

Prof. MARIO ENRICO PÈ

Personal data

Date and place of birth:

Nationality:

Civil Status:

Address.

Position: Full Professor of Genetics at the Institute of Life Sciences, Scuola Superiore Sant'Anna

Studies and Qualifications

2013 – 2016: Director of the Institute of Life Sciences

2007 – : Full professor of Genetics at Scuola Superiore Sant'Anna di Pisa, Italy

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)

2000: Associate professor of Agricultural Genetics at University of Milan, Italy

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 Center of the Indonesian National Institute for the Development and Application of Biotechnology, Serpong, Indonesia

1986: Assistant professor of Genetics at the University of Milan, Italy

Teaching Experience

A long standing teaching activity in the field of Genetics, Plant Genetics, Plant Breeding, Plant Genomics, including both introductory and advanced courses.

Research activity

Prof. M. Enrico Pè research activity involves two major areas, each represented by complementary research lines.

Genetic basis of complex traits in cereals

1. *Studies on the genetic control of yield and yield components in cereals*

2. *Applying genetics and genomics for the analysis of genome structure in cereals and the dissection of complex traits in mendelian factors*

3. *Genetic and molecular analysis of heterosis in maize*

4. *Characterization and exploitation of genetic resources in cereals and in orphan crops*

Structural and functional characterization of non-coding RNAs

1. *Structural and functional characterization of microRNAs and other non-coding RNAs*

2. *The role of non-coding RNAs in plant response to drought*

Relevant Publications

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*: 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

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*, pp1-1310.1111/pbi.12538

- Baute J, Herman D, Coppens F, De Block J, Slabbinck B, Matteo Dell'Acqua M, Pè ME, Maere S, Nelissen H, Inzé D (2015) Correlation Analysis of the Transcriptome of Growing Leaves with Mature Leaf Parameters in a Maize RIL Population. *Genome Biology* 16: 168
- Dell'Acqua M, Gatti DM, Pea G, Cattonaro F, Coppens F, Magris G, Hlaing AL, Aung HH, Nelissen H, Baute J, Frascaroli E, Churchill GA, Inzé D, Morgante M, Pè ME (2015) Genetic properties of the MAGIC maize population: a new platform for high definition QTL mapping in *Zea mays*. *Genome Biology* 16: 167
- Olango TM, Bizuayehu T, Pagnotta MA, Pè ME, Catellani M (2015) Development of SSR markers and genetic diversity analysis in enset (*Ensete ventricosum* (Welw.) Cheesman), an orphan food security crop from Southern Ethiopia. *BMC Genetics* 16: 98-114
- Baroncelli R, Piaggieschi G, Fiorini L, Bertolini E, Zapparata A, Pè ME, Sarrocco S, Vannacci G (2015) Draft whole-genome sequence of the biocontrol agent *Trichoderma harzianum* T6776. *Genome Announcements: Genome Announc* 3:e 00647-15. doi:10.1128/genomeA.00647-15.
- Mengistu DK, Kiroso AY, Pè ME (2015) Phenotypic diversity in Ethiopian durum wheat (*Triticum turgidum* var. *durum*) landraces. *The Crop Journal* 3:190-199
- Belli Kullán J, Lopes Paim Pinto D, Bertolini E, Fasoli M, Zenoni S, Tornielli GB, Pezzotti M, Meyers BC, Farina L, Pè ME, Mica E (2015) miRVine: a microRNA expression atlas of grapevine based on small RNA sequencing. *BMC Genomics* 16: 393
- Dell'Acqua M, Zuccolo A, Tuna M, Gianfranceschi L, Pè ME (2014) Targeting environmental adaptation in the monocot model *Brachypodium distachyon*: a multi-faceted approach. *BMC Genomics* 15: 801
- Olango TM, Bizuayehu T, Catellani M, Pè ME (2014) Indigenous knowledge, use and on-farm management of enset (*Ensete ventricosum* (Welw.) Cheesman) diversity in Wolaita, Southern Ethiopia. *Journal of Ethnobiology and Ethnomedicine* 10: 41
- Pea G, Aung HH, Frascaroli E, Landi P, Pè ME (2013) Extensive genomic characterization of a set of near-isogenic lines for heterotic QTL in maize (*Zea mays* L.). *BMC Genomics* 14: 61
- Bertolini E, Verelst W, Horner DW, Gianfranceschi L, Piccolo V, Inzé D, Pè ME, Mica E (2013) Addressing the role of microRNAs in reprogramming leaf growth during drought stress in *Brachypodium distachyon*. *Mol. Plant* 6: 423-443
- Verelst W, Bertolini E, De Bodt S, Vandepoele K, Demeulenaere M, Pè ME, Inzé D (2013) Molecular and physiological analysis of growth-limiting drought stress in *Brachypodium distachyon* leaves. *Mol. Plant* 6: 311-322
- Sheferaw E, Pè ME, Porceddu E, Ponnaiah M (2012) Exploring the genetic diversity of Ethiopian grass pea (*Lathyrus sativus* L.) using EST-SSR markers. *Mol Breeding* 2: :789-797
- Frascaroli E, Canè M, Pè ME, Pea G, Landi P (2012) Characterization of heterotic quantitative trait loci in maize by evaluation of near-isogenic lines and their crosses at two competition levels. *TAG: 124: 35-47*
- Carra A, Mica E, Gambino G, Pindo M, Moser C, Pè ME, Schubert A (2009) Cloning and characterization of small non-coding RNAs from grape. *Plant Journal* 59: 750-763
- Mica E, Piccolo V, Delledonne M, Ferrarini A, Pezzotti M, Casati C, Del Fabbro C, Valle G, Policriti A, Morgante M, Pesole G, Pè ME, Horner DS (2010) Correction: High throughput approaches reveal splicing of primary microRNA transcripts and tissue specific expression of mature microRNAs in *Vitis vinifera*. *BMC Genomics*, 11: 109
- Frascaroli E, Canè MA, Pè ME, Pea G, Morgante M, Landi P (2009) QTL detection in maize testcross progenies as affected by related and unrelated testers. *TAG*. 118: 993-1004.
- Pea G, Paulstephenraj P, Canè MA, Savo Sardaro ML, Landi P, Morgante M, Porceddu E, Pè ME, Frascaroli E. (2009) Recombinant near-isogenic lines: a resource for the mendelization of heterotic QTL in maize. *Mol. Gen. and Genomics* 281: 447-457
- Marino M, Ponnaiah M, Krajewski P, Frova C, Gianfranceschi L, Pè ME, Sari-Gorla M (2009) Addressing drought tolerance in maize by transcriptional profiling and mapping. *Mol-Gen and Genomics* 281: 163-179

- Balint-Kurti PJ, Zwonitzer JC, Pè ME, Pea G, Lee M, Cardinal AJ (2008) Identification of Quantitative Trait Loci for resistance to southern leaf blight and days to anthesis in two maize recombinant inbred line populations. *Phytopathology* 99: 315-319.
- Pea G, Ferron S, Gianfranceschi L, Krajewski P, Pè ME (2008) Gene expression non-additivity in immature ears of a heterotic F1 maize hybrid. *Plant Science* 174:17-24. IF: 1.795
- Jaillon O, Aury JM, Noel B, Policriti A, et al, Pè ME, et al, Quetier F, Wincker P (2007) The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. *Nature* 449: 463-467
- Frascaroli E, Canè MA, Landi P, Pea G, Gianfranceschi L, Villa M, Morgante M, Pè ME (2007). Classical and QTL genetic analysis of heterosis in a maize hybrid between two elite inbred lines. *Genetics* 176: 625-644
- Gallavotti A, Zhao Q, Kyozukas J, Meeley RB, Ritter MK, Doebley JF, Pè ME, Schmidt RJ (2004) The role of barren stalk in shaping maize architecture. *Nature* 432: 630-635.