BIO-Sketch of Giampiero Valè

- Personal Information

From December 28th 2018, Associate professor in Genetics (Bio/18), Università del Piemonte Orientale, Dipartimento per lo Sviluppo Sostenibile e la Transizione Ecologica (DiSSTE), Polo S. Giuseppe, piazza S. Eusebio 5, 13100, Vercelli (Italy).
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- Academic age: years from the beginning of scientific activity: 31
- Previous positions

- May 2017 - December 2018, responsible of the Vercelli side office of CREA-CI, (Italy);
- January 2011 - April 2017, acting director of the CREA-Rice research unit of Vercelli, (Italy);
- 1991 – December 2010, researcher at the Genomics research centre of the CREA, Fiorenzuola d'Arda (PC), (Italy)

- Prizes and awards

- Winner of a bimonthly NATO-CNR Senior fellowship for international research institutions on June1999
- National scientific qualification to full professor for the disciplinary scientific sector AGR/07 (Agricultural genetics) from 10/04/2017 to 10/04/2023
- Eligible for direction of the Genomics and bioinformatics research centre of CREA (CREA-GB), from 23-5-2017 to 23-5-2025
- National scientific qualification to full professor for the disciplinary scientific sector BIO/18 (Genetics), from 15/04/2021 to 15/04/2030

- Visiting academic positions

- July 1999 – March 2000, visiting postdoctoral scientist at the Sainsbury Laboratory of John Innes Centre in Norwich, (UK);
- 2015, invited visiting at China Agricultural University, Beijing and Academy of Agricultural Sciences, Nanjing (China), title of presentation: "Priorities for rice research in Italy and Europe".

- Teaching activities and PhD supervision

- 2005-2010, Molecular Plant Pathology and Plant Genomics at the Faculty of Biology of the University of Parma (Italy);
- 2003-2006, Plant Molecular Biology at the Faculty of Agriculture of the University of Modena e Reggio Emilia (Italy).

2019-present: Genetica (9 CFU), Genetica II (6 CFU), Plant Genetics (3 CFU) at Università del Piemonte Orientale;

- Supervisor/co-tutor of the following PhD students: Elena Dall'Aglio, PhD Biotecnologie Industriali e Ambientali, Università degli Studi di Verona, 2005-2008; Davide Bulgarelli, PhD Biologia Vegetale e Produttività della Pianta Coltivata, Università degli Studi di Milano, 2006-2009; Simona Urso, PhD Biologia Vegetale, Università degli Studi di Parma, 2008-2011; Letizia Bernardo, PhD Biochimica e Biotecnologie, Università degli Studi di Padova, 2009-2012; Chiara Biselli, PhD Biochimica e Biologia Molecolare, Università degli Studi di Parma, 2009-2012; Jacopo Trotti, PhD Chemistry and Biology, UPO, 2022-present.

- Education

- 1994 PhD in Applied Genetics (70/70), University of Milan, Italy;
- 1990 Laurea cum laude in Agricultural Sciences, Catholic University of Piacenza (Italy).

- Administrative role and position responsibility

- 2010, member of the national delegation visiting Agriculture and Agri-Food Canada and participation to round tables and meetings with the Canadian colleagues to define bilateral collaborations between Italy and Canada on agricultural research;
- 2011-2012, member of the working group appointed to define a revision of the criteria for registration of rice varieties to the "Registro Nazionale delle varietà di riso" to be proposed to the "Commissione Sementi of MiPAAF";
- from September 2013 to September 2015, member of the SIGA (Società Italiana di Genetica Agraria) Executive Board;

- since 2013, member of the Expert Working group (EWG) “Durum Wheat Genomics and Breeding” of the consortium the “Wheat Initiative” (www.wheatinitiative.org);
- since 2016, member of Working Group on Rice Authentication of ICC (International Association for Cereal Science and Technology) Technical Committee;
- 2019-present, Referent Teacher of the Master Degree in Food Health and Environment;
- 2020-present, Member of the Didactic Committee of the PhD program in Chemistry and Biology, University of Piemonte Orientale;
- 2022-present, Director of the international Master of Science in Food, health and environment, University of Piemonte Orientale.

➢ Scientific organisations

- 2002, member of the international organizing committee of the Eucarpia (European Association for Research on Plant Breeding) international congress “From biodiversity to genomics: breeding strategies for small grain cereals in the third millennium”, Salsomaggiore (PR), Italy;
- 2014, member of the international organizing committee of the IWBLD (1st International Workshop on Barley Leaf Diseases) international congress, SalsomaggioreTerme, (http://www.iwbld.org/) and chairman of the Session 6 on “Durable resistance in barley”; Italy, June 3-6, 2014;
- 2014, invited speaker at the congress “Rice International Conference From Staple to Innovation” (http://www.rice2014.com/en/index.php), Session 2 “Rice breeding and agricultural practices to meet processing and product requirements”, Pingtung, Taiwan, title of presentation: “Breeding for quality- and functional-related traits in European temperate japonica rice”.

➢ Editorial activity

- since 1998, reviewer of scientific publications for several indexed scientific journals;
- since 2017, member of the Frontiers in Plant Science Editorial Board (associate editor), specialty section Crop Science and Horticulture;
- 2021-2022, Guest Editor of the MDPI journal Agriculture on “Breeding and Genetics to shape rice production systems in the new climatic scenario”;
- 2021-2022, Topic Editor of the Frontiers in Plant Science article collection on “Disease Resistance in Rice”.

➢ Membership of scientific societies

- 1993-present, member of the Italian Society for Agricultural Genetics (SIGA);
- from 2007 to 2015, member of the “International society for Molecular Plant-Microbe Interactions”.

➢ Fundings (current and past)

GV has been Principal investigator/Coordinator/WP leader in 24 National/International projects (Ministry of Agricultural, Food and Forestry Policies, Regions Emilia-Romagna and Lombardia, AGER-Foundation, Cariplo and Agripolis Foundations, ERA-NET, H2020), and 1 Project with a national private company. Co-owner of Community plant variety rights for three rice varieties: Ducato (decision n. 33458), Salvo (decision n. 33457) (2012) e Onice (decision n. 34408) (2013)

Main Fund raising; among parentheses are indicated the amount (€) funded to GV, funding organizations and number of partners:

- 2001-2005, responsible of research unit, PROMAR, a project on plant protection by using marker-assisted selection (100.710 € funded to GV), (MiPAF, 6 partners);
- 2005-2007, responsible of research unit, CEREALAB, a project on the identification of useful traits for the seed companies (91.200 € funded to GV), (Regione Emilia-Romagna, 5 partners);
- 2005-2010, responsible of research unit, PROM, a project on structural and functional genomics of horticultural plants (112.900 € funded to GV) (MiPAF, 36 partners);
- 2005-2009, responsible of research unit, PROTEOSTRESS, a project on proteins and genes involved in plant protection from pathogens (210.000 € funded to GV) (MiPAF, 9 partners);
- 2009-2011, coordinator, RESPAT, a project dedicated to the identification of genes involved in plant-pathogens interactions (35.000 funded to GV) (MiPAAF, 9 partners);
- 2008-2012, responsible of research unit, “Progetto internazionale sequenziamento genoma frumenti: la mappa fisica del cromosoma 5A”, a project on the realization of the bread wheat chromosome 5A physical map (600.000 € funded to GV) (MiPAF, 10 partners);
- 2009-2011, responsible of research unit, CITRUSTART, a project on Citrus resistance to CTV (70.000 funded to GV) (MiPAF, 4 partners);

- 2011-2013, responsible of research unit, RGV-FAO, a project dedicated to characterization and exploitation of genetic resources (60.000 € funded to GV) (MiPAF, 26 partners);
- 2012-2014, responsible of research unit, CANADAIR, a project devoted to research on wheat within an Italy-Canada collaboration (450.000 funded to GV) (MiPAF, 4 partners);
- 2011-2014, coordinator, RISINNOVA, Integrated Genetic and Genomic Approaches for New Italian Rice Breeding Strategies, a project dedicated to genetics and genomics research of rice adaptation to abiotic and biotic stresses, (410.000 € funded to GV) (AGER foundation, 12 partners);
- 2011-2013, responsible of research unit and WP leader, POLORISO, scientific research on genetics and technology of rice, (151.000 € funded to GV) (MiPAF, 10 partners);
- 2012-2016, responsible of research unit, GS-RUSE, Genomic selection for resources use efficiency in rice, (48.000 € funded to GV) (Cariplo and Agripolis Foundations; 7 partners);
- 2014-2016, responsible of research unit, RGV-FAO, a project dedicated to characterization and exploitation of genetic resources (56.000 € funded to GV) (MiPAF, 26 partners);
- 2014-2017responsible of research unit and WP leader, GreenRice, Sustainable and environmental friendly rice cultivation systems in Europe, (100.100 € funded to GV) (FACCE-JPI ERA Net+, 7 partners);
- 2015-2019, responsible of agreement with a private seed company, ViNaRes, a project dedicated to pyramiding of blast resistance genes into a traditional Italian rice variety (40.000 € funded to GV) (national private company);
- 2016-2020, responsible of research unit, NEURICE, New commercial EUropean RICE (Oryza sativa) harbouring salt tolerance alleles to protect the rice sector against climate change and apple snail (Pomacea insularum) invasion, H2020 call SFS-05-2015 (350.036 € funded to GV) (13 partners);
- 2017-2020, responsible of research unit, RGV-FAO, a project dedicated to characterization and exploitation of genetic resources (51.000 € funded to GV) (MiPAF, 26 partners);
- 2017-2020, coordinator, RISO-BIOSYSTEMS, a project dedicated to research and dissemination on organic rice (167.731 € funded to GV) (MiPAF, 6 partners);
- 2023-2024, responsible of research unit, "FUTUREGRAIN: Exploring Rice diversity in agricultural systems and nutritional quality towards healthier food with a lower environmental impact" (42.255 € funded to GV) (Swedish private agency Ekhagastiftelsen, 2 partners).

➢Research Interests

Research is related to plant breeding and genetics: about 30 years of experience in plant breeding and genetics: conventional breeding, molecular genetics, transcriptome analysis, quantitative genetics, map-based cloning, marker-assisted selection, with focus on biotic and abiotic stresses tolerance, resource use efficiency and plant microbiota. Expertise in genetic data analyses: construction of genetic maps, mapping of single genes and quantitative traits, association mapping for agronomical and quality traits in rice.

➢Bibliometric data (Source Scopus)

- H-Index (in Scopus): 26
- Total number of publications in peer-reviewed journals: 86

➢Main scientific publications

More than 130 publications in international-national Journals and book chapters.

Publications on peer-reviewed Journals

1. Marè C, Zampieri E, Cavallaro V, Frouin J, Grenier C, Courtois B, Brottier L, Tacconi G, Finocchiaro F, Serrat X, Nogués S, Bundó M, San Segundo B, Negrini N, Pesenti M, Sacchi GA, Gavina G, Bovina R, Monaco S, Tondelli A, Cattivelli L, Valè G (2023) Marker-assisted introgression of the salinity tolerance locus Saltol in temperate japonica rice. Rice, 16:2. DOI: 10.1186/s12284-023-00619-2

2. Hester ER, Vaksmaa A, Vale' G, Monaco S, Jetten MSM, Lüke C (2022) Effect of water management on microbial diversity and composition in an Italian rice field system. FEMS Microbiology Ecology, 98:1–11; DOI: 10.1093/femsec/fiac018
3. Puglisi D, Visioni A, Ozkan H, Kara I, Lo Piero AR, Ezzahra Rachdad F, Tondelli A, Vale` G, Cattivelli L, Fricano A (2022) High accuracy of genome-enabled prediction of belowground and physiological traits in barley seedlings. G3, 12(3), jkac022; DOI: 10.1093/g3journal/jkac022
4. Bez C, Esposito A, Thuy H-D, Hong M-N, Valè G, Licastro D, Bertani I, Piazza S, Venturi V (2021) The rice foot rot pathogen Dickeya zeae alters the in-field plant microbiome. Environmental Microbiology, 23(12): 7671-7687; DOI: 10.1111/1462-2920.15726
5. Monaco S, Volante A, Orasen G, Cochrane N, Oliver V, Price AH, Teh YA, Martínez-Eixarch M, Thomas C, Courtois B, Valè G (2021) Effects of the application of a moderate alternate wetting and drying technique on the performance of different European varieties in Northern Italy rice system. Field Crops Research 270: 108220. DOI: 10.1016/j.fcr.2021.108220
6. Mongiano G, Zampieri E, Morcia C, Titone P, Volante A, Terzi V, Tamborini V, Valè G, Monaco S (2021) Application of plant-derived bioactive compounds as seed treatments to manage the rice pathogen Fusarium fujikuroi. Crop Protection 148: 105739. DOI: 10.1016/j.cropro.2021.105739
7. Puglisi D, Delbono S, Visioni A, Ozkan H, Kara I, Casas AM, Igartua E, Valè G, Lo Piero AR, Cattivelli L, Tondelli A, Fricano A (2021) Genomic prediction of grain yield in a barley MAGIC population modelling genotype per environment interaction. Frontiers in Plant Science 12: 664148. DOI: 10.3389/fpls.2021.664148
8. Maghrebi M, Baldoni E, Lucchini G, Vigani G, Valè G, Sacchi GA, Nocito FF (2021) Analysis of Cadmium Root Retention for Two Contrasting Rice Accessions Suggests an Important Role for OsHMA2. Plants 10: 806. DOI: 10.3390/plants10040806
9. Desiderio F, Bourras S, Mazzucotelli E, Rubiales D, Keller B, Cattivelli L, Valè G (2021) Characterization of the resistance to powdery mildew and leaf rust carried by the bread wheat cultivar Victo. International Journal of Molecular Sciences 22(6):3109. DOI: 10.3390/ijms22063109
10. Faccini N, Delbono S, Çelik Oguz A, Cattivelli L, Valè G, Tondelli A (2021) Resistance of European spring 2-row barley cultivars to Pyrenophora graminea and detection of associated loci. Agronomy 11(2):374. DOI: 10.3390/agronomy11020374
11. Volante A, Tondelli A, Desiderio F, Abbruscato P, Menin B, Biselli C, Casella L, Singh N, McCouch SR, Tharreau D, Zampieri E, Cattivelli L, Valè G (2020) Genome wide association studies for japonica rice resistance to blast in field and controlled conditions. Rice 13:71. DOI: 10.1186/s12284-020-00431-2
12. Barabaschi D, Tondelli A, Valè G, Cattivelli L (2020) Fitness cost shapes differential evolutionary dynamics of disease resistance genes in cultivated and wild plants. Molecular Plant 13:1-3. DOI: 10.1016/j.molp.2020.09.003
13. Orasen G, De Nisi P, Lucchini G, Abruzzese A, Pesenti M, Maghrebi M, Kumar A, Nocito FF, Baldoni E, Morgutti S, Negrini N, Valè G, Sacchi GA (2019) Continuous flooding or alternate wetting and drying differently affect the accumulation of health-promoting phytochemicals and minerals in rice brown grain. Agronomy 9: 628. DOI:10.3390/agronomy9100628
14. Andreozzi A, Prieto P, Mercado-Blanco J, Monaco S, Zampieri E, Romano S, Valè G, Defez R, Bianco C (2019) Efficient colonization of the endophytes Herbaspirillum huttiense RCA24 and Enterobacter cloacae RCA25 influences the physiological parameters of Oryza sativa L. cv. Baldo rice. Environmental Microbiology 21(9): 3489–3504. DOI: 10.1111/1462-2920.14688
15. Oliver V, Cochrane N, Magnusson J, Brachi E, Monaco S, Volante A, Courtois B, Valè G, Price A, Teh YA (2019) Effects of water management and cultivar on carbon dynamics, plant productivity and biomass allocation in European rice systems. Science of the Total Environment 685: 1139–1151. DOI: 10.1016/j.scitotenv.2019.06.110.

16. Biselli C, Volante A, Desiderio F, Tondelli A, Gianinetti A, Finocchiaro F, Taddei F , Gazza L, Sgrulletta D, Cattivelli L, Valè G (2019) GWAS for Starch-Related Parameters in JaponicaRice (Oryza sativa L.). Plants, 8, 292. DOI:10.3390/plants8080292
17. Nghi KN, Tondelli A, Valè G, Tagliani A, Marè C, Perata P, Pucciariello C (2019) Dissection of coleoptile elongation in japonica rice under submergence through integrated genome-wide association mapping and transcriptional analyses. Plant Cell Environment, 42:1832–1846. DOI: 10.1111/pce.13540
18. Hu X, Rocheleau H, McCartney C, Biselli C, Balcerzak M, Fedak G, Yan Z, Valè G, Khanizadeh S, Ouellet T (2019) Identification and mapping of espresse genes associated with the 2DL QTL for fusarium head blight resistance in the wheat line Wuhan 1. BMC Genetics,20:47. DOI: 10.1186/s12863-019-0748-6.
19. Borrelli GM, Mazzucotelli E, Marone D, Crosatti C, Michelotti V, Valè G, Mastrangelo AM (2018) Regulation and Evolution of NLR Genes: A Close Interconnection for Plant Immunity. The International Journal of Molecular Sciences, 19:1662. DOI: 10.3390/ijms19061662
20. Ben Hassen M, Bartholomé J, Valè G, Cao TV, Ahmadi N (2018) Genomic Prediction accounting for Genotype by Environment Interaction Offers an Effective Framework for Breeding Simultaneously for Adaptation to an Abiotic Stress and Performance Under Normal Cropping Conditions in Rice. G3: Genes, Genomes, Genetics, 8: 2319-2332. DOI: 10.1534/g3.118.200098.
21. Gianinetti A, Finocchiaro F, Bagnaresi P, Zechini A, Faccioli P, Cattivelli L, Valè G, Biselli C (2018) Seed dormancy involves a transcriptional program that supports early plastid functionality during imbibition. Plants, 7: 35. DOI: 10.3390/plants7020035
22. Buerstmayr M, Steiner B, Wagner C, Schwarz P, Brugger K, Barabaschi D, Volante A, Valè G, Cattivelli L, Buerstmayr H (2018) High-resolution mapping of the of the peri-centromeric region on wheat chromosome arm 5AS harboring the Fusarium head blight resistance QTL Qfhs.ifa-5A. Plant Biotechnology Journal, 16:1046-1056. DOI: 10.1111/pbi.12850
23. Biselli C, Bagnaresi P, Faccioli P, Hu X, Balcerzark M, Mattera GM, Yan Z, Ouellet T, Cattivelli L, Valè G (2018) Comparative transcriptome profiles of near-isogenic hexaploid wheat lines differing for effective alleles at the 2DL FHB resistance QTL. Frontiers in Plant Science, 9:37. DOI: 10.3389/fpls.2018.00037.
24. Ben Hassen M, Cao T-V, Bartholomé J, Orasen G, Colombi C, Rakotomalala J, Razafinimpiaza L, Bertone C, Biselli C, Volante A, Desiderio F, Jacquin JL, Valè G, Ahmadi N (2018) Rice diversity panel provides accurate genomic predictions for complex traits in the progenies of biparental crosses involving members of the panel. Theoretical and Applied Genetics, 131(2): 417-435. DOI: 10.1007/s00122-017-3011-4.
25. Vaksmaa A, van Alen TA, Ettwig KF, Lupotto E, Valè G, Jetten MSM, Lüke C (2017) Stratification of diversity and activity of methanogenic and methanotrophic microorganisms in a nitrogen-fertilized Italian paddy soil. Frontiers in Microbiology, 8:2127. DOI: 10.3389/fmicb.2017.02127
26. Volante A, Desiderio F, Tondelli A, Perrini R, Orasen G, Biselli C, Riccardi P, Vattari A, Cavalluzzo D, Urso S, Ben Hassen M, Fricano A, Piffanelli P, Cozzi P, Biscarini F, Sacchi GA, Cattivelli L, Valè G (2017) Genome-wide analysis of japonica rice performance under limited water and permanent flooding conditions. Frontiers in Plant Science, 8:1862. DOI: 10.3389/fpls.2017.01862.
27. Volante A, Tondelli A, Aragona M, Valente MT, Biselli C, Desiderio F, Bagnaresi P, Matic S, Gullino ML, Infantino A, Spadaro D, Valè G (2017) Identification of bakanae disease resistance loci in japonica rice through genome wide association study. Rice 10:29. DOI: 10.1186/s12284-017-0168-z.
28. Valente MT, Desiderio F, Infantino A, Valè G, Abbruscato P, Aragona M (2017) Genetic variability of Fusarium fujikuroi populations associated with bakanae of rice in Italy. Plant Pathology, 66(3): 469-479; DOI: 10.1111/ppa.12575.
29. Ben Hassen M, Monaco F, Facchi A, Romani M, Valè G, Sali G (2017) Economic performance of traditional and modern rice varieties under different water management systems. Sustainability 9(3): 347; doi:10.3390/su9030347.

30. Vaksmaa A, Lüke C, van Alen T, Valè G, Lupotto E, Jetten MSM, Ettwig KF (2016) Distribution and activity of the anaerobic methanotrophic community in a nitrogen-fertilized Italian paddy soil. FEMS Microbiology Ecology, 92(12), DOI:10.1093/femsec/fiw181
31. Barchi L, Rotino GL, Toppino L, Valè G, Acciarri N, Ciriaci T, Portis E, Lanteri S (2016) SNP mapping and identification of QTL for horticultural key breeding traits in eggplant (Solanum melongena L.). Acta Horticulturae, 1145:9-15, DOI: 10.17660/ActaHortic.2016.1145.2; ISSN: 05677572 ISBN: 978-946261134-4.
32. Matić S, Bagnaresi P, Biselli C, Orrù L, Carneiro GA, Siciliano I, Valé G, Gullino ML, Spadaro D (2016) Comparative transcriptome profiling of resistant and susceptible rice genotypes in response to the seedborne pathogen Fusarium fujikuroi. BMC Genomics, 17(1):608, DOI: 10.1186/s12864-016-2925-.
33. Monaco F, Sali G, Ben Hassen M, Facchi A, Romani M, Valè G (2016) Water management options for rice cultivation in a temperate area: a multi-objective model to explore economic and water saving results. Water, 8(8), 336, doi: 10.3390/w8080336; ISSN 2073-4441
34. Mazza G, Agnelli AE, Orasen G, Gennaro M, Valè G, Lagomarsino A (2016) Reduction of Global Warming Potential from rice under alternate wetting and drying practice in a sandy soil of northern Italy. Italian Journal of Agrometeorology, 21(2): 35-44, DOI: 10.19199/2016.2.2038-5625.035; ISSN 2038-5625.
35. Biscarini F, Cozzi P, Casella L, Riccardi P, Vattari A, Orasen G, Perrini R, Tacconi G, Tondelli A, Biselli C, Cattivelli L, Spindel J, McCouch S, Abbruscato P, Valè G, Piffanelli P, Greco R (2016) Genome-wide association study for traits related to plant and grain morphology, and root architecture in temperate rice accessions. PLoS ONE, 11(5): e0155425, doi:10.1371/journal.pone.0155425
36. Barbierato V, Toppino L, Rinaldi P, Sala T, Bassolino L, Valè G, Ferrarini A, Delledonne M, Bagnaresi P, Rotino GL (2016) Phenotype and gene expression analyses of the Rfo-sa1 resistant aubergine interaction with Fusarium oxysporum f. sp. melongenae and Verticillium dahliae. Plant Pathology, 65(8): 1297-1309, Doi: 10.1111/ppa.12518.
37. Carletti G, Carra A, Allegro G, Vietto L, Desiderio F, , Bagnaresi P, Cattivelli L, Valè G, Nervo G (2016) QTLs for Woolly Poplar Aphid (Phloeomyzus passerinii L.) resistance Detected in an Inter-Specific Populus deltoides X P. nigra Mapping Population. PLoS ONE, 11(3): e0152569; DOI: 10.1371/journal.pone.0152569.
38. Pessina S, Lenzi L, Perrazzolli M, Campa M, Dalla Costa L, Urso S, Valè G, Salamini F, Velasco R, Malnoy M (2016) Knockdown of MLO genes reduces susceptibility to powdery mildew in grapevine. Horticulture Research, 3, 16016; doi: 10.1038/hortres.2016.16
39. Laino P, Russo M P, Guardo M, Reforgiato-Recupero G, Valè G, Cattivelli L, Moliterni VMC (2016) Rootstock-scion interaction affecting citrus response to CTV infection: a proteomic view. Physiologia Plantarum, 156: 444–467, DOI:10.1111/ppl.12395
40. Urso S, Biselli C, Desiderio F, Bagnaresi P, Crispino L, Piffanelli P, Abbruscato P, Assenza F, Guarnieri G, Cattivelli L., Valè G (2016). Genetic analysis of durable resistance to Magnaporthe oryzae in the rice accession Gigante Vercelli identified two blast resistance loci. Molecular Genetics and Genomics, 291:17-32, DOI 10.1007/s00438-015-1085-8
41. Barabaschi D, Tondelli A, Desiderio F, Volante A, Vaccino P, Valè G, Cattivelli L (2016) Next generation breeding. Plant Science, 242: 3-13, DOI: http://dx.doi.org/10.1016/j.plantsci.2015.07.010
42. Biselli C, Bagnaresi P, Cavalluzzo D, Urso S, Desiderio F, Orasen G, Gianinetti A, Righettini F, Gennaro M, Ben Hassen M, Sacchi GA, Cattivelli L, Valè G (2015) Deep sequencing transcriptional fingerprinting of rice kernels for dissecting grain quality traits. BMC Genomics, 16:1091, DOI 10.1186/s12864-015-2321-7.
43. Barabaschi D, Magni F, Volante A, Gadaleta A, Šimková H, Scalabrin S, Prazzoli ML, Bagnaresi P, Lacrima K, Michelotti V, Desiderio F, Orrù L, Mazzamurro V, Fricano A, Mastrangelo AM, Tononi P, Vitulo N, Jurman I, Frenkel Z, Cattonaro F, Morgante M, Blanco A, Doležel J, Delledonne M, Stanca AM, Cattivelli L, Valè G (2015). Physical mapping of bread wheat chromosome 5A: an integrated approach. The Plant Genome, 8:3, DOI: 10.3835/plantgenome2015.03.0011

44. Gadaleta A, Giancaspro A, Nigro D, Giove SL, Incerti O, Simeone R, Piarulli L, Colasuonno P, Valè G, Cattivelli L, Blanco A (2014). A new genetic and deletion map of wheat chromosome 5A to detect candidate genes for quantitative traits. Molecular Breeding, 34: 1599-1611, DOI: 10.1007/s11032-014-0185-1
45. Desiderio F, Guerra D, Rubiales D, Piarulli L, Pasquini M, Mastrangelo AM, Simeone R, Blanco A, Cattivelli L, Vale' G (2014). Identification and mapping of quantitative trait loci for leaf rust resistance derived from a tetraploid wheat Triticum dicoccum accession. Molecular Breeding, 34:1659-1675, DOI: 10.1007/s11032-014-0186-0
46. Aragona M, Minio A, Ferrarini A, Valente MT, Bagnaresi P, Orrù L, Tononi P, Zamperin G, Infantino A, Valè G, Cattivelli L, Delledonne M. (2014) De novo genome assembly of the soil-borne fungus and tomato pathogen Pyrenochaeta lycopersici. BMC Genomics, 15:313, DOI: 10.1186/1471-2164-15-313
47. Portis E, Barchi L, Toppino L, Lanteri S, Acciarri N, Felicioni N, Fusari F, Barbierato V,Cericola F, Valè G, Rotino GL. (2014) QTL Mapping in eggplant reveals cluster of yield - related loci and orthology with the tomato genome. PLoS ONE, 9(2): e89499. DOI: 10.1371/journal.pone.0089499
48. Biselli C, Cavalluzzo D, Perrini R, Gianinetti A, Bagnaresi P, Urso S, Orasen G, Lupotto E, Cattivelli L, Valè G (2014) Improvement of marker-based predictability of Apparent Amylose Content in japonica rice through GBSSI allele mining. Rice, 7:1, DOI: 10.1186/1939-8433-7-1
49. Biselli C, Urso S, Tacconi G, Steuernagel B, Schulte D, Gianinetti A, Bagnaresi P, Stein N, Cattivelli L, Valè G. (2013) Haplotype variability and identification of new functional alleles at the Rdg2a leaf stripe resistance gene locus. Theoretical and Applied Genetics 126:1575–1586, DOI 10.1007/s00122-013-2075-z
50. Urso S, Zottini M, Ruberti C, Lo Schiavo F, Stanca AM, Cattivelli L, Valè G. (2013) An Agrobacterium tumefaciens-mediated gene silencing system for functional analysis in grapevine leaves. Plant Cell Tissue and Organ Culture 114: 49-60. DOI: 10.1007/s11240-013-0305-3.
51. Campos-Soriano L, Valè G, Lupotto E, San Segundo B (2013) Investigation of rice blast development in susceptible and resistant rice cultivars using a gfp-expressing Magnaporthe oryzae strain. Plant Pathology, 62: 1030-1037, DOI: 10.1111/ppa.12023
52. Bagnaresi P, Biselli C, Orrù L, Urso S, Crispino L, Abbruscato P, Piffanelli P, Lupotto E, Cattivelli L, Valè G (2012) Comparative transcriptome profiling of the early response to Magnaporthe oryzae in durable resistant vs susceptible rice (Oryza sativa L.) genotypes. PLoS ONE, 7(12): e51609. DOI: 10.1371/journal.pone.0051609
53. Bernardo L, Prinsi B, Negri AS, Cattivelli L, Espen L, Valè G. (2012) Proteomic characterization of the Rph15 barley resistance gene-mediated responses to leaf rust. BMC Genomics, 13: 642. DOI: 1471-2164/13/642
54. Gadaleta A., Giancaspro A., Giove S.L., Zacheo S., Incerti O., Simeone R., Colasuonno P., Nigro D.,, Valè G., Cattivelli L. , Stanca M. , Blanco A. (2012) Development of a deletion and genetic linkage map for the 5A and 5B chromosomes of wheat (Triticum aestivum L.). Genome, 55(6): 417-427. DOI:10.1139/G2012-028
55. Barchi L, Lanteri S, Portis E, Valè G, Volante A, Pulcini L, Ciriaci T, Acciarri N, Barbierato V, Toppino L, Rotino GL (2012) A RAD Tag derived marker based eggplant linkage map and the location of QTLs determining anthocyanin pigmentation. PLoS ONE 7(8): e43740. DOI: 10.1371/journal.pone.0043740
56. Barabaschi D., Guerra D., Lacrima K., Laino P., Michelotti V., Urso S., Valè G., Cattivelli L. (2012) Emerging Knowledge from Genome Sequencing of Crop Species. Mol Biotech 50: 250-266. DOI 10.1007/s12033-011-9443-1
57. Barchi L., Lanteri S., Portis E., Acquadro A., Valè G., Toppino L., Rotino G.L. (2011) Identification of SNP and SSR markers in eggplant using RAD tag sequencing. BMC Genomics, 12: 304. DOI: 1471-2164/12/304
58. Bulgarelli D, Biselli C, Collins NC, Consonni G, Stanca AM, Schulze-Lefert P, Valè G (2010) The CC-NB-LRR-type Rdg2a resistance gene confers immunity to the seed-borne barley leaf stripe pathogen in the

absence of hypersensitive cell death. PLoS ONE, 5:e12599, DOI:10.1371/journal.pone.0012599. ISSN 1932-6203

59. Barchi L, Lanteri S, Portis E, Stàgel A, Valè G, Toppino L, Rotino GL (2010) Segregation distortion and linkage analysis in eggplant (Solanum melongena L.). Genome, 53:805-815. DOI:10.1139/G10-073

60. Tacconi G, Baldassarre V, Lanzanova C, Faivre-Rampant O, Cavigiolo S, Urso S, Lupotto E, Valè G (2010) Polymorphism analysis of genomic regions associated with broad-spectrum effective blast resistance genes for marker development in rice. Molecular Breeding, 26:595–617, ISSN : 1380-3743. DOI:10.1007/s11032-010-9394-4

61. Biselli C, Urso S, Bernardo L, Tondelli A, Tacconi G, Martino V, Grando S, Valè G (2010) Identification and mapping of the leaf stripe resistance gene Rdg1a in Hordeum spontaneum. Theoretical and Applied Genetics, 120: 1207-1218, DOI:10.1007/s00122-009-1248-2. ISSN 0040-5752.

62. Haegi A., Bonardi V., Dall'Aglio E., Glissant D., Tumino G., Collins N., Bulgarelli D., Infantino A., Stanca A.M., Delledonne M., Valè G. (2008). Histological and molecular analysis of Rdg2a barley resistance to leaf stripe. Molecular Plant Pathology, 9(4): 463-478. DOI:10.1111/J.1364-3703.2008.00479.X

63. Toppino L., Valè G., Rotino GL., (2008). Inheritance of Fusarium wilt resistance introgressed from Solanum aethiopicum Gilo and Aculeatum groups into cultivated eggplant (S. melongena) and development of associated PCR-based markers. Molecular Breeding, 22: 237-250. DOI:10.1007/s11032-008-9170-x

64. Licciardello C, Russo MP, Valè G, Reforgiato-Recupero G (2008). Identification of differentially expressed genes in the flesh of blood and common oranges. Tree Genetics and Genomes, 4: 315-331. DOI:10.1007/s11295-007-0111-3

65. Terzi V, Morcia C, Faccioli P, Valè G, Tacconi G, Malnati M, (2007). In vitro antifungal activity of the Tea Tree (Melaleuca alternifolia) essential oil and its major components against plant pathogens. Letters of Applied Microbiology 44: 613-618. DOI:10.1111/j.1472-765X.2007.02128.x

66. Barabaschi D, Campani L, Francia E, Toubia-Rahme H, Valè G, Gianinetti A, Delogu G, Stanca AM, Pecchioni N. (2007). Haplotype structure around the nud locus in barley and its association with resistance to leaf stripe (Pyrenophora graminea). Plant Breeding 126: 24-29. DOI: 10.1111/j.1439-0523.2007.01340.

67. Tacconi G, V. Baldassarre, N. C. Collins, D. Bulgarelli, A. M. Stanca, and G. Valè (2006). Haplotype characterization and markers at the barley Mlo powdery mildew resistance locus as tools for marker-assisted selection, Genome 49: 864-872. DOI:10.1139/G06-044

68. Regis, C., Laura M., Morreale G., Valè G., Allavena A. (2006). Screening of viviparous plantlet formation-related genes in Kalanchoe daigremontiana by SSH analysis. Acta Horticulturae 714, 155-161. ISSN: 05677572 ISBN: 9066055499;978-906605549-0

69. Rotino GL, Sihachakr D, Rizza F, Valè G, Tacconi MG, Alberti P, Mennella G, Sabatini E, Toppino L, D'Alessandro A, Acciarri N (2005). Current status in production and utilization of dihaploids from somatic hybrids between eggplant (Solanum melongena L.) and its wild relatives. Acta Physiologiae Plantarum 27: 723-733. DOI: 10.1007/s11738-005-0077-4

70. Francia E., Tacconi G., Crosatti C., Bulgarelli D., Barabaschi D., Dall'Aglio E., G. Valè (2005). Marker-assisted selection in crop plants. Plant Cell Tissue and Organ Culture 82: 317-342. DOI:10.1007/s11240-005-2387-z

71. Bulgarelli D., N.C. Collins, G. Tacconi, E. Dall'Aglio, R. Brueggeman, A. Kleinhofs, A.M. Stanca, G. Valè (2004). High-resolution genetic mapping of the leaf stripe resistance gene Rdg2a in barley. Theoretical and Applied Genetics,108: 1401-1408. DOI:10.1007/s00122-003-1557-9

72. Arru L., N. Faccini, C. Govoni, L. Cattivelli, N. Pecchioni, G. Delogu, A.M. Stanca, G. Valè (2003). The PCR-based marker MWG2018 linked to the Rdg2a leaf stripe resistance gene is a useful tool for assesing barley resistance in breeding programs. Crop Science, 43, 1036-1042. DOI:10.2135/cropsci2003.1036

73. Müller K.J., G. Valè, D. Enneking (2003): Selection of resistant spring-barley accessions after natural infection with leaf stripe (Pyrenophora graminea) under organic farming conditions in Germany and by sandwich test. Journal of Plant Pathology, 85/1, 9-14
74. Orru L., R.E. Nicks, P. Lindhout, G. Valè, E. Francia, N. Pecchioni (2002). Genomic regions determining resistance to leaf stripe (Pyrenophora graminea) in barley. Genome 45: 460-466. DOI:10.1139/G02-004
75. Baldi P., G. Valè, E. Mazzucotelli, C. Govoni, P. Faccioli, A.M. Stanca, L. Cattivelli (2001). The transcripts of several components of the protein synthesis machinery are cold-regulated in a chloroplast-dependent manner in barley and wheat. Journal of Plant Physiology 158: 1541-1546. DOI:10.1078/0176-1617-00591
76. Tacconi G., L. Cattivelli, N. Faccini, N. Pecchioni, A.M. Stanca, G. Valè (2001). Identification and mapping of a new leaf stripe resistance gene in barley (Hordeum vulgare L.). Theoretical and Applied Genetics 102: 1286-1291. DOI:10.1007/s001220000510
77. Zhou F., J. Kurth, F. Wei, C. Elliot, G. Valè, N. Yahiaoui, B. Keller, S. Somerville, R. Wise, P. Schulze-Lefert (2001). Cell-autonomous Expression of Barley Mla1 Confers Race-specific Resistance to the Powdery Mildew Fungus via a Rar1 Independent Signaling Pathway. Plant Cell 13: 337-350. DOI: http://dx.doi.org/10.1105/tpc.13.2.337
78. Pecchioni N., G. Tacconi, L. Arru, L. Bellini, G. Valè (2000). The resistance of barley to leaf stripe caused by Pyrenophora graminea. Czech Journal of Genetics and Plant Breeding, 36: 88-91; ISSN 1212-1975
79. Baldi P., M. Grossi, N. Pecchioni, G. Valè, L. Cattivelli (1999). High expression level of a gene coding for a chloroplastic amino acid selective channel protein is correlated to cold acclimation in cereals. Plant Molecular Biology 41: 233-243. DOI:10.1023/A:1006375332677
80. Pecchioni N., L. Arru, L. Bellini, A.M. Stanca, G. Valè (1999). The wheat leaf rust resistance gene Lrk10 maps to barley chromosome 1HS. Journal of Genetics and Breeding, 53: 113-119; ISSN: 03949257
81. Pecchioni N., G. Valè, H. Toubia-Rahme, P. Faccioli, V. Terzi, G. Delogu (1999). Barley-Pyrenophora graminea interaction: QTL analysis and gene mapping. Plant Breeding, 118: 29-35. DOI:10.1046/j.1439-0523.1999.118001029.
82. Valè G, M. Aragona, E. Torrigiani, L. Cattivelli, M. Montigiani, A. Porta-Puglia (1998). Characterization of a hypovirulent insertional mutant of Pyrenophora graminea and analysis of the barley defence response after inoculation. Plant Pathology, 47: 657-664. DOI:10.1046/j.1365-3059.1998.00290.
83. Valè G, H. Thoubia-Rahme, G. Delogu, P. Faccioli, V. Terzi, N. Pecchioni (1997). Molecular mapping of genes conferring resistance to Pyrenophora graminea. Journal of Applied Genetics 38B: 7-15; ISSN 1234-1983
84. Pecchioni N., P. Faccioli, H. Toubia-Rahme, G. Valè, V. Terzi (1996). Quantitative resistance to barley leaf stripe (Pyrenophora graminea) is dominated by one major locus. Theoretical and Applied Genetics, DOI:93: 97-101. 10.1007/BF00225733
85. Valè G, E. Torrigiani, L. Cattivelli, G. Delogu (1994). Molecular study on barley-Drechslera graminea interaction. Genetica Polonica 35B, pp. 31-37 ISSN 0016-6715
86. Valè G, E. Torrigiani, A. Gatti, G. Delogu, A. Porta-Puglia, G. Vannacci, L. Cattivelli (1994). Activation of genes in barley roots in response to infection by two Drechslera graminea isolates. Physiological and Molecular Plant Pathology, 44 : 207-215; DOI: 10.1016/S0885-5765(05)80005-0