

Curriculum vitae of Dr. Andrea Zuccolo

-Personal data:

Present Address: KAUST G3805C, Thuwal, Kingdom of Saudi Arabia

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Nationality: Italian

Present position: -Research Scientist at KAUST, Saudi Arabia;

-Assistant Professor (tenured) at Scuola Superiore Sant'Anna, Pisa-Italy (on leave of absence)

-Languages Knowledge:

Italian: native

English: read, spoken and written

SCIENTIFIC ACTIVITY

-Education:

-2003: PhD in Plant Biotechnologies, at the University of Udine (Italy). Title of the thesis defended: "Characterisation of the repetitive fraction in plant genomes" under the supervision of Prof. Michele Morgante

-1998: MSc Degree in Biological Sciences (5 years course), with full marks (110/110), at the University of Trieste (Italy). Title of the experimental thesis defended: "Cloning and characterization of highly repeated DNA in Norway spruce (*Picea abies* K.)" under the supervision of Prof. Michele Morgante

-Professional appointments:

-Since May 2019: Research Scientist at KAUST, Saudi Arabia

-Since June 2015: Tenured Assistant Professor at Scuola Superiore Sant'Anna, Pisa, Italy

-December 2011-June 2015: Assistant Professor at Scuola Superiore Sant'Anna, Pisa, Italy

-June 2011-December 2011: Senior Scientist at the Applied Genomics Institute, Udine, Italy

-July 2006-May 2011: Coordinator of the Bioinformatics Team at the Arizona Genomic Institute (The University of Arizona, Tucson, AZ, USA)

-November 2004-July 2006: Research Associate at the Arizona Genomics Institute (The University of Arizona, Tucson, AZ, USA)

-June 2003-October 2004: Research Associate in the Plant Molecular Breeding Laboratory (Department of Crop Science and Agricultural Engineering, University of Udine)

-Qualifications:

-Italian National scientific qualification to function as associate professor ("abilitazione scientifica") in Genetics (05/11), obtained in 2017

-Italian National scientific qualification to function as associate professor (“abilitazione scientifica”) in Molecular Biology (05/E2), obtained in 2013

-Italian National scientific qualification to function as associate professor (“abilitazione scientifica”) in Agricultural Genetics (07/E1), obtained in 2013

-Papers published in peer-reviewed journals, book chapters:

53 papers, 4 book chapters; H index: 28 (Scopus); Total citations: 10,239; 7 papers as first author; 9 papers as corresponding author

-53) K. Sedeek, **A. Zuccolo**, A. Fornasiero, A. Weber, K. Sanikommu, S. Sampathkumar, L. Rivera Serna, H. Butt, S. Mussurova, A. Alhabsi, N. Nurmansyah, E. Ryan, R. Wing, M. Mahfouz. Multi-omics resources for targeted agronomic improvement of pigmented rice. **Nat Food** 2023

-52) Zhou Y, Yu Z, Chebotarov D, Chougule K, Lu Z, Rivera LF, Kathiresan N, Al-Bader N, Mohammed N, Alsantely A, Mussurova S, Santos J, Thimma M, Troukhan M, Fornasiero A, Green CD, Copetti D, Kudrna D, Llaca V, Lorieux M, **Zuccolo A***, Ware D, McNally K, Zhang J, Wing RA. Pan-genome inversion index reveals evolutionary insights into the subpopulation structure of Asian rice. **Nat Commun.** 2023 Mar 21;14(1):1567. doi: 10.1038/s41467-023-37004-y.

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-51) **A. Zuccolo***, S. Mfarrej, M. Celii, S. Mussurova, L.F. Rivera, V. Llaca, N. Mohammed, A. Pain, A. F. Alrefaei, A. F. Alrefaei, Wing R.A (2023), The gyrfalcon (*Falco rusticolus*) genome, **G3 Genes|Genomes|Genetics**, jkad001

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-50) M. Ventimiglia, G. Marturano, A. Vangelisti, G. Usai, S. Simoni, A. Cavallini, T. Giordani, L. Natali, **A. Zuccolo***, F. Mascagni. Genome-wide identification and characterisation of exapted transposable elements in the large genome of sunflower (*Helianthus annuus* L.), **The Plant Journal** Dec. 2022

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-49) Alsantely, A., Gutaker, R., Navarrete Rodríguez, M. E., ArrietaEspinoza, G., Fuchs, E. J., Costa de Oliveira, A., Tohme, J., **Zuccolo, A.**, Wing, R. A., & Fornasiero, A. (2022). The International Oryza Map Alignment Project (IOMAP): The Americas – Past achievements and future directions. **Journal of Experimental Botany**.

-48) S. Niu, J. Li, W. Bo, W. Yang, **A. Zuccolo**, S. Giacomello, X. Chen, F. Han, J. Yang, Y. Song, Y. Nie, B. Zhou, P. Wang, Q. Zuo, H. Zhang, J. Ma, J. Wang, L. Wang, Q. Zhu, H. Zhao, Z. Liu, X. Zhang, T. Liu, S. Pei, Z. Li, Y. Hu, Y. Yang, W. Li, Y. Zan, L. Zhou, J. Lin, T. Yuan, W. Li, Y. Li, H. Wei, H. Wu “The Chinese pine genome and methylome unveil key features of conifer evolution” **Cell** 2021 <https://doi.org/10.1016/j.cell.2021.12.006>.

-47) R. Lehmann, A. Kovařík, K. Ocalewicz, L. Kirtiklis, **A. Zuccolo**, J. Tegner, J. Wanzenböck, L. Bernatchez, D. Lamatsch, R. Symonová “DNA transposon expansion is associated with genome size increase in mudminnows” **Genome Biology and Evolution**. 2021 <https://doi.org/10.1093/gbe/evab228>

-46) Song J.-M., Xie W.-Z., Wang S., Guo Y.-X., Koo D.-H., Kudrna D., Gong C., Huang Y., Feng J.-W., Zhang W., Zhou Y., **Zuccolo A.**, Long E., Lee S., Talag J., Zhou R., Zhu X.-T., Yuan D., Udall J., Xie W., Wing R.A., Zhang Q., Poland J., Zhang J., and Chen L.-L. “Two Gap-free Reference Genomes and a Global View of the Centromere Architecture in Rice” **Molecular Plant**.

2021 <https://doi.org/10.1016/j.molp.2021.06.018>

-45) H. Yu, T. Lin, X. Meng, H. Du, J. Zhang, G. Liu, M. Chen, Y. Jing, L. Kou, X. Li, Q. Gao, Y. Liang, X. Liu, Z. Fan, Y. Liang, Z. Cheng, M. Chen, Z. Tian, Y. Wang, C. Chu, J. Zuo, J. Wan, Q. Qian, B. Han, **A. Zuccolo**, R.A. Wing, C. Gao, C. Liang, J. Li "A route to de novo domestication of wild allotetraploid rice" **Cell** 2021 Mar 4;184(5):1156-1170.e14.

-44) S. Mussurova, N. Al-Bader, **A. Zuccolo***, R.A. Wing "Potential of platinum standard reference genomes to exploit natural variation in the wild relatives of rice" **Frontiers in Plant sciences** 2020 September 15, doi: 10.3389/fpls.2020.579980

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-43) S. Pinosio, F. Marroni, **A. Zuccolo**, N. Vitulo, S. Mariette, G. Sonnante, F. A. Aravanopoulos, I. Ganopoulos, M. Palasciano, M. Vidotto, G. Magris, A. Iezzoni, G. G. Vendramin, M. Morgante "A draft genome of sweet cherry (*Prunus avium* L.) reveals genome-wide and local effects of domestication" **The Plant Journal** 2020 May 11; <https://doi.org/10.1111/tpj.14809>

-42) Y. Zhou, D. Chebotarov, D. Kudrna, V. Llaca, S. Lee, S. Rajasekar, N. Mohammed, N. Al-Bader, C. Sobel-Sorenson, P. Parakkal, L.J. Arbelaez, N. Franco, N. Alexandrov, N.R. Sackville Hamilton, H. Leung, R. Mauleon, M. Lorieux, **A. Zuccolo***, K. McNally, J. Zhang, R.A. Wing "A platinum standard pan-genome resource that represents the population structure of Asian rice" **Sci. Data** 2020 volume 7, Article number: 113

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-41) G. Usai, F. Mascagni, T. Giordani, A. Vangelisti, E. Bosi, **A. Zuccolo**, M. Ceccarelli, R. King, K. Hassani-Pak, L.S. Zambrano, A. Cavallini, L. Natali "Epigenetic patterns within the haplotype phased fig (*Ficus carica* L.) genome" **The Plant Journal** 2019 Dec. 5; doi.org/10.1111/tpj.14635

-4) G. Marturano, C. Canovi, F. Rossi, **A. Zuccolo*** "Transposable Elements in Spruce" (2020) "The Spruce Genome" pages 37-49 Springer Nature Switzerland AG, Editors: I. M. Porth and A. R. De la Torre

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-40) Y. Lin, J. Wang, N. Delhomme, B. Schiffthaler, G. Sundström, **A. Zuccolo**, B. Nystedt, T.R. Hvidsten, A. de la Torre, R.M. Cossu, M.P. Hoepfner, H. Lantz, D.G. Scofield, N. Zamani, A. Johansson, C. Mannapperuma, K.M. Robinson, N. Mähler, I.J. Leitch, J. Pellicer, E. Park, M. Van Montagu, Y. Van de Peer, M. Grabherr, S. Jansson, P.K. Ingvarsson, N. Street. "Functional and evolutionary genomic inferences in *Populus* through genome and population sequencing of American and European aspen" **Proc Natl Acad Sci USA**. 2018 Nov 13;115(46):E10970-E10978

-39) J. Stein, Y. Yu, D. Copetti, D. Zwickl, L. Zhang, C. Zhang, K. Chougule, D. Gao, A. Iwata, J. Goicoechea, S. Wei, J. Wang, Y. Liao, M. Wang, J. Jacquemin, C. Becker, D. Kudrna, J. Zhang, C. Maldonado, X. Song, S. Lee, P. Sanchez, **A. Zuccolo**, J. Ammiraju, J. Talag, A. Danowitz, L. Rivera, A. Gschwend, C. Noutsos, C. Wu, S. Kao, J. Zeng, F. Wei, Q. Zhao, Q. Feng, M. el Baidouri, M. Carpentier, E. Lasserre, R. Cooke, D. Farias, L. Maia, R. dos Santos, K. Nyberg, C. Fan, D. Weigel, K. Jena, T. Wicker, M. Chen, B. Han, R. Henry, Y. Hsing, N. Kurata, A. de Oliveira, O. Panaud, S. Jackson, C. Machado, M. Sanderson, M. Long, D. Ware, K. McNally, R. Mauleon, N. Alexandrov, J. Schmutz, D. Flowers, R. Wing. "Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus *Oryza*" - **Nature Genetics** – Nat Genet. 2018 Jan 22

-38) R.M. Cossu, C. Casola, S. Giacomello, A. Vidalis, D.G. Scofield, **A. Zuccolo***. "LTR retrotransposons show low levels of unequal recombination and high rates of intraelement gene

conversion in large plant genomes" **Genome Biology and Evolution** 2017 Dec 1;9(12):3449-3462 *Co-Corresponding author

-37) A. Lwin, E. Bertolini, M.E. Pè, **A. Zuccolo*** "Genomic skimming for identification of medium/highly abundant Transposable Elements in *Arundo donax* and *Arundo plinii*" - **Molecular Genetics and Genomics** 2017 Feb;292(1):157-171 10.1007/s00438-016-1263-3.
*Corresponding author

-36) T. Wicker, Y. Yu, G.Haberer, K.F.X. Mayer, P. Reddy Marri, S. Rounsley, M. Chen, **A. Zuccolo**, O. Panaud, R.A. Wing, S. Roffler. "DNA transposon activity is associated with increased mutation rates in genes of rice and other grasses" **Nature Communications** 7, 2016 Article number: 12790 doi:10.1038/ncomms127902016

-3) **A. Zuccolo*** "Repetitive Sequences" (2016) "The Kiwifruit Genome", pages 115-123. Springer International Publishing, Editors: R. Testolin, H. Huang and R. Ferguson.
*Corresponding author

-35) D. Cukrov, M. Zemiani, S. Brizzolara, A. Cestaro, F. Licausi, C. Luchinat, C. Santucci, C. Tenori, H. Van Veen, **A. Zuccolo**, B. Ruperti, P. Tonutti "Extreme hypoxic conditions induce selective molecular responses and metabolic reset in detached apple fruit" -. **Frontiers in Plant Sciences** 2016, 7: 146 10.3389/fpls.2016.00146

-34) Y.G. Gebre, E. Bertolini, M.E. Pè, **A. Zuccolo*** "Identification and characterization of abundant repetitive sequences in *Eragrostis tef* cv. Enatite genome" . **BMC Plant Biology** 2016, 16(1):39. doi: 10.1186/s12870-016-0725-4.
*Corresponding author

-33) D. Copetti, J. Zhang, M. El Baidouri, D. Gao, J. Wang, E. Barghini, R. Cossu, A. Angelova, C. Maldonado, S. Roffler, H. Ohyanagi, T. Wicker, C. Fan, **A. Zuccolo**, M. Chen, A. Costa de Oliveira, B. Han, R. Henry, Y. Hsing, N. Kurata, W. Wang, S. Jackson, O. Panaud, Rod A. Wing. "RiTE database: a resource database for genus-wide rice genomics and evolutionary biology" **BMC Genomics** 2015, 16:538

-32) **A. Zuccolo***, D. G. Scofield, E. De Paoli, M. Morgante. "The Ty1-*cop* LTR retroelement family PARTC is highly conserved in conifers over 200 MY of evolution" **Gene** 2015 (14 May 2015)

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-31) M. Dell'Acqua, **A. Zuccolo**, M. Tuna, L. Gianfranceschi, ME Pè. "Targeting environmental adaptation in the monocot model *Brachypodium distachyon*: a multi-faceted approach" **BMC Genomics** 2014, 15:801

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-29) M. Wang, Y. Yu, G. Haberer, P. Marri, C. Fan, J.L. Goicoechea, **A. Zuccolo**, X. Song, D. Kudrna, J. Ammiraju, R.M. Cossu, C. Maldonado, J. Chen, S. Lee, N. Sisneros, K. de Baynast, W. Golser, M. Wissotski, W. Kim, P. Sanchez, M. Ndjiondjop, K. Sanni, M. Long, J. Carney, O. Panaud, T. Wicker, C. Machado, M. Chen, K. Mayer, S.Rounsley, R. Wing. "The genome sequence of African rice (*Oryza glaberrima*) and evidence for independent domestication" **Nature Genetics** 2014 Sep;46(9):982-8

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-27) J. Stival Sena, I. Giguère, B. Boyle, P. Rigault, I. Birol, **A. Zuccolo**, K. Ritland, C. Ritland, J. Bohlmann, S. Jones, J. Bousquet, J. Mackay. "Evolution of gene structure in the conifer *Picea glauca*: a comparative analysis of the impact of intron size." **BMC Plant Biology**, 2014 Apr 16;14(1):95

-26) B. Nystedt, N. Street, A. Wetterbom*, **A. Zuccolo***, Y. Lin*, D. Scofield*, F. Vezzi, N. Delhomme, S. Giacomello, A. Alexeyenko, R. Vicedomini, K. Sahlin, E. Sherwood, M. Elfstrand, L. Gramzow, K. Holmberg, J. Hällman, O. Keech, L. Klasson, M. Koriabine, M. Kucukoglu, M. Käller, J. Luthman, F. Lysholm, T. Niittylä, A. Olson, N. Rilakovic, C. Ritland, J. Rosselló, J. Sena, T. Svensson, C. Talavera-López, G. Theißen, H. Tuominen, K. Vanneste, Z. Wu, B. Zhang, P. Zerbe, L. Arvestad, R. Bhalariao, J. Bohlmann, J. Bousquet, R. Garcia Gil, T. Hvidsten, P. de Jong, J. MacKay, M. Morgante, K. Ritland, B. Sundberg, S. Lee Thompson, Y. Van de Peer, B. Andersson, O. Nilsson, P. Ingvarsson, J. Lundeberg, S. Jansson. "The Norway spruce genome sequence and conifer genome evolution." **Nature**, 2013 May 30;497(7451):579-84
*joint second author

-25) The International Peach Genome Initiative, I. Verde, A. Abbott, S. Scalabrin, S. Jung, S. Shu, F. Marroni, T. Zhebentyayeva, M. Dettori, J. Grimwood, F. Cattonaro, **A. Zuccolo**, L. Rossini, J. Jenkins, E. Vendramin, L. Meisel, V. Decroocq, B. Sosinski, S. Prochnik, T. Mitros, A. Policriti, G. Cipriani, L. Dondini, S. Ficklin, D. Goodstein, P. Xuan, C. Del Fabbro, V. Aramini, D. Copetti, S. Gonzalez, D. Horner, R. Falchi, S. Lucas, E. Mica, J. Maldonado, B. Lazzari, D. Bielenberg, R. Pirona, M. Miculan, A. Barakat, R. Testolin, A. Stella, S. Tartarini, P. Tonutti, P. Arús, A. Orellana, C. Wells, D. Main, G. Vizzotto, S. Silva, F. Salamini, J. Schmutz, M. Morgante & D. Rokhsar "The high-quality draft genome of peach (*Prunus persica*) identifies unique patterns of genetic diversity, domestication and genome evolution" **Nature genetics** 2013 May;45(5):487-94

-24) K. Mayer, R. Waugh, P. Langridge, T. Close, R. Wise, A. Graner, T. Matsumoto, K. Sato, A. Schulman, R. Ariyadasa, D. Schulte, N. Poursarebani, R. Zhou, B. Steuernagel, M. Mascher, U. Scholz, B. Shi, K. Madishetty, J. Svensson, P. Bhat, M. Moscou, J. Resnik, G. Muehlbauer, P. Hedley, H. Liu, J. Morris, Z. Frenkel, A. Korol, H. Bergès, S. Taudien, M. Felder, M. Groth, M. Platzer, A. Himmelbach, S. Lonardi, D. Duma, M. Alpert, F. Cordero, M. Beccuti, G. Ciardo, Y. Ma, S. Wanamaker, F. Cattonaro, V. Vendramin, S. Scalabrin, S. Radovic, R. Wing, M. Morgante, T. Nussbaumer, H. Gundlach, M. Martis, J. Poland, M. Pfeifer, C. Moisy, J. Tanskanen, **A. Zuccolo**, M. Spannagl, J. Russell, A. Druka, D. Marshall, M. Bayer, D. Swarbreck, D. Sampath, S. Ayling, M. Febrer, M. Caccamo, T. Tanaka, S. Wannamaker, T. Schmutz, J. Brown, G. Fincher, N. Stein "A physical, genetic and functional sequence assembly of the barley genome" **Nature** 2012 November 29 Volume 491, Issue 7426, Pages 711-716

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- 22) **A. Zuccolo**, J.E. Bowers, J.C. Estill, Z. Xiong, M. Luo, A. Sebastian, J.L. Goicoechea, K. Collura, Y. Yu, Y. Jiao, J. Duarte, H. Tang, S. Ayyampalayam, S. Rounsley, D. Kudrna, A.H. Paterson, J.C. Pires, A. Chanderbali, D.E. Soltis, S. Chamala, B. Barbazuk, P.S. Soltis, V.A. Albert, H. Ma, D. Mandoli, J. Banks, J.E. Carlson, J. Tomkins, C.W. Depamphilis, R.A. Wing, J. Lebens-Mack. "A physical map for the *Amborella trichopoda* genome sheds light on the evolution of angiosperm genome structure" **Genome Biology** 2011 May 27;12(5):R48.
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- 20) **A. Zuccolo**, A. Sebastian, Y. Yu, S. Jackson, S. Rounsley, D. Billheimer and R.A. Wing "Assessing the Extent of Substitution Rate Variation of Retrotransposon Long Terminal Repeat Sequences in *Oryza sativa* and *Oryza glaberrima*" - **RICE** 2010, 10.1007/s12284-010-9046-7
- 19) L. Lin, G.J. Pierce, J.E. Bowers, J.C. Estill, R.O. Compton, L.K. Rainville, C. Kim, C. Lemke, J. Rong, H. Tang, X. Wang, M. Braidotti, A.H. Chen, K. Chicola, K. Collura, E. Epps, W. Golser, C. Grover, J. Ingles, S. Karunakaran, D. Kudrna, J. Olive, N. Tabassum, E. Um, M. Wissotski, Y. Yu, **A. Zuccolo**, M.U. Rahman, D.G. Peterson, R.A. Wing, J.F. Wendel and A.H. Paterson "A draft physical map of a D-genome cotton species (*Gossypium raimondii*)"- **BMC Genomics** 2010, 11:395
- 18) B. Hurwitz, D. Kudrna, Y. Yu, A. Sebastian, **A. Zuccolo**, S. Jackson, D. Ware, R. Wing, S. Lincoln "Rice structural variation: a comparative analysis of structural variation between rice and three of its closest relatives in the genus *Oryza*" -2010 **The Plant Journal**
- 17) P.S. Schnable, D. Ware, R.S. Fulton, J.C. Stein, F. Wei, S. Pasternak, C. Liang, J. Zhang, L. Fulton, T.A. Graves, P. Minx, A. D. Reily, L. Courtney, S.S. Kruchowski, C. Tomlinson, C. Strong, K. Delehaunty, C. Fronick, B. Courtney, S. M. Rock, E. Belter, F. Du, K. Kim, R.M. Abbott, M. Cotton, A. Levy, P. Marchetto, K. Ochoa, S.M. Jackson, B. Gillam, W. Chen, L. Yan, J. Higginbotham, M. Cardenas, J. Waligorski, E. Applebaum, L. Phelps, J. Falcone, K. Kanchi, T. Thane, A. Scimone, N. Thane, J. Henke, T. Wang, J. Ruppert, N. Shah, K. Rotter, J. Hodges, E. Ingenthron, M. Cordes, S. Kohlberg, J. Sgro, B. Delgado, K. Mead, A. Chinwalla, S. Leonard, K. Crouse, K. Collura, D. Kudrna, J. Currie, R. He, A. Angelova, S. Rajasekar, T. Mueller, R. Lomeli, G. Scara, A. Ko, K. Delaney, M. Wissotski, G. Lopez, D. Campos, M. Braidotti, E. Ashley, W. Golser, H. Kim, S. Lee, J. Lin, Z. Dujmic, W. Kim, J. Talag, **A. Zuccolo**, C. Fan, A. Sebastian, M. Kramer, L. Spiegel, L. Nascimento, T. Zutavern, B. Miller, C. Ambroise, S. Muller, W. Spooner, A. Narechania, L. Ren, S. Wei, S. Kumari, B. Faga, M.J. Levy, L. McMahan, P. Van Buren, M. W. Vaughn, K. Ying, C. Yeh, S.J. Emrich, Y. Jia, A. Kalyanaraman, A. Hsia, W.B. Barbazuk, R.S. Baucom, T.P. Brutnell, N.C. Carpita, C. Chaparro, J. Chia, J. Deragon, J.C. Estill, Y.Fu, J.A. Jeddeloh, Y. Han, H. Lee, P. Li, D.R. Lisch, S. Liu, Z. Liu, D.H. Nagel, M.C. McCann, P. SanMiguel, A.M. Myers, D. Nettleton, J. Nguyen, B.W. Penning, L. Ponnala, K.L. Schneider, D.C. Schwartz, A. Sharma, C. Soderlund, N.M. Springer, Q. Sun, H. Wang, M. Waterman, R. Westerman, T.K. Wolfgruber, L. Yang, Y. Yu, L. Zhang, S. Zhou, Q. Zhu, J.L. Bennetzen, R.K. Dawe, J. Jiang, N. Jiang, G.G. Presting, S.R. Wessler, S. Aluru, R.A. Martienssen, S.W. Clifton, W.R. McCombie, R.A. Wing, R.K. Wilson "The B73 Maize Genome: Complexity, Diversity, and Dynamics" -**Science** 326, 1112 (2009)
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- 15) H. Zhang, J. K. DiBaise, **A. Zuccolo**, D. Kudrna, M. Braidotti, Y. Yu, P. Parameswaran, M. D. Crowell, R. Wing, B. E. Rittmann, and R. Krajmalnik-Brown- "Human gut microbiota in obesity and after gastric bypass" **Proc Natl Acad Sci U S A.** 2009 Feb 17;106(7):2365-70

- 14) L. Natali, M. Ceccarelli, T. Giordani, V. Sarri, **A. Zuccolo**, I. Jurman, M. Morgante, A. Cavallini, and P. G. Cionini "Phylogenetic relationships between annual and perennial species of *Helianthus*: evolution of a tandem repeated DNA sequence and cytological hybridization experiments"- **Genome**. 2008 Dec; 51(12):1047-1053
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- 12) V. Sarri, S. Minelli, F. Panara, M. Morgante, I. Jurman, **A. Zuccolo**, P.G. Cionini. "Characterization and chromosomal organization of satellite DNA sequences in *Picea abies*"- **Genome**. 2008 Sep;51(9):705-13.
- 11) **A. Zuccolo**, S. Jetty, H. Kim, A. Sanhyal, S. Jackson R.A. Wing "Rapid and differential proliferation of the Ty3-Gypsy LTR-retrotransposon *Atlantys* in the genus *Oryza*" – "**RICE**", 2008 Aug 10.1007/s12284-008-9002-y
- 10) Soltis D, Albert V, Leebens-Mack J, Palmer JD, Wing RA, dePamphilis CW, Ma H, Carlson JE, Altman N, Kim S, Kerr Wall P, **A. Zuccolo** and Soltis PS "The *Amborella* genome: an evolutionary reference for plant biology" **Genome Biology** 2008, 9:402
- 9) JA Schlueter, JL Goicoechea, K Collura, N Gill, J Lin, Y Yu, D Kudrna, **A Zuccolo**, CE Vallejos, M Muñoz-Torres, MW Blair, J Tohme, J Tomkins, P McClean, RA Wing, S A Jackson "BAC-end Sequence Analysis and a Draft Physical Map of the Common Bean (*Phaseolus vulgaris* L.) Genome Status" **Tropical Plant Biology** 2008 10.1007/s12042-007-9003-9
- 8) Rice Annotation Project, Tanaka T, Antonio BA, Kikuchi S, Matsumoto T, Nagamura Y, Numa H, Sakai H, Wu J, Itoh T, Sasaki T, Aono R, Fujii Y, Habara T, Harada E, Kanno M, Kawahara Y, Kawashima H, Kubooka H, Matsuya A, Nakaoka H, Saichi N, Sanbonmatsu R, Sato Y, Shinso Y, Suzuki M, Takeda J, Tanino M, Todokoro F, Yamaguchi K, Yamamoto N, Yamasaki C, Imanishi T, Okido T, Tada M, Ikeo K, Tateno Y, Gojobori T, Lin YC, Wei FJ, Hsing YI, Zhao Q, Han B, Kramer MR, McCombie RW, Lonsdale D, O'Donovan CC, Whitfield EJ, Apweiler R, Koyanagi KO, Khurana JP, Raghuvanshi S, Singh NK, Tyagi AK, Haberer G, Fujisawa M, Hosokawa S, Ito Y, Ikawa H, Shibata M, Yamamoto M, Bruskiwich RM, Hoen DR, Bureau TE, Namiki N, Ohyanagi H, Sakai Y, Nobushima S, Sakata K, Barrero RA, Sato Y, Souvorov A, Smith-White B, Tatusova T, An S, An G, Oota S, Fuks G, Fuks G, Messing J, Christie KR, Lieberherr D, Kim H, **A. Zuccolo**, Wing RA, Nobuta K, Green PJ, Lu C, Meyers BC, Chaparro C, Piegu B, Panaud O, Echeverria M. "The Rice Annotation Project Database (RAP-DB): 2008 update" **Nucleic Acids Research**. 2008 Jan;36(Database issue): D1028-33. Epub 2007 Dec 17
- 7) **A. Zuccolo**, Sebastian A., Talag J., Yu Y., Kim H., Collura K., Kudrna D., Wing R. "Transposable element distribution, abundance and role in genome size variation in the genus *Oryza*" **BMC Evolutionary Biology** 2007, 7:152
- 6) Jetty S.*, **A. Zuccolo***, Yu Y., Song X., Piegu B., Chevalier F., Walling J., Ma J., Talag J., Brar D., SanMiguel P., Jiang N., Jackson S., Panaud O., Wing R. "Evolutionary dynamics of an ancient retrotransposon family provides insights into evolution of genome size in the genus *Oryza*" **The plant Journal** 2007 Oct;52(2):342-51
* These two authors equally contributed to this work.
- 5) Ceccarelli M, Sarri V, Natali L, Giordani T, Cavallini A, **A. Zuccolo**, Jurman I, Morgante M, Cionini PG. "Characterization of the chromosome complement of *Helianthus annuus* by in situ

hybridization of a tandemly repeated DNA sequence." **Genome**. 2007 May;50(5):429-34.

-4) Chaparro C., Guyot R., **A. Zuccolo**, Piegue B. and O. Panaud "RetrOryza: a database of the rice LTR-retrotransposons" **Nucleic Acids Research** 2007 Jan; 35(Database issue): D66-D70.

-2) Wing, R.A., H.R. Kim, J.L. Goicoechea, Y. Yu, D. Kudrna, **A. Zuccolo**, S.S. Ammiraju Jetty, M. Luo, W. Nelson C. Soderlund, P. SanMiguel, N. Gill, J. Walling, S. Jackson, B. Hurwitz, D. Ware, L. Stein, D. Brar, D. Mackill. (2006) "The Oryza Map Alignment Project (OMAP): A new resource for comparative genome studies within Oryza." "Rice Genetics V", pages 51-64. The International Rice Research Institute Press, Editors: G.S. Khush, D.S. Brar and B. Hardy.

-1) Wing, R.A., H.R. Kim, J.L. Goicoechea, Y. Yu, D. Kudrna, **A. Zuccolo**, S.S. Ammiraju Jetty, M. Luo, W. Nelson C. Soderlund, P. SanMiguel, N. Gill, J. Walling, S. Jackson, B. Hurwitz, D. Ware, L. Stein, D. Brar, D. Mackill. (2006). "The Oryza Map Alignment Project (OMAP): A new resource for comparative genome studies within Oryza" "Rice Functional Genomics Challenges, Progress and Prospects", pages 395-410, Editor Upadhyaya Narayana (Springer) 2007

-3) Luo M., Kim H., Kudrna D., Sisneros NB, Lee S., Mueller C., Collura K., **A. Zuccolo**, Buckingham B., Grim S.M., Yanagiya K., Inoko H, Shiina T., Flajnik M.F., Wing R.A. and Ohta Y. "Construction of a Nurse Shark (*Ginglymostoma cirratum*) Bacterial Artificial Chromosome (BAC) Library and a Preliminary Genome Survey" **BMC Genomics**, 2006 May 3;7:106

-2) Policriti A., Vitacolonna N., Morgante M., **A. Zuccolo**, "Structured motif search" **Journal of Computational Biology** 2005 Oct;12(8):1065-82.

-1) Morgante M., Brunner S., Pea G., Fengler K., **A. Zuccolo**, Rafalski A. "Gene duplication and exon shuffling by helitron-like transposons generate intraspecies diversity in maize" **Nature Genetics** 2005 Sep;37(9):997-1002

-Research grants:

2012-2015 APOMIS2013 40.000 Euros from Scuola Superiore Sant'Anna, Italy, to support the following research project: "Genomics study of apomictic species"

-Ad hoc reviewer for Journals:

Nature Communications, The Plant Cell, Plant Physiology, The Plant Journal, Trends in Plant Sciences, Molecular Ecology, Molecular Plant, Genome Biology and Evolution, GigaScience, Genomics, BMC Genomics, BMC Evolutionary Biology, BMC Plant Biology, BMC Bioinformatics, Frontiers in Plant Sciences, Frontiers in Genetics, Frontiers in Microbiology, Plant Science, Molecular Genetics and Genomics, PlosONE, Annals of Botany, Journal of Plant Physiology, Tree Genetics and Genomes, Journal of Heredity, Plant Cell Reports, Plant Genetics Resources, Genes and Genomics, Postharvest Biology and Technology, PeerJ, Gene, Plant Gene, Genetica, Genome, Plant Ecology and Diversity, Genetics and Molecular Biology, Zeitschrift für Naturforschung C, Biologia Plantarum, Open Biology, Plant Systematics and Evolution, Biology (MDPI), Journal of Medicinal Plant Research, Journal of Advanced Research

Agencies:

- USA National Science Foundation grant proposals;
- Italian Ministry of Education, University and Research FIRB grant proposals
- Italian Ministry of Education, University and Research, VQR (Research Quality evaluation)

-Associate editor:

- Frontiers in Plant Bioinformatics (2021-present)
- BMC Genomics (2018-present)
- The Scientific World Journal (2011-2022),
- Dataset Papers in Biology (2011-2016)

-Review editor:

- Frontiers in Plant Science (2017-present)

-Faculty committees:

-Member of the Scientific Board of the PhD program in Agrobiosciences at the Scuola Superiore Sant'Anna, Pisa Italy (Since December 2011)

-Member of the Scientific Board of the PhD program in Agrobiodiversity at the Scuola Superiore Sant'Anna, Pisa Italy (December 2011-April 2022)

-Member of the Scientific Board of the PhD program in Translational Medicine at the Scuola Superiore Sant'Anna, Pisa Italy (December 2011-April 2022)

-Supervision of Postdoctoral Fellows:

- 2012-2013 Dr. Stefania Giacomello
- 2014-2015 Dr. Rosa Maria Cossu

-Participation to Practical Courses, Workshops and Genome Annotation jamboree:

-“UCSD Next-Gen Sequencing meeting”- San Diego, CA, November 9-10, 2008

-“Computational and Comparative genomics”- practical course, Cold Spring Harbor Laboratory, NY USA, November 8-14, 2006

-“Rice annotation project 2” Tsukuba, Japan February 1-3, 2006

-“Acquiring and analyzing genomic sequence data” - practical course, Cold Spring Harbor Laboratory, NY USA, March 9-26, 2002

-“Introduction to Biosafety and Risk Assessment for the Environmental Release of Genetically Modified Organisms (GMOs): Theoretical Approach and Scientific Background”, workshop, Trieste, AREA science park, International Centre for Genetic Engineering and Biotechnology-ICGEB Italy, March 5-9 2001

-“Bioinformatics: Computer methods in molecular biology”, Practical course, AREA science park, International Centre for Genetic Engineering and Biotechnology-ICGEB, Trieste, July 9-16 1999

-“Bioinformatics: the functional characterisation of the biosequences with the employing of computer”, University of Udine, January 14,15 and 16, 1997

-Congress and workshop oral communications, invited lectures and seminars:

-Oral communication:“Disentangling the Genome Wide Contribute of Structural Variations and Transposable Elements to Drought Resistance in the Model Species Rice” “Plant and Animal

Genome XXX Conference”, San Diego, CA, January 13-18, 2023

-Oral communication: “Structural Variant identification and preliminary characterization in two *Oryza alta* accessions” 19th International Symposium on Rice Functional Genomics, Phuket, Thailand, November 4th 2022

-Oral communication: “Detecting Structural Variants (SVs) using Pacbio HiFi reads” 19th International Symposium on Rice Functional Genomics, Phuket, Thailand, November 4th 2022

-Seminar: “TEs dynamics in spruce: a better genome assembly to test previous hypotheses and address new questions” KAW Conifer Genomics project meeting, Umea University, Sweden, April 25th, 2022

-Seminar: “Transposable elements in plants: from comparative analyses to a potential exploitation as a source of genetic variability” School of Sciences and Humanities, Nazarbayev University Kazakhstan April 22nd, 2022

-Seminar: “Transposable elements in plants: from comparative analyses to a potential exploitation as a source of genetic variability” Spring Lecture Series, Center for Desert Agriculture, KAUST, Saudi Arabia March 25th, 2021

-Seminar: “Whole genome sequencing: the importance and application in life sciences”; webseminar as part of webinar series of Genetics and Molecular Biotechnology research group at the Institut Teknologi Bandung School of Life Sciences and Technology, Indonesia, November 6th, 2020

-Seminar: “Low Levels of Unequal Recombination and High Rates of Intraelement Gene Conversion affecting LTR retrotransposons in Large Plant Genomes” Applied Genomics Institute, Udine, Italy, October 12th 2018

-Seminar: “The role of methylation in the interplay between Low Levels of Unequal Recombination and High Rates of Intraelement Gene Conversion affecting LTR retrotransposons in Large Plant Genomes”. “Plant Epigenetics at the Botanical Garden” University of Padova, Padova, Italy, September 14th 2018

-Oral communication: “Unequal recombination targeting LTR-retrotransposons is greatly reduced in conifers” **A. Zuccolo**, R.M. Cossu, S. Giacomello- “2nd Conifer Genome Summit” Forêt Montmorency, Québec, Canada 16-18 June 2014.

-Oral communication: “A comparative overview of Transposable Elements distribution and dynamics in conifers.” **A. Zuccolo**, S. Giacomello- “The 2013 Conifer Genome Sequencing Summit” Björkliden, Lapland, Sweden June 14 - 17 2013.

-Seminar: “The repetitive fraction of the Norway spruce genome (and other conifers...)”. Arizona Genomics Institute (The University of Arizona), Tucson, AZ, USA, November 28th, 2012

-Seminar: “Bioinformatics approaches to plant comparative genomics.” 5th International PhD School in Plant Development, Pontignano, Siena-Italy, September 2012

-Seminar: “The Transposable Element landscape of the genus *Oryza*: a comparative approach”. Parco Tecnologico Padano, Lody-Italy, May 3rd 2012

-Oral communication: “*Oryza* TE-DB: a database of Transposable Elements in the *Oryza* spp.” **A.**

Zuccolo, M. Braidotti, A. Sebastian, A. Angelova, C. Chaparro, F. Sabot, O. Panaud and Rod A. Wing- "Plant and Animal Genome XIX Conference", San Diego, CA, January 15-19, 2011

-Seminar: "Comparative Analysis of Transposable Elements in the Genus *Oryza*" Scuola Superiore Sant'Anna, Pisa, Italy September 10th, 2009

-Oral communication: "Assessment of the extent of substitution rate variation of Long Terminal Repeat sequences in *Oryza sativa* and *Oryza glaberrima*" **A. Zuccolo**, A. Sebastian, Y. Yu, R.A. Wing-"Western American Society of Plant Biologists-Annual Meeting" Tucson, AZ, April 25-26, 2009

-Oral communication: "A Preliminary Survey Of The Structure And Content Of The *Amborella* Genome: Characterization Of The Repeat Landscape And Identification Of Syntenic Blocks With Rice, Arabidopsis And Poplar" **A. Zuccolo**, A. Sebastian, ..., J. Leebens-Mack, R. Wing-"Plant and Animal Genome XVI Conference", San Diego, CA, January 12-16, 2008

-Oral communication: "Characterisation, genomic organisation and phylogenetic analysis of repetitive DNA in Norway spruce"-F. Cattonaro, I. Jurman, **A. Zuccolo**, M. Vizzi, M. Morgante-IUFRO conference: "Genetic response of forest systems to changing environmental conditions - analysis and management" University of Munich, Germany, September 12-17, 1999

-Participation to Congresses and Meetings:

-“Plant and Animal Genome XXX Conference”, San Diego, CA, January 13-18, 2023

-19th International Symposium on Rice Functional Genomics, Phuket, Thailand, November 4th-7th 2022

-“Transposable Elements” Cold Spring Harbor Laboratory, NY, USA October 11 - 15 2022

-“18th International Symposium on Rice Functional Genomics”, Barcelona, Spain, November 3-5, 2021

-“Transposable Elements- Virtual meeting” Cold Spring Harbor Laboratory, NY, USA, November 6th-9th, 2020

-“Annual PacBio EMEA User Group Meeting (UGM)”-Milan, Italy, November 14-25 2019

-“Transposable Elements” Cold Spring Harbor Laboratory, NY, USA November 1-4 2018

-“Plant Genomes in a Changing Environment 2018”-Hinxton, Cambridge UK 24-26 October 2018

-“2nd Uppsala Transposon Symposium” Uppsala, Sweden, October 4-5 2018

-“Plant Genomes & Biotechnology: from genes to networks” – Cold Spring Harbor Laboratory, NY, USA, November 29th-December 2nd, 2017

-“LXI annual congress of the Italian Society of Agriculture Genetics” - Pisa, Italy, September 19-22 2017

-“Annual meeting of the Society for Molecular Biology and Evolution-SMBE”, Wien, Austria 12-16 July 2015

-“IUFRO Tree Biotechnology Conference: Forests: the importance to the planet and society”, Florence, Italy 8-12 June 2015

-“2nd Conifer Genome Summit” Forêt Montmorency, Québec, Canada 16-18 June 2014

-“The 2013 Conifer Genome Sequencing Summit” Björkliden, Lapland, Sweden June 14 - 17 2013

-“Plant and Animal Genome XX Conference”, San Diego, CA, January 14-18, 2012

-“Plant and Animal Genome XIX Conference”, San Diego, CA, January 15-19, 2011

-“Western American Society of Plant Biologists-Annual Meeting”-Tucson, AZ, April 25-26, 2009

-“2nd International Conference and Workshop Genomic Impact of Eukaryotic Transposable Elements”- Asilomar, CA, February 6-10, 2009

-“UCSD Next-Gen Sequencing meeting”- San Diego, CA, November 9-10, 2008

-“Plant and Animal Genome XVI Conference”, San Diego, CA, January 12-16, 2008

-“5th Plant Genomics European Meeting” Venice, Italy, October 11-14, 2006

- “4th International Symposium on Rice Functional Genomics” Montpellier, France, October 9-11th, 2006
- “Genomes, Evolution and Bioinformatics” Tempe, AZ USA May 24-28, 2006
- “Genomics of closely related organisms” Tucson, AZ USA January 12-14, 2006
- “2nd International Symposium on Rice Functional Genomics” Tucson, AZ USA, November 15-17th, 2004
- “XLVIII annual; congress of the Italian Society of Agriculture Genetics” - Lecce, Italy, September 15-18 2004
- “V convegno della Federazione Italiana Scienze della Vita, FISV” – Rimini, Italy, October 10-13 2003
- “XLVII annual congress of the Italian Society of Agriculture Genetics” – Verona, Italy, September 24-27 2003
- “Molecular Evolution; Evolution, Genomics, Bioinformatics”- Sorrento (Naples) June 13-16 2002
- “XLV annual congress of the Italian Society of Agriculture Genetics” Salsomaggiore Terme, Italy, September 26-29 2001
- “Annual congress of the Italian Society of Agriculture Genetics”- Bologna, Italy, September 20-23 2000
- “Genetic response of forest systems to changing environmental conditions - analysis and management”, IUFRO conference University of Munich, Germany, September 12-17 1999

DIDACTIC ACTIVITY

-Teaching and mentoring:

- “Transposable elements” 101 module as part of the Molecular Genetics course at KAUST, Kingdom of Saudi Arabia, 2020-2022
- “Advanced Genomics” course at University of Pisa, Italy, 2014-2020 (MSc students)
- “Complement of Bioinformatics” at the Scuola Superiore Sant’Anna, Pisa-Italy 2016-2019 (Msc and PhD students)
- “Introduction to Bioinformatics” at the Scuola Superiore Sant’Anna, Pisa-Italy 2013-2015 (MSc and PhD students)
- “Applied Bioinformatics” at the Scuola Superiore Sant’Anna, Pisa-Italy- 2013-2015 (MSc and PhD students)
- “Bioinformatics” at University of Pisa, Italy, 2014-2018 (MSc students)
- “Integrative Biomedicine II” at the Scuola Superiore Sant’Anna, Pisa-Italy, 2014 (MD students)
- “Elements of Evolutionary Biology” at the Scuola Superiore Sant’Anna, Pisa-Italy, 2015, 2016, 2018 (MSc and PhD students)
- “Bioinformatics I” at the University of Udine-Italy, 2004 (BSc students)

-PhD and MSc thesis supervised:

- “Characterization of Long Terminal Repeat Retroelements and identification of exaptation events involving Transposable Elements in conifer genomes: a comparative approach”. PhD student: Giovanni Marturano; Advisor: Dr. **Andrea Zuccolo**; PhD Programme in Agrobiosciences, Scuola Superiore Sant’Anna, Pisa. Graduated in May 2020 with *Summa cum Laude*

-”Transcriptome Sequencing and Characterization of the Repetitive Landscape in the Orphan Crop *Eragrostis tef*”. PhD student: Yohannes Gebre; Advisors: Dr. **Andrea Zuccolo**, Prof. Mario Enrico Pè; PhD Programme in Agrobiosciences, Scuola Superiore Sant’Anna, Pisa February 2018

-”The repetitive component of giant reed genome *Arundo donax* L.” PhD Student: Aung Kyaw Lwin; Advisors: Dr. **Andrea Zuccolo**, Prof. Mario Enrico Pè; PhD Programme in Agrobiosciences, Scuola Superiore Sant’Anna, Pisa, May 2016

-”Identification and characterization of Transposable Element exaptation events in the *Oryza sativa* genome” MSc student: Elisabetta Caciolli; Advisors: Dr. **Andrea Zuccolo**, Dr. Giovanni Marturano, Dipartimento di Biologia, University of Pisa and Life Sciences Institute Scuola Sant’Anna, Pisa (MSc thesis, expected: April 2021)

-”Identification and characterization of LINE retroelements in conifer genomes” MSc student: Camilla Canovi; Advisors: Dr. **Andrea Zuccolo**, Dr. Rodolfo Bernardi, Dipartimento di Scienze Agrarie, Alimentari e Agro-ambientali, University of Pisa, May 2018 (MSc thesis)

-”sRNA role in regulating Transposable Elements activity in *Picea abies* genome” MSc student: Federico Rossi; Advisors: Dr. **Andrea Zuccolo**, Dr. Rodolfo Bernardi, Dipartimento di Scienze Agrarie, Alimentari e Agro-ambientali, University of Pisa, October 2015 (MSc thesis)

-”Structured motifs search in DNA sequences”; MSc Student: Simone Scalabrin; Advisors: Professor Alberto Policriti; Coauthors: Dr. Nicola Vitacolonna, Dr. **Andrea Zuccolo**. Department of Mathematics and Computer Science at University of Udine, April 2003 (MSc thesis)

-”A database to store and to manage nucleotidic sequences”; MSc Student: Michele Braidotti; Advisor: Professor Angelo Montanari; Coauthor: Dr. **Andrea Zuccolo**. Department of Mathematics and Computer Science at University of Udine, July 2002 (MSc thesis)

-Participation to PhD and MSc thesis defense committees

- Member of evaluation committee for Pamela Vetrano, Camilla Vullo, “Licenza Magistrale” degree (MSc degree) Plant sciences and Plant Biotechnologies, Scuola Sant’Anna Pisa, Italy, June 15th 2022

-Member of evaluation committee for Aseel Alsantely, MSc degree, King Abdullah University of Science and Technology Thuwal, Kingdom of Saudi Arabia November 10th 2020

-Member of evaluation committee for Liubov Gapa, MSc degree, King Abdullah University of Science and Technology Thuwal, Kingdom of Saudi Arabia November 19th 2019

-Member of evaluation committee for Camilla Canovi, MSc degree in Plant and Microbial Biotechnologies, Università di Pisa, Italy, May 22nd 2018

-Opponent in the doctoral examination procedure for Chiara Mancini, PhD program in Agrobiosciences, Scuola Superiore Sant’Anna, Pisa, Italy, February 5th 2018

- Opponent in the doctoral examination procedure for Yohannes Gebre, PhD program in Agrobiodiversity, Scuola Superiore Sant'Anna, Pisa, Italy, February 2018
- Opponent in the doctoral examination procedure for Benedetta Svezia, PhD program in Agrobiodiversity, Scuola Superiore Sant'Anna, Pisa, Italy, October 2017
- Opponent in the doctoral examination procedure for Alice Brunazzi, PhD program in Agrobiosciences, Scuola Superiore Sant'Anna, Pisa, Italy, September 19th 2017
- doctoral examination procedure for Aung Kyaw Lwin, PhD program in Agrobiodiversity, Scuola Superiore Sant'Anna, Pisa, Italy, May 3rd 2016
- Opponent in the doctoral examination procedure for Flavia Mascagni, PhD program in "Scienza delle Produzioni Vegetali" ("Plant and crop sciences"), Università di Pisa, Italy, January 29th 2016
- Member of evaluation committee for Federico Rossi, MSc degree in Plant and Microbial Biotechnologies, Università di Pisa, Italy, October 17th 2015
- Opponent in the doctoral examination procedure for Daniela Lopez Pam Pinto, PhD program in "Agrobioscienze" ("Agrobiosciences"), Scuola Superiore Sant'Anna, Pisa, Italy, September 29th 2015
- Opponent in the doctoral examination procedure for Elena Barghini, PhD program in "Biotecnologie Molecolari" ("Molecular Biotechnologies"), Università di Pisa, Italy, March 18th 2014
- Opponent in the doctoral examination procedure for Marco Pietrella, PhD program in Agrobiodiversity, Scuola Superiore Sant'Anna, Pisa, Italy, June 24th 2013
- Opponent in the doctoral examination procedure for Rosa Maria Cossu, PhD program in "Biotecnologie Molecolari" ("Molecular Biotechnologies"), Università di Pisa, Italy, March 23rd 2012
- doctoral examination procedure for Federico Manuel Giorgi , PhD Program in "Molekulare Pflanzenphysiologie" ("Molecular Plant Physiology"), Potsdam University, Germany, October 2011