

Mario Enrico Pè – Curriculum vitae

PERSONAL DETAILS

Name: Mario Enrico Pè, former Full Professor Settore Concorsuale **07E1 – Chimica Agraria**, **Genetica Agraria**, **Pedologia**, Settore Scientifico disciplinare **AGR/07 – Genetica Agraria** (Agricultural Genetics)

PROFILE

- Current position: Full professor of Agricultural Genetics (Genetica Agraria AGR/07) associated to the Institute of Plant Sciences of Scuola Superiore Sant'Anna in Pisa
- President of the Interuniversity Consortium for Plant Molecular Biology
- 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"
- Member of the Task Force on Sustainable Agriculture and Innovation of the Europena incubator RE-Imagine Europa

EDUCATION

- 2021 2024 President of the Interuniversity Consortium for Plant Molecular Biology
- 2007 2024: 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

- 2019 2024 (May): Scientific coordinator of the International Doctoral Programme in Agrobiodiversity
- 2021 current Member of the Special Programme "AfricaConnect
- 2019 2021: President of the Italian Society of Agricultural Genetics (SIGA)
- 2019 2021: in the board of the Itaian Federation of Live Sciences (FISV)
- 2016 2021: Dean of the Academic Class of Experimental Sciences

- 2016 2021: member of the Academic Senate of Scuola Superiore Sant'Anna
- 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.

Statistics according to Scopus:

N° of pubblications = 89, Citations = 6,725, h-index = 36

Pubblications 2019–2025

- Ferguson J, Caproni L, ... **Pè ME**, et al. (2025) A deficient CP24 allele in maize defines genetic variation for non-photochemical quenching and photosystem II efficiency. The Plant Cell: in press
- Tran, TN, Lanubile A, Marocco A, **Pè ME**, Dell'Acqua M, Miculan M (2024) Transcriptome profiling of eight *Zea mays* lines identifies genes responsible for the resistance to *Fusarium verticillioides*. BMC Plant Biology 24: 1107 DOI: 10.1186/s12870-024-05697-y
- Tamang A, Macharia MW, Caproni L, Miculan M, Mageri S, Seid Ahmed J, Yangzome T, **Pè ME**, Dell'Acqua M (2024) Genomic, climatic, cultural diversity of maize landraces from the Himalayan Kingdom of Bhutan. Plants People Planet 1–14. DOI: 10.1002/ppp3.10513
- Seid Ahmed J, Buizza R, Dell'Acqua M, Demissie T, **Pè ME** (2024) Evaluation of ERA5 and CHIRPS rainfall estimates against observations across Ethiopia. Metereology and Atmosferic Physiscs 136: 17 https://doi.org/10.1007/s00703-024-0100
- Barravecchia I, De Cesari C, Guadagni V, Signore G, Bertolini E, Giannelli SG, Scebba F, Martini D, **Pè ME**, Broccoli V, Massimiliano M, DeboraAngeloni D, Demonti GC (2023) Increasing cell culture density during a developmental window prevents fated rod precursors derailment toward hybrid rod-glia cells. Scientific Reports, DOI 10.1038/s41598-023-32571-y
- Caproni L, Lakew BF, Kassaw SA, Miculan M, Ahmed JS, Grazioli S, Kidane YG, Fadda C, **Pè ME**, Dell'Acqua M (2023) The genomic and bioclimatic characterization of Ethiopian barley (*Hordeum vulgare* L.) unveils challenges and opportunities to adapt to a changing climate. Global Change Biology 29: 2335–2350, DOI: 10.1111/gcb.16560
- Gesesse CA, Nigir B, de Sousa, Gianfranceschi L, Gallo GA, Poland J, Kidane YG, Abate E, Fadda C, Pè ME, Dell'Acqua M (2023) Genomics-driven breeding for local adaptation of durum wheat is enhanced by farmers' traditional knowledge. PNAS 120 (14) e2205774119
- van Etten J, de Sousa K, Cairnsc JE, Dell'Acqua M, Fadda C, Guereñaf D, van Heerwaardeng J, Assefah T, Mannersi R, Müllera A, **Pè ME**, Polar V, Julian Ramirez-Villegas JR, Solberg SØ, Teekenl B, and Tufanm HA (2023) Data-driven approaches can harness crop diversity to address heterogeneous needs for breeding products. PNAS 120 (14) e2205771120
- Woldeyohannes AB, Iohannes SA, Miculan M, Caproni L, Ahmed JS, de Sousa K, Desta EA, Fadda C, Pè ME, Dell'Acqua M (2022). Data-driven, participatory characterization of farmer varieties discloses teff breeding potential under current and future climates. eLife 11: e80009. DOI: https://doi.org/10.7554/eLife.80009
- Woldeyohannes AB, Desta EA, Fadda C, **Pè ME**, Dell'Acqua M (2022). Value of teff (*Eragrostis tef*) genetic resources to support breeding for conventional and smallholder farming: a review. CABI Agriculture and Bioscience 3: 27. https://doi.org/10.1186/s43170-022-00076-9
- Barravecchia I, De Cesari C, Forcato M, Scebba F, Pyankova OV, Bridger JM, Foster HA, Signore G, Borghini A, Andreassi M, Andreazzoli M, Bicciato S, **Pè ME**, Angeloni D (2021) Microgravity and space radiation inhibit autophagy in human capillary endothelial cells, through either opposite or synergistic effects on specific molecular pathways. Cell Mol Life Sci: 28. doi: 10.1007/s00018-021-04025
- de Sousa K, van Etten J, Poland J, Fadda C, Jannik JL, Kidane YG, Mengistu DK, **Pè ME**, Solberg SØ, Dell'Acqua M (2021) Data-driven decentralized breeding increases prediction accuracy in a challenging crop production environment. Communication Biology 4: 944, doi: 10.1038/s42003-021-02463-w
- Miculan M, Nelissen H, Hassen MB, Marroni F, Inzé D, **Pè ME**, Dell'Acqua M (2021) A forward genetics approach integrating genome-wide association study and expression quantitative trait locus mapping to dissect leaf development in maize (*Zea mays*). Plant Journal: 107: 1056-1071, doi: 10.1111/tpj.15364
- McLean-Rodriguez FD, Costich DE, Camacho-Villa TC, **Pè ME**, Dell'Acqua M (2021). Genetic diversity and selection signatures in maize landraces compared across 50 years of in situ and ex situ conservation. Heredity 126: 913-928, doi.org/10.1038/s41437-021-00423-y
- Occelli M, Mantino A, Ragaglini G, Dell'Acqua M, Fadda C, **Pè ME**, Nuvolari A (2021). Traditional knowledge affects soil management ability of smaller farmers in marginal areas. Agronomy for sustainable development 41, ISSN 1774-0746, doi: 10.1007/s13593-020-00664-x
- 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 185:102947, 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 (*Eragrostis 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 oft he 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, **Pè 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-
- 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