

Massimo Delledonne

Professor of Genetics

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Born in Cortemaggiore, Piacenza, Italy, 17 February 1963
Resident in via Lazzaretto 7, Verona, Italy
Married, 2 daughters

EDUCATION

1988: Laurea degree in Agricultural Sciences, Catholic University, Piacenza (Italy)
1994: Ph.D. in Molecular Biotechnologies, Catholic University, Piacenza (Italy)

RESEARCH ACTIVITY ABROAD

1991: Research Associate, Iowa State University, Ames, Iowa (USA)
1995: NATO-CNR Post-doc fellow, Salk Institute for Biological Studies, La Jolla, California (USA)
1997: NATO-CNR Post-doc fellow, Salk Institute for Biological Studies, La Jolla, California (USA)
1998: Research Associate, Salk Institute for Biological Studies, La Jolla, California (USA)
1999: Visiting scientist, University of Edinburgh, Edinburgh, Scotland (UK)
2002: Professeur invitee, Université de Nice - Sophia Antipolis (France)

PROFESSIONAL CAREER

1994-2001 Researcher of Plant Genetics at Institute of Genetics, Università Cattolica S.C., Piacenza (Italy)
2001-2011 Associate Professor of Plant Genetics at the Faculty of Science, Dept. of Biotechnologies, University of Verona (Italy)

2012-now Full Professor of Genetics at the Faculty of Science, Dept. of Biotechnologies,
University of Verona

APPOINTMENTS

2004-2012 Chair of the PhD Course in Applied Biotechnologies of University of Verona

2007- Director, Functional Genomic Centre of University of Verona

2010-now National Expert, members of the European Food Safety Agency (EFSA) Scientific
Network on Risk Assessment of GMOs

2013-2016 Chair of the PhD School of Science Medicine Engineering of University of Verona

2015-now Chair of the PhD Course in Biotechnologies of University of Verona

2015-now Director of the Core Facilities of University of Verona (<http://cpt.univr.it/>)

TEACHING ACTIVITY

I currently teach Genetics (40 hrs, Degree in Biotechnology and Degree in Bioinformatics),
Genomics and transcriptomics (40h Master in Agri-Food Biotechnology) and Structure and
function of genomes (40 hrs, Masters in Bioinformatics and Medical Biotechnology)

ITALIAN UNIVERSITY 3rd MISSION: ACCOMPLISHMENTS

2012 - 2018 Founder, CEO and Scientific Director of Personal Genomics SRL, Spin-off of
University of Verona (www.personalgenomics.it)

2014 Founder of Biodiversa SRL (www.biodiversa.it)

HONOURS AND AWARDS

2003 EMBO Young Investigator

2008 Assunta Baccharini Melandri award from Italian Society of Plant Biology

2011 Antico Fattore award from Accademia del Georgofili

2013 Assoenologi (winemakers) award for scientific research in viticulture

CURRENT AND RECENT MISCELLANEOUS ACTIVITY

Editorial: I have been a member of the Advisory Board of The Plant Journal and of the Editorial
Board of the Biotechnology Journal and of BMC Plant Biology. I served as referee for: Journal of

Experimental Botany, Molecular Plant-Microbe Interactions, The Plant Cell, Plant Physiology, The Plant Journal, Trends in Plant Science, BMC Genomics, PLoS ONE, Science, Nature Genetics, Nature.

Scientific societies: I'm a member of: Italian Genetics Association, Italian Society of Plant Genetics, Human Genome Organization, American Society of Human Genetics.

RESEARCH GRANTS (last 5 years)

2019. JointProject 2018 – “CanGenome: The genome of Cangrande della Scala: DNA as historical source”;
RiBa 2018 – “NEBBIOLO GENOMICS: structural and functional genomics to explain phenotypic and pathological features”
2018. PRIN 2017 Sensaging (partner) (c.a. €330.000)
- 2016 Valorization of Italian OLive products through INnovative analytical tools – VIOLIN. Fondazione in Rete per la Ricerca Agroalimentare – AGER (100,000)
“Development and application of Novel, Integrated Tools for monitoring and managing Catchments – INTCATCH”. EU project 689341-2 (c.a. 350.000 euro)
- 2015 “The continuum between healthy ageing and idiopathic Parkinson Disease within a propagation perspective of inflammation and damage: the search for new diagnostic, prognostic and therapeutic targets — PROPAG-AGEING”. EU project 634821 (about 550.000 euro)
“Physical Activity and Nutrition INfluences In ageing – PANINI”. EU project 675003 (c.a. 200.000 euro)
Verona Nanomedicine Initiative. Fondazione Cariverona. (about 200.000 euro)

CHAIRMAN (last 5 years)

- London Calling. Nanopore sequencing. London, 14-15 May 2015
- II International Symposium on Postharvest Pathology: Using Science to Increase Food Availability. Bari (Italy), 7 - 11 June 2015
- 12th International Conference on Reactive Oxygen and Nitrogen Species in Plants: from model systems to field. Verona, 22-24 June 2015
- Solanaceae Conference 2016, Davis, CA, 13-16 Sept 2016
- The Future of Medicine Starts Now: how science and new technology are reshaping health science. Genova, Italy, 29-30 June 2017
- Corso avanzato di biologia molecolare, Genova, 25 January 2018

INVITED SPEAKER (last 5 years)

- 2015 Pipeline bioinformatiche del Whole-Exome Sequencing e software di interpretazione dei dati NGS. *NGS-PTL for Personalized Therapy of Leukemia: Bioinformatic Tools for NGS Data Analysis*, Bologna, January 29
- My beautiful genome. *SAS Forum 2015 – Analytics for everyone*, Milano, April 22
- An Eggplant (*Solanum melongena* L.) High Quality Genome Draft. *3rd Plant Genomic Congress*. London, May 11-12
- Sequencing in the field. *London Calling. Nanopore sequencing*. London, May 14-15
- Sequencing your own genome. *Danish Congress in Clinical Biochemistry 2015*, Vejle, Denmark, May 27-29
- Next Generation Sequencing for next generation crops. *II International Symposium on Postharvest Pathology: Using Science to Increase Food Availability*. Bari (Italy), June 7 - 11
- Genetic predisposition of grapevine to polyphenols accumulation. *Redox biology meets nutrition*. Stuttgart (DE), September 1-4
- From next generation sequencing to next generation diagnostic and therapy. *Anticipation and Medicine*. Delmenhorst (DE), September 28-30
- Tecnologie di Nuova Generazione per una Medicina di Nuova Generazione. 5° workshop nazionale di Ematologia Traslazionale. Pisa (Italy), October 29-30
- 2016 *(Im)precision Genomics*. 18^a Giornata di Studio sulle Cellule Staminali. Milano (Italy), January 22
- Geni e genomi: la bellezza nascosta del nostro DNA*. SAP Executive Summit. Cernobbio, Como (Italy) March 11-12
- MinION: a portable experience*. Oxford Nanopore Sequencing. Keygene, Wageningen, (NL) April 14, 2016
- Next Generation Sequencing*. La sclerosi multipla: nuove prospettive. Verona (Italy) April 15
- Solanum melongena: an Illumina/BioNano Genomics integrated approach for a high quality assembly of the Eggplant genome*. *4th Plant Genomic Congress*. London, May 9-10
- Genomica: quali applicazioni e quale futuro*. XLI Congresso Nazionale Associazione Italiana Ematologia Oncologia Pediatrica. Verona, May 22-24
- La ricerca genetica per il miglioramento della qualità della vita*. XXXIX Congresso Associazione Nazionale Direttori Amministrativi e Finanziari. Catania, October 22-23
- (Im)Precision Genomics*. XIX Congresso Nazionale Società italiana Genetica Umana. Torino, November 23-26
- 2017 *(Im)precision Genomics*. Illumina User Group Meeting. Malaga (Spain), March 2-3
- Le mappe ottiche nella caratterizzazione strutturale dei genomi, nell'assemblaggio de novo e nel miglioramento genetico*. Oltre il Transgenico: Nuovi approcci sostenibili per una Moderna Agricoltura. Palermo, March 27
- L'oracolo del DNA*. Festival della Scienza Medica, Bologna, April 20-23

Next generation sequencing for next generation medicine. Meeting on standard NGS protocols for clinical tissues, CRO Aviano, Pordenone, April 26-27

Methods, Instruments and Results: the relevance of governing the machinery to address the right question. The Future of Medicine Starts Now: how science and new technology are reshaping health science. Genova, Italy, June 29-30

2018 *Dai geni ai genomi.* Stati Generali della ricerca. Piacenza, Italy, June 15-16

Enhanced targeted resequencing by optimization of DNA insert length. European Human Genetics Conference. Milan, June 16-19

From medical genetics to medical genomics. The fourth Edition of The pelvis as a Mother International Meeting on "Journey to the Center of A.R.T.". Bari, Italy, September 24-25

From medical genetics to medical genomics. XXI Congresso Nazionale Società Italiana Genetica Umana. Catania, Italy, October 25-27

2019 *Enhanced targeted resequencing by optimization of DNA insert length.* Advances in Genome Biology and Technology (AGBT). Marcos Island, Florida February 27th March 2nd

Superuomini? Quali scenari per migliorare geneticamente l'uomo. Festival della Scienza Medica, Bologna, May 10-12

Superuomini: come modificare geneticamente l'uomo. Stati Generali della ricerca. Piacenza, Italy, May 31 – June 1

Development of a portable genomic laboratory for water metagenomic analysis. International Conference on Smarter Catchment Monitoring: Cleaner Water. London, UK, Sept 4-6

One reference genome is not enough: integration of multiple technologies for de-novo assembly of individuals. LXIII Conv. Soc. Ital. Gen. Agraria, Napoli, 10-13 Sept.

Genome Sequencing Technology Assessment. The Future of Medicine Starts Now: how science and new technology are reshaping health science. Genova, 25-27 Sept.

Integration of multiple technologies for de-novo assembly of complex genomes. Joint Meeting AGI - SIMAG. Cortona (Ar) 26-28 Sept.

Medical genetics and genomics in IVF laboratory. 3rd Med Alpregio Congress 2019, Bolzano, 11-12 Oct.

Genomics goes (in the) wild: on site sequencing for biodiversity studies. International Conference on Bioinformatics, Montevideo, UY, 28-30 Oct.

The effect of fragment size on whole exome sequencing efficiency using Twist Target Capture kits. XXII Congresso Soc. Ital. Gen. Umana, Roma, 13-16 Nov.

(Im)precision genomics. ELIXIR INNOVATION AND SME FORUM. Data management in the life sciences - a driver for innovation. Milan, Ita, 27 - 28 Nov.

RESEARCH INTEREST

During the last 10 years, I had the opportunity to develop a vigorous research program that emphasizes interdisciplinary approaches to understanding the genome biology of living organisms.

In 2006 my lab participated to the sequencing of the *Vitis vinifera* and *Bifidobacterium dentium* genomes and, since then, performed an impressive number of microarray analyses of genome wide gene expression. The development of very high density microarrays led us to implement technologies for comparative genome hybridization, chromatin immunoprecipitation and sequence capture for targeted resequencing with 2nd generation sequencing technologies (NGS) that we adopted since they became available. As NGS has the ability to generate digital and quantitative information and to discover previously unknown genes, in 2008 we embraced gene expression analysis based on deep sequencing of the transcriptome (RNA-Seq). Since then, my lab has continued implementing and developing new wet-lab methodologies and bioinformatic pipelines for expression data analysis on genomic scales.

As the sequencing costs dropped, we begun involved in sequencing a number of bacterial, fungal and plant genomes. With surprise, we found that our experience on sequencing assembling and annotating the genome of "difficult" fungi and plants allowed us to smoothly approach human whole genome sequencing (WGS) and interpretation. Thanks to a lab composed by fantastic and enthusiastic people with different skills and very much different backgrounds (bioengineers, human and plant bioinformaticians, computer scientists, biotechnologists and geneticists), we are now taking full advantage of our understanding of the complexity of different living organisms. It's quite interesting to see how much it can be learned when in the same lab people work on bacteria, plants and humans. A striking example is the comparison of genetic diversity in plant and humans: due to the young age (~60.000 years), to the fact that population has rapidly increased in the last 200 years or so and to the continuous moving (and mating) of people all over the world, human genetic diversity is much limited compared to plants. *Vitis vinifera* for instance, like *Arabidopsis* and poplar, is a dicotyledonous plant that diverged from monocotyledons about 130–240 Myr ago. Being propagated asexually, each variety maintains a genetic diversity that goes beyond simple allele variation. The discovery that plant varieties/ecotypes can be characterized by sets of proprietary genes and not only by a proprietary combination of different alleles of the same set of genes (like humans do) required a tremendous effort, as we had to adapt technologies mainly developed for human genomics that are based on resequencing and that therefore do not allow to characterize what is lacking in the reference genome, forcing us to develop a "lateral thinking" approach that is now an integral component of each of our research projects.

De-novo assembly of complex genomes is currently performed with Illumina paired ends and mate pairs (we produce MP up to 20 kb long), Illumina combined with 10x genomics libraries and of course PacBio, both RSII and Sequel. We are also producing optical maps with BioNano

Genomics for pseudomolecules reconstruction and scaffold anchoring. Genome annotation is based on the extensive use of directional RNA-Seq data. We sequence whole human genomes (WGS) and exomes (WES) as well as plants, algae, fungi and bacteria genomes and transcriptomes with Illumina, and we perform targeted resequencing based on hybridization probes and amplicons. We also take advantage of long reads generated by PacBio and Oxford Nanopore.

Comparison of the different technologies available and testing of new emerging technologies for DNA sequencing and analysis is another integral part of our research studies. For example, we are deeply involved in bringing nanopore sequencing to maturity, and to improve its use in addressing the Darwinian shortfall in tropical countries by speeding up the organism's barcoding rate and comprehensive phylogenetic reconstruction, key components in the measurement of the values associated with the term biodiversity. Our mobile DNA sequencing laboratory was proven successful for sequencing in extreme field conditions, such as in the tropical rainforests of Tanzania, Congo and Borneo.

We are now part of Taxon Expedition, an organization which focuses on education and biodiversity discovery harnessing the power of citizen science, and the next goal is to train citizen scientists to sequence wild species in the field (our metabarcoding) on site sequencing.

PUBLICATIONS

Scopus statistics February 26th, 2020:

- h index: 54
- citations: 13794

Rank 20 among the Top Italian Scientists (via-academy.org)

1. Xu X., Dietrich C.R., Delledonne M., Xia Y., Wen T., Robertson D., Nikolau B., Schnable P. (1997). Sequence analysis of the cloned *glossy8* gene of maize suggests that it may code for a β -ketoacyl reductase required for the biosynthesis of cuticular waxes. **Plant Physiol.** 115:501-510.
2. Confalonieri M., Allegro G., Balestrazzi A., Fogher C. & Delledonne M. (1998). Regeneration of *Populus nigra* transgenic plants expressing a Kunitz proteinase inhibitor (*KTI₃*) gene. **Mol. Breed.** 4:137-145.
3. Delledonne M., Xia Y., Dixon R. and Lamb C. (1998). Nitric oxide functions as a signal in plant disease resistance. **Nature** 394:585-558.

4. Solomon M., Belenghi B., Delledonne M., Levine A. (1999) The involvement of cysteine proteases and protease inhibitor genes in the regulation of programmed cell death in plants. **Plant Cell** 11:431-443.
5. Tosca A., Delledonne M., Furini A., Belenghi B., Fogher C., Frangi P. (2000). Transformation of Korean chrysanthemum (*Dendranthema zawadskii* X *D. X grandiflorum*) and insertion of the maize autonomous element *Ac* using *Agrobacterium tumefaciens*. **J. Genetics and Breed.** 54: 19-24.
6. Confalonieri M., Belenghi B., Balestrazzi A., Negri S., Facciotto G., Schenone G., Delledonne M. (2000). Transformation of elite white poplar (*Populus alba* L.) cv. 'Villafranca' and evaluation of herbicide resistance. **Plant Cell Rep.** 19: 978-982
7. Marchetti S., Delledonne M., Fogher C., Chiabà C., Chiesa F., Savazzini F., Giordano A. (2000). Soybean Kunitz, C-II and Pi-IV inhibitor genes confer different levels of insect resistance to tobacco and potato transgenic plants. **Theor. Appl. Genet.** 101: 519-526
8. Delledonne M., Allegro G., Belenghi B., Balestrazzi A., Picco F., Levine A., Zelasco S., Calligari P., Confalonieri M. (2001) Transformation of white poplar (*Populus alba* L.) with a novel *Arabidopsis thaliana* cysteine proteinase inhibitor and analysis of insect pest resistance. **Mol. Breed.** 7: 35-42
9. Caccia R., Delledonne M., Levine A., De Pace C. and Mazzucato A. (2001). Apoptosis-like DNA fragmentation in leaves and floral organs precedes their developmental senescence. **Plant Biosystems** 135: 183-190
10. Delledonne M., Zeier J., Marocco A., Lamb C. (2001). Signal interactions between nitric oxide and reactive oxygen intermediates in the plant hypersensitive disease resistance response. **Proc. Natl. Acad. Sci. USA** 98:13454-13459
11. Delledonne M., Murgia I., Ederle D., Sbicego P.F., Biondani A., Polverari A., Lamb C. (2002). Reactive oxygen intermediates modulate nitric oxide signaling in the plant hypersensitive disease resistance response. **Plant Physiol. Biochem.** 40: 605-610
12. Murgia I., Delledonne M., Soave C. (2002). Nitric oxide mediates iron-induced ferritin accumulation in *Arabidopsis thaliana*. **Plant J.** 30: 521-528
13. Delledonne M., Polverari A., Murgia I. (2003). Nitric oxide-mediated signaling functions and change in genes expression during the plant hypersensitive response. **Antioxid. Redox Signal.** 5: 33-42
14. Belenghi B., Acconcia F., Trovato M., Perazzolli M., Bocedi A., Polticelli F., Ascenzi P., Delledonne M. (2003). AtCYS1, a cystatin from *Arabidopsis thaliana*, suppresses hypersensitive cell death. **Eur. J. Biochem.** 270: 2593-2604
15. Polverari A., Molesini B., Pezzotti M., Buonauro R., Marte M., Delledonne M. (2003). Nitric oxide-mediated transcriptional changes in *Arabidopsis thaliana*. **Mol. Plant-Microbe Interact.** 16: 1094-1105

16. Romero-Puertas M.C., Delledonne M. (2003). Nitric oxide signaling in plant-pathogens interaction. **IUBMB Life**. 55: 579-583
17. Murgia I., de Pinto M.C., Delledonne M., Soave C., De Gara L. (2004) Comparative effects of various nitric oxide donors on ferritin regulation, programmed cell death and cell redox state in plant cells. **J. Plant Physiol**. 161: 777-783.
18. Romero-Puertas M.C., Perazzolli M., Zago E., Delledonne M. (2004) Nitric oxide signaling functions in plant-pathogen interactions. **Cell. Microbiol**. 6: 795-803
19. Zeier J., Delledonne M., Severi E., Sonoda M., Lamb C. (2004) Genetic elucidation of nitric oxide signaling in incompatible plant-pathogen interactions. **Plant Physiol**. 136: 2875-2886.
20. Perazzolli M., Dominici P., Romero-Puertas M., Zago E., Zeier J., Sonoda M., Lamb C., Delledonne M. (2004) *Arabidopsis* non-symbiotic hemoglobin AHb1 modulates nitric oxide bioactivity. **Plant Cell** 16: 2785-2794.
21. Delledonne M. (2005) NO news is good news for plants. **Curr. Opin. Plant Biol**. 8: 390-396
22. Boccarda M., Mills C., Zeier J., Anzi C., Lamb C., Poole R., Delledonne M. (2005) Flavohaemoglobin HmpX from *Erwinia chrysanthemi* confers nitrosative stress tolerance and affects the plant hypersensitive reaction by intercepting nitric oxide produced by the host. **Plant J**. 43:226-237
23. Perazzolli M., Romero-Puertas M., Delledonne M. (2006). Modulation of nitric oxide bioactivity by plant haemoglobins. **J. Exp. Bot**. 57:479-488
24. Zaninotto F., La Camera S., Polverari A., Delledonne M. (2006). Cross-talk between reactive nitrogen and oxygen species during the hypersensitive disease resistance response. **Plant Physiol**. 141: 379-383
25. Zago E., Morsa S., Dat J.F., Alard P., Ferrarini A., Inzè D., Delledonne M., Van Breusegem F. (2006) Nitric oxide- and hydrogen peroxide-responsive gene regulation during cell death induction in tobacco. **Plant Physiol**. 141: 404-411
26. Belenghi B., Romero-Puertas M., Vercammen D., Brackener A., Inzé D., Delledonne M., Van Breusegem F. (2007). Metacaspase activity of *Arabidopsis thaliana* is regulated by S-nitrosylation of a critical cysteine residue. **J Biol. Chem**. 282: 1352-1358
27. Innocenti G, Pucciariello C, Le Gleuher M, Hopkins J, de Stefano M, Delledonne M, Puppo A, Baudouin E, Frendo P. (2007). Glutathione synthesis is regulated by nitric oxide in *Medicago truncatula* roots. **Planta** 225: 1597-1602
28. Jaillon O, Aury JM, Noel B, Policriti A, Clepet C, Casagrande A, Choisne N, Aubourg S, Vitulo N, Jubin C, Vezzi A, Legeai F, Huguency P, Dasilva C, Horner D, Mica E, Jublot D, Poulain J, Bruyère C, Billault A, Segurens B, Gouyvenoux M, Ugarte E, Cattonaro F, Anthouard V, Vico V, Del Fabbro C, Alaux M, Di Gaspero G, Dumas V, Felice N, Paillard S, Juman I, Moroldo M, Scalabrin S, Canaguier A, Le Clainche I, Malacrida G, Durand E, Pesole G, Laucou V, Chatelet P,

- Merdinoglu D, Delledonne M, Pezzotti M, Lecharny A, Scarpelli C, Artiguenave F, Pè ME, Valle G, Morgante M, Caboche M, Adam-Blondon AF, Weissenbach J, Quétier F, Wincker P. (2007). The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. **Nature** 449: 463-467
29. Romero-Puertas M.C., Laxa M., Mattè A., Zaninotto F., Finkemeier I., Jones A.M.E., Perazzolli M., Vandelle E., Dietz K.J., Delledonne M. (2007). S-nitrosylation of peroxiredoxin II E promotes peroxynitrite-mediated tyrosine nitration. **Plant Cell** 19: 4120-4130
30. Romero-Puertas M.C., Campostrini N., Mattè A., Righetti P.G., Perazzolli M., Zolla L., Roepstorff P., Delledonne M. (2008). Proteomic analysis of S-nitrosylated proteins in *Arabidopsis thaliana* undergoing hypersensitive response. **Proteomics** 8: 1459-1469
31. Ferrarini A., De Stefano M., Baudouin E., Pucciariello C., Polverari A., Puppo A., Delledonne M (2008). Expression of *Medicago truncatula* genes responsive to nitric oxide, in pathogenic and symbiotic conditions. **Mol. Plant-Microbe Interact.** 21: 781-790
32. Vandelle E. and Delledonne M. (2008). Methods for nitric oxide detection during plant-pathogen interactions. **Methods in Enzymol.** 437: 575-594
33. Haegi A., Bonardi V., dall'Aglio E., Glissant D., tumino G., Collins N., bulgarelli D., Infantino A., Stanca M., Delledonne M., Valè G. (2008) Histological and molecular analysis of Rdg2a barley 1 resistance to leaf stripe. **Mol. Plant Pathol.** 9: 463-478
34. Denoeud F., Aury JM., Da Silva C., Noel B., Rogier O., Delledonne M., Morgante M., Valle G., Wincker P., Scarpelli C., Jaillon O., Artiguenave F. (2008) Annotating genomes with massive-scale RNA-sequencing. **Genome Biology** 9: R175
35. Zamboni A., Minoia L., Ferrarini A., Tornielli G.B., Zago E., Delledonne M. and Pezzotti M. (2008) Molecular analysis of post-harvest withering in grape by AFLP transcriptional profiling. **J. Exp. Bot.** 59: 4145-4159
36. De Michele R., Formentin E., Todesco M., Toppo S., Carimi F., Zottini M., Barizza E., Ferrarini A., Delledonne M., Fontana P., Lo Schiavo F. (2009) Transcriptome analysis of *Medicago truncatula* leaf senescence: similarities and differences in metabolic and transcriptional regulations as compared to Arabidopsis, nodule senescence, and nitric oxide signalling. **New Phytol.** 181: 563-575
37. Omrane S., Ferrarini A., D'Apuzzo E., Rogato A, Delledonne M., Chiurazzi M. (2009) Nitrogen status and symbiotic competence, a transcriptomic analysis in *Lotus japonicus*. **New Phytol.** 183: 380-394
38. Cecconi D., Orzetti S., Vandelle E., Rinalducci S., Zolla L., Delledonne M. (2009) Protein nitration during defence response in *Arabidopsis thaliana*. **Electrophoresis** 14: 2460-2468
39. Leitner M., Vandelle E., Gaupels F., Bellin D., Delledonne M. (2009) NO signals in the haze. **Curr. Opin. Plant Biol.** 12: 451-458
40. Mica E., Piccolo V., Delledonne M., Ferrarini A., Pezzotti M., Casati C., Del Fabbro C., Valle G.,

- Policriti A., Morgante M., Pesole G., Pè M.E., Horner D.S. (2009). High throughput approaches reveal splicing of primary microRNA transcripts and tissue specific expression of mature microRNAs in *Vitis vinifera*. **BMC Genomics** 10: 558
41. Bellin D., Ferrarini A., Chimento A., Kaiser O., Levenkova N., Bouffard P., Delledonne M. (2009). Combining next-generation pyrosequencing with microarray for large scale expression analysis in non-model species. **BMC Genomics** 10: 555
42. Ventura M., Turrone F., Zomer A., Foroni E., Giubellini V., Bottacini F., Canchaya C., Claesson M.J., He F., Mantzourani M., Mulas L., Ferrarini A., Gao B., Delledonne M., Henrissat B., Coutinho P., Oggioni M., Gupta R.S., Zhang Z., Bighton D., Fitzgerald G.F., O'Toole P.W., van Sinderen D. (2009). The *Bifidobacterium dentium* Bd1 genome sequence reflects its genetic adaptation to the human oral cavity. **PLoS Genetics** 5 (12): e1000785
43. Polesani M., Bortesi L., Ferrarini A., Zamboni A., Fasoli M., Zadra C., Lovato A., Pezzotti M., Delledonne M., Polverari A. (2010). General and species-specific transcriptional responses to downy mildew infection in a susceptible (*Vitis vinifera*) and a resistant (*V. riparia*) grapevine species. **BMC Genomics** 11: 117
44. Zenoni S., Ferrarini A., Giacomelli E., Xumerle L., Fasoli M., Malerba G., Bellin D., Pezzotti M., Delledonne M. (2010). Characterization of transcriptional complexity during berry development in *Vitis vinifera* using RNA-Seq. **Plant Physiol** 152: 1787-1795
45. The International Cancer Genome Consortium. (2010). International network of cancer genome projects. **Nature** 464: 993-998
46. Turrone F., Foroni E., O'Connell Motherway M., Bottacini F., Giubellini V., Zomer A., Ferrarini A., Delledonne M., Zhang Z., van Sinderen D., Ventura M. (2010). Characterization of the serpin-encoding gene of *Bifidobacterium breve* 210B. **Appl. Environ. Microbiol.** 76: 3206-19
47. Zamboni A., Di Carli M., Guzzo F., Stocchero M., Zenoni S., Ferrarini A., Tononi P., Toffali K., Desiderio A., Lilley K., Pè E., Benvenuto E., Delledonne M., Pezzotti M. (2010). Identification of putative stage-specific grapevine berry biomarkers and omics data integration into networks. **Plant Physiol.** 154:1439-1459
48. De Matteo A., Sacco A., Anacleria M., Pezzotti M., Delledonne M., Ferrarini A., Frusciante L., Barone A. (2010). The ascorbic acid content of tomato fruits is associated with the expression of genes involved in pectin degradation. **BMC Plant Biology** 10: 163
49. Turrone F., Bottacini F., Foroni E., Mulder I., Kim J.H., Zomer A., Garcia B.S., Bidossi A., Ferrarini A., Giubellini V., Delledonne M., Henrissat B., Coutinho P., Oggioni M., Fitzgerald G.F., Mills D., Margolles A., Kelly D., van Sinderen D., Ventura M. (2010). Genome analysis of *Bifidobacterium bifidum* PRL2010 reveals metabolic pathways for host-derived glycan foraging. **Proc Natl Acad Sci. USA** 107: 19514–19519
50. Soverini S., Score J., Iacobucci I., Poerio A., Lonetti A., Gnani A., Colarossi S., Ferrari A., Castagnetti F., Rosti G., Cervantes F., Hochhaus A., Delledonne M., Ferrarini A., Sazzini M., Luiselli D., Baccharani M., Cross N.C., Martinelli G. (2011). IDH2 somatic mutations in chronic myeloid leukemia patients in blast crisis. **Leukemia** 25:178-181

51. Sestili S.I, Polverari A., Luongo L., Ferrarini A., Scotton M., Hussain J., Delledonne M., Ficcadenti N., Belisario A. (2011). Distinct colonization patterns and cDNA-AFLP transcriptome profiles in compatible and incompatible interactions between melon and different races of *Fusarium oxysporum* f. sp. *melonis*. **BMC Genomics** 12:122
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