 Member of the InRoad Project, University of Pavia  
 2016 to present Member of the "Commissione Risorse" for the Dep. Of Biology and Biotechnology, University of Pavia  
 2015 *Ad hoc* reviewer for the Netherlands Organization for Scientific Research, VICI Scheme  
 2014 NIH-NIAD review panel member for R13 and "International Collaborations in Infectious Diseases Research" U01 and U19 grants

### PROFESSIONAL SERVICES

2014 to present Invited Associate Editor for PLoS Neglected Tropical Diseases  
 2012-current Associate Editor for BMC Genetics  
 2007 to present Scientific Reviewer 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, Parasite and Vectors and Heredity

### ACADEMIC COURSES

From 2015 Zoology (Modulo, 6 CFU Corso B) Laurea triennale in Scienze Biologiche  
 Molecular Entomology (6 CFU) Laurea Magistrale in "Molecular Biology and Genetics"  
 May 2017 Lecture in the course "Frontiers in Molecular Biology, Model systems in molecular biology research: from basic processes to human diseases", Dottorato in Genetica, Biologia Molecolare e Cellulare, Universita' degli Studi di Pavia  
 2014-2015 Applied Zoology (Modulo, 6 CFU Corso B) Laurea triennale in Scienze Biologiche  
 2014 Guest Lectures in Vector Biology, Human Parasitology, University of California at Irvine

### MENTORING ACTIVITIES

2017 to present Elisa Pischedda, post graduate researcher in Bioinformatics  
 2016 to present Michele Marconici, PhD student Dottorato in Genetica, Biologia Molecolare e Cellulare, Universita' degli Studi di Pavia

2015 to present	Federica Valerio, Umberto Palatini, Giuseppe Iovino, Alessandra Tancredi, Master Students in Molecular Biology and Genetics, University of Pavia
2015-2016	Rebeca Carballar, postdoc University of Pavia
2012-2013	Joshua Hartsel, postdoc, University of California at Irvine
2004-2005	Francesca Scolari, Master student in Scienze Naturali, University of Pavia
2004-2005	Ines Lara Bellazzi, Master student in Biologia, University of Pavia
2002-2004	Frederick N. Baliraine, PhD student, Nairobi Kenya
2002-2003	Stefania Moltoni, Master Student in Biologia, University of Pavia

## CONTRIBUTION TO SCIENCE

A well-known idiom dictates that “prevention is better than cure”. There are limited vaccines and no 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 *Ceratitis* and *Bactrocera*. Later I included also vectors for human diseases, which are now the main focus of my research.

My specific contributions are listed below, following broadly a chronological order and starting from the most recent projects:

### Contribution 1. Co-evolution between arthropod vectors and arboviruses.

Emerging or resurging infectious diseases include several caused by arthropod-borne viruses (arboviruses). An example is dengue, with 100 million people infected annually. Despite having different replication strategies, all arboviruses are maintained in a natural cycle involving transmission by the bite of an infected hematophagous arthropod (vector) to a vertebrate host. Once infected with an arbovirus, the vector becomes persistently infected for life. Mosquito competence for arboviruses is a complex and evolving phenotype because it depends on the interaction of genetic factors from both mutation-prone RNA viruses and mosquito vectors with environmental variables. Understanding the genetic components of vector competence and how these genetic elements are distributed in natural populations and interact with environmental factors is essential for predicting the risk of arboviral diseases and for developing new transmission-blocking strategies. I use the tools from a number of scientific disciplines to probe the complicated biology of vector-mediated pathogen transmission, with a current focus on mosquito genomics and immunity pathways.

#### Key citations:

- Olson and Bonizzoni, 2017. Nonretroviral integrated RNA viruses in arthropod vectors: an occasional event or something more? *Curr Op Insect Sci* 22: 45-53.
- Palatini et al., 2017. Comparative genomics shows that viral integrations are abundant and express piRNAs in the arboviral vectors *Aedes aegypti* and *Aedes albopictus*. *BMC Genomics* 18: 512.
- Bonizzoni et al., 2012. Complex modulation of the *Aedes aegypti* transcriptome in response to dengue virus infection. *PLoS One* 7: e50512.

### Contribution 2. Insecticide resistance in vectors.

Insecticide resistance is recognized as one of the main obstacles in the malaria elimination/eradication agenda. Understanding the molecular mechanisms of insecticide resistance will provide the tools to derive markers to predict resistance and possibly identify targets for novel insecticide formulations. I applied transcriptomics and molecular ecology approaches to study insecticide resistance mechanisms and the emergence of resistance in malaria and arboviral

vectors.

Key citations:

- 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.
- 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 3. 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:

- Manni et al., Genetic evidence for a worldwide chaotic dispersion pattern of the arbovirus vector, *Aedes albopictus*. *PLoS Negl Trop Dis* 10: e0005332.
- Bonizzoni et al., 2013. Probing functional polymorphisms in the dengue vector, *Aedes aegypti*. *BMC Genomics* 14:739.
- 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.
- Bonizzoni et al. 2004. On the origins of medfly invasion and expansion in Australia. *Mol Ecol* 13: 3845-3855;

Contribution 4. 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 Mol Biol* 16: 645-650.
- Ameyya et al., 2010. Comparative Fitness Assessment of *Anopheles stephensi* Transgenic Lines Receptive to Site-Specific Integration. *Insect Mol Biol* 19: 263-269.

Contribution 5. 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.

## LIST OF PEER REVIEWED PUBLICATIONS (h-index scopus: 24, as of Sept. 2017)

1. Bonizzoni M, Attardo G. Editorial overview: Vectors and medical and veterinary entomology: Becoming vectors or victims, the intriguing interplay between insects and viruses. (2017) *Current Opinion in Insect Science* 22:v-vii.
2. Palatini U, Miesen P, Carballar-Lejarazu R, Ometto L, Rizzo E, Tu Z, van Rij RP, Bonizzoni M. Comparative genomics shows that viral integrations are abundant and express piRNAs in the arboviral vectors *Aedes aegypti* and *Aedes albopictus*. (2-17) *BMC Genomics* 18:512.
3. Olson, K.E., Bonizzoni, M. Nonretroviral integrated RNA viruses in arthropod vectors: an occasional event or something more? (2017) *Current Opinion in Insect Science* 22, pp. 45-53.
4. Manni, M., Guglielmino, C.R., Scolari, F., Vega-Rúa, A., Failloux, A.-B., Somboon, P., Lisa, A., Savini, G., Bonizzoni, M., Gomulski, L.M., Malacrida, A.R., Gasperi, G. Genetic evidence for a worldwide chaotic dispersion pattern of the arbovirus vector, *Aedes albopictus* (2017) *PLoS Neglected Tropical Diseases*, 11 (1), art. no. e0005332.
5. Xu, J., Bonizzoni, M., Zhong, D., Zhou, G., Cai, S., Li, Y., Wang, X., Lo, E., Lee, R., Sheen, R., Duan, J., Yan, G., Chen, X.-G. Multi-country Survey Revealed Prevalent and Novel F1534S Mutation in Voltage-Gated Sodium Channel (VGSC) Gene in *Aedes albopictus* (2016) *PLoS Neglected Tropical Diseases*, 10 (5), art. no. e0004696.
6. Chang, X., Zhong, D., Lo, E., Fang, Q., Bonizzoni, M., Wang, X., Lee, M.-C., Zhou, G., Zhu, G., Qin, Q., Chen, X., Cui, L., Yan, G. Landscape genetic structure and evolutionary genetics of insecticide resistance gene mutations in *Anopheles sinensis* (2016) *Parasites and Vectors*, 9 (1), art. no. 228.
7. Chen, X.-G., Jiang, X., Gu, J., Xu, M., Wu, Y., Deng, Y., Zhang, C., Bonizzoni, M., Dermauw, W., Vontas, J., Armbruster, P., Huang, X., Yang, Y., Zhang, H., He, W., Peng, H., Liu, Y., Wu, K., Chen, J., Lirakisi, M., Topalis, P., Van Leeuwen, T., Hall, A.B., Jiang, X., Thorpe, C., Mueller, R.L., Sun, C., Waterhouse, R.M., Yan, G., Tu, Z.J., Fang, X., James, A.A. Genome sequence of the Asian tiger mosquito, *Aedes albopictus*, reveals insights into its biology, genetics, and evolution (2015) *Proceedings of the National Academy of Sciences of the United States of America*, 112 (44), pp. E5907-E5915.
8. Bonizzoni, M., Ochomo, E., Dunn, W.A., Britton, M., Afrane, Y., Zhou, G., Hartsel, J., Lee, M.-C., Xu, J., Githeko, A., Fass, J., Yan, G. 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 (2015) *Parasites and Vectors*, 8 (1), art. no. 474.
9. Evans, B.R., Gloria-Soria, A., Hou, L., McBride, C., Bonizzoni, M., Zhao, H., Powell, J.R. A multipurpose, high-throughput single-nucleotide polymorphism chip for the dengue and yellow fever mosquito, *Aedes aegypti* (2015) *G3: Genes, Genomes, Genetics*, 5 (5), pp. 711-718.
10. Manni, M., Lima, K.M., Guglielmino, C.R., Lanzavecchia, S.B., Juri, M., Vera, T., Cladera, J., Scolari, F., Gomulski, L., Bonizzoni, M., Gasperi, G., Silva, J.G., Malacrida, A.R. Relevant genetic differentiation among brazilian populations of *Anastrepha fraterculus* (Diptera, tephritidae) (2015) *ZooKeys*, 2015 (540), pp. 157-173.
11. Macias, V., Coleman, J., Bonizzoni, M., James, A.A. piRNA pathway gene expression in the malaria vector mosquito *Anopheles stephensi* (2014) *Insect Molecular Biology*, 23 (5), pp. 579-586.
12. Bonizzoni, M., Britton, M., Marinotti, O., Dunn, W.A., Fass, J., James, A.A. Probing functional polymorphisms in the dengue vector, *Aedes aegypti* (2013) *BMC Genomics*, 14 (1), art. no. 739.
13. Bonizzoni, M., Gasperi, G., Chen, X., James, A.A. The invasive mosquito species *Aedes albopictus*: Current knowledge and future perspectives (2013) *Trends in Parasitology*, 29 (9), pp. 460-468.
14. Zhong, D., Lo, E., Hu, R., Metzger, M.E., Cummings, R., Bonizzoni, M., Fujioka, K.K., Sorvillo, T.E., Klueh, S., Healy, S.P., Fredregill, C., Kramer, V.L., Chen, X., Yan, G. Genetic

- Analysis of Invasive *Aedes albopictus* Populations in Los Angeles County, California and Its Potential Public Health Impact (2013) PLoS ONE, 8 (7), art. no. e68586.
15. Zhong, D., Chang, X., Zhou, G., He, Z., Fu, F., Yan, Z., Zhu, G., Xu, T., Bonizzoni, M., Wang, M.-H., Cui, L., Zheng, B., Chen, B., Yan, G. Relationship between Knockdown Resistance, Metabolic Detoxification and Organismal Resistance to Pyrethroids in *Anopheles sinensis* (2013) PLoS ONE, 8 (2), art. no. e55475.
  16. Bonizzoni, M., Dunn, W.A., Campbell, C.L., Olson, K.E., Marinotti, O., James, A.A. Complex Modulation of the *Aedes aegypti* Transcriptome in Response to Dengue Virus Infection (2012) PLoS ONE, 7 (11), art. no. e50512.
  17. Bonizzoni, M., Afrane, Y., Dunn, W.A., Atieli, F.K., Zhou, G., Zhong, D., Li, J., Githeko, A., Yan, G. Comparative Transcriptome Analyses of Deltamethrin-Resistant and -Susceptible *Anopheles gambiae* Mosquitoes from Kenya by RNA-Seq (2012) PLoS ONE, 7 (9), art. no. e44607.
  18. Liu, C., Mauk, M.G., Hart, R., Bonizzoni, M., Yan, G., Bau, H.H. A low-cost microfluidic chip for rapid genotyping of malaria-transmitting mosquitoes (2012) PLoS ONE, 7 (8), art. no. e42222.
  19. Bonizzoni, M., Augustine Dunn, W., Campbell, C.L., Olson, K.E., Marinotti, O., James, A.A. Strain variation in the transcriptome of the dengue fever vector, *Aedes aegypti* (2012) G3: Genes, Genomes, Genetics, 2 (1), pp. 103-114.
  20. Bonizzoni, M., Bourjea, J., Chen, B., Crain, B.J., Cui, L., Fiorentino, V., Hartmann, S., Hendricks, S., Ketmaier, V., Ma, X., Muths, D., Pavesi, L., Pfautsch, S., Rieger, M.A., Santonastaso, T., Sattabongkot, J., Taron, C.H., Taron, D.J., Tiedemann, R., Yan, G., Zheng, B., Zhong, D. Permanent genetic resources added to Molecular Ecology Resources Database 1 April 2011-31 May 2011 (2011) Molecular Ecology Resources, 11 (5), pp. 935-936.
  21. Zhong, D., Bonizzoni, M., Zhou, G., Wang, G., Chen, B., Vardo-Zalik, A., Cui, L., Yan, G., Zheng, B. Genetic diversity of *Plasmodium vivax* malaria in China and Myanmar (2011) Infection, Genetics and Evolution, 11 (6), pp. 1419-1425.
  22. Bonizzoni, M., Dunn, W.A., Campbell, C.L., Olson, K.E., Dimon, M.T., Marinotti, O., James, A.A. RNA-seq analyses of blood-induced changes in gene expression in the mosquito vector species, *Aedes aegypti* (2011) BMC Genomics, 12, art. no. 82.
  23. Bertin, S., Scolari, F., Guglielmino, C.R., Bonizzoni, M., Bonomi, A., Marchini, D., Gomulski, L.M., Gasperi, G., Malacrida, A.R., Matessi, C. Sperm storage and use in polyandrous females of the globally invasive fruitfly, *Ceratitis capitata* (2010) Journal of Insect Physiology, 56 (11), pp. 1542-1551.
  24. Baliraine, F.N., Afrane, Y.A., Amenity, D.A., Bonizzoni, M., Vardo-Zalik, A.M., Menge, D.M., Githeko, A.K., Yan, G. A cohort study of *Plasmodium falciparum* infection dynamics in Western Kenya Highlands (2010) BMC Infectious Diseases, 10, art. no. 283.
  25. Khatoon, L., Baliraine, F.N., Bonizzoni, M., Malik, S.A., Yan, G. Genetic structure of *Plasmodium vivax* and *Plasmodium falciparum* in the Bannu district of Pakistan (2010) Malaria Journal, p. 112.
  26. Amenity, D.A., Bonizzoni, M., Isaacs, A.T., Jasinskiene, N., Chen, H., Marinotti, O., Yan, G., Jamesti, A.A. Comparative fitness assessment of *Anopheles stephensi* transgenic lines receptive to site-specific integration (2010) Insect Molecular Biology, 19 (2), pp. 263-269.
  27. Bonizzoni, M., Afrane, Y., Yan, G. Loop-mediated isothermal amplification (LAMP) for rapid identification of *Anopheles gambiae* and *Anopheles arabiensis* mosquitoes (2009) American Journal of Tropical Medicine and Hygiene, 81 (6), pp. 1030-1034.
  28. Khatoon, L., Baliraine, F.N., Bonizzoni, M., Malik, S.A., Yan, G. Short report: Prevalence of antimalarial drug resistance mutations in *Plasmodium vivax* and *P. falciparum* from a malaria-endemic area of Pakistan (2009) American Journal of Tropical Medicine and Hygiene, 81 (3), pp. 525-528.
  29. Bonizzoni, M., Afrane, Y., Baliraine, F.N., Amenity, D.A., Githeko, A.K., Yan, G. Genetic structure of *Plasmodium falciparum* populations between lowland and highland sites and antimalarial drug resistance in Western Kenya (2009) Infection, Genetics and Evolution, 9 (5), pp. 806-812.

30. Baliraine, F.N., Afrane, Y.A., Ameyna, D.A., Bonizzoni, M., Menge, D.M., Zhou, G., Zhong, D., Vardo-Zalik, A.M., Githeko, A.K., Yan, G. High prevalence of asymptomatic *Plasmodium falciparum* Infections in a highland area of western Kenya: A cohort study (2009) *Journal of Infectious Diseases*, 200 (1), pp. 66-74.
31. Bonizzoni, M., Gomulski, L.M., Malacrida, A.R., Capy, P., Gasperi, G. Highly similar piggyBac transposase-like sequences from various *Bactrocera* (Diptera, Tephritidae) species (2007) *Insect Molecular Biology*, 16 (5), pp. 645-650.
32. Aketarawong, N., Bonizzoni, M., Thanaphum, S., Gomulski, L.M., Gasperi, G., Malacrida, A.R., Guglielmino, C.R. Inferences on the population structure and colonization process of the invasive oriental fruit fly, *Bactrocera dorsalis* (Hendel) (2007) *Molecular Ecology*, 16 (17), pp. 3522-3532.
33. Malacrida, A.R., Gomulski, L.M., Bonizzoni, M., Bertin, S., Gasperi, G., Guglielmino, C.R. Globalization and fruitfly invasion and expansion: The medfly paradigm (2007) *Genetica*, 131 (1), pp. 1-9.
34. Bonizzoni, M., Gomulski, L.M., Bertin, S., Scolari, F., Guglielmino, C.R., Yuval, B., Gasperi, G., Malacrida, A.R. Unfaithful Mediterranean fruit fly *Ceratitis capitata* females: Impact on the SIT? (2007) *Area-Wide Control of Insect Pests: From Research to Field Implementation*, pp. 175-182.
35. Aketarawong, N., Bonizzoni, M., Malacrida, A.R., Gasperi, G., Thanaphum, S. Seventeen novel microsatellite markers from an enriched library of the pest species *Bactrocera dorsalis* sensu stricto (2006) *Molecular Ecology Notes*, 6 (4), pp. 1138-1140.
36. Bonizzoni, M., Gomulski, L.M., Mossinson, S., Guglielmino, C.R., Malacrida, A.R., Yuval, B., Gasperi, G. Is polyandry a common event among wild populations of the pest *Ceratitis capitata*? (2006) *Journal of Economic Entomology*, 99 (4), pp. 1420-1429.
37. Torti, C., Gomulski, L.M., Bonizzoni, M., Murelli, V., Moralli, D., Guglielmino, C.R., Raimondi, E., Crisafulli, D., Capy, P., Gasperi, G., Malacrida, A.R. Cchobo, a hobo-related sequence in *Ceratitis capitata* (2005) *Genetica*, 123 (3), pp. 313-325.
38. Bonizzoni, M., Guglielmino, C.R., Smallridge, C.J., Gomulski, M., Malacrida, A.R., Gasperi, G. On the origins of medfly invasion and expansion in Australia (2004) *Molecular Ecology*, 13 (12), pp. 3845-3855.
39. Kanzok, S.M., Hoa, N.T., Bonizzoni, M., Luna, C., Huang, Y., Malacrida, A.R., Zheng, L. Origin of toll-like receptor-mediated innate immunity (2004) *Journal of Molecular Evolution*, 58 (4), pp. 442-448.
40. Baliraine, F.N., Bonizzoni, M., Guglielmino, C.R., Osir, E.O., Lux, S.A., Mulaa, F.J., Gomulski, L.M., Zheng, L., Quilici, S., Gasperi, G., Malacrida, A.R. Population genetics of the potentially invasive African fruit fly species, *Ceratitis rosa* and *Ceratitis fasciventris* (Diptera: Tephritidae) (2004) *Molecular Ecology*, 13 (3), pp. 683-695.
41. Gomulski, L.M., Torti, C., Murelli, V., Bonizzoni, M., Gasperi, G., Malacrida, A.R. Medfly transposable elements: Diversity, evolution, genomic impact and possible applications (2004) *Insect Biochemistry and Molecular Biology*, 34 (2), pp. 139-148.
42. Shao, Z.-Y., Mao, H.-X., Fu, W.-J., Ono, M., Wang, D.-S., Bonizzoni, M., Zhang, Y.-P. Genetic Structure of Asian Populations of *Bombus ignitus* (Hymenoptera: Apidae) (2004) *Journal of Heredity*, 95 (1), pp. 46-52.
43. Baliraine, F.N., Bonizzoni, M., Osir, E.O., Lux, S.A., Mulaa, F.J., Zheng, L., Gomulski, L.M., Gasperi, G., Malacrida, A.R. Comparative analysis of microsatellite loci in four fruit fly species of the genus *Ceratitis* (Diptera: Tephritidae) (2003) *Bulletin of Entomological Research*, 93 (1), pp. 1-10.
44. Bonizzoni, M., Katsoyannos, B.I., Marguerie, R., Guglielmino, C.R., Gasperi, G., Malacrida, A., Chapman, T. Microsatellite analysis reveals remating by wild Mediterranean fruit fly females, *Ceratitis capitata* (2002) *Molecular Ecology*, 11 (10), pp. 1915-1921.
45. Bonizzoni, M., Zheng, L., Guglielmino, C.R., Haymer, D.S., Gasperi, G., Gomulski, L.M., Malacrida, A.R. Microsatellite analysis of medfly bioinvasions in California (2001) *Molecular Ecology*, 10 (10), pp. 2515-2524.
46. Gomulski, L.M., Torti, C., Bonizzoni, M., Moralli, D., Raimondi, E., Capy, P., Gasperi, G., Malacrida, A.R. A new basal subfamily of mariner elements in *Ceratitis rosa* and other tephritid flies (2001) *Journal of Molecular Evolution*, 53 (6), pp. 597-606.

47. Luna, C., Bonizzoni, M., Cheng, Q., Robinson, A.S., Aksoy, S., Zheng, L. Microsatellite polymorphism in tsetse flies (Diptera: Glossinidae) (2001) *Journal of Medical Entomology*, 38 (3), pp. 376-381.
48. Bonizzoni, M., Malacrida, A.R., Guglielmino, C.R., Gomulski, L.M., Gasperi, G., Zheng, L. Microsatellite polymorphism in the mediterranean fruit fly, *Ceratitis capitata* (2000) *Insect Molecular Biology*, 9 (3), pp. 251-261.

#### INVITED SPEAKER AT THE FOLLOWING INTERNATIONAL CONGRESSES:

- Palatini U, Pischedda E, Bonizzoni M. Nonretroviral integrated RNA viruses in the genome of mosquito vectors: a new form of immunity? Second Joint Meeting of Societe Zoologique de France and Unione Zoologia Italiana (Torino, 18-23 Settembre 2017)
- Palatini U, Pischedda E, Bonizzoni M. Comparative genomics of viral integrations in mosquitoes. EMBO Conference "Molecular and Population Biology of Mosquitoes and other disease vectors" (Kolymbari, Greece, July 24-28, 2017).
- Bonizzoni M. Viral integrations are abundant in the genome of *Aedes* mosquitoes. 3rd International Workshop on *Aedes albopictus*, the Asian tiger mosquito (Pavia, April 10-14 2017)
- Bonizzoni M. Non-retroviral RNA virus integrations in *Aedes albopictus*. Symposium 394 "the Role of Microbiota in Vectors". XXV International Congress of Entomology 2016 (Orlando, FL Sept. 25-30, 2016)
- Bonizzoni M. Resistance to pyrethroids in *Aedes albopictus*: results from a multycountry survey. Congresso "Facing the invasion of alien arthropods species" (Trento, Nov. 07-09 - 2016)
- Bonizzoni M. Control of the Dengue vectors *Aedes aegypti* and *Aedes albopictus*: challenges of insecticide resistance and alternative methods. Gordon Research Conference "Drug Resistance" (University of New England, Biddeford Maine, June 12-17 2016)
- Bonizzoni M. Assessing functional polymorphism in the dengue vector *Aedes aegypti* by RNA-Seq. 9th Annual Meeting of NIAID Regional Centers of Excellence for Biodefense and Emerging Infectious Disease Research (Seattle, April 7-9, 2013)
- Bonizzoni M. Transcriptional analyses of the dengue vector *Aedes aegypti* supports a transgenic approach for vector control. 6th International Congress of the Society for Vector Ecology (La Quinta, CA, Sept. 22-27th 2013)
- Bonizzoni M. Profiling the mosquito transcriptome: case studies of *Aedes aegypti* and *Anopheles gambiae*. XXIV International Congress of Entomology (Daegu, Korea, 19-25 August 2012)
- Bonizzoni M, Li J & Yan G. Comparative transcriptome analyses of pyrethroid - resistant and -susceptible *Anopheles gambiae* mosquitoes. 59th Annual Meeting of the Entomological Society of America (Reno, USA, 13-16 November 2011)
- Bonizzoni M, Gomulski LM, Bertin S, Scolari F, Matessi C, Gasperi G. Remating and sperm use in medfly females. Eighth Annual Exotic Fruit Fly Symposium (Riverside, California, 7-9 March 2005)
- Bonizzoni M, Guglielmino R, Gomulski LM, Smallridge C, Malacrida AR & Gasperi G. Genetic status of medfly in Australia as inferred from microsatellite markers. XXII International Congress of Entomology (Brisbane, Australia, August 15-21, 2004)
- Baliraine FN, Bonizzoni M, Osir EO, Lux SA, Mulaa FJ, Quilici S, Gomulski LM, Gasperi G & Malacrida AR. Medfly microsatellite markers for species diagnosis and population genetics analysis in three tephritid fruit fly species. 6<sup>th</sup> International Symposium on Fruit Fly of Economic Importance pp. 2 (Stellenbosch, South Africa, May 6-10, 2002)
- Bonizzoni M, Marchini D, Dallai R, Malacrida AR & Gasperi G. Progress in the analysis of sperm use in medfly. 2002 Annual Exotic Fruitfly Symposium (Riverside, California, USA, September 14-16, 2002)
- Bonizzoni M, Murelli V, Guglielmino CR, Chapman T, Haymer DS, Katsoyannos BI, Zheng L, Gasperi G & Malacrida AR. SSR genotyping in the medfly *Ceratitis capitata* as a tool to



interpret bioinvasion processes and remating frequency. 2001 Annual Exotic Fruitfly Symposium (Tampa, Florida, USA; December 2-4, 2001)