GIOVANNI MALERBA

Date of birth: 11 August 1971
Place of birth: Verona, Italy.
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Studi

	1990	High School Diploma, at the Liceo Piccole Figlie di S. Giuseppe in Verona
	01/03/1996	Degree in Biological Sciences (March 1996), at the University of Padua, with a thesis entitled "Analysis of mutations in candidate genes in some respiratory diseases: examination of cystic Fibrosis, alpha1-antitrypsin and alpha1-antichymotrypsin genes"
15/10/2000	15/10/2000	Diploma of Specialization in Medical Genetics - technical degree, at the University of Verona with a thesis entitled "Study of linkage of the NOS2 gene and of the 19 chromosome in allergic asthma and use of the simulation to estimate the power of statistical analysis"
	15/05/2006	PhD in Biotechnology Applied to Biomedical Sciences at the University of Verona with a thesis entitled "Genomic scan for allergic asthma in a sample of Italian asthmatic families"

Qualification

	1997	Qualification to practice the profession of Biologist achieved in the first session of the year 1997

Posizioni Lavorative

1996	2003	Biologist Collaborator, at the Biology and Genetics Section of the Mother and Child and of Biology and Genetics Department of the University of Verona (Prof. Pier Franco Pignatti). During this time Giovanni was the winner of scholarships for linkage and association studies of the genetic factor with complex characters and he obtained the Specialization in Medical Genetics - Technical degree.
2003 (apr)	2006 (feb)	Position of Technician / Administrative (level D) in which computational and statistical biology methods were developed and implemented for the study of phenotypic and genotypic variability in Mendelian diseases and complex traits.
2006 (mar)	2014 (ago)	Assistant Professor (SSD: MED / 03, Medical Genetics) - at the Biology and Genetics Section of the Mother and Child and of Biology and Genetics Department, University of Verona
2014 (sep 1st)	today	Associate Professor (SSD: MED / 03, Medical Genetics) - Department of Neurosciences, Biomedicine and Movement, University of Verona.

Attività di ricerca presso istituti di ricerca esteri

15/10/1997	14/02/1998	Fox Chase Cancer Center (Phyladelphia, USA) for genome-wide linkage studies in families with asthma-affected siblings.
10/01/2008	20/04/2008	Stephan Weiland Fellowship (Progetto EU Gabriel), for the study entitled “Pooled analysis of

		genome-wide linkage scans from 3 European family samples" (Prof. F. Demenais, Foundation Jean Dausset-Centre d'Etude du Polymorphisme Humain - CEPH- , Paris, FranceParigi)
05/05/2009	30/06/2009	INSERM U794, CEPH institute, Paris (Prof. Florence Demenais) for a meta-analysis study of linkage studies on allergic asthma in European families.
05/10/2009	30/03/2010	INSERM U794, CEPH institute, Paris (Prof. Florence Demenais). ERS/AIMAR fellowship for a study on the effects of imprinting in allergic asthma based on linkage and association analysis at the genomic level.
15/09/2010	20/10/2010	Sanger Center, Hinxton, UK (Prof. Nicole Soranzo) for a study on the quality control of genotyping obtained through DNA arrays in a sample of 1000 Italian individuals and subsequent imputation of genotypes through the reference panel of the HAPMAP2 project
02/10/2010	30/10/2010	Sanger Center, Hinxton, UK (Prof. Nicole Soranzo) for a study on the lipid profile of individuals of the INCIPE cohort (4000 individuals) and imputation of all genotyped individuals using the panels of the 1000 genomes project and of the UK10K study

Summary of Scientific Activity

I started my scientific activity as a university student in Biology studying the genetic component of multifactorial respiratory diseases (September 1994 - March 1996). During the following years, duing and after the specialization in Medical Genetics, I deepened my knowledge on statistical methods to characterize and study the genetic component both in Mendelian and in complex diseases.
In 1997 I joined the bioinformatics group of Dr. KH. Buetow, an expert in the biomedical research community for the integration and analysis of genetic data and their application to patient care, at the Fox Chase Cancer Center (Philadelphia, USA) for 4 months (October 1997 - February 1998) . During that time I had the opportunity to learn to program with different computer programming languages and to understand the logic of the statistical methods applied to linkage analysis at the genomic level. During the time of specialization I was able to increase my knowledge of computer science (programming in bioinformatics with different languages, management and administration of databases and web applications) combining them with the knowledge of medical genetics. In the same years I improved my knowledge in computational genomics and biostatistics. This knowledge allowed me to collaborate with research groups at the University of Verona and in other Italian Universities.
From January to April 2008, I joined the research group of Prof. Demenais in Paris (INSERM U794, CEPH Institute) where I improve my knowledge in genetic epidemiology through the application of different statistical approaches to study linkage and association with complex phenotypes in family studies. I was then able to re-join the group of Prof. Demenais from November 2009 to March 2010 to define and implement statistical models suitable for studying preferential allelic transmissions from a single parent in childhood asthma.
From September 2010 to October 2010, I joined the group of Dr. Nicole Soranzo of the Sanger Center (Hinxton, United Kingdom) where I worked on genetic and phenotypic data for the realization of a genomic scan (millions of DNA markers) in a sample of about 1000 Italians (cohort of the INCIPE study, aimed at the study of different aspects of kidney disease - referents: prof Lupo, prof Gambaro). At the Sanger Center I learned to use sophisticated bioinformatics and statistical tools to carry out quality controls on the data that precede the association study and to impute genotypes starting from a panel of well-characterized individuals at the genomic level (the samples of Hapmap project first and 1000 genome project later). During this experience I learned to use computer clusters dedicated to high performance computing.
Starting from 2009 I had the opportunity to work on the data produced by the recent platforms dedicated to the high throughput sequencing (next generation sequencing, NGS). Being a new technology, we had to develop bioinformatical and statistical tools to work on the data obtained. The interest was initially directed to studies of human transcriptome (autism spectrum diseases, Alzheimer's, coronary disease, lymphomas, leukemia, kidney transplants) and also some plants. In 2010, taking advantage of what I learned during my previous stay at the Sanger Center, I joined the international consortia CKDGen and GUGC as researcher involved in the statistical analysis of data for the study of the genetic component of the phenotypes associated with renal function. These consortia include many international groups contributing to realize the genetic association meta-analysis of hundreds of thousands of individuals. Starting from 2010 I started to work on the genetic data produced by NGS platforms. Over the time I have been able to conduct studies on cohorts of exomes, of transcriptomes and more recently of methylomes, always in the context of a linkage study or association of the genetic factor with a complex phenotype.

Reviewer for International scientic journals

2005	oggi	Allergy, American Journal of Case Reports,American Journal of Respiratory and Critical Care Medicine, American Journal of Respiratory and Critical Care, Clinical Chemistry, Experimental Biology and Medicine, Gene, Human Genetics, Journal of Human Genetics, Journal of Nutrition and Matabolism, Nutrition & Metabolism, Plos One, Respiratory Research e The Pharmacogenomics Journal

Book chapters

Chapter 17. “Tecniche Genomiche, bioinformatica e statistica abbinata alla genetica” (Pp 369-397)
of the book “Nutrigenomica ed epigenetica. Dalla biologia alla clinica” by Damiano Galimberti, Giovanni Battista Gidaro, Vittorio Calabrese.
Publisher: Edra
Date of publication: June 2017
EAN: 9788821442353, ISBN: 8821442357

Pubblications on scientic journals (june 12, 2018)

H-index (Scopus): 34
N. of citations (Scopus): 3702

Total Impact Factor: 742.866

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2. Andreini A, Zampieri N, Costantini C, **Malerba G**, Bruno C, Salvagno G, Francia G, Gottardi M, Rimondini M, Ferrarini I, Lippi G, Ambrosetti A, Benedetti F, Tecchio C. Chronic graft versus host disease is associated with erectile dysfunction in allogeneic hematopoietic stem cell transplant patients: a single-center experience. Leuk Lymphoma. 2018 Mar 21:1-4. doi: 10.1080/10428194.2018.1443338. [Epub ahead of print] PubMed PMID: 29561209. [IF: 2.755]
3. Cecconi D, Carbonare LD, Mori A, Cheri S, Deiana M, Brandi J, Degaetano V, Masiero V, Innamorati G, Mottes M, **Malerba G**, Valenti MT. An integrated approach identifies new oncotargets in melanoma. Oncotarget. 2017 Dec 15;9(14):11489-11502. doi: 10.18632/oncotarget.23727. eCollection 2018 Feb 20. PubMed PMID: 29545914; PubMed Central PMCID: PMC5837771. [IF: 5.168]
4. Kraja AT, Cook JP, Warren HR, Surendran P, Liu C, Evangelou E, Manning AK, Grarup N, Drenos F, Sim X, Smith AV, Amin N, Blakemore AIF, Bork-Jensen J, Brandslund I, Farmaki AE, Fava C, Ferreira T, Herzig KH, Giri A, Giulianini F, Grove ML, Guo X, Harris SE, Have CT, Havulinna AS, Zhang H, Jørgensen ME, Käräjämäki A, Kooperberg C, Linneberg A, Little L, Liu Y, Bonnycastle LL, Lu Y, Mägi R, Mahajan A, **Malerba G**, Marioni RE, Mei H, Menni C, Morrison AC, Padmanabhan S, Palmas W, Poveda A, Rauramaa R, Rayner NW, Riaz M, Rice K, Richard MA, Smith JA, Southam L, Stančáková A, Stirrups KE, Tragante V, Tuomi T, Tzoulaki I, Varga TV, Weiss S, Yiorkas AM, Young R, Zhang W, Barnes MR, Cabrera CP, Gao H, Boehnke M, Boerwinkle E, Chambers JC, Connell JM, Christensen CK, de Boer RA, Deary IJ, Dedoussis G, Deloukas P, Dominiczak AF, Dörr M, Joehanes R, Edwards TL, Esko T, Fornage M, Franceschini N, Franks PW, Gambaro G, Groop L, Hallmans G, Hansen T, Hayward C, Heikki O, Ingelsson E, Tuomilehto J, Jarvelin MR, Kardia SLR, Karpe F, Kooner JS, Lakka TA, Langenberg C, Lind L, Loos RJF, Laakso M, McCarthy MI, Melander O, Mohlke KL, Morris AP, Palmer CNA, Pedersen O, Polasek O, Poulter NR, Province MA, Psaty BM, Ridker PM, Rotter JI, Rudan I, Salomaa V, Samani NJ, Sever PJ, Skaaby T, Stafford JM, Starr JM, van der Harst P, van der Meer P; Understanding Society Scientific Group, van Duijn CM, Vergnaud AC, Gudnason V, Wareham NJ, Wilson JG, Willer CJ, Witte DR, Zeggini E, Saleheen D, Butterworth AS, Danesh J, Asselbergs FW, Wain LV, Ehret GB, Chasman DI, Caulfield MJ, Elliott P, Lindgren CM, Levy D, Newton-Cheh C, Munroe PB, Howson JMM; CHARGE EXOME BP, CHD Exome+, Exome BP, GoT2D:T2DGenes Consortia, The UK Biobank Cardio-Metabolic Traits Consortium Blood Pressure Working Group†. New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. Circ Cardiovasc Genet. 2017 Oct;10(5). pii: e001778. doi: 10.1161/CIRCGENETICS.117.001778. PubMed PMID: 29030403; PubMed Central PMCID: PMC5776077. [IF: 4.743]
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