

Massimo Delledonne

Professor of Genetics

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Born in Cortemaggiore, Piacenza, Italy, 17 February 1963

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 Dept. of Biotechnologies, University of Verona

APPOINTMENTS

- 2004-2012 Chair of the PhD Course in Applied Biotechnologies of University of Verona
- 2010-2016 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
- 2015-2018 Chair of the PhD Course in Biotechnologies of University of Verona
- 2015-2018 Director of the Core Facilities of University of Verona (<http://cpt.univr.it/>)
- 2019 - Member of the Working Group 4 “Good Genomic Practice”, 1+ Million Genomes Initiative
- 2021 - National delegate, Working Group 7 “Involvement of the private sector”, 1+ Million Genomes Initiative

TEACHING ACTIVITY

I currently teach Genetics (48 hrs, Degree in Biotechnology and Degree in Bioinformatics), Human Genomics and Epigenomics (48h Master in Medical Bioinformatics) and Human Genome Sequencing and Interpretation (48 hrs, Masters in Molecular 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). The company has been acquired by the SOL group (www.solgroup.com) in 2017
- 2014 Founder of Biodiversa SRL (www.biodiversa.it)
- 2019 Founder of Genartis SRL

HONOURS AND AWARDS

- 2003 EMBO Young Investigator
- 2008 Assunta Baccarini Melandri award from Italian Society of Plant Biology
- 2011 Antico Fattore award from Accademia dei 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)

- 2022 "Development of an integrated tool based on genetic, epigenetic and clinical analysis to optimize the diagnosis, prognosis and treatment of myotonic dystrophies (GEPINDM)" PNRR Malattie rare (c.a. 115.000 euro)
- 2021 "Innovative technologies to unravel the complexity of myotonic dystrophy repeats". Muscular Dystrophy Association USA. Idea Grant Program (25.000 \$)
RESO - RESilienza e SOstenibilità delle filiere ortofrutticole e cerealicole per valorizzare i territori. PON Agrifood (c.a. 65.000 euro)
- 2020 Garding – Gene barcoding: next generation pathogen identification . Lombardia Region (~ 550,000 €)
- 2019 JointProject 2018 – "CanGenome: The genome of Cangrande della Scala: DNA as historical source" (~ 25,000 €);
RiBa 2018 – "NEBBIOLO GENOMICS: structural and functional genomics to explain phenotypic and pathological features" (~ 50,000 €)
- 2018 PRIN (from Italian Ministry of University and Research) 2017 Sensaging (~ 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 H2020 project 689341-2 (~ 350,000 €)

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

- Advanced Course in Molecular Biology, Genova, 25 January 2018

INVITED SPEAKER (last 5 years)

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.

Integration of multiple technologies for de-novo genome assembly. 11th Annual Next Generation Sequencing & Clinical Diagnostics and 7th Annual Single Cell Analysis Congress, London, UK, 7-8 Nov.

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.

2020 *Characterization of long DNA regions by short and long reads*. Oxford Global Digital Workshop on Long and short read sequencing. NextGen Omics UK Series, 30 Sept.

Accurate genome reconstruction of Sars-Cov-2 for the analysis of intrahost and interhost viral populations. 12th Annual Next Generation Sequencing & Clinical Diagnostics Congress. Virtual, 4-6 Nov.

2021 *Sequencing (re)volution in genomics screening*. Meet in Italy for Life Sciences 2021. Genova, 29 Sept – 1 Oct.

Big data e analytics trasformeranno il Sistema Sanitario Nazionale. Forum PA Sanità. Virtual 27-28 Oct.

Cooperation of short and long reads in genome de novo assembly, targeted resequencing and transcript reconstruction. 13th Annual Next Generation Sequencing & Clinical Diagnostics Congress, London, UK, 4-5 Nov.

No fragments left behind: increased WES performance of the new Twist Bioscience Enrichment Protocol v2.0. XXIV Congresso Soc. Ital. Gen. Umana, Virtual, 17-19 Nov.

WES performance of Roche KAPA HyperExome. XXIV Congresso Soc. Ital. Gen. Umana, Virtual, 17-19 Nov.

2022 *No Fragment left behind - Performance Evaluation of the Twist Exome 2.0*. 11emes Assises de Genetique Humaine et Medicale, Rennes, F, 1-3 Feb.

Characterization of CNBP expansions in Myotonic Dystrophy type 2 patients using nanopore Cas9-targeted sequencing. AGBT General Meeting 2022, Orlando FL – USA (selected from posters)

Genomic technologies. NextGen Omics UK, Oxford Global. 14 June, virtual

De novo genome assembly across multiple species. Italian Society of Bioinformatics annual meeting, Verona, 24-27 June

Characterization of CNBP expansions in Myotonic Dystrophy type 2 patients by Cas9-enrichment and nanopore sequencing. American Society of Human Genetics 2022, Los Angeles, USA 25-29 October

On site sequencing for biodiversity studies. Philippine Symposium on Freshwater Biodiversity and Ecosystems (PSFBE) 2022, Manila, Philippine, 09-11 November

2023 *On-site racehorses whole genome sequencing with the P2 suggests a need for a horse pangenome*. Plant Animal Genome Conference 30, 13-17 January

High quality racehorses genome assemblies pave the way to the horse pangenome construction. Nanopore Day, Bologna 2023, 19 September

Le tecnologie NGS. Nuove sfide, prospettive e soluzioni nella diagnostica fitopatologica nel florovivaismo. Padova, 22 September

Sequencing (r)evolution. XXVI Convegno nazionale Società Italiana di Genetica Umana (SIGU) Rimini, 4-6 October

Le prospettive del sequenziamento in Italia. III Annual meeting rete IRCCS delle neuroscienze e della neuroriabilitazione. Roma, 30 November – 1 December

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 combined with Oxford Nanopore or PacBio (either CLR or HiFi) scaffolded with BioNano Genomics optical maps and then assembled in pseudomolecules by Hi-C. Genome annotation is based on the extensive use of directional RNA-Seq data, both Illumina and PacBio (Iso-Seq). We sequence whole human genomes (WGS) and exomes (WES) as well as plants, algae, fungi and bacteria. genomes and transcriptomes, and we perform targeted resequencing based on Cas-9 enrichment, hybridization probes and amplicons.

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 02, 2024:

- h index: 67
- citations: 20,402

PUBLICATIONS

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. Boccara 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., Inzé 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., Brackeiner 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, Hugueney 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., Beighton 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**

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., Baccarani 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
52. Gaupels F., Spiazzi-Vandelle E., Yang D., Delledonne M. (2011). Detection of peroxynitrite accumulation in *Arabidopsis thaliana* during the hypersensitive defense response. **Nitric Oxide** 25:222-228
53. Malacarne G, Vrhovsek U, Zulini L, Cestaro A, Stefanini M, Mattivi F, Delledonne M, Velasco R, Moser C. (2011) Resistance to *Plasmopara viticola* in a grapevine segregating population is associated with stilbenoid accumulation and with specific host transcriptional responses. **BMC Plant Biol.** 2011 11:114
54. Mele C., Iatropoulos P., Donadelli R., Calabria A., Maranta R., Cassis P., Buelli S., Tomasoni S., Piras R., Krendel M., Bettoni S., Morigi M., Delledonne M., Pecoraro C., Abbate I., Capobianchi M.R., Hildebrandt F., Otto E., Schaefer F., Macciardi F., Ozaltin F., Emre S., Ibsirlioglu T., Benigni A., Remuzzi G. and Noris M. (2011). MYO1E mutations and childhood familial focal segmental glomerulosclerosis. **New Engl J Med** 365:295-306
55. Zenoni S, D'Agostino N, Tornielli GB, Quattrocchio F, Chiusano ML, Koes R, Zethof J, Guzzo F, Delledonne M, Frusciante L, Gerats T, Pezzotti M. (2011). Revealing impaired pathways in the an11 mutant by high-throughput characterization of *Petunia axillaris* and *Petunia inflata* transcriptomes. **Plant J.** 68: 11-27
56. Turrone F, Foroni E, Serafini F, Viappiani A, Montanini B, Bottacini F, Ferrarini A, Bacchini PL, Rota C, Delledonne M, Ottonello S, van Sinderen D, Ventura M. (2011). Ability of *Bifidobacterium breve* to grow on different milk types: exploring milk metabolism through genome analysis. **Appl Environ Microbiol.** 77:7408-7417
57. Vandelle E., Delledonne M. (2011). Peroxynitrite formation in plants. **Plant Sci** 181: 534-539
58. Turrone F., Foroni E., Montanini B., Viappiani A., Strati F., Duranti S., Ferrarini A., Delledonne M., Ottonello S., van Sinderen D., Ventura M. (2011). Global genome transcription profiling of *Bifidobacterium bifidum* PRL2010 under in vitro conditions and identification of reference genes for quantitative Real-Time PCR. **Appl Environ Microbiol.** 77: 8578-8587
59. Iacobucci I., Ferrarini A., Sazzini M., Giacomelli E., Xumerle L., Lonetti A., Ferrari A., Papayannidis C., Malerba G., Luisella D., Boattini A., Garagnani P., Vitale A., Soverini S., Foà R., Baccarani M, Delledonne M., Martinelli G. (2012). Application of the Whole Transcriptome Shotgun Sequencing approach to the study of Philadelphia-Positive Acute Lymphoblastic Leukemia". **Blood Cancer J.** 2: e61

60. Abate F., Acquaviva A., Paciello G., Ficarra E., Ferrarini A., Delledonne M., Soverini S., Martinelli G, Macii E. (2012). Bellerophonotes: A RNA-Seq data analysis framework for chimeric transcript discovery based on accurate fusion model. **Bioinformatics** 28: 2114-2121
61. Bottacini F., Milani C., Turrone F., Sanchez B., Foroni E., Duranti S., Serafini F., Viappiani A., Strati F, Ferrarini A., Delledonne M., Henrissat B., Coutinho P., Fitzgerald G.F., Margolles A., van Sinderen D., Ventura M. (2012). *Bifidobacterium asteroides* PRL2011 genome analysis reveals clues for colonization of the insect gut. **PLoS One** 7: e44229
62. Fasoli M., Dal Santo S., Zenoni S., Tornielli GB, Farina L., Zmboni A., Porceddu A., Venturini L., Bicego M., Murino V., Ferrarini A., Delledonne M., Pezzotti M. (2012). The grapevine expression atlas reveals a deep transcriptome shift driving the entire plant into a maturation program. **Plant Cell** 24: 3489-3505
63. Bicego M., Lovato P., Perina A., Fasoli M., Delledonne M., Pezzotti M., Polverari A., Murino V. Investigating topic models' capabilities in expression microarray data classification. (2012) **IEEE/ACM Trans Comput Biol Bioinform.** 9: 1831-1836
64. Perazzolli M., Moretto M., Fontana P., Ferrarini A., Velasco R., Moser C., Delledonne M., Pertot I. (2012). Downy mildew resistance induced by *Trichoderma harzianum* T39 in susceptible grapevines partially mimics transcriptional changes of resistant genotypes. **BMC Genomics** 13: 660
65. Duranti S., Turrone F., Milani C., Foroni E., Bottacini F., Dal Bello F., Ferrarini A., Delledonne M., van Sinderen D., Ventura M. (2013). Exploration of genomic diversity and core genome of the *Bifidobacterium adolescentis* phylogenetic group by means of a polyphasic approach. **Appl Environ Microbiol.** 79: 336-46
66. Bellin D., Asai S., Delledonne M., Yoshioka H. (2013) Nitric Oxide as a Mediator for Defense Responses. **Mol Plant-Microbe Interact** 26: 271-277
67. Boscari A., del Giudice J., Ferrarini A., Venturini L., Zaffini A-L, Delledonne M., Puppo A. (2013). Expression dynamics of the *Medicago truncatula* transcriptome during the symbiotic interaction with *Sinorhizobium meliloti*: which role for nitric oxide? **Plant Physiol** 161: 425-439
68. Venturini L, Ferrarini A, Zenoni S, Tornielli GB, Fasoli M, Santo SD, Minio A, Buson G, Tononi P, Zago. Zamperin G., Bellin D., Pezzotti M., Delledonne M. (2013). De novo transcriptome characterization of *Vitis vinifera* cv. Corvina unveils varietal diversity. **BMC Genomics** 14: 41
69. Donà M., Confalonieri M., Minio A., Biggiogera M., Buttafava A., Raimondi E., Delledonne M., Ventura L., Sabatini M.E., Macovei A., Giraffa G., Carbonera D., Balestrazzi A. (2013). RNA-Seq analysis discloses early senescence and nucleolar dysfunction triggered by *Tdp1α* depletion in *Medicago truncatula*. **J. Exp. Bot.** 64: 1941-1951
70. Dal Santo S., Tornielli G., Zenoni S., Fasoli M., Farina L., Anesi A., Guzzo F., Delledonne M., Pezzotti M. (2013). The plasticity of the grapevine berry transcriptome. **Genome Biol.** 14: R54
71. Garagnani P., Giuliani C., Pirazzini C., Olivieri F., Bacalini M.G., Ostan R., Mari D., Passarino G., Monti D., Bonfigli A.R.O, Boemi M., Ceriallo A., Genovese S., Sevini F., Luiselli D., Tieri P., Capri

- M., Salvioli S., Vijg J., Suh Y., Delledonne M., Testa R., Franceschi C. (2013). Centenarians as super-controls to assess the biological relevance of genetic risk factors for common age-related diseases: A proof of principle on type 2 diabetes. **Aging** 5: 373-385
72. Correa-Aragunde N., Foresi N., Delledonne M., Lamattina L. (2013). Auxin induces redox regulation of ascorbate peroxidase 1 activity by S-nitrosylation/denitrosylation balance resulting in changes of root growth pattern in *Arabidopsis*. **J. Exp. Bot.** 64: 3339-3349
 73. Turrone F., Serafini F., Foroni E., Duranti S., O'Connell Motherway M., Taverniti V., Mangifesta M., Milani C., Viappiani A., Roversi T., Sánchez B., Santoni A., Gioiosa L., Ferrarini A., Delledonne M., Margolles A., Piazza L., Palanza P., Bolchi A., Guglielmetti S., van Sinderen D., Ventura M. (2013). The role of sortase-dependent pili of *Bifidobacterium bifidum* PRL2010 in modulating bacterium-host interactions. **Proc Natl Acad Sci. USA** 110: 11151-11156
 74. Landoni M., De Francesco A., Bellatti S., Delledonne M., Ferrarini A., Venturini L., Pili R., Bononi M., Tonelli C. (2013). A mutation in the *FZL* gene of *Arabidopsis* causing alteration in chloroplast morphology results in a lesion mimic phenotype. **J. Exp. Bot.** 64: 4313-4328
 75. Storci G., Bertoni S., De Carolis S., Papi A., Nati M., Ceccarelli C., Pirazzini C., Garagnani P., Ferrarini A., Buson G., Delledonne M., Fiorentino M., Capizzi E., Gruppioni E., Taffurelli M., Santini D., Franceschi C., Bandini G., Bonifazi F., Bonafé M. (2013). Slug/beta-catenin-dependent DNA damage signalling induces pro-inflammatory phenotype in hypoxic breast cancer stem cells. **Am J Pathol.** 183: 1688-1697
 76. Licciardello C., Torrisi B., Allegra M., Sciacca F., Roccuzzo G., Intrigliolo F., Reforgiato Recupero G., Tononi P., Delledonne M., Muccilli V. (2013). A Transcriptomic Analysis of Sensitive and Tolerant Citrus Rootstocks under Natural Iron Deficiency Conditions. **J. Amer. Soc. Hort. Sci.** 138: 487-498
 77. de Pinto M.C., Locato V., Sgobba A., Romero-Puertas M.D., Gadadeta C., Delledonne M., De Gara L. (2013). S-nitrosylation of ascorbate peroxidase is part of the programmed cell death signaling in tobacco BY-2 cells. **Plant Physiol** 163: 1766-1775
 78. Da Silva C., Zamperin G., Ferrarini A., Minio A., Dal Molin A., Venturini L., Buson G., Tononi P., Avanzato C., Zago E., Boido E., Dellacassa E., Gaggero C., Pezzotti M., Carrau F., Delledonne M. (2013). The high polyphenol content of *Vitis vinifera* cv. Tannat berries is conferred mostly by genes that are not shared with the reference genome. **Plant Cell** 25: 4777-4788
 79. Gauthier A., Trouvelot S., Kelloniemi J., Frettinger P., Wendehenne D., Daire X., Joubert J-M., Ferrarini A., Delledonne M., Flors V., Poinssot B. (2014). The sulfated laminarin triggers a stress transcriptome before priming the SA- and ROS-dependent defenses during grapevine's induced resistance against *Plasmopara viticola*. **PLoS ONE** 9: e88145
 80. Ercolano M.R., Sacco A., Ferriello F., D'Alessandro R., Tononi P., Traini A., Barone A., Zago E., Chiusano M.L., Buson G., Delledonne M., Frusciante L. (2014). Patchwork sequencing of tomato San Marzano and Vesuviano varieties highlights genome-wide variations. **BMC Genomics** 15: 138
 81. Garagnani P., Pirazzini C., Giuliani C., Candela M., Brigidi P., Sevin F., Luiselli D., Bacalini M.G., Salvioli S., Capri M., Monti D., Mari D., Collino S., Delledonne M., Descombes P., Franceschi C. (2014). The three genetics (nuclear DNA, mitochondrial DNA and gut microbiome) of longevity in humans considered as metaorganisms. **BioMed Res Int** 2014: 560340
 82. Aragona M., Minio A., Ferrarini A., Valente M.T., 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

83. Bellucci E., Bitocchi E., Ferrarini A., Benazzo A., Biagetti E., Klie S., Minio A., Rau D., Rodriguez M., Panziera A., Venturini L., Attene G., Albertini E., Jackson S.A., Nanni L., Fernie A.R., Nikoloski Z., Bertorelle G., Delledonne M., Papa R. (2014). Decreased Nucleotide and Expression Diversity and Modified Coexpression Patterns Characterize Domestication in the Common Bean. **Plant Cell** 26: 1901–1912
84. Chen J., Vandelle E., Bellin D., Delledonne M. (2014). Detection and function of nitric oxide during the hypersensitive response in *Arabidopsis thaliana*: Where there's a will there's a way. **Nitric Oxide** 43: 81-88
85. Bulgari D., Minio A., Casati P., Quaglino F., Delledonne M., Bianco PA. (2014). *Curtobacterium* sp. genome sequencing underlines plant growth promotion-related traits. *Genome Announc.* e00592-14
86. Lanubile A., Ferrarini A., Maschietto V., Delledonne M., Marocco A., Bellin D. (2014). Functional genomic analysis of constitutive and inducible defense responses to *Fusarium verticillioides* infection in maize genotypes with contrasting ear rot resistance. **BMC Genomics**. 15:710
87. Degu A., Hochberg U., Sikron N., Venturini L., Buson G., Ghan R., Plaschkes I., Batushansky A., Chalifa-Caspi V., Mattivi F., Delledonne M., Pezzotti M., Rachmilevitch S., Cramer G.R., Fait A. (2014). Metabolite and transcript profiling of berry skin during fruit development elucidates differential regulation between Cabernet Sauvignon and Shiraz cultivars at branching points in the polyphenol pathway. **BMC Plant Biol.** 14: 188
88. Cramer G.R., Ghan R., Schlauch K.A., Tillett R.L., Heymann H., Ferrarini A., Delledonne M., Zenoni S., Fasoli M., Pezzotti M. (2014). Transcriptomic analysis of the late stages of grapevine (*Vitis vinifera* cv. Cabernet Sauvignon) berry ripening reveals significant induction of ethylene signaling and flavor pathways in the skin. **BMC Plant Biology** 2014, 14:370
89. Siozios S., Tosi L., Ferrarini A., Ferrari A., Tononi P., Bellin D., Gessler C., Maurhofer M., Delledonne M., Pertot I. (2015). Transcriptional reprogramming of the mycoparasitic fungus *Ampelomyces quisqualis* during the powdery mildew host-induced germination. **Phytopathology** 105: 199-209
90. Venturini L., Delledonne M. (2015). Symbiotic plant-fungi interactions stripped down to the root. **Nat Genet.** 2015 47: 309-310
91. Udali S., Guarini P., Ruzzenente A., Ferrarini A., Guglielmi A., Lotto V., Tononi P., Pattini P., Moruzzi S., Campagnaro T., Conci S., Olivieri O., Corrocher R., Delledonne M., Choi S., Friso S. (2015). DNA methylation and gene expression profiles show novel regulatory pathways in hepatocellular carcinoma. **Clinical Epigenetics** 7: 43
92. Moliterni VM., Paris R., Onofri C., Orrù L., Cattivelli L., Pacifico D., Avanzato C., Ferrarini A., Delledonne M., Mandolino G. (2015). Early transcriptional changes in *Beta vulgaris* in response to low temperature. **Planta**. 242: 187-201
93. Aversano R., Contaldi F., Ercolano M.R., Grosso V., Iorizzo M., Tatino F., Xumerle L., Dal Molin A., Avanzato C., Ferrarini A., Delledonne M., Sanseverino W., Aiese Cigliano R., Capella-Gutierrez S., Gabaldón T., Frusciante L., Bradeen J.M., Carputo D. (2015). *The Solanum commersonii* Genome Sequence Provides Insights into Adaptation to Stress Conditions and Genome Evolution of Wild Potato Relatives. **Plant Cell** 7: 954–968
94. Ferrarini A., Xumerle L., Griggio F., Garonzi M., Cantaloni C., Centomo C., Vargas SM., Descombes P., Marquis J., Collino S., Franceschi C., Garagnani P., Salisbury BA., Harvey JM., Delledonne M. (2015). The Use of Non-Variant Sites to Improve the Clinical Assessment of Whole-Genome Sequence Data. **PLoS One** 10:e0132180

95. Bartoletti-Stella A., Chiaro G., Calandra-Buonaura G., Contin M., Scaglione C., Barletta G., Cecere A., Garagnani P., Tieri P., Ferrarini A., Piras S., Franceschi C., Delledonne M., Cortelli P., Capellari S. (2015). A patient with *PMP22*-related hereditary neuropathy and *DBH*-gene-related dysautonomia. **J Neurol.** 262:2373-2381
96. Raggi S., Ferrarini A., Delledonne M., Dunand C., Ranocha P., De Lorenzo G., Cervone F., Ferrari S. (2015). The *Arabidopsis thaliana* Class III Peroxidase *AtPRX71* Negatively Regulates Growth under Physiological Conditions and in Response to Cell Wall Damage. **Plant Physiol.** 169: 2513-2525
97. Barabaschi D., Magni F., Volante A., Gadaleta A., Šimková H., Scalabrin S., Prazzoli M. L., Bagnaresi P., Lacrima K., Michelotti V., Desiderio F., Orrù L., Mazzamurro V., Fricano A., Mastrangelo A., Tononi P., Vitulo N., Jurman I., Frenkel Z., Cattonaro F., Morgante M., Blanco A., Doležel J., Delledonne M., Stanca A. M., Cattivelli L., Valè G. (2015). Physical Mapping of Bread Wheat Chromosome 5A: An Integrated Approach. **Plant Genome**, vol. 8, no. 3: 1-24
98. Horvath S., Pirazzini C., Bacalini M.G., Gentilini D., Di Blasio A.M., Delledonne M., Mari D., Arosio B., Monti D., Passarino G., De Rango F., D'Aquila P., Giuliani C., Marasco E., Collino S., Descombes P., Garagnani P., Franceschi C. (2015). Decreased epigenetic age of PBMCs from Italian semi-supercentenarians and their offspring. **Aging** 7:1159-1170
99. Sabatini ME, Donà M, Leonetti P, Minio A, Delledonne M, Carbonera D, Confalonieri M, Giraffa G, Balestrazzi A. (2016). Depletion of tyrosyl-DNA phosphodiesterase 1 α (MtTdp1 α) affects transposon expression in *Medicago truncatula*. **J Integr Plant Biol.** 58:618-622
100. Badar S., Busti F., Ferrarini A., Xumerle L., Bozzini P., Capelli P., Pozzi-Mucelli R., Campostrini N., De Matteis G., Marin Vargas S., Giorgetti A., Delledonne M., Olivieri O., Girelli D. (2016). Identification of novel mutations in hemochromatosis genes by targeted next generation sequencing in Italian patients with unexplained iron overload. **Am J Hematol.** 91: 420-425
101. Bassi D., Colla F., Gazzola S., Puglisi E., Delledonne M., Cocconcelli PS. (2016). Transcriptome analysis of *Bacillus thuringiensis* spore life, germination and cell outgrowth in a vegetable-based food model. **Food Microbiol.** 55: 73-85
102. Turroni F., Milani C., Duranti S., Mancabelli L., Mangifesta M., Viappiani A., Lugli G.A., Ferrario C., Gioiosa L., Ferrarini A., Li J., Palanza P., Delledonne M., van Sinderen D., Ventura M. (2016). Deciphering bifidobacterial-mediated metabolic interactions and their impact on gut microbiota by a multi-omics approach. **ISME J.** 10:1656-1668
103. Delaney S.K., Hultner M.L., Jacob H.J., Ledbetter D.H., McCarthy J.J., Ball M., Beckman K.B., Belmont J.W., Bloss C.S., Christman M.F., Cosgrove A., Damiani S.A., Danis T., Delledonne M., Dougherty M.J., Dudley J.T., Faucett W.A., Friedman J.R., Haase D.H., Hays T.S., Heilsberg S., Huber J., Kaminsky L., Ledbetter N., Lee W.H., Levin E., Libiger O., Linderman M., Love R.L., Magnus D.C., Martland A., McClure S.L., Megill S.E., Messier H., Nussbaum R.L., Palaniappan L., Patay B.A., Popovich B.W., Quackenbush J., Savant M.J., Su M.M., Terry S.F., Tucker S., Wong W.T., Green R.C. (2016). Toward clinical genomics in everyday medicine: perspectives and recommendations. **Expert Rev Mol Diagn.** 16: 521-532
104. Bellin D., Delledonne M., Vandelle E. (2016). Detection of Peroxynitrite in Plants Exposed to Bacterial Infection. **Methods Mol Biol.** 1424: 191-200
105. Bombarely A., Moser M., Amrad A., Bao M., Bapaume L., Barry C.S., Bliet M., Boersma M.R., Borghi L., Bruggmann R., Bucher M., D'Agostino N., Davies K., Druege U., Dudareva N., Egea-Cortines M., Delledonne M., Fernandez-Pozo N., Franken P., Grandont L., Heslop-Harrison

- J.S., Hintzsche J., Johns M., Koes R., Lv X., Lyons E., Malla D., Martinoia .E, Mattson N.S., Morel P., Mueller L.A., Muhlemann J., Nouri E., Passeri V., Pezzotti M., Qi Q., Reinhardt D., Rich M., Richert-Pöggeler K.R., Robbins T.P., Schatz M.C., Schranz M.E., Schuurink R.C., Schwarzacher T., Spelt K., Tang H., Urbanus S.L., Vandenbussche M., Vijverberg K., Villarino G.H., Warner R.M., Weiss J., Yue Z., Zethof J., Quattrocchio F., Sims T.L., Kuhlemeier C. (2016). Insight into the evolution of the Solanaceae from the parental genomes of *Petunia hybrida*. **Nature Plants**. 2: 16074
106. Pezzini F., Bettinetti L., Di Leva F., Bianchi M., Zoratti E., Carrozzo R., Santorelli F.M., Delledonne M., Lalowski M., Simonati A. (2016). Transcriptomic Profiling Discloses Molecular and Cellular Events Related to Neuronal Differentiation in SH-SY5Y Neuroblastoma Cells. **Cell Mol Neurobiol**. 37: 665-668
 107. Ferbo L., Manzini P.M., Badar S., Campostrini N., Ferrarini A., Delledonne M., Francisci T., Tassi V., Valfrè A., Dall'omo A.M., D'antico S., Girelli D., Roetto A., De Gobbi M. (2016) Detection of a rare mutation in the ferroportin gene through targeted next generation sequencing. **Blood Transfus**. 14: 531-534
 108. Tadiello A., Longhi S., Moretto M., Ferrarini A., Tononi P., Farneti B., Busatto N., Vrhovsek U., Dal Molin A., Avanzato C., Biasioli F., Cappellin L., Scholz M., Velasco R., Trainotti L., Delledonne M., Costa F. (2016). Interference with ethylene perception at receptor level sheds light on auxin and transcriptional circuits associated with climacteric ripening of apple fruit (*Malus x domestica* Borkh.). **The Plant Journal** 88: 963-975
 109. Chin C.S., Peluso P., Sedlazeck F.J., Nattestad M., Concepcion G.T., Clum A., Dunn C., O'Malley R., Figueroa-Balderas R., Morales-Cruz A., Cramer G.R., Delledonne M., Luo C., Ecker J.R., Cantu D., Rank D.R., Schatz M.C. (2016). Phased diploid genome assembly with single-molecule real-time sequencing. **Nat Methods**. 13: 1050-1054.
 110. do Valle Í.F., Giampieri E., Simonetti G., Padella A., Manfrini M., Ferrari A., Papayannidis C., Zironi I., Garonzi M., Bernardi S., Delledonne M., Martinelli G., Remondini D., Castellani G. (2016) Optimized pipeline of MuTect and GATK tools to improve the detection of somatic single nucleotide polymorphisms in whole-exome sequencing data. **BMC Bioinformatics**. 17: 341.
 111. Gagliardi S., Ricca I., Ferrarini A., Valente M., Grieco G.S., Piccolo G., Alfonsi E., Delledonne M., Cereda C. (2017) Palmoplantar Keratoderma and Charcot-Marie-Tooth: combination of two independent genetic diseases? Identification of two point mutations in CMT2 and PPK genes by whole exome sequencing. **Br J Dermatol**. 177(1):284-286
 112. Kumar A., Castellano I., Patti F.P., Delledonne M., Abdelgawad H., Beemster G.T.S., Asard H., Palumbo A., Buia M.C. (2017) Molecular response of *Sargassum vulgare* to acidification at volcanic CO₂ vents: insights from de novo transcriptomic analysis. **Mol Ecol**. 26: 2276-2290
 113. D'Esposito D., Ferriello F., Molin A.D., Diretto G., Sacco A., Minio A., Barone A., Di Monaco R., Cavella S., Tardella L., Giuliano G., Delledonne M., Frusciante L., Ercolano M.R. (2017) Unraveling the complexity of transcriptomic, metabolomic and quality environmental response of tomato fruit. **BMC Plant Biol**. 17: 66
 114. Giuliani C., Pirazzini C., Delledonne M., Xumerle L., Descombes P., Marquis J., Mengozzi G., Monti D., Bellizzi D., Passarino G., Luiselli D., Franceschi C., Garagnani P. (2017) Centenarians as extreme phenotypes: An ecological perspective to get insight into the relationship between the genetics of longevity and age-associated diseases. **Mech Ageing Dev**. 165(Pt B):195-201
 115. Piubelli C., Castagna A., Marchi G., Rizzi M., Busti F., Badar S., Marchetti M., De Gobbi M.,

- Roetto A., Xumerle L., Suku E., Giorgetti A., Delledonne M., Olivieri O., Girelli D. (2017) Identification of new BMP6 pro-peptide mutations in patients with iron overload. **Am J Hematol.** 92(6):562-568
116. Menegon M., Cantaloni C., Rodriguez-Prieto A., Centomo C., Abdelfattah A., Rossato M., Bernardi M., Xumerle L., Loader S., Delledonne M. (2017). On site DNA barcoding by nanopore sequencing. **PLoS One.** 12(10):e0184741.
 117. Pezzini F., Bianchi M., Benfatto S., Griggio F., Doccini S., Carrozzo R., Dapkunas A., Delledonne M., Santorelli F.M., Lalowski M.M., Simonati A. (2017). The Networks of Genes Encoding Palmitoylated Proteins in Axonal and Synaptic Compartments Are Affected in PPT1 Overexpressing Neuronal-Like Cells. **Front Mol Neurosci.** 10: 266.
 118. Whittaker A.C., Delledonne M., Finni T., Garagnani P., Greig C., Kallen V., Kokko K., Lord J., Maier A.B., Meskers C.G.M., Santos N.C., Sipila S., Thompson J.L., van Riel N. (2017). Physical Activity and Nutrition INfluences In ageing (PANINI): consortium mission statement. **Aging Clin Exp Res.** 6:685-692. doi: 10.1007/s40520-017-0823-7
 119. Di Donato A., Andolfo G., Ferrarini A., Delledonne M., Ercolano M.R. (2017). Investigation of orthologous pathogen recognition gene-rich regions in solanaceous species. **Genome.** 60: 850-859.
 120. Chitarra W., Perrone I., Avanzato C.G., Minio A., Boccacci P., Santini D., Gilardi G., Siciliano I., Gullino M.L., Delledonne M., Mannini F., Gambino G. (2017). Grapevine Grafting: Scion Transcript Profiling and Defense-Related Metabolites Induced by Rootstocks. **Front Plant Sci.** 8: 654
 121. Ling T, Bellin D, Vandelle E, Imanifard Z, Delledonne M. (2017). Host-Mediated S-Nitrosylation Disarms the Bacterial Effector HopAI1 to Reestablish Immunity. **Plant Cell** 11:2871-2881
 122. Gambino G, Dal Molin A, Boccacci P, Minio A, Chitarra W, Avanzato CG, Tononi P, Perrone I, Raimondi S, Schneider A, Pezzotti M, Mannini F, Gribaudo I, Delledonne M. (2017). Whole-genome sequencing and SNV genotyping of 'Nebbiolo' (*Vitis vinifera* L.) clones. **Sci Rep.** Dec 11;7(1):17294. doi: 10.1038/s41598-017-17405-y.
 123. Martinelli G., Mancini M., De Benedittis C., Rondoni M., Papayannidis C., Manfrini M., Meggendorfer M., Calogero R., Guadagnuolo V., Fontana M.C., Bavaro L., Padella A., Zago E., Pagano L., Zanotti R., Scaffidi L., Specchia G., Albano F., Merante S., Elena C., Savini P., Gangemi D., Tosi P., Ciceri F., Poletti G., Riccioni L., Morigi F., Delledonne M., Haferlach T., Cavo M., Valent P., Soverini S. (2018). SETD2 and histone H3 lysine 36 methylation deficiency in advanced systemic mastocytosis. **Leukemia** 32: 139-148
 124. Busatto N., Farneti B., Commisso M., Bianconi M., Iadarola B., Zago E., Ruperti B., Spinelli F., Zanella A., Velasco R., Ferrarini A., Chitarrini G., Vrhovsek U., Delledonne M., Guzzo F., Costa G., Costa F. (2018). Apple fruit superficial scald resistance mediated by ethylene inhibition is associated with diverse metabolic processes. **Plant J.** 93: 270-285
 125. Dal Molin A, Minio A, Griggio F, Delledonne M, Infantino A, Aragona M. (2018). The genome assembly of the fungal pathogen *Pyrenochaeta lycopersici* from Single-Molecule Real-Time sequencing sheds new light on its biological complexity. **PLoS One** Jul 6;13(7):e0200217. doi: 10.1371/journal.pone.0200217. eCollection 2018.
 126. Remo A, Manfrin E, Parcesepe P, Ferrarini A, Han HS, Mickys U, Laudanna C, Simbolo M, Malanga D, Mendes Oliveira D, Baritono E, Colangelo T, Sabatino L, Giuliani J, Molinari E, Garonzi M, Xumerle L, Delledonne M, Giordano G, Ghimenton C, Lonardo F, D'angelo F, Grillo

- F, Mastracci L, Viglietto G, Ceccarelli M, Colantuoni V, Scarpa A, Pancione M. (2018). Centrosome Linker-induced Tetraploid Segregation Errors Link Rhabdoid Phenotypes and Lethal Colorectal Cancers. **Mol Cancer Res.** doi: 10.1158/1541-7786.MCR-18-0062.
127. Kamga PT, Dal Collo G, Bassi G, Midolo M, Delledonne M, Chilosi M, Bonifacio M, Krampera M. (2018). Characterization of a new B-ALL cell line with constitutional defect of the Notch signaling pathway. **Oncotarget** 9(26):18341-18350. doi: 10.18632/oncotarget.24836. eCollection 2018 Apr 6.
 128. Cecchin M, Benfatto S, Griggio F, Mori A, Cazzaniga S, Vitulo N, Delledonne M, Ballottari M. (2018). Molecular basis of autotrophic vs mixotrophic growth in *Chlorella sorokiniana*. **Sci Rep.** 8(1):6465. doi: 10.1038/s41598-018-24979-8.
 129. Kurtas N, Arrigoni F, Errichiello E, Zucca C, Maghini C, D'Angelo MG, Beri S, Giorda R, Bertuzzo S, Delledonne M, Xumerle L, Rossato M, Zuffardi O, Bonaglia MC. (2018). Chromothripsis and ring chromosome 22: a paradigm of genomic complexity in the Phelan-McDermid syndrome (22q13 deletion syndrome). **J Med Genet.** 55(4):269-277. doi: 10.1136/jmedgenet-2017-105125.
 130. Errichiello E, Gorgone C, Giuliano L, Iadarola B, Cosentino E, Rossato M, Kurtas NE, Delledonne M, Mattina T, Zuffardi O. (2018). SOX2: Not always eye malformations. Severe genital but no major ocular anomalies in a female patient with the recurrent c.70del20 variant. **Eur J Med Genet.** 61(6):335-340. doi: 10.1016/j.ejmg.2018.01.011.
 131. Passera A, Marcolungo L, Casati P, Brasca M, Quagliano F, Cantaloni C, Delledonne M. (2018). Hybrid genome assembly and annotation of *Paenibacillus pasadenensis* strain R16 reveals insights on endophytic life style and antifungal activity. **PLoS One.** 2018 Jan 19;13(1):e0189993. doi: 10.1371/journal.pone.0189993.
 132. Papaiani M, Contaldi F, Fulgione A, Woo SL, Casillo A, Corsaro MM, Parrilli E, Marcolungo L, Rossato M, Delledonne M, Garonzi M, Iannelli D, Capparelli R. (2018). Role of phage $\phi 1$ in two strains of *Salmonella Rissen*, sensitive and resistant to phage $\phi 1$. **BMC Microbiol.** 2018 Dec 7;18(1):208. doi: 10.1186/s12866-018-1360-z.
 133. Kurtas NE, Xumerle L, Leonardelli L, Delledonne M, Brusco A, Chrzanowska K, Schinzel A, Larizza D, Gueneri S, Natacci F, Bonaglia MC, Reho P, Manolakos E, Mattina T, Soli F, Provenzano A, Al-Rikabi AH, Errichiello E, Nazaryan-Petersen L, Giglio S, Tommerup N, Liehr T, Zuffardi O. (2019). Small supernumerary marker chromosomes: A legacy of trisomy rescue? **Hum Mutat.** 40(2):193-200
 134. Kurtas NE, Xumerle L, Giussani U, Pansa A, Cardarelli L, Bertini V, Valetto A, Liehr T, Clara Bonaglia M, Errichiello E, Delledonne M, Zuffardi O. (2019). Insertional translocation involving an additional nonchromothriptic chromosome in constitutional chromothripsis: Rule or exception? **Mol Genet Genomic Med.** Feb; 7(2): e00496
 135. Busatto N, Farneti B, Tadiello A, Oberkofler V, Cellini A, Biasioli F, Delledonne M, Cestaro A, Noutsos C, Costa F. (2019). Wide transcriptional investigation unravel novel insights of the on-tree maturation and postharvest ripening of 'Abate Fetel' pear fruit. **Hortic Res.** 6: 32
 136. Rau D, Murgia ML, Rodriguez M, Bitocchi E, Bellucci E, Fois D, Albani D, Nanni L, Gioia T, Santo D, Marcolungo L, Delledonne M, Attene G, Papa R. (2019). Genomic dissection of pod shattering in common bean: mutations at non-orthologous loci at the basis of convergent phenotypic evolution under domestication of leguminous species. **Plant J.** 97(4):693-714
 137. Licciardello C, Tononi P, Rossato M, Delledonne M, Caruso P. (2019) A transcriptional analysis reveals an extensive range of genes responsible for increasing the tolerance of Carrizo

138. Maestri S, Cosentino E, Paterno M, Freitag H, Garces JM, Marcolungo L, Alfano M, Njunjić I, Schilthuizen M, Slik F, Menegon M, Rossato M, Delledonne M. (2019). A Rapid and Accurate MinION-Based Workflow for Tracking Species Biodiversity in the Field. **Genes** Jun 20;10(6)
139. Passera A, Compant S, Casati P, Maturo MG, Battelli G, Quaglino F, Antonielli L, Salerno D, Brasca M, Toffolatti SL, Mantegazza F, Delledonne M, Mitter B. (2019). Not Just a Pathogen? Description of a Plant-Beneficial *Pseudomonas syringae* Strain. **Front Microbiol.** Jun 21;10:1409.
140. Barchi L, Pietrella M, Venturini L, Minio A, Toppino L, Acquadro A, Andolfo G, Aprea G, Avanzato C, Bassolino L, Comino C, Molin AD, Ferrarini A, Maor LC, Portis E, Reyes-Chin-Wo S, Rinaldi R, Sala T, Scaglione D, Sonawane P, Tononi P, Almekias-Siegl E, Zago E, Ercolano MR, Aharoni A, Delledonne M, Giuliano G, Lanteri S, Rotino GL. (2019). A chromosome-anchored eggplant genome sequence reveals key events in Solanaceae evolution. **Sci Rep.** Aug 13;9(1):11769. (co-corresponding)
141. Morani F, Doccini S, Sirica R, Paterno M, Pezzini F, Ricca I, Simonati A, Delledonne M, Santorelli FM. (2019). Functional Transcriptome Analysis in ARSACS KO Cell Model Reveals a Role of Sacs in Autophagy. **Sci Rep.** Aug 15;9(1):11878
142. Cecchin M, Marcolungo L, Rossato M, Girolomoni L, Cosentino E, Cuine S, Li-Beisson Y, Delledonne M, Ballottari M. (2019). *Chlorella vulgaris* genome assembly and annotation reveals the molecular basis for metabolic acclimation to high light conditions. **Plant J.** 100(6):1289-1305
143. Corbett MA, Kroes T, Veneziano L, Bennett MF, Florian R, Schneider AL, Coppola A, Licchetta L, Franceschetti S, Suppa A, Wenger A, Mei D, Pendziwiat M, Kaya S, Delledonne M, Straussberg R, Xumerle L, Regan B, Crompton D, van Rootselaar AF, Correll A, Catford R, Bisulli F, Chakraborty S, Baldassari S, Tinuper P, Barton K, Carswell S, Smith M, Berardelli A, Carroll R, Gardner A, Friend KL, Blatt I, Iacomino M, Di Bonaventura C, Striano S, Buratti J, Keren B, Nava C, Forlani S, Rudolf G, Hirsch E, Leguern E, Labauge P, Balestrini S, Sander JW, Afawi Z, Helbig I, Ishiura H, Tsuji S, Sisodiya SM, Casari G, Sadleir LG, van Coller R, Tijssen MAJ, Klein KM, van den Maagdenberg AMJM, Zara F, Guerrini R, Berkovic SF, Pippucci T, Canafoglia L, Bahlo M, Striano P, Scheffer IE, Brancati F, Depienne C, Gecz J. (2019). Intronic ATTTC repeat expansions in STARD7 in familial adult myoclonic epilepsy linked to chromosome 2. **Nat Commun.** Oct 29; 10(1): 4920.
144. Freitag H, Molls C, Bouma AM, Garces JM, Rossato M, Cosentino E, Delledonne M. (2019). Additional new species of *Grouvellinus* Champion 1923 (Insecta, Coleoptera, Elmidae) discovered by citizen scientists and DNA barcoded in the field applying a novel MinION-based workflow, **Journal of Natural History**, 53:41-42, 2593-2620, DOI: 10.1080/00222933.2019.1709669
145. Pagliarini C, Boccacci P, Chitarra W, Cosentino E, Sandri M, Perrone I, Mori A, Cuozzo D, Nerva L, Rossato M, Zuccolotto P, Pezzotti M, Delledonne M, Mannini F, Griboudo I, Gambino G. (2019). Distinct Metabolic Signals Underlie Clone by Environment Interplay in "Nebbiolo" Grapes Over Ripening. **Front Plant Sci.** 10:1575. doi: 10.3389/fpls.2019.01575
146. Bizzarri M, Delledonne M, Ferrarini A, Tononi P, Zago E, Vittori D, Damiani F, Paolocci F (2020). Whole-Transcriptome Analysis Unveils the Synchronized Activities of Genes for Fructans in Developing Tubers of the Jerusalem Artichoke. **Front Plant Sci.** doi: 10.3389/fpls.2020.00101

147. Giné-Bordonaba J, Busatto N, Larrigaudière C, Lindo-García V, Echeverría G, Vrhovsek U, Farneti B, Biasioli F, De Quattro C, Rossato M, Delledonne M, Costa F. (2020). Investigation of the transcriptomic and metabolic changes associated with superficial scald physiology impaired by lovastatin and 1-methylcyclopropene in pear fruit (cv. "Blanquilla"). **Hortic Res.** 2020 Apr 1;7:49. doi: 10.1038/s41438-020-0272-x. eCollection 2020. PMID: 32257235
148. Iadarola B, Xumerle L, Lavezzari D, Paterno M, Marcolungo L, Beltrami C, Fortunati E, Mei D, Vetro A, Guerrini R, Parrini E, Rossato M, Delledonne M. (2020). Shedding light on dark genes: enhanced targeted resequencing by optimizing the combination of enrichment technology and DNA fragment length. **Sci Rep.** 2020 Jun 10;10(1):9424. doi: 10.1038/s41598-020-66331-z. PMID: 32523024
149. Sazzini M, Abondio P, Sarno S, Gnecci-Ruscione GA, Ragno M, Giuliani C, De Fanti S, Ojeda-Granados C, Boattini A, Marquis J, Valsesia A, Carayol J, Raymond F, Pirazzini C, Marasco E, Ferrarini A, Xumerle L, Collino S, Mari D, Arosio B, Monti D, Passarino G, D'Aquila P, Pettener D, Luiselli D, Castellani G, Delledonne M, Descombes P, Franceschi C, Garagnani P. (2020). Genomic history of the Italian population recapitulates key evolutionary dynamics of both Continental and Southern Europeans. **BMC Biol.** 2020 May 22;18(1):51. doi: 10.1186/s12915-020-00778-4. PMID: 32438927
150. Cecchin M, Berteotti S, Paltrinieri S, Vigliante I, Iadarola B, Giovannone B, Maffei ME, Delledonne M, Ballottari M. (2020). Improved lipid productivity in *Nannochloropsis gaditana* in nitrogen-replete conditions by selection of pale green mutants. **Biotechnol Biofuels.** 2020 Apr 21;13:78. doi: 10.1186/s13068-020-01718-8. eCollection 2020.
151. Massonnet M, Cochetel N, Minio A, Vondras AM, Lin J, Muyle A, Garcia JF, Zhou Y, Delledonne M, Riaz S, Figueroa-Balderas R, Gaut BS, Cantu D. (2020) The genetic basis of sex determination in grapes. **Nat Commun.** 2020 Jun 9;11(1):2902. doi: 10.1038/s41467-020-16700-z. PMID: 32518223
152. Zombardo A, Crosatti C, Bagnaresi P, Bassolino L, Reshef N, Puccioni S, Faccioli P, Tafuri A, Delledonne M, Fait A, Storch P, Cattivelli L, Mica E. (2020) Transcriptomic and biochemical investigations support the role of rootstock-scion interaction in grapevine berry quality. **BMC Genomics.** 2020 Jul 8;21(1):468. doi: 10.1186/s12864-020-06795-5. PMID: 32641089
153. Cassuto D, Delledonne M, Zaccaria G, Illiano I, Giori AM, Bellia G. (2020) Safety Assessment of High- and Low-Molecular-Weight Hyaluronans (Prophilo®) as Derived from Worldwide Postmarketing Data. **Biomed Res Int.** 2020 Jun 20;2020:8159047. doi: 10.1155/2020/8159047. eCollection 2020. PMID: 32685528 Free PMC article.
154. Maestri S, Maturo MG, Cosentino E, Marcolungo L, Iadarola B, Fortunati E, Rossato M, Delledonne M. (2020) A Long-Read Sequencing Approach for Direct Haplotype Phasing in Clinical Settings. **Int J Mol Sci.** 2020 Dec 1;21(23):9177. doi: 10.3390/ijms21239177. PMID: 33271988 Free PMC article.
155. Passera A, Rossato M, Oliver JS, Battelli G, Shahzad GI, Cosentino E, Sage JM, Toffolatti SL, Lopatriello G, Davis JR, Kaiser MD, Delledonne M, Casati P. (2020). Characterization of *Lysinibacillus fusiformis* strain S4C11: In vitro, in planta, and in silico analyses reveal a plant-beneficial microbe. **Microbiol Res.** 2020 Dec 5;244:126665. doi: 10.1016/j.micres.2020.126665. Online ahead of print. PMID: 33340794
156. Pirazzini C, Azevedo T, Baldelli L, Bartoletti-Stella A, Calandra-Buonaura G, Molin AD, Dimitri GM, Doykov I, Gómez-Garre P, Hägg S, Hällqvist J, Halsband C, Heywood W, Jesús S, Jylhävä J, Kwiatkowska KM, Labrador-Espinosa MA, Licari C, Maturo MG, Mengozzi G, Meoni G, Milazzo M, Perrián-Tocino MT, Ravaioli F, Sala C, Sambati L, Schade S, Schreglmann S, Spasov

- S, Tenori L, Williams D, Xumerle L, Zago E, Bhatia KP, Capellari S, Cortelli P, Garagnani P, Houlden H, Liò P, Luchinat C, Delledonne M, Mills K, Mir P, Mollenhauer B, Nardini C, Pedersen NL, Provini F, Strom S, Trenkwalder C, Turano P, Bacalini MG, Franceschi C; PROPAG-AGEING Consortium (2020) A Geroscience approach for Parkinson's Disease: conceptual framework and design of PROPAG-AGEING project. **Mech Ageing Dev.** 2020 Dec 29:111426. doi: 10.1016/j.mad.2020.111426. Online ahead of print. PMID: 33385396 Review.
157. Vittori VD, Bitocchi E, Rodriguez M, Alseekh S, Bellucci E, Nanni L, Gioia T, Marzario S, Logozzo G, Rossato M, De Quattro C, Murgia ML, Ferreira JJ, Campa A, Xu C, Fiorani F, Sampathkumar A, Fröhlich A, Attene G, Delledonne M, Usadel B, Fernie AR, Rau D, Papa R. (2020). Pod indehiscence in common bean is associated to the fine regulation of PvMYB26. **J Exp Bot.** 2021 Feb 27;72(5):1617-1633. doi: 10.1093/jxb/eraa553. PMID: 33247939
 158. Freitag H, de Vries R, Paterno M, Maestri S, Delledonne M, Thompson CG, Lamed H, Lambert R, Fox MF, Gonzalez MC, Delocado ED, Sabordo MR, Pangantihon CV, Njunjić I. (2021). *Hydraena* (s.str.) *dinarica*, new species (Coleoptera: Hydraenidae) along with further records of *Hydraena* spp. from Durmitor National Park, Montenegro and comments on the DNA barcoding problem with the genus. **Biodivers Data J.** 2021 Jan 12;9:e59892. doi: 10.3897/BDJ.9.e59892. eCollection 2021. PMID: 33519262
 159. Santangelo A, Rossato M, Lombardi G, Benfatto S, Lavezzari D, De Salvo GL, Indraccolo S, Dehecchi MC, Prandini P, Gambari R, Scapoli C, Di Gennaro G, Caccese M, Eoli M, Rudà R, Brandes AA, Ibrahim T, Rizzato S, Lolli I, Lippi G, Delledonne M, Zagonel V, Cabrini G (2021). A molecular signature associated with prolonged survival in glioblastoma patients treated with regorafenib. **Neuro Oncol.** 2021 Feb 25;23(2):264-276. doi: 10.1093/neuonc/noaa156. PMID: 32661549
 160. Di Vittori V, Bitocchi E, Rodriguez M, Alseekh S, Bellucci E, Nanni L, Gioia T, Marzario S, Logozzo G, Rossato M, De Quattro C, Murgia ML, Ferreira JJ, Campa A, Xu C, Fiorani F, Sampathkumar A, Fröhlich A, Attene G, Delledonne M, Usadel B, Fernie AR, Rau D, Papa R. (2021). Pod indehiscence in common bean is associated with the fine regulation of PvMYB26. **J Exp Bot.** 72:1617-1633. doi: 10.1093/jxb/eraa553. PMID: 33247939 Free PMC article.
 161. Passera A, Rossato M, Oliver JS, Battelli G, Shahzad GI, Cosentino E, Sage JM, Toffolatti SL, Lopatriello G, Davis JR, Kaiser MD, Delledonne M, Casati P. (2021). Characterization of *Lysinibacillus fusiformis* strain S4C11: In vitro, in planta, and in silico analyses reveal a plant-beneficial microbe. **Microbiol Res.** 244:126665. doi: 10.1016/j.micres.2020.126665. PMID: 33340794
 162. Degli Esposti C, Iadarola B, Maestri S, Beltrami C, Lavezzari D, Morini M, De Marco P, Erminio G, Garaventa A, Zara F, Delledonne M, Ognibene M, Pezzolo A. (2021) Exosomes from Plasma of Neuroblastoma Patients Contain Double stranded DNA Reflecting the Mutational Status of Parental Tumor Cells. **Int J Mol Sci.** 2021 Apr 1;22(7):3667. doi: 10.3390/ijms22073667. PMID: 33915956
 163. Garagnani P, Marquis J, Delledonne M, Pirazzini C, Marasco E, Kwiatkowska KM, Iannuzzi V, Bacalini MG, Valsesia A, Carayol J, Raymond F, Ferrarini A, Xumerle L, Collino S, Mari D, Arosio B, Casati M, Ferri E, Monti D, Nacmias B, Sorbi S, Luiselli D, Pettener D, Castellani G, Sala C, Passarino G, De Rango F, D'Aquila P, Bertamini L, Martinelli N, Girelli D, Olivieri O, Giuliani C, Descombes P, Franceschi C. (2021). Whole-genome sequencing analysis of semi-supercentenarians. **Elife.** 2021 May 4;10: e57849. doi: 10.7554/eLife.57849. PMID: 33941312
 164. Marcolungo L, Beltrami C, Esposti CD, Lopatriello G, Piubelli C, Mori A, Pomari E, Deiana M, Scarso S, Bisoffi Z, Grosso V, Cosentino E, Maestri S, Lavezzari D, Iadarola B, Paterno M, Segala

- E, Giovannone B, Gallinaro M, Rossato M, Delledonne M. (2021). ACoRE: Accurate SARS-CoV-2 genome reconstruction for the characterization of intra-host and inter-host viral diversity in clinical samples and for the evaluation of re-infections. **Genomics**. 2021 Apr 8:S0888-7543(21)00134-8. doi: 10.1016/j.ygeno.2021.04.008. Online ahead of print. PMID: 33839270
165. Baldelli L, Schade S, Jesús S, Schreglmann SR, Sambati L, Gómez-Garre P, Halsband C, Calandra-Buonaura G, Adarmes-Gómez AD, Sixel-Döring F, Zenesini C, Pirazzini C, Garagnani P, Bacalini MG, Bhatia KP, Cortelli P, Mollenhauer B, Franceschi C; PROPAG-AGEING consortium, Mir P, Trenkwalder C, Provini F. (2021) Heterogeneity of prodromal Parkinson symptoms in siblings of Parkinson disease patients. **NPJ Parkinsons Dis**. 7:78. doi: 10.1038/s41531-021-00219-1. PMID: 34493736
 166. Grosso V, Marcolungo L, Maestri S, Alfano M, Lavezzari D, Iadarola B, Salviati A, Mariotti B, Botta A, D'Apice MR, Novelli G, Delledonne M, Rossato M. (2021). Characterization of FMR1 Repeat Expansion and Intragenic Variants by Indirect Sequence Capture. **Front Genet**. 2021 Sep 27;12:743230. doi: 10.3389/fgene.2021.743230. eCollection 2021. PMID: 34646309
 167. Iadarola B, Lavezzari D, Modi A, Degli Esposti C, Beltrami C, Rossato M, Zaro V, Napione E, Latella L, Lari M, Caramelli D, Salviati A, Delledonne M. (2021). Whole-exome sequencing of the mummified remains of Cangrande della Scala (1291-1329 CE) indicates the first known case of late-onset Pompe disease. **Sci Rep**. 2021 Oct 26;11(1):21070. doi: 10.1038/s41598-021-00559-1. PMID: 34702906
 168. Bellucci E, Mario Aguilar O, Alseekh S, Bett K, Brezeanu C, Cook D, De la Rosa L, Delledonne M, Dostatny DF, Ferreira JJ, Geffroy V, Ghitarrini S, Kroc M, Kumar Agrawal S, Logozzo G, Marino M, Mary-Huard T, McClean P, Meglič V, Messer T, Muel F, Nanni L, Neumann K, Servalli F, Străjeru S, Varshney RK, Vasconcelos MW, Zaccardelli M, Zavarzin A, Bitocchi E, Frontoni E, Fernie AR, Gioia T, Graner A, Guasch L, Prochnow L, Oppermann M, Susek K, Tenaillon M, Papa R. (2021). The INCREASE project: Intelligent Collections of food-legume genetic resources for European agrofood systems. **Plant J**. doi: 10.1111/tpj.15472. Online ahead of print. PMID: 34427014
 169. Maguolo A, Rodella G, Giorgetti A, Nicolodi M, Ribeiro R, Dianin A, Cantalupo G, Monge I, Carcereri S, De Bernardi ML, Delledonne M, Pasini A, Campostrini N, Ion Popa F, Piacentini G, Teofoli F, Vincenzi M, Camilot M, Bordugo A. (2022). A Gain-of-Function Mutation on BCKDK Gene and Its Possible Pathogenic Role in Branched-Chain Amino Acid Metabolism. **Genes (Basel)**; 13(2):233. doi: 10.3390/genes13020233. PMID: 35205278
 170. Marcolungo L, Passera A, Maestri S, Segala E, Alfano M, Gaffuri F, Marturano G, Casati P, Bianco PA, Delledonne M. (2022). Real-Time On-Site Diagnosis of Quarantine Pathogens in Plant Tissues by Nanopore-Based Sequencing. **Pathogens**; 11(2):199. doi: 10.3390/pathogens11020199. PMID: 35215142
 171. Maestri S, Gambino G, Lopatriello G, Minio A, Perrone I, Cosentino E, Giovannone B, Marcolungo L, Alfano M, Rombauts S, Cantu D, Rossato M, Delledonne M, Calderón L. (2022). 'Nebbiolo' genome assembly allows surveying the occurrence and functional implications of genomic structural variations in grapevines (*Vitis vinifera* L.). **BMC Genomics**; 23(1):159. doi: 10.1186/s12864-022-08389-9. PMID: 35209840
 172. Ramsey KA, Meskers CGM, Trappenburg MC, Bacalini MG, Delledonne M, Garagnani P, Greig C, Kallen V, van Meeteren N, van Riel N, Correia Santos N, Sipilä S, Thompson JL, Whittaker AC, Maier AB (2022). The Physical Activity and Nutritional INfluences in Ageing (PANINI) Toolkit: A Standardized Approach towards Physical Activity and Nutritional Assessment of Older Adults. **Healthcare** 10(6):1017.

<https://doi.org/10.3390/healthcare10061017>

173. Schilthuizen M, Thompson CG, de Vries R, van Peursen ADP, Paterno M, Maestri S, Marcolongo L, Esposti CD, Delledonne M, Njunjić I (2022). A new giant keelback slug of the genus *Limax* from the Balkans, described by citizen scientists. **Biodivers. Data J.** 10: e69685. <https://doi.org/10.3897/BDJ.10.e69685>
174. Maestri S, Grosso V, Alfano M, Lavezzari D, Piubelli C, Bisoffi Z, Rossato M, Delledonne M. (2022). STArS (STrain-Amplicon-Seq), a targeted nanopore sequencing workflow for SARS-CoV-2 diagnostics and genotyping. **Biol Methods Protoc.** 7(1): bpac020. doi: 10.1093/biomethods/bpac020.
175. Alfano M, De Antoni L, Centofanti F, Visconti VV, Maestri S, Degli Esposti C, Massa R, D'Apice MR, Novelli G, Delledonne M, Botta A, Rossato M (2022). Characterization of full-length CNBP expanded alleles in myotonic dystrophy type 2 patients by Cas9-mediated enrichment and nanopore sequencing. **Elife.** 11: e80229. doi: 10.7554/eLife.80229.
176. Marcolungo L, Vincenzi L, Ballottari M, Cecchin M, Cosentino E, Mignani T, Limongi A, Ferraris I, Orlandi M, Rossato M, Delledonne M. (2023). Structural Refinement by Direct Mapping Reveals Assembly Inconsistencies near Hi-C Junctions. **Plants** (Basel). Jan 10;12(2):320. doi: 10.3390/plants12020320.
177. Lopatriello G, Maestri S, Alfano M, Papa R, Di Vittori V, De Antoni L, Bellucci E, Pieri A, Bitocchi E, Delledonne M, Rossato M (2023). CRISPR/Cas9-Mediated Enrichment Coupled to Nanopore Sequencing Provides a Valuable Tool for the Precise Reconstruction of Large Genomic Target Regions. **Int J Mol Sci.** Jan 5;24(2):1076. doi: 10.3390/ijms24021076.
178. Giovenino C, Trajkova S, Pavinato L, Cardaropoli S, Pullano V, Ferrero E, Sukarova-Angelovska E, Carestiatu S, Salmin P, Rinninella A, Battaglia A, Bertoli L, Fadda A, Palermo F, Carli D, Mussa A, Dimartino P, Bruselles A, Froukh T, Mandrile G, Pasini B, De Rubeis S, Buxbaum JD, Pippucci T, Tartaglia M, Rossato M, Delledonne M, Ferrero GB, Brusco A. (2023). Skewed X-chromosome inactivation in unsolved neurodevelopmental disease cases can guide re-evaluation For X-linked genes. **Eur J Hum Genet.** Mar 6. doi: 10.1038/s41431-023-01324-w. PMID: 36879111
179. Schilthuizen M, Berenyi S, Ezzwan NSMN, Hamdani NIAA, Wu H, De Antoni L, Vincenzi L, de Gier W, van Peursen ADP, Njunjić I, Delledonne M, Slik F, Grafe U, Cicuzza D (2023) A new semi-slug of the genus *Microparmarion* from Brunei, discovered, described and DNA-barcoded on citizen-science 'taxon expeditions' (Gastropoda, Stylommatophora, Ariophantidae). **Biodivers. Data J.** 11: e101579. <https://doi.org/10.3897/BDJ.11.e101579>
180. Melo US, Jatzlau J, Prada-Medina CA, Flex E, Hartmann S, Ali S, Schöpflin R, Bernardini L, Ciolfi A, Moeinzadeh MH, Klever MK, Altay A, Vallecillo-García P, Carpentieri G, Delledonne M, Ort MJ, Schwestka M, Ferrero GB, Tartaglia M, Brusco A, Gossen M, Strunk D, Geißler S, Mundlos S, Stricker S, Knaus P, Giorgio E, Spielmann M. (2023) Enhancer hijacking at the ARHGAP36 locus is associated with connective tissue to bone transformation. **Nat Commun.** 2023 Apr 11;14(1):2034. doi: 10.1038/s41467-023-37585-8. PMID: 37041138
181. Rossato M, Marcolungo L, De Antoni L, Lopatriello G, Bellucci E, Cortinovis G, Frascarelli G, Nanni L, Bitocchi E, Di Vittori V, Vincenzi L, Lucchini F, Bett KE, Ramsay L, Konkin DJ, Delledonne M, Papa R. (2023) CRISPR-Cas9-based repeat depletion for high-throughput genotyping of complex plant genomes. **Genome Res.** 2023 May;33(5):787-797. doi: 10.1101/gr.277628.122. Epub 2023 May 1. PMID: 37127332
182. Toffali L, D'Ulivo B, Giagulli C, Montresor A, Zenaro E, Delledonne M, Rossato M, Iadarola B,

Sbarbati A, Bernardi P, Angelini G, Rossi B, Lopez N, Linke WA, Unger A, Di Silvestre D, Benazzi L, De Palma A, Motta S, Constantin G, Mauri P, Laudanna C. (2023) An isoform of the giant protein titin is a master regulator of human T lymphocyte trafficking. **Cell Rep.** 2023 May 30;42(5):112516. doi: 10.1016/j.celrep.2023.112516. Epub 2023 May 18. PMID: 37204926

183. Lavezzari D, Mori A, Pomari E, Deiana M, Fadda A, Bertoli L, Sinigaglia A, Riccetti S, Barzon L, Piubelli C, Delledonne M, Capobianchi MR, Castillette C. (2023) Comparative analysis of bioinformatics tools to characterize SARS-CoV-2 subgenomic RNAs. **Life Sci Alliance.** 2023 Sep 25;6(12):e202302017. doi: 10.26508/lsa.202302017. Print 2023 Dec. PMID: 37748810
184. Sillo F, Neri L, Calvo A, Zampieri E, Petruzzelli G, Ferraris I, Delledonne M, Zaldei A, Gioli B, Baraldi R, Balestrini R. (2023) Correlation between microbial communities and volatile organic compounds in an urban soil provides clues on soil quality towards sustainability of city flowerbeds. *Heliyon.* 2023 Dec 12;10(1):e23594. doi: 10.1016/j.heliyon.2023.e23594. eCollection 2024 Jan 15. PMID: 38205296