Mario Enrico Pè – Curriculum vitae

PERSONAL DETAILS

Name: Mario Enrico Pè, Professor

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PROFILE

Current position: Dean of the Academic Class of Experimental Sciences at Scuola Superiore Sant'Anna

- Component of the Academic Senate of Scuola Superiore Sant'Anna
- Full professor of Agricultural Genetics
- Coordinator of the International Doctoral Programme in Agrobiodiversity, Scuola Superiore Sant'Anna
- President of the Italian Society of Agricultural Genetics (SIGA)
- Member of the Italian Academy of Grape and Wine "Accademia Nazionale della Vite e del Vino"
- Member of the National Academy "Accademia dei Georgofili"
- Member of the national Academy "Accademia dei Fisiocritici"
- Coordinator of the Genetics Lab at the Institute of Life Sciences, Scuola Superiore Sant'Anna.

Currently the group is composed by two Assistant Professors, three Post-doctoral fellows and 7 PhD students

EDUCATION

- 2007: Full professor of Genetics at Scuola Superiore Sant'Anna di Pisa, Italy
- 2000: Associate professor of Agricultural Genetics at University of Milan, Italy
- 1984: Assistant professor of Genetics at the University of Milan, Italy
- 1979: Master degree in Agricultural Sciences *cum laude*

PROFESSIONAL EXPERIENCE

- 2013 2016: Director of the Institute of Life Sciences
- 2007 2009: Vice president of the Italian Society of Agricultural Genetics (SIGA)
- 2005: National coordinator of the French-Italian initiative for the structural and functional characterization of the grapevine genome (VIGNA)
- 2000 2002: In the Board of the Italian Association of Genetics (AGI)
- 1999: Visiting scientist at University of California San Diego
- 1997: Visiting scientist of Ministry of Agriculture, Forestry and Fishery of Japan at the Rice Genome Project, Tsukuba, Japan
- 1994-1996 Scientific advisor in Genetics and Molecular Biology at the Indonesian National Institute for the Development and Application of Biotechnology, Serpong, Indonesia

Mario Enrico Pè's research activity involves two major research areas, each represented by complementary research lines.

AREA 1 Genetic and molecular bases of complex traits in crops

This area comprises several research lines, in which methods and concepts of classical and modern quantitative genetics, based on the use of molecular markers for the identification of chromosomal regions involved in phenotypic variation of quantitative traits are applied. A recent development is the production and characterization of a MAGIC population of maize for the fine dissection of traits of agronomic interest in maize. From this MAGIC population a Recombinant Intercrossed (RIX) population has been also developed to study phenotypic variation in heterozygous maize genotypes. The specific research lines are listed here below.

- 1.1.Studies on yield component and yield stability in cereals
- 1.2 Analysis of genome structure in crops and dissection of complex traits in mendelian factors
- 1.3 Genetic and molecular analysis of heterosis in maize
- 1.4 Characterization and valorization of cereal genetic resources (maize, wheat, barley, teff, millet)

AREA 2 The role of non-coding RNA in the regulation of gene expression

Research area within this area started with the launch of the French-Italian bilateral program aimed at the characterization of the grapevine (*Vitis vinifera*) genome.During this initiative a deep interest in understanding the role of small non-coding RNAs in the fine regulation of gene expression during development and in response to stresses arose. This research line grew to encompass the long non-coding RNA component of this complex regulatory network.

2.1. Characterization of small non-coding RNAs in model and crop species

- 2.2 The role of ncRNAs during plant development and in response to environmental stresses
- 2.3 Characterization of long ncRNAs in cereals

All the above mentioned research lines are or were funded by International and National Agencies.

Pubblications 2016 – 2020

- Teferi ET, Kassie GT, **Pè ME**, Fadda C (2020) Are farmers willing to pay for climate related traits of wheat? Evidence from rural parts of Ethiopia. Agricultural systems. DOI: 10.1016/j.agsy.2020.102947
- Fadda C, Mengistu DK, Kidane YG, Dell'Acqua M, **Pè ME**, Van Etten J (2020) Integrating conventional and participatory crop improvement for smallholder agriculture using the seeds for needs approach: a review. Frontiers in Plant Sciences 11. DOI: 10.3389/fpls.2020.559515
- Woldeyohannes AB, Accotto C, Desta EA, Kidane YG, Fadda C, Pè ME, Dell'Acqua M (2020) Current and projected eco-geographic adaptation and phenotypic diversity of Ethiopian teff (*Eragrostic teff*) across its cultivation range. Agriculture, Ecosystems, Environment 300:107020.DOI: 10.1016/j.agee.2020.107020
- Talini R, Brandolini A, Miculan M, Brunazzi A, Vaccino P, **Pè ME**, Dell'Acqua M (2020) Genome wide association study of agronomic and quality traits in a world collection of the wild wheat relative *Triticum urartu*. Plant J. 102: 555-568, DOI 10.1111/tpj.14650
- Svezia B, Cabiati M, Matteucci M, Passino C, **Pè ME**, Lionetti V, Del Ry S (2019) Tuscany Sangiovese grape juice imparts cardioprotection by regulating gene expression of cardioprotective C-type natriuretic peptide. European Journal of Nutrition. 2019 Nov. DOI: 10.1007/s00394-019-02134-x.
- Fiore Mc, Mercati F, Spina A, Blagiforti S, Venora G, Dell'Acqua M, Lupini A, Preiti G, Monti M, **Pè ME**, Sunseri F (2019) High-throughput genotype, morphology, and quality traits evaluation for the assessment of genetic diversity of wheat landraces from Sicily. Plants 8: 116. DOI 10.3390/plants8050116
- Septiani P, Lanubile A, Stagnati L, Busconi M, Nelissen H, **Pè ME**, Dell'Acqua M, Marocco A (2019) Unravelling the genetic basis of Fusarium seedling rot resistance in the MAGIC maize population: novel targets for breeding. Scientific Rep 9: (1). DOI 10.1038/s41598-019-42248-0

- van Etten J, de Sousa K, Aguilarc A, Barriosc M, Cotoa A, Dell'Acqua M, Fadda C, Gebrehawaryate Y, van de Gevelf J, Guptag A, Kirosh AY, Madriza B, Mathurg P, Mengistu DK, Mercado L, Mohammedh JN, Paliwalg A, Pe` ME, Quiros CF, Rosas JC, Sharmag N, Singh SS, Solanki IS, Steinke J (2019) Crop variety management for climate adaptation supported by citizen science. PNAS 116: 4194-4199. DOI 10.1073/pnas.1813720116
- McLean-Rodríguez FD, Camacho-Villa TC, Almekinders CJM, **Pè ME**, Dell'Acqua M, Costich DE (2019) The abandonment of maize landraces over the last 50 years in Morelos, Mexico: a tracing study using a multi-level perspective. Agriculture and Human Values X: 1-18. DOI 10.1007/s10460-019-09932-3
- Lazzaro MT, Bàrberi P, Dell'Acqua M, **Pè ME**, Limonta M, Barabaschi D, Cattivelli L, Laino P, Vaccino P (2019) Unraveling diversity in wheat competitive ability traits can improve integrated weed management. Agronomy for Sustainable Development 39: 6. DOI 10.1007/s13593-018-0551-1
- Kidane Y, Gesesse CA, Hailemariam B, Desta EA, Mengistu DK, Fadda C, **Pè ME**, Dell'Acqua M (2019) A large nested association mapping population for breeding and quantitative trait locus mapping in Ethiopian durum wheat. Plant Biotechnology Journal pp. 1–14. DOI 10.1111/pbi.13062
- Barravecchia I, De Cesari C, Pyankova OV, Scebba F, Pè ME, Forcato M, Bicciato S, Foster HA, Bridger JM, Angeloni D (2018) A comprehensive molecular and morphological study off he effects of space flight on human capillary endothelial cells: sample quality assessment and preliminary results. Frontiers in Physiology 9 DOI: 10.3389/conf.fphys.2018.26.00050
- Pieri A, Pè ME, Bertolini E (2018) Long non-coding RNAs in wild wheat progenitors. BioR□iv DOI 10.1101/301804
- Brunazzi A, Scaglione D, Talini R, Miculan M, Magni F, Poland J, **Pè ME**, Brandolini B, Dell'Acqua M (2018) Molecular diversity and landscape genomics of the crop wild relative *Triticum urartu* across the Fertile Crescent. Plant J 94: 670-684. DOI 10.1111/tpj.13888
- De Quattro CS, Pè ME Bertolini E (2017). Long noncoding RNAs in the model species *Brachypodium distachyon*. Scientific Reports 7: 11252. DOI 10.1038/s41598-017-11206-z
- Kidane YG, Hailemariam BN, Mengistu DK, Fadda C, Pè ME, Dell'Acqua M (2017). Genome-Wide Association Studies of Septoria tritici blotch resistance in Ethiopian durum wheat landraces. Frontiers in Plant Science 8:1586. DOI 10.3389/fpls.2017.01586
- Kidane YG, Mancini C, Mengistu DK, Frascaroli E, Fadda C, **Pè ME**, Dell'Acqua M (2017) Genome Wide Association Study to identify the genetic base of smallholder Farmer preferences of durum wheat traits. Frontiers in Plant Science 8: 1230, DOI 10.3389/fpls.2017.01230
- Mancini C, Kidane YC, Mengistu DK, **Pè ME**, Fadda C, Melfa and Workaye Farmer Community Dell'Acqua M (2017) Joining smallholder farmers' traditional knowledge with metric traits to select better varieties of Ethiopian wheat. Scientific Reports 7: 9129. DOI 10.1038/s41598-017-07628-4
- Lwin AK, Bertolini E, **Pè ME**, Zuccolo A (2017) Genomic skimming for identification of medium/highly abundant transposable elements in *Arundo donax* and *Arundo plinii*. Mol Genet Genomics 292: 157-171. DOI 10.1007/s00438-016-1263-3
- Lopes Paim Pinto D, Brancadoro L, Dal Santo S, De Lorenzis G, Pezzotti M, Blake M, **Pè ME**, Mica E (2016) The influence of genotype and environment on small RNA profiles in grapevine berry. Frontiers in Plant Science 7: 1459. DOI 10.3389/fpls.2016.01459
- Mengistu DK, Kidane YG, Fadda C, Pè ME (2016) Genetic diversity in Ethiopian durum wheat (*Triticum turgidum* var *durum*) inferred from phenotypic variations. Plant Genetic Resources 1-11. DOI 10.1017/S1479262116000393
- Mengistu DK, **Pè ME** (2016) Revisiting the ignored Ethiopian durum wheat (*Triticum turgidum* var *durum*) landraces for genetic diversity exploitation in future wheat breeding programs. Journal of Plant Breeding and Crop Science 8: 45-59. DOI 10.5897/JPBCS2015.0542
- Baute J, Herman D, Coppens F, De Block J, Slabbinck B, Dell'Acqua M, Pè ME, Maere S, Nelissen H, Inzé D (2016) Combined large-scale phenotyping and transcriptomics in maize reveals a robust growth regulatory network. Plant Phys 170: 1848-1867. DOI 10.1104/pp.15.01883

- Gebre YG, Bertolini E, **Pè ME**, Zuccolo A (2016) Identification and characterization of abundant repetitive sequences in *Eragrostis tef* cv. Enatite genome. BMC Plant Biology 16: 39. DOI 10.1186/s12870-016-0725-4
- Mengistu DK, Kidane YG, Catellani M, Frascaroli E, Fadda C, **Pè ME**, Dell'Acqua M (2016) High-density molecular characterization and association mapping in Ethiopian durum wheat landraces reveals high diversity and potential for wheat breeding. Plant Biotechnology Journal 14:1800-1812. DOI 10.1111/pbi.12538

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