

# Plant Abiotic Stress Responses

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Contributor: Luca Ambrosino, Maria Luisa Chiusano

Abiotic stresses are among the principal limiting factors for productivity in agriculture. In the current era of continuous climate changes, the understanding of the molecular aspects involved in abiotic stress response in plants is a priority.

The rise of -omics approaches provides key strategies to promote effective research in the field, facilitating the investigations from reference models to an increasing number of species, tolerant and sensitive genotypes. Integrated multilevel approaches, based on molecular investigations at genomics, transcriptomics, proteomics and metabolomics levels, are now feasible, expanding the opportunities to clarify key molecular aspects involved in responses to abiotic stresses. To this aim, bioinformatics has become fundamental for data production, mining and integration, and necessary for extracting valuable information and for comparative efforts, paving the way to the modeling of the involved processes.

We provide here an overview of bioinformatics resources for research on plant abiotic stresses, describing collections from -omics efforts in the field, ranging from raw data to complete databases or platforms, highlighting opportunities and still open challenges in abiotic stress research based on -omics technologies.

Keywords: bioinformatics ; genomics ; transcriptomics ; proteomics ; metabolomics ; data integration ; stress

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## 1. Introduction

Plants display an amazing diversity and, owing to their sessile nature, they evolved a broad range of molecular mechanisms to respond to complex network of environmental signals, which activate multiple pathways, modulated by different responsive genes, in case conferring tolerance to the pressure determined by stressor factors <sup>[1][2][3]</sup>.

Abiotic stresses, such as heat and cold, drought, salinity and flooding <sup>[4][5][6][7]</sup>, however, dramatically affect plant growth and crop yield <sup>[2][8][9][10][11][12][13][14][15][16]</sup>, and these are among the reasons why abiotic stress management is one of the most important challenges in agriculture. In current climate change scenarios, exposure to abiotic stresses is more frequent and the consequent effects are so relevant also considering the exponential increase of the world food supply due to the rapid population growth <sup>[2][9][12][13][17][18][19][20][21]</sup>, and the widespread attention to promote a sustainable productivity. This is why extensive studies have been focused on understanding the molecular basis of abiotic stress response and the research for improved, productive plants, adapted for stress tolerance <sup>[10][13][20][22]</sup>. These activities were strongly favored by the evolving -omics technologies, which provide key strategies to promote molecular investigations on plant organization and functionality, also under stress conditions<sup>[23][24][25][26]</sup>, and novel approaches for omics assisted crop improvement<sup>[27][28]</sup>. Since their initial introduction, they permitted unexpected views on different levels of cell functionality, ranging from genome to transcriptome, to proteome and metabolome, and more recently covering also investigation on chromatin organization by epigenome approaches <sup>[29][30][31][32]</sup>.

These approaches, that cover different levels of biological functionalities, enable deeper investigations at each level, also offering the opportunity of integrated views <sup>[33][34][35]</sup>, to study the complexity of the molecular response of plants and to abiotic stresses as well. Moreover, the technological evolution and cheaper methodologies offer faster and more accessible approaches favoring research considering an increasing number of crops<sup>[36][37]</sup>.

## 2. Bioinformatics Resources for Plant Abiotic Stress Responses

The so-called “Next Generation Sequencing” (NGS) technologies, as one of the major examples, largely favored deeper insights on plant genome organization <sup>[38][39][40][41][42][43]</sup> and on functional responses to variable environmental parameters, elucidating the first level of gene expression, i.e., the transcriptome analysis, by promoting the transition from expressed sequence tags (ESTs) and microarray based techniques <sup>[44][45]</sup>, to more powerful approaches such as RNA-seq <sup>[46][47][48]</sup> and associated technologies <sup>[29][49][50]</sup>.

Simultaneously, the development of proteomics procedures by 2D-Gels coupled to mass spectrometry (MS) [51] or, more recently, via high-throughput shotgun approaches [52], and robust LC–MS (liquid chromatography-mass spectrometry) [53] and GC–MS (gas chromatography-mass spectrometry) [54] metabolomics technologies, able to unravel fluctuations of non-volatile and volatile metabolites, are paving the way to a deep understanding of the effects of the biological processes under investigation [33].

In this context, the integration of results from different levels of molecular information favors holistic views to decipher key components that are playing roles in complex molecular processes involved in plant responses to unfavorable or changing environmental conditions [55][56][57].

Bioinformatics is necessary for data production in support of the different omics technologies, fundamental for data organization and for data mining. It favors the data sharing, the interpretation of the massive amount of information provided by high throughput technologies, permitting the filtering of valuable information for human driven interpretation, therefore assisting single level approach and multilevel data integration for comprehensive views on systems functionality [34][35][58].

Moreover, bioinformatics also provides overwhelming amount of accessible resources to the scientific community, driving pioneering research based either on the exploitation of -omics technologies [33][59][60][61], or of the manifold resources that may support specific subsequent analyses, such as those based on sequence comparisons, gene family investigations and molecular modeling [62][63][64].

Bioinformatics resources implementation and maintenance, and data sharing, are therefore among the main drivers of the success of this research field and of the evolution of the omics technologies, since the data exploitation revealed to be a very powerful approach to support the overall scientific community.

One of the key points to carefully sustain to this aim remains data accessibility and care. Data collection should be reliable and interoperable, suitable to be compared, touching the new challenges in the field, which mainly fall in the so called integrative bioinformatics [65]. However, data exploitation is today still relying on scientist consciousness about the opportunities and limits offered by the different data sources, about the sensitivity and specificity of the different technologies, and about the quality of the organized results. Additionally, inexperienced users must be aware of the opportunities and rules in the field, to profitably handle, analyze and compare data from the available resources and to obtain novel insights into the organization and functionality of the biological systems. This requires education, collaborative efforts, transdisciplinarity.

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## References

1. Takashi Hirayama; Kazuo Shinozaki; Research on plant abiotic stress responses in the post-genome era: past, present and future. *The Plant Journal* **2010**, *61*, 1041-1052, [10.1111/j.1365-3113.2010.04124.x](https://doi.org/10.1111/j.1365-3113.2010.04124.x).
2. Jun You; Zhulong Chan; ROS Regulation During Abiotic Stress Responses in Crop Plants. *Frontiers in Plant Science* **2015**, *6*, 1925, [10.3389/fpls.2015.01092](https://doi.org/10.3389/fpls.2015.01092).
3. Potters, G.; Jansen, M.; Guisez, Y.; Pasternak, T.. Stress drives plant cells to take the road towards embryogenesis; Global Science Books Ltd: London, 2006; pp. 289-294.
4. Colin R Cavanagh; Matthew Morell; Ian J. Mackay; Wayne Powell; From mutations to MAGIC: resources for gene discovery, validation and delivery in crop plants. *Current Opinion in Plant Biology* **2008**, *11*, 215-221, [10.1016/j.pbi.2008.01.002](https://doi.org/10.1016/j.pbi.2008.01.002).
5. Chinnusamy, Viswanathan, and Jian-Kang Zhu; Epigenetic regulation of stress responses in plants. *Current opinion in plant biology* **2009**, *12*(2), 133-139, <https://doi.org/10.1016/j.pbi.2008.12.006>.
6. R. Mittler; Eduardo Blumwald; Genetic Engineering for Modern Agriculture: Challenges and Perspectives. *Annual Review of Plant Biology* **2010**, *61*, 443-462, [10.1146/annurev-arplant-042809-112116](https://doi.org/10.1146/annurev-arplant-042809-112116).
7. Munns, Rana; Tester, Mark; Mechanisms of Salinity Tolerance. *Annu. Rev. Plant Biol.* **2008**, *59*, 651-681, [10.1146/annurev-arplant.59.032607.092911](https://doi.org/10.1146/annurev-arplant.59.032607.092911).
8. Hyacinthe Le Gall; Florian Philippe; Jean-Marc Domon; Françoise Gillet; Jérôme Pelloux; Catherine Rayon; Cell Wall Metabolism in Response to Abiotic Stress. *Plants* **2015**, *4*, 112-166, [10.3390/plants4010112](https://doi.org/10.3390/plants4010112).
9. Kemal Kazan; Diverse roles of jasmonates and ethylene in abiotic stress tolerance. *Trends in Plant Science* **2015**, *20*, 219-229, [10.1016/j.tplants.2015.02.001](https://doi.org/10.1016/j.tplants.2015.02.001).

10. Rajesh Kumar; Role of MicroRNAs in Biotic and Abiotic Stress Responses in Crop Plants. *Applied Biochemistry and Biotechnology* **2014**, 174, 93-115, [10.1007/s12010-014-0914-2](https://doi.org/10.1007/s12010-014-0914-2).
11. Gulzar S Sanghera; Shabir H Wani; Waseem Hussain; Naorem Brajendra Singh; Engineering Cold Stress Tolerance in Crop Plants. *Current Genomics* **2011**, 12, 30-43, [10.2174/138920211794520178](https://doi.org/10.2174/138920211794520178).
12. Anita Tripathi; Kavita Goswami; Neeti Sanan-Mishra; Role of bioinformatics in establishing microRNAs as modulators of abiotic stress responses: the new revolution. *Frontiers in Physiology* **2015**, 6, 78, [10.3389/fphys.2015.00286](https://doi.org/10.3389/fphys.2015.00286).
13. Jian-Kang Zhu; Abiotic Stress Signaling and Responses in Plants.. *Cell* **2016**, 167, 313-324, [10.1016/j.cell.2016.08.029](https://doi.org/10.1016/j.cell.2016.08.029).
14. Rudy Dolferus; To grow or not to grow: A stressful decision for plants. *Plant Science* **2014**, 229, 247-261, [10.1016/j.plantsci.2014.10.002](https://doi.org/10.1016/j.plantsci.2014.10.002).
15. Akanksha Sehgal; Kumari Sita; Kadambot H. M. Siddique; Rakesh Kumar; Sailaja Bhogireddy; Rajeev K. Varshney; Bindumadhava Hanumantharao; Ramakrishnan M. Nair; P. V. Vara Prasad; Harsh Nayyar; et al. Drought or/and Heat-Stress Effects on Seed Filling in Food Crops: Impacts on Functional Biochemistry, Seed Yields, and Nutritional Quality. *Frontiers in Plant Science* **2018**, 9, 1705, [10.3389/fpls.2018.01705](https://doi.org/10.3389/fpls.2018.01705).
16. Khader Shameer; Mahantesha B N Naika; K. Mohamed Shafi; Ramanathan Sowdhamini; Decoding systems biology of plant stress for sustainable agriculture development and optimized food production. *Progress in Biophysics and Molecular Biology* **2019**, 145, 19-39, [10.1016/j.pbiomolbio.2018.12.002](https://doi.org/10.1016/j.pbiomolbio.2018.12.002).
17. Rafi Shaik; Wusirika Ramakrishna; Machine learning approaches distinguish multiple stress conditions using stress-responsive genes and identify candidate genes for broad resistance in rice.. *Plant Physiology* **2013**, 164, 481-95, [10.1104/pp.113.225862](https://doi.org/10.1104/pp.113.225862).
18. Benjamin I. Cook; Toby R. Ault; Jason E. Smerdon; Unprecedented 21st century drought risk in the American Southwest and Central Plains. *Science Advances* **2015**, 1, e1400082-e1400082, [10.1126/sciadv.1400082](https://doi.org/10.1126/sciadv.1400082).
19. Patrick Gerland; Adrian E Raftery; Hana Ševčíková; Nan Li; Danan Gu; Thomas Spoorenberg; Leontine Alkema; Bailey K Fosdick; Jennifer Chunn; Nevena Lalic; et al. World population stabilization unlikely this century. *Science* **2014**, 346, 234-237, [10.1126/science.1257469](https://doi.org/10.1126/science.1257469).
20. Jack Grundy; Claire Stoker; Isabelle Carre; Circadian regulation of abiotic stress tolerance in plants. *Frontiers in Plant Science* **2015**, 6, 648, [10.3389/fpls.2015.00648](https://doi.org/10.3389/fpls.2015.00648).
21. David B. Lobell; Sharon M. Gourdji; The Influence of Climate Change on Global Crop Productivity1. *Plant Physiology* **2012**, 160, 1686-1697, [10.1104/pp.112.208298](https://doi.org/10.1104/pp.112.208298).
22. Nobuhiro Suzuki; Rosa M. Rivero; Vladimir Shulaev; Eduardo Blumwald; Ron Mittler; Abiotic and biotic stress combinations. *New Phytologist* **2014**, 203, 32-43, [10.1111/nph.12797](https://doi.org/10.1111/nph.12797).
23. Kamila Bokszczanin; Sotirios Fragkostefanakis; Perspectives on deciphering mechanisms underlying plant heat stress response and thermotolerance. *Frontiers in Plant Science* **2013**, 4, 315, [10.3389/fpls.2013.00315](https://doi.org/10.3389/fpls.2013.00315).
24. Uday Chand Jha; Abhishek Bohra; Rintu Jha; Swarup Kumar Parida; Salinity stress response and 'omics' approaches for improving salinity stress tolerance in major grain legumes. *Plant Cell Reports* **2019**, 38, 255-277, [10.1007/s00299-019-02374-5](https://doi.org/10.1007/s00299-019-02374-5).
25. Tong Li; Ya-Hui Wang; Jie-Xia Liu; Kai Feng; Zhi-Sheng Xu; Ai-Sheng Xiong; Advances in genomic, transcriptomic, proteomic, and metabolomic approaches to study biotic stress in fruit crops.. *Critical Reviews in Biotechnology* **2019**, 39, 680-692, [10.1080/07388551.2019.1608153](https://doi.org/10.1080/07388551.2019.1608153).
26. Anna Piasecka; Piotr Kachlicki; Maciej Stobiecki; Analytical Methods for Detection of Plant Metabolomes Changes in Response to Biotic and Abiotic Stresses. *International Journal of Molecular Sciences* **2019**, 20, 379, [10.3390/ijms20020379](https://doi.org/10.3390/ijms20020379).
27. Federico Scossa; Yariv Brotman; Francisco De Abreu E Lima; Lothar Willmitzer; Zoran Nikoloski; Takayuki Tohge; Alisdair R. Fernie; Genomics-based strategies for the use of natural variation in the improvement of crop metabolism. *Plant Science* **2016**, 242, 47-64, [10.1016/j.plantsci.2015.05.021](https://doi.org/10.1016/j.plantsci.2015.05.021).
28. Tariq Shah; Jinsong Xu; Xi-Ling Zou; Yong Cheng; Mubasher Nasir; Xuekun Zhang; Omics Approaches for Engineering Wheat Production under Abiotic Stresses. *International Journal of Molecular Sciences* **2018**, 19, 2390, [10.3390/ijms19082390](https://doi.org/10.3390/ijms19082390).
29. Kamila Bokszczanin; SPOT-ITN Consortium (Solanaceae Pollen Thermotolerance Initial Training Network Consortium)SPOT-ITN Consortium (Solanaceae Pollen Thermotolerance Initial Training Network Consortium); Nicolas Krezdorn; Sotirios Fragkostefanakis; Sören Müller; Lukas Rycak; Yuanyuan Chen; Klaus Hoffmeier; Jutta Kreutz; Marine J. Paupière; et al. Identification of novel small ncRNAs in pollen of tomato. *BMC Genomics* **2015**, 16, 714, [10.1186/s12864-015-1901-x](https://doi.org/10.1186/s12864-015-1901-x).

30. Alex Boyko; Igor Kovalchuk; Genome instability and epigenetic modification—heritable responses to environmental stress?. *Current Opinion in Plant Biology* **2011**, 14, 260-266, [10.1016/j.pbi.2011.03.003](https://doi.org/10.1016/j.pbi.2011.03.003).
31. Akihiro Matsui; Motoaki Seki; The Involvement of Long Noncoding RNAs in Response to Plant Stress.. *Breast Cancer* **2019**, 1933, 151-171, [10.1007/978-1-4939-9045-0\\_8](https://doi.org/10.1007/978-1-4939-9045-0_8).
32. Kamlesh K. Meena; Ajay M. Sorty; Utkarsh M. Bitla; Khushboo Choudhary; Priyanka Gupta; Ashwani Pareek; Dhananjaya P. Singh; Ratna Prabha; Pramod K. Sahu; Vijai Kumar Gupta; et al. Abiotic Stress Responses and Microbe-Mediated Mitigation in Plants: The Omics Strategies. *Frontiers in Plant Science* **2017**, 8, 3291, [10.3389/fpls.2017.00172](https://doi.org/10.3389/fpls.2017.00172).
33. Mario Keller; SPOT-ITN Consortium; Stefan Simm; Kamila Bokszczyńska; The coupling of transcriptome and proteome adaptation during development and heat stress response of tomato pollen.. *BMC Genomics* **2018**, 19, 447, [10.1186/s12864-018-4824-5](https://doi.org/10.1186/s12864-018-4824-5).
34. Anil Kumar; Rajesh Kumar Pathak; Sanjay Mohan Gupta; Vikram Singh Gaur; Dinesh Pandey; Systems Biology for Smart Crops and Agricultural Innovation: Filling the Gaps between Genotype and Phenotype for Complex Traits Linked with Robust Agricultural Productivity and Sustainability. *OMICS: A Journal of Integrative Biology* **2015**, 19, 581-601, [10.1089/omi.2015.0106](https://doi.org/10.1089/omi.2015.0106).
35. Ryo Nakabayashi; Kazuki Saito; Integrated metabolomics for abiotic stress responses in plants. *Current Opinion in Plant Biology* **2015**, 24, 10-16, [10.1016/j.pbi.2015.01.003](https://doi.org/10.1016/j.pbi.2015.01.003).
36. Maria Raffaella Ercolano; Adriana Sacco; Francesca Ferriello; Raffaella D'Alessandro; Paola Tononi; Alessandra Traini; Amalia Barone; Elisa Zago; Maria Luisa Chiusano; Genny Buson; et al. Patchwork sequencing of tomato San Marzano and Vesuviano varieties highlights genome-wide variations. *BMC Genomics* **2014**, 15, 138-138, [10.1186/1471-2164-15-138](https://doi.org/10.1186/1471-2164-15-138).
37. Valentina Tranchida-Lombardo; R. Aiese Cigliano; Irantzu Anzar; Simone Landi; SamuelA Palombieri; Chiara Colantuono; Hamed Bostan; Pasquale Termolino; Riccardo Aversano; Giorgia Batelli; et al. Whole-genome re-sequencing of two Italian tomato landraces reveals sequence variations in genes associated with stress tolerance, fruit quality and long shelf-life traits. *Current Neuropharmacology* **2017**, 25, 149-160, [10.1093/dnares/dsx045](https://doi.org/10.1093/dnares/dsx045).
38. Carlos Alonso-Blanco; 1,135 Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis thaliana. *Cell* **2016**, 166, 481-491, [10.1016/j.cell.2016.05.063](https://doi.org/10.1016/j.cell.2016.05.063).
39. Maria José Aranzana; Véronique Decroocq; Elisabeth Dirlwanger; Iban Eduardo; Zhong Shan Gao; Ksenija Gasic; Amy Iezzoni; Sook Jung; Cameron Peace; Humberto Prieto; et al. Prunus genetics and applications after de novo genome sequencing: achievements and prospects. *Horticulture Research* **2019**, 6, 58, [10.1038/s41438-019-0140-8](https://doi.org/10.1038/s41438-019-0140-8).
40. Huan Liu; Huan Liu; Liu Min; Xuezhu Liao; Sunil Kumar Sahu; Yuan Fu; Bo Song; Shifeng Cheng; Robert Kariba; Samuel Muthemba; et al. The draft genomes of five agriculturally important African orphan crops.. *GigaScience* **2019**, 8, giy152, [10.1093/gigascience/giy152](https://doi.org/10.1093/gigascience/giy152).
41. Ying-Hui Li; Guangyu Zhou; Jianxin Ma; Wen-Kai Jiang; Long-Guo Jin; Zhouhao Zhang; Yong Guo; Jinbo Zhang; Yi Sui; Liangtao Zheng; et al. De novo assembly of soybean wild relatives for pan-genome analysis of diversity and agronomic traits. *Nature Biotechnology* **2014**, 32, 1045-1052, [10.1038/nbt.2979](https://doi.org/10.1038/nbt.2979).
42. Cameron Peace; Luca Bianco; Michela Troggio; Eric Van De Weg; Nicholas P. Howard; Amandine Cornille; Charles-Eric Durel; Sean Myles; Zoë Migicovsky; Robert J. Schaffer; et al. Apple whole genome sequences: recent advances and new prospects. *Horticulture Research* **2019**, 6, 59, [10.1038/s41438-019-0141-7](https://doi.org/10.1038/s41438-019-0141-7).
43. Norman J. Wickett; Siavash Mirarab; Nam Nguyen; Tandy Warnow; Eric Carpenter; Naim Matasci; Saravanaraj Ayyampalayam; Michael S. Barker; J. Gordon Burleigh; Matthew A Gitzendanner; et al. Phylotranscriptomic analysis of the origin and early diversification of land plants.. *Proceedings of the National Academy of Sciences* **2014**, 111, E4859-68, [10.1073/pnas.1323926111](https://doi.org/10.1073/pnas.1323926111).
44. Alfredo Ambrosone; Giorgia Batelli; Hamed Bostan; Nunzio D'A; gostino; Maria Luisa Chiusano; Gaetano Perrotta; Antonietta Leone; Stefania Grillo; Antonello Costa; et al. Distinct gene networks drive differential response to abrupt or gradual water deficit in potato. *Gene* **2017**, 597, 30-39, [10.1016/j.gene.2016.10.024](https://doi.org/10.1016/j.gene.2016.10.024).
45. Julia C Redman; Brian J Haas; Gene Tanimoto; Christopher D Town; Development and evaluation of anArabidopsiswhole genome Affymetrix probe array. *The Plant Journal* **2004**, 38, 545-561, [10.1111/j.1365-313x.2004.02061.x](https://doi.org/10.1111/j.1365-313x.2004.02061.x).
46. Paolo Iovieno; Paola Punzo; Gianpiero Guida; Carmela Mistretta; Michael Van Oosten; Roberta Nurcato; Hamed Bostan; Chiara Colantuono; Antonello Costa; Paolo Bagnaresi; et al. Transcriptomic Changes Drive Physiological Responses to Progressive Drought Stress and Rehydration in Tomato. *Frontiers in Plant Science* **2016**, 7, 371, [10.3389/fpls.2016.00371](https://doi.org/10.3389/fpls.2016.00371).

47. Yuwen Liu; Jie Zhou; Kevin P. White; RNA-seq differential expression studies: more sequence or more replication?. *Bioinformatics* **2013**, 30, 301-304, [10.1093/bioinformatics/btt688](#).
48. Zhong Wang; Mark Gerstein; Michael Snyder; RNA-Seq: a revolutionary tool for transcriptomics. *Nature Reviews Microbiology* **2009**, 10, 57-63, [10.1038/nrg2484](#).
49. J. Delanne; S. Nambot; A. Chassagne; O. Putois; A. Pelissier; C. Peyron; E. Gautier; J. Thevenon; E. Cretin; A.L. Bruel; et al. Secondary findings from whole-exome/genome sequencing evaluating stakeholder perspectives. A review of the literature. *European Journal of Medical Genetics* **2019**, 62, 103529, [10.1016/j.ejmg.2018.08.010](#).
50. Minmin Liu; Huiyang Yu; Gangjun Zhao; Qiufeng Huang; Yongen Lu; Bo Ouyang; Profiling of drought-responsive microRNA and mRNA in tomato using high-throughput sequencing. *BMC Genomics* **2017**, 18, 481, [10.1186/s12864-017-3869-1](#).
51. Thierry Rabilloud; How to Use 2D Gel Electrophoresis in Plant Proteomics. *Advanced Structural Safety Studies* **2013**, 1072, 43-50, [10.1007/978-1-62703-631-3\\_4](#).
52. Soon-Wook Kwon; Mijeong Kim; Hijin Kim; Joohyun Lee; Shotgun Quantitative Proteomic Analysis of Proteins Responding to Drought Stress in Brassica rapa L. (Inbred Line "Chiifu"). *International Journal of Genomics* **2016**, 2016, 4235808-9, [10.1155/2016/4235808](#).
53. Tiago Jorge; João A. Rodrigues; Camila Caldana; Romy Schmidt; Joost T. Van Dongen; Carla Antonio; Jane Thomas-Oates; Mass spectrometry-based plant metabolomics: Metabolite responses to abiotic stress. *Mass Spectrometry Reviews* **2015**, 35, 620-649, [10.1002/mas.21449](#).
54. Takayuki Tohge; Alisdair R. Fernie; Metabolomics-Inspired Insight into Developmental, Environmental and Genetic Aspects of Tomato Fruit Chemical Composition and Quality. *Plant And Cell Physiology* **2015**, 56, 1681-1696, [10.1093/pcp/pcv093](#).
55. Angelo D'Alessandro; Manel Taamalli; Federica Gevi; Anna Maria Timperio; Lello Zolla; Tahar Ghnaya; Cadmium Stress Responses in Brassica juncea: Hints from Proteomics and Metabolomics. *Journal of Proteome Research* **2013**, 12, 4979-4997, [10.1021/pr400793e](#).
56. Setsuko Komatsu; Akifumi Yamamoto; Takuji Nakamura; Mohammad-Zaman Nouri; Yohei Nanjo; Keito Nishizawa; Kiyoshi Furukawa; Comprehensive Analysis of Mitochondria in Roots and Hypocotyls of Soybean under Flooding Stress using Proteomics and Metabolomics Techniques. *Journal of Proteome Research* **2011**, 10, 3993-4004, [10.1021/pr2001918](#).
57. Anna Michaletti; Mohammad Reza Naghavi; Mahmoud Toorchi; Lello Zolla; Sara Rinalducci; Metabolomics and proteomics reveal drought-stress responses of leaf tissues from spring-wheat. *Scientific Reports* **2018**, 8, 5710, [10.1038/s41598-018-24012-y](#).
58. Maria Luisa Chiusano; Nunzio D'A; gostino; Alessandra Traini; Concetta Licciardello; Enrico Raimondo; Mario Aversano; Luigi Frusciante; Luigi Monti; ISOL@: an Italian SOLanaceae genomics resource. *BMC Bioinformatics* **2008**, 9, S7-S7, [10.1186/1471-2105-9-S2-S7](#).
59. Hong-Kyu Choi; Translational genomics and multi-omics integrated approaches as a useful strategy for crop breeding. *Genes & Genomics* **2018**, 41, 133-146, [10.1007/s13258-018-0751-8](#).
60. Almudena Gonzalez-Mula; Marta Torres Bejar; Denis Faure; Integrative and deconvolution omics approaches to uncover the Agrobacterium tumefaciens lifestyle in plant tumors.. *Plant Signaling & Behavior* **2019**, 14, e1581562-2, [10.1080/15592324.2019.1581562](#).
61. Darren C J Wong; Harnessing Integrated Omics Approaches for Plant Specialized Metabolism Research: New Insights into Shikoin Biosynthesis. *Plant And Cell Physiology* **2018**, 60, 4-6, [10.1093/pcp/pcy230](#).
62. Concetta Licciardello; Nunzio D'A; gostino; Alessandra Traini; Giuseppe Reforgiato Recupero; Luigi Frusciante; Maria Luisa Chiusano; Characterization of the glutathione S-transferase gene family through ESTs and expression analyses within common and pigmented cultivars of Citrus sinensis (L.) Osbeck. *BMC Plant Biology* **2014**, 14, 39-39, [10.1186/1471-2229-14-39](#).
63. Evangelina Lopez De Maturana; Lola Alonso; Pablo Alarcón; Isabel Adoración Martín-Antoniano; Silvia Pineda; Lucas Piorno; M.Luz Calle; Nuria Malats; Challenges in the Integration of Omics and Non-Omics Data.. *Genes* **2019**, 10, 238, [10.3390/genes10030238](#).
64. Francesco Monticolo; Chiara Colantuono; Maria Luisa Chiusano; Shaping the evolutionary tree of green plants: evidence from the GST family. *Scientific Reports* **2017**, 7, 14363, [10.1038/s41598-017-14316-w](#).
65. Hoe-Han Goh; Integrative Multi-Omics Through Bioinformatics. *Plant Promoters and Transcription Factors* **2018**, 1102, 69-80, [10.1007/978-3-319-98758-3\\_5](#).

