Curriculum Vitae of Michele Morgante

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Appointments and qualifications:
1983-1987: Laurea in Forest Sciences, Università di Padova, Italy
1988-1990 Research Fellow of Regione FVG at the Dipartimento di Produzione Vegetale e Tecnologie Agrarie, University of Udine, Italy.
1990-1992 Research Fellow in Agricultural Genetics of the "V.V. Landi" Foundation of the Accademia Nazionale dei Lincei
1992-1994 Postdoctoral Visiting Scientist at Agricultural Products Department - Biotechnology Research, E.I. du Pont de Nemours & Co., Wilmington, DE
1994-2000 Tenured Assistant Professor, Genetics, at the Dipartimento di Produzione Vegetale e Tecnologie Agrarie, University of Udine, Italy (on leave of absence from 02/1998 to 10/2000)
1998-2002 Senior Scientist, Agricultural Products Department - Biotechnology Research, E.I. du Pont de Nemours & Co., Wilmington, DE
2000- 2005 Associate Professor, Plant Genetics, at the Dipartimento di Produzione Vegetale e Tecnologie Agrarie, University of Udine, Italy (part-time appointment until 11/2002)
2005- current Full Professor, Genetics, Università di Udine
2005- 2009 Guest Professor, Umea Plant Science Center, Umea University, Sweden
2006- current Scientific Director, Istituto di Genomica Applicata, Parco Scientifico Luigi Danieli, Udine
2008-2013 Rector Delegate for Research and Technology Transfer, Università di Udine
2010- Associate Researcher, Istituto di Genetica Vegetale, CNR
2013-2013 Vice Rector (Prorettore Vicario), Università di Udine
2013- 2019 President, Consorzio InnovaFVG
2013-2015 President elect, Società Italiana di Genetica Agraria
2015-2017 President, Società Italiana di Genetica Agraria
2015-current Board member, Area Science Park, Trieste

Awards and honors

- 2018 Elected Member Academia Europaea
- 2015 Elected Member, Accademia Nazionale di Agricoltura
- 2011 European Research Council Advanced Grant Award
- 2010 Elected Member, Accademia Italiana della Vite e del Vino
- 2007 Elected Member, Accademia Nazionale dei Lincei (Italian National Academy of Sciences)
- 2006 Elected Member, Accademia Italiana di Scienze Forestali
- 2005 Medal for Physical and Natural Sciences, Accademia delle Scienze detta dei XL
- 2003 DuPont Young Professor Award
- 1990 Research Fellowhsip, Accademia Nazionale dei Lincei

Recent miscellaneous activity
Editorial:
Associate Editor, Theoretical and Applied Genetics (2005-2009); Associate Editor, Tree Genetics and Genomes (2005-2009); Associate Editor, BMC Genetics (2010-2011); Section Editor, BMC Genetics (2011-); Associate Editor, BMC Plant Biology (2010-)
Scientific Advisory Boards:
Dipartimento Agroalimentare, Consiglio Nazionale delle Ricerche (2006-2012);
IBERS, Aberystwyth University, UK (2008-);
UPSC Research School in Forest Genetics, Umea, Sweden (2005-2009);
IRTA (Instituto de Recerca i Tecnologia Agroalimentaries), Barcelona (2010-)

SMARTForest Project, GenomeCanada, Canada, (2011-)
French Plant Genomic Resources Center (CNRGV), Francia (2013-)
CREA (Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria) (2017-current)
Board of Directors:
Area Science Park, Trieste (2008-2011)
IGA Technology Services Srl (2013-)
Area Science Park, Trieste (2015-2018)
Grant Advisory Panels:
ERC, Advanced Grants Life Sciences 8: Evolutionary, Population and Environmental Biology (2008-2011); ERC Consolidator Grants Life Sciences 9: Applied Life Sciences and Biotechnology (2013-2018); ERC Advanced Grants Life Sciences 9: Applied Life Sciences and Biotechnology Qualitative Assessment of Completed Projects (2019-present); NSF Plant Genome Panel (2006); Generation Challenge Program Panel (2004); Agence Nationale de la Recherche, Biotechnology and Bioresource Engineering (2010-2011); EU FPVII-Infrastructures (2010-2011); Chile Genome Program CONICYT (2008-2013), NWO (Olanda) (2014, 2015, 2017), Experimental Plant Science Doctorate School (Olanda) (2015), Commissione MIUR per progetti PON distretti e laboratory pubblico-privato (2013-), ICREA (Catalan Institution for Research and Advanced Studies) Spagna (2015, 2017).

Grant Funding

Recent:
ERANET-Plant Genomics Research project: “Genomics-assisted dissection of barley morphology and development” P.I. (2007-2011) 429000 EU
MIPAF Progetto Speciale DRUPOMICS “Sequenziamento del genoma del pesco ed utilizzo della sequenza in programmi di miglioramento della qualità del frutto del pesco e della resistenza alle malattie” P.I. (2008-2010) 690000 EU
MIPAF Progetto Speciale Cromosoma 5A Frumento “Mappa fisica del cromosoma 5A dei frumenti”: P.I. (2008-2011) 200000 EU
MIPAF Special Project CITROMICS "Citrus genome sequencing and applications to functional genomics and breeding" (2009-2011) 320000 EU
PRIN 2008 "Towards the elucidation of the molecular bases of heterosis in cultivated plants: global molecular characterization of hybrids and discovery of genes involved in heterosis" PI and national coordinator (2010-2012) 34000 EU
NOVELTREEBREEDING “Novel tree breeding strategies” EU FPVII, P.I. (2008-2012) 233000 EU
ENERGYPOPLAR "Enhancing Poplar Traits for Energy Applications" EU FPVII, P.I. (2008-2012) 428000 EU
TRITICEAEGENOME "Genomics for Triticeae improvement" EU FPVII, P.I. (2008-2012) 528000 EU
MIPAF Special Project OLEA "Genomics and breeding of olive tree" (2011-2012) 310000 EU
AGER project "From Seed to Pasta: integrated research for the production of high quality durum wheat": P.I. (2010-2013) 470000 EU
MIPAF Special Project VITIGNO "Analysis and evaluation of Italian autoctonous grapevine varieties" (2011-2013) 330000 EU
MIUR Progetto Bandiera Epigenomica: "Next generation sequencing for epigenomic analysis" (2012-2018) 5000000 EU
European Research Council Advanced Grant: "NOVABREED: Novel variation in plant breeding and the plant pan-genomes" (2012-2017) 2473500 EU
WATBIO “Development of improved perennial non-food biomass and bioproduct crops for water stressed environments”, EU FPVII, P.I. (2012-2017) 900000 EU
GENTREE “Optimizing the management and sustainable use of forest genetic resources in Europe”, EU-Horizon2020, P.I. (2016-2020) 903000 EU
EPIDIVERSE Marie Curie Innovative Training Network “Linking Ecology, Molecular Biology and Bioinformatics in plant epigenetic research”, EU-Horizon2020, P.I. (2017-2021) 560000 EU
PRIN 2017 “Regulation of gene expression in grapevine: analysis of genetic and epigenetic determinants”, MIUR, National Coordinator (2019-2022) 271000 EU

Patents

I am inventor on 16 US and international patents concerning genome analysis methods and the use of genes in plant breeding and transgenic applications and on 10 plant variety rights for 10 grapevine varieties resistant to downy and powdery mildew.

Tutoring activity
I have been PhD thesis advisor for 20 students (2 current) and of 30 postdocs (3 current) many of which have continued in a successful science career with positions at University of Arizona, Scuola Superiore Sant'Anna di Pisa, INRA, IASMA, Danforth Plant Science Center or in private companies.

Publications
As of 01/09/2019 I have more than 140 publications (3 in Nature, 3 in Nature Genetics, 3 in Nature Biotechnology, 2 in Nature Reviews Genetics, 3 in PNAS) indexed in Web of Science starting in 1991 that have attracted in Google Scholar 29272 citations for an H-index of 73.

Research interests
Structural and functional genomics, genome evolution, epigenetic variation, variation of gene regulation, transposable elements and their role in regulating gene expression, molecular breeding, new breeding technologies.

Seminars/Invited lectures (last 10 years)
01/2008 Invited lecture, "Transposable Elements, Functional Variation And The Plant Pan-Genomes", Mutation Screening Workshop, Plant & Animal Genome XVI Conference, San Diego, USA
01/2008 Invited lecture, "Sequence And Analysis Of The Grape Genome: Product Of A Public Consortium", Grape Genomics Workshop, Plant & Animal Genome XVI Conference, San Diego, USA
01/2008 Invited seminar, "Transposable Elements, Functional Variation And The Plant Pan-Genomes" Unitè de Recherche de Genomique Vegetale, CNRS-INRA, Evry,Paris, France
02/2008 Invited lecture, "The application of DNA markers to monitoring adaptation and migration of forest tree species", 13th meeting of the Subsidiary Body on Scientific, Technical and Technological Advice (SBSTTA) of the Convention on Biological Diversity, FAO, Rome, Italy
02/2008 Invited seminar, "Transposable Elements, Genetic Variation And The Plant Pan-Genomes", Istituto Genetica e Biofisica, CNR, Naples, Italy
02/2008 Invited lecture, "Una Visione Genomica Della Biodiversità Nelle Piante", Seminario Accademia Lincei: La Biodiversità, Accademia Nazionale dei Lincei, Roma, Italy
03/2008 Invited lecture, Meeting Tuning The Taste Of Wine: The results of the French-Italian grape genome sequencing project and their potential for applications, "How Genomics Is Changing Our View Of Plant Science And Breeding", Udine, Italy
05/2008 Invited lecture, "Genetic and genomic approaches enabling rapid poplar improvement for bioenergy", EPSO Workshop on Biofuels, Royal Society, London, UK
06/2008 Invited lecture, "Transposable Elements and the Plant Pan-Genomes", Annual Meeting of the Society for Molecular Biology and Evolution, Barcellona, Spain
07/2008 Invited lecture, "The structural and transcriptional landscape of the grape genome" Gatersleben lecture on Plant Genomics, IPK, Gatersleben, Germany
08/2008 Invited lecture, "The analysis of gymnosperm genomes: is their structure and history making them easier to sequence?" IUFRO-CTIA 2008 Joint Conference Quebec City, Canada
09/2008 Invited lecture, "Maize domestication and breeding", Symposium on "New trends in plant biology and biotechnology", French Academy of Sciences, Paris, France
09/2008 Invited lecture, "Transposable elements and the plant pan-genomes", X Annual Congress Federazione Italiana Scienze della Vita, Riva del Garda, Italy
10/2008 Invited lecture, "From genomics to breeding: problems and perspectives", InnovaChile-Chilean Economic Development Agency) meeting on Initiative Genome Chile, Santiago, Chile.
11/2008 Invited lecture, "The plant pan-genomes, transposable elements and functional variation", Uppsala University Evolutionary Biology Center graduate School on The Genomics of Phenotypic Diversity in Natural Populations, Uppsala, Sweden
02/2009 Invited lecture, "Transposable elements, functional variation and the plant pan-genomes", Ramon Areces International Symposium on New frontiers in forest genomics: sequencing and functional understanding of the conifer genome, Madrid, Spain.

04/2009 Invited lecture, "Assessing nucleotide and structural variation in grapevine by CGH and resequencing", 2nd Illumina European User Meeting, Crete, Greece
06/2009 Invited lecture, "Applications of next generation sequencing technologies in plant genetics and breeding", Keygene Strategic Research Meeting, Wageningen, Netherlands.
07/2009 Invited lecture, "From genomics to plant breeding: how to make the best use of genetic variation", 1st Annual Congress of Italian Society of Plant Biology (SIBV), Verona, Italy
07/2009 Invited lecture, "The plant pan-genomes: structure, diversity and function", Plant Genome and Beyond Meeting, Paris, France
09/2009 Invited lecture "Maize genomics", EPSO workshop 'Plant Productivity for Food – from Model to Crop', Gent, Belgium.
10/2009 Invited lecture on Genome structure, evolution and comparative genomics, Plant Gem Meeting 2009, Lisbon, Portugal.
10/2009 Invited lecture, "Grape Genome Structure", Symposium on Structural Genomics, International Plant Molecular Biology Congress, St. Louis, MO
10/2009 Invited lecture, "From Genomics to Plant Breeding", Symposium on Genomics-Assisted Breeding, International Plant Molecular Biology Congress, St. Louis, MO
11/2009 Invited lecture, "A Genome Based View Of Plant Biodiversity", European Academies Science Advisory Council International Workshop on "Plant Genetic Resources for Food and Agriculture: General aspects and research opportunities", Accademia Nazionale dei Lincei, Rome, Italy
03/2010 Keynote lecture, "From genomics to plant breeding: new avenues to food innovations through the use of genetic variation", Netherlands Biotechnology Congress-13, Ede-Wageningen, The Netherlands.
03/2010 Keynote lecture, "The Pan-Genome Concept In Plants: Origin, Structure And Function Of The Dispensable Genome", Maize Genetics Meeting, Riva del Garda, Italy
04/2010 Invited lecture, "From genomics to breeding: how to make the best use of genetic resources", 2nd International Symposium on Genomics of Plant Genetic Resources, Bologna, Italy.
08/2010 Invited lecture, 28th International Horticultural Congress, Lisbon, Portugal
09/2010 Keynote lecture, Queenstown Molecular Biology Meeting 2010, Queenstown, New Zealand
09/2010 Invited lecture, 14th International Biotechnology Congress, Rimini, Italy
09/2010 Keynote lecture, ASIC 23rd International Conference on Coffee Science, Bali, Indonesia.
10/2010 Keynote Lecture, German Society for Plant Breeding Conference on Genomics based breeding, Giessen, Germany
11/2010 Invited lecture, 10th Gatersleben Research Conference; Gatersleben, Germany
05/2011 Invited lecture, PlantGEM 2011 Meeting, Istanbul, Turkey
05/2011 Invited lecture, New Phytologist Symposium on Bioenergy Trees, Nancy, France
10/2011 Invited lecture, 3rd Next Generation Sequencing Workshop, Bari, Italy
11/2011 Invited lecture, 25th Colloquium, "Crop plants: biodiversity and genomics", University of Hohenheim, Germany
11/2011 Invited lecture, Symposium on "Plant Breeding in the genomics era", University of Wageningen, The Netherlands
04/2012 Invited lecture, 4th StatSeq Cost Action workshop, Verona, Italy
07/2012 Keynote lecture, International Conference on Arabidopsis Research 2012, Vienna, Austria
09/2012 Invited seminar, VIB, University of Gent, Gent, Belgium
10/2012 Invited lecture, Conference "The future of plant genomes. Harvesting genes for agriculture" Barcelona, Spain
10/2012 Invited lecture, Conference "Plant Science for Future Needs" Linnean Centre for Plant Biology, University of Uppsala, Uppsala, Sweden
10/2012 Invited lecture, Workshop on Genome analysis tools applied to forest tree breeding, The Finnish Forest Research Institute - METLA, Helsinki, Finnland
11/2012 Invited lecture, International Workshop: "Crop Improvement in a Changing Environment", Venice, Italy
12/2012 Invited seminar, Centre d'Etude de la Foret, Quebec City, Canada
12/2012 Invited lecture, Annual meeting of the Italian Society for Evolutionary Biology, Ferrara, Italy
01/2013 Keynote lecture, XXI Plant and Animal Genome Meeting
05/2013 Invited lecture, The Plant Genomics Congress, London, UK

05/2013 Keynote lecture, Next NGS Challenge Conference, Valencia, Spain
06/2013 Invited seminar, SciLifeLab The Svedbergh seminar, Uppsala University, Sweden
09/2013 Keynote lecture, Plant Genome Evolution 2013, Amsterdam, The Netherlands
11/2013 Plenary lecture, International Conference on Development and Genetics, Isle sur la Sorgue, France
11/2013 Invited lecture, 5th Annual Next Generation Sequencing Congress, London,UK
01/2014 Keynote lecture, Annual Plant Biotech Denmark meeting, Copenhagen, Denmark
06/2014 Keynote lecture, Plant Genomes Day, Toulouse, France
06/2014 Keynote lecture, 4th Banff Conference on Plant Metabolism, Banff, Canada
10/2014 Invited seminar, Vienna Graduate School for Population Genetics, Vienna, Austria
10/2014 Invited lecture, Translational Research Workshop, Clermont-Ferrand, France
03/2015 Plenary lecture, BDEBATE "Evolution of plant phenotypes, from genomes to traits. A symposium and public workshop", Barcelona, Spain
05/2015 EXPO 2015 Water and Food Security International Conference, Venice, Italy
06/2015 Keynote lecture, IUFRO Tree Biotechnology Conference, Florence, Italy
06/2015 Keynote lecture, XIV Eucarpia Symposium on Fruit Breeding and Genetics, Bologna, Italy
07/2015 Invited lecture, EC-EPSO EXPO Conference on plant breeding techniques, Milan, Italy
09/2015 Plenary lecture, International botanical Congress, Munich, Germany
01/2016 Keynote lecture, Dutch Graduate School of Experimental Plant Sciences Annual Meeting, Wageningen, Netherlands
02/2016 Invited seminar, Michigan State University, East Lansing, USA
03/2016 Plenary lecture, German Plant Breeding Society Congress, Bonn, Germany
04/2016 Plenary lecture, International Transposable Element Meeting, Saint Malò, France
09/2016 Plenary lecture, 18th annual Donald Danforth Plant Science Center Fall Symposium, "Genetics and Genomics of Crop Improvement", St. Louis, USA
09/2017 Keynote lecture, 4th International Symposium on Genomics of Plant Genetic Resources, Giessen, Germany
09/2017 Plenary lecture, Bioenergy Genomics Meeting, Oxford, UK
09/2017 Plenary lecture, The 6th EU-US DNA Repair Meeting 2017, Udine, Italy

Publication list, Michele Morgante

P1. **MORGANTE M.**, G.G. VENDRAMIN, R. GIANNINI, 1989. Genetics of 6PGD and SKDH in Norway spruce (*Picea abies* K.). **Journal of Genetics & Breeding**, 43:67-72.

P2. **MORGANTE M.**, G.G. VENDRAMIN, 1990. Analyse der Genressourcen von *Pinus leucodermis* Ant., einer Art mit kleinem Verbreitungsgebiet. In: H.H. Hattemer (ed.), **Erhaltung forstlicher Genressourcen**, pp. 87-98. Schriftenreihe aus der Forstlichen Fakultaet der Universitaet Goettingen und der Niedersaechsischen Forstlichen Versuchsanstalt, Band 98. J.D. Sauerlaender's Verlag, Frankfurt am Main, Germany.

P3. FINESCHI S., M.E. MALVOLTI, **M. MORGANTE**, G.G. VENDRAMIN, M. PACIUCCI, 1990. Erhaltung von Genressourcen bei der Kastanie (*Castanea sativa* Mill.). In: H.H. Hattemer (ed.), **Erhaltung forstlicher Genressourcen**, pp. 155-164. Schriftenreihe aus der Forstlichen Fakultaet der Universitaet Goettingen und der Niedersaechsischen Forstlichen Versuchsanstalt, Band 98. J.D. Sauerlaender's Verlag, Frankfurt am Main, Germany.

P4. GIANNINI R., **M. MORGANTE**, G.G. VENDRAMIN, 1990. A putative gene duplication in Norway spruce for 6PGD and its phylogenetic implications. In: S. Fineschi, M.E. Malvolti, F. Cannata and H.H. Hattemer (eds**.), Biochemical markers in the population genetics of forest trees**, pp. 21-27. SPB Academic Publishing BV, The Hague, The Netherlands.

P5. GIANNINI R., **M. MORGANTE**, G.G. VENDRAMIN, 1991. Allozyme variation in italian populations of *Picea abies* K. **Silvae Genetica**, 40:160-166.

P6. MESSINA R., R. TESTOLIN, **M. MORGANTE**, 1991. Isozymes for cultivar identification in kiwifruit. **HortScience**, 26:899-902.

P7. **MORGANTE M.**, G.G. VENDRAMIN, A.M. OLIVIERI, 1991. Mating system analysis in *Pinus leucodermis* Ant.: detection of self-fertilization in natural populations. **Heredity**, 67:197-203.

P8. **MORGANTE M.**, G.G. VENDRAMIN, P. ROSSI, 1991. Effects of stand density on outcrossing rate in two Norway spruce (*Picea abies*) populations. **Canadian J. of Botany** 69:2704-2708.

P9. **MORGANTE M.**, G.G. VENDRAMIN, 1991. Genetic variation in italian populations of *Picea abies* (L.) Karst. and *Pinus leucodermis* Ant. In: G. Mueller-Starck and M. Ziehe (eds.), **Genetic variation in european populations of forest trees**, pp. 205-227. J.D. Sauerlaender's Verlag, Frankfurt am Main, Germany.

P10. TILL-BOTTRAUD I., **M. MORGANTE**, R.A. CURIEL, I. DAJOZ, R. GIANNINI, M.L. GONZALES, P.H. GOUYON, A.M. OLIVIERI, V.D.E. SOLORZANO, G.G. VENDRAMIN, 1992. Pollen and ovules in evolutionary studies. In E. Ottaviano, D. Mulcahy, M. Sari Gorla, G. Bergamini Mulcahy (eds**.), Angiosperm Pollen and Ovules: Basic and Applied Aspects**. Springer Verlag, New York, NY, pp. 451-455.

P11. **MORGANTE M.**, A.M. OLIVIERI, 1993. PCR-amplified microsatellites as markers in plant genetics. **The Plant Journal**, 3:175-182.

P12. **MORGANTE M.**, G.G. VENDRAMIN, P. ROSSI, A.M. OLIVIERI, 1993. Selection against inbreds in early life-cycle phases in *Pinus leucodermis* Ant. **Heredity**, 70:622-627.

P13. **MORGANTE M.**, G.G. VENDRAMIN, R. GIANNINI, 1993. Inheritance and linkage relationships of isozyme variants of *Pinus leucodermis* Ant. **Silvae Genetica**, 42:231-237.

P14. CIPRIANI C., **M. MORGANTE** 1993. Evidence of chloroplast DNA variation in the genus Actinidia revealed by restriction analysis of PCR-amplified fragments. **Journal of Genetics & Breeding,** 47:319-326.

P15. BOSCHERINI G., **M. MORGANTE**, P. ROSSI, G.G. VENDRAMIN 1994. Allozyme and chloroplast DNA variation in italian and greek populations of *Pinus leucodermis* Ant. **Heredity**, 73:284-290.

P16. FINESCHI S., M.E. MALVOLTI, **M. MORGANTE**, G.G. VENDRAMIN 1994. Allozyme variation within and among cultivated varieties of sweet chestnut (Castanea sativa Mill.). **Canadian Journal of Forest Research**, 24:1160-1165.

P17. **MORGANTE M.**, A. RAFALSKI, P. BIDDLE, S.V. TINGEY, A.M. OLIVIERI 1994. Genetic mapping and variability of seven soybean simple sequence repeat loci. **Genome**, 37:763-769.

P18. **MORGANTE M.**, P. ROSSI, G.G. VENDRAMIN, G. BOSCHERINI 1994. Low levels of outcrossing in *Pinus leucodermis* Ant.: further evidences in artificial stands. **Canadian Journal of Botany**, 72:1289-1293.

P19. BOSCHERINI G., **M. MORGANTE**, P. ROSSI, G.G. VENDRAMIN, F. VICARIO 1994. Detection of DNA polymorphisms in *Pinus leucodermis* Ant. using random amplification. **Forest Genetics**, 1:131-137.

P20. CIPRIANI G., R. TESTOLIN, **M. MORGANTE** 1995. Paternal inheritance of plastids in interspecific hybrids of the genus *Actinidia* revealed by PCR-amplification of chloroplast DNA fragments. **Molecular & General Genetics**, 247:693-697.

P21. POWELL W., **M. MORGANTE**, R. MCDEVITT, G.G. VENDRAMIN, J.A. RAFALSKI 1995. Polymorphic simple sequence repeat regions in chloroplast genomes: applications to the population genetics of pines. **Proceedings National Academy of Science of the USA (PNAS)**, 92:7759-7763.

P22. POWELL W., **MORGANTE M.**, ANDRE C., MCNICOL G. DOYLE J.J., RAFALSKI J.A. 1995. Hypervariable microsatellites provide a general source of polymorphic DNA markers for the chloroplast genome. **Current Biology**, 5:1023-1029.

P23. MALVOLTI M.E., S. FINESCHI, **M.MORGANTE**, G.G. VENDRAMIN 1995. Mating system of a naturalised *Juglans regia* population in Italy. In: Ph. Baradat, W.T. Adams, G. Muller-Starck (Eds.) **Population genetics and genetic conservation of forest trees**, SPB Academic Publishing, The Hague, The Netherlands, pp. 305-308.

P24. RAFALSKI A. , J.M. VOGEL, **M. MORGANTE**, W. POWELL, S.V. TINGEY 1996. Generating and using DNA markers in plants. In: B. Birren, E. Lai (Eds.), **Non-mammalian Genomic Analysis: A Practical Guide**, Academic Press, pp. 75-134.

P25. **MORGANTE M**., PFEIFFER A., COSTACURTA A., OLIVIERI A.M. 1996. Molecular tools for population and ecological genetics in coniferous trees. **Phyton**, 36:133-142.

P26. VENDRAMIN G.G., LELLI L., ROSSI P., **MORGANTE M.** 1996. A set of primers for the amplification of 20 chloroplast microsatellites in *Pinaceae*. **Molecular Ecology**, 5: 595-598.

P27. PROVAN J., CORBETT J., WAUGH R., MCNICOL J.W., **MORGANTE M.**, POWELL W. 1996. DNA fingerprints of rice (*Oryza sativa*) obtained from hypervariable chloroplast simple sequence repeats. **Proc. Roy. Soc. London B: Biological Sciences**, 263: 1275-1281.

P28. SHI L., ZHU T., **MORGANTE M.**, RAFALSKI J.A., KEIM P. 1996. Soybean chromosome painting: a strategy for somatic cytogenetics. **J. Heredity**, 87: 308-313.

P29. POWELL W., **M. MORGANTE**, C. ANDRE, M. HANAFEY, J. VOGEL, S.V. TINGEY, J.A. RAFALSKI 1996. The comparison of RFLP, RAPD, AFLP and SSR (microsatellite) markers for germplasm analysis. **Molecular Breeding**, 2: 225-238.

P30. POWELL W., **MORGANTE M.**, DOYLE J.J., MCNICOL J.W., TINGEY S.V., RAFALSKI J.A. 1996. Genepool variation in genus *Glycine* sub-genus *Soja* revealed by polymorphic nuclear and chloroplast microsatellites. **Genetics**, 144: 793-803.

P31. **M. MORGANTE**, A. PFEIFFER, A. COSTACURTA, A.M. OLIVIERI, W. POWELL, G.G. VENDRAMIN, J.A. RAFALSKI 1996. Polymorphic Simple Sequence Repeats in nuclear and chloroplast genomes: applications to the population genetics of trees. In: R. Ahuja, W. Boerjan, D. Neale (Eds.): **Somatic Cell Genetics and Molecular Genetics of Trees**, Kluwer Academic Publishers, pp. 233-238.

P32. **MORGANTE M.**, JURMAN I., SHI L., ZHU T., KEIM P, RAFALSKI J.A. 1997. The STR120 satellite DNA of soybean: organization, evolution and chromosome specificity. **Chromosome Research**, 5: 363-373.

P33. PFEIFFER A., A.M. OLIVIERI, **M. MORGANTE** 1997. Identification and characterization of microsatellites in Norway spruce (*Picea abies* K.). **Genome**, 40: 411-419.

P34. ARP A., K.J. EDWARDS, M. BRUFORD, FUNK S., B. VOSMAN, **M. MORGANTE**, O. SEBERG, A. KREMER, P. BOURSOT, P. ARCTANDER, D. TAUTZ, G. HEWITT 1997. Newer molecular technologies for biodiversity evaluation: opportunities and challenges. **Nature Biotechnology**, 15: 625-628.

P35. E SIMONE M., **M. MORGANTE**, M. LUCCHIN, P. PARRINI, A. MAROCCO 1997. A first linkage map of *Cichorium intybus* L. using a one-way pseudo-testcross and PCR-derived markers. **Molecular Breeding**, 3:415-425.

P36. **MORGANTE M.**, A. PFEIFFER, I. JURMAN, G.P. PAGLIA, A.M. OLIVIERI 1998. Microsatellite markers in plants. In: A. Karp, P.G. Isaac, D.S. Ingram (eds.), **Molecular tools for screening biodiversity: plants and animals**, Chapman and Hall, London, UK, pp. 288-296.

P37. **MORGANTE M.**, N. FELICE, G. G. VENDRAMIN 1998. Analysis of hypervariable chloroplast microsatellites in *Pinus halepensis* reveals a dramatic genetic bottleneck: a case study. In: A. Karp, P.G. Isaac, D.S. Ingram (eds.), **Molecular tools for screening biodiversity: plants and animals**, Chapman and Hall, London, UK, pp 407-412.

P38. DOYLE J.J., **M. MORGANTE**, S. V. TINGEY, W. POWELL 1998. Size homoplasy in chloroplast microsatellites of wild perennial relatives of soybean (*Glycine* subgenus *Glycine*). **Molecular Biology & Evolution**, 15: 215-218.

P39. PAGLIA G.P., **M. MORGANTE** 1998. PCR-based multiplex DNA fingerprinting techniques for the analysis of conifer genomes. **Molecular Breeding**, 4:173-177.

P40. PAGLIA G.P., A.M. OLIVIERI, **M. MORGANTE** 1998. Towards second generation STS (sequence-tagged sites) linkage maps in conifers: a genetic map of Norway spruce (*Picea abies* K.). **Molecular & General Genetics**, 258: 466-478.

P41. PEAKALL R., S. GILMORE, W. KEYS, **M. MORGANTE**, A. RAFALSKI 1998. Cross-species amplification of Soybean (*Glycine max*) simple-sequence-repeats (SSRs) within the genus and other legume genera: implications for the transferability of SSRs in plants. **Molecular Biology & Evolution**, 15: 1275-1287.

P42. PEJIC I., AJMONE-MARSAN P., **MORGANTE M.**, KOZUMPLICK V., CASTIGLIONI P., TARAMINO G., MOTTO M. 1998. Comparative analysis of genetic similarity among maize inbred lines detected by RFLPs, RAPDs, SSRs, and AFLPs. **Theoretical & Applied Genetics**, 97: 1248-1255.

P43. HUANG WG., CIPRIANI G., **MORGANTE M.**, TESTOLIN R. 1998. Microsatellite DNA in Actinidia chinensis: isolation, characterisation, and homology in related species **Theoretical & Applied Genetics**, 97: 1269-1278.

P44. GEBUREK T., S. MOTTINGER-KROUPA, **M. MORGANTE**, K. BURG 1998. Genetic variation of Norway spruce (*Picea abies* [L.] Karst.) populations in Austria II. Microspatial patterns derived from nuclear sequence tagged microsatellite sites. **Forest Genetics**, 5:231-237.

P45. RAMSAY L., MACAULAY M., CARDLE L., **MORGANTE M.**, DEGLI IVANISSEVICH S., MAESTRI E., POWELL W., WAUGH R. 1999. Intimate association of microsatellite repeats with retrotransposons and other dispersed repetitive elements in barley. **The Plant Journal**, 17:415-425.

P46. TENZER I., DEGLI IVANISSEVICH S., **MORGANTE M.**, GESSLER C. 1999. Identification of microsatellite markers and their application to population genetics of *Venturia inaequalis*. **Phytopathology**, 89:748-753.

P47. PROVAN J., SORANZO N., WILSON N.J., MCNICOL J.W., **MORGANTE M.**, POWELL W. 1999. The use of uniparentally inherited simple sequence repeat markers in plant population studies and systematics. In: P.M. Hollingsworth, R.M. Bateman, R.J. Gornall (Eds.): **Molecular Systematics and Plant Evolution**, Taylor and Francis Limited, pp. 35-50.

P48. PROVAN J., LAWRENCE P., YOUNG G., WRIGHT F., BIRD R., PAGLIA G.P., CATTONARO F., **MORGANTE M.**, POWELL W. 1999. Analysis of the genus *Zea* (Poaceae) using polymorphic chloroplast simple sequence repeats. **Plant Systematics & Evolution**, 218: 245-256.

P49. RAMSAY, L., M. MACAULAY, S. DEGLI IVANISSEVICH, K. MACLEAN, L. CARDLE, J. FULLER, K. J. EDWARDS, S. TUVESSON, **M. MORGANTE**, A. MASSARI, E. MAESTRI, N. MARMIROLI, T. SJAKSTE, M. GANAL, W. POWELL, R. WAUGH 2000. A simple sequence repeat-based linkage map of barley. **Genetics**, 156:1997-2005.

P50. ZAVODNA, M; KRAIC, J; PAGLIA, G; GREGOVA, E; **MORGANTE, M** 2000 Differentiation between closely related lentil (*Lens culinaris* MEDIK.) cultivars using DNA markers **Seed Science And Technology**, 28: 217-219

P51. MEYERS B.C., TINGEY S.V., **MORGANTE M**. 2001. Abundance, distribution and transcriptional activity of repetitive elements in the maize genome. **Genome Research**, 11:1660-1676.

P52. **MORGANTE M.**, HANAFEY M., POWELL W. 2002. Microsatellites are preferentially associated with non repetitive DNA in plant genomes. **Nature Genetics**, 30:194-200.

P53. SCOTTI I., PAGLIA G.P., MAGNI F., **MORGANTE M.** 2002. Efficient development of dinucleotide microsatellite markers in Norway spruce (*Picea abies* Karst.) through dot-blot selection. **Theoretical & Applied Genetics**, 104: 1035-1041.

P54. VAN BUUREN ML, SALVI S, **MORGANTE M**, SERHANI B. AND TUBEROSA R. 2002. Comparative genomic mapping between a 4 cM region flanking DREB1 in *Arabidopsis thaliana* and maize. **Plant Molecular Biology**, 48: 741-750.

P55. SCOTTI I., MAGNI F., PAGLIA G.P., **MORGANTE M.** 2002. Trinucleotide microsatellites in Norway spruce (*Picea abies*): their features and the development of molecular markers. **Theoretical & Applied Genetics**, 106: 40-50,.

P56. MEYERS B.C., **MORGANTE M**. MICHELMORE R.W. 2002. TIR-X and TIR-NBS proteins: Two new families related to disease resistance TIR-NBS-LRR proteins encoded in Arabidopsis and other plant genomes. **The Plant Journal**, 32:77-92.

P57. CHING A., CALDWELL K., JUNG M., DOLAN M., SMITH H., TINGEY S., **MORGANTE M.**, RAFALSKI A. 2002. SNP frequency and haplotype structure of 18 maize genes. **BMC Genetics**, 3:19.

P58. HOTH S., **MORGANTE M.**, SANCHEZ J-P., HANAFEY M., TINGEY S.V., CHUA N-H 2002. Genome-wide gene expression profiling in Arabidopsis thaliana revealed new targets of abscisic acid and largely impaired gene regulation in the abi1-1 mutant. **Journal of Cell Science**, 115:4891-4900.

P59. **MORGANTE M.**, SALAMINI F. 2003 From plant genomics to breeding practice. **Current Opinion in Biotechnology**, 14:214-219.

P60. VISCHI M., JURMAN I., BIANCHI G., **MORGANTE M.** 2003 Karyotype of Norway spruce by multicolor FISH. **Theoretical & Applied Genetics**, 107:591-7.

P61. PALAISA K., **MORGANTE M.**, WILLIAMS M., RAFALSKI A. 2003 Contrasting effects of selection on sequence diversity and linkage disequilibrium at two phytoene synthase loci. **Plant Cell** 15:1795-806.

P62. STEFAN HOTH, YOSHIHISA IKEDA, **MICHELE MORGANTE**, XIUJIE WANG, JIANRU ZUO, MICHAEL K. HANAFEY, TERRY GAASTERLAND, SCOTT V. TINGEY AND NAM-HAI CHUA 2003 Monitoring genome-wide changes in gene expression in response to endogenous cytokinin reveals targets in *Arabidopsis thaliana*. **FEBS Letters**, 554:373-380.

P63. RAFALSKI A., **MORGANTE M.** 2004 Corn and humans: recombination and linkage disequilibrium in two genomes of similar size. **Trends in Genetics**, 20: 103-111.

P64. JACK GARDINER, STEVEN SCHROEDER, MARY L. POLACCO, HECTOR SANCHEZ-VILLEDA, ZHIWEI FANG, **MICHELE MORGANTE**, TIM LANDEWE, KEVIN FENGLER, FRANCISCO USECHE, MICHAEL HANAFEY, SCOTT TINGEY, HUGH CHOU, ROD WING, CAROL SODERLUND, AND EDWARD H. COE JR. 2004 Anchoring 9,371 Maize EST Unigenes to the BAC Contig Map by Two-Dimensional Overgo Hybridization. **Plant Physiology**, 134: 1317-1326.

P65. PALAISA K., **MORGANTE M**., TINGEY S., RAFALSKI J. 2004 Long range patterns of diversity and LD surrounding the maize Y1 gene are indicative of an asymmetric selective sweep. **Proceedings National Academy of Science of the USA (PNAS)**, 101:9885-9890.

P66. MEYERS B.C., SCALABRIN S., **MORGANTE M**. 2004 Mapping and sequencing complex genomes: Let's get physical! **Nature Reviews Genetics**, 5: 578-588.

P67. JUNG M., CHING A., BHATTRAMAKKI D., DOLAN M., TINGEY S., **MORGANTE M**., RAFALSKI A. 2004 Linkage disequilibrium and sequence diversity in a 500 kb region around the adh1 locus in maize elite germplasm. **Theoretical & Applied Genetics**, 109:681-689.

P68. BRUNNER S, FENGLER K, **MORGANTE M,** TINGEY SV AND RAFALSKI A. 2005 Evolution of DNA Sequence Non-Homologies Among Maize Inbreds. **Plant Cell,** 17:343-360.

P69. **MORGANTE M,** BRUNNER S, PEA G, FENGLER K, ZUCCOLO A, RAFALSKI A. 2005 Gene duplication and exon shuffling by helitron-like transposons generate intraspecies diversity in maize. **Nature Genetics** 37: 997-1002.

P70. **MORGANTE M,** POLICRITI A, VITACOLONNA N, ZUCCOLO A. 2005 Structured motifs search. **Journal Computational Biology** 12: 1065-1082.

P71. SCOTTI I., BURELLI A., CATTONARO F., CHAGNÉ D., FULLER J., HEDLEY P.E., JANSSON G., LALANNE C., MADUR D., NEALE D., PLOMION C., POWELL W., TROGGIO M., **MORGANTE M.** 2005 Analysis of the distribution of marker classes in a genetic linkage map: a case study in Norway spruce (*Picea abies* Karst). **Tree Genetics and Genomes** 1: 93 – 102.

P72. **MORGANTE M**. 2006 Plant genome organisation and diversity: the year of the junk! **Current Opinion in Biotechnology**, 17:168-73.

P73. SCOTTI I., PAGLIA G., MAGNI F., **MORGANTE M.** 2006 Population genetics of Norway spruce (*Picea abies* Karst.) at regional scale: sensitivity of different microsatellite motif classes in detecting differentiation. **Annals of Forest Science** 63:485-491.

P74. HEUERTZ M, DE PAOLI E, KALLMAN T, LARSSON H, JURMAN I, **MORGANTE M**, LASCOUX M, GYLLENSTRAND N. 2006 Multilocus patterns of nucleotide diversity, linkage disequilibrium and demographic history of Norway spruce [Picea abies (L.) Karst]. **Genetics** 174:2095-2105.

P75. **MORGANTE M,** DE PAOLI E, RADOVIC S. 2007 Transposable elements and the plant pan-genomes. **Curr Opin Plant Biol**. 10:149-155.

P76. E. FRASCAROLI, M. A. CANÈ, P. LANDI, G. PEA, L. GIANFRANCESCHI, M. VILLA, **M. MORGANTE**, M.E. PÈ 2007 Classical genetic and QTL analyses of heterosis in a maize hybrid between two elite inbred lines. **Genetics**, 176: 625–644.

P77. M. CECCARELLI, V. SARRI, L. NATALI, T. GIORDANI, A. CAVALLINI, A. ZUCCOLO, I. JURMAN, **M. MORGANTE**, P.G. CIONINI 2007 Characterization of the chromosome complement of Helianthus annuus by in-situ hybridization of a tandem repeated DNA sequence**. Genome**, 50:429-434.

P78. S. SALVI, G. SPONZA, **M. MORGANTE** , D. TOMES , X. NIU , K.A.FENGLER , R. MEELEY , E.V. ANANIEV , S. SVITASHEV , E. BRUGGEMANN , B. LI , C.F. HAINEY , S. RADOVIC , G. ZAINA , J.A. RAFALSKI , S.V. TINGEY , G.H. MIAO , R.L. PHILLIPS , R. TUBEROSA 2007 Conserved non-coding genomic sequences associated with a flowering time QTL in maize. **Proceedings National Academy of Science of the USA**, 104:11376-11381.

P79. M. TROGGIO, G. MALACARNE, G. COPPOLA, C. SEGALA, D.A. CARTWRIGHT, M. PINDO, M. STEFANINI, R. MANK, M. MOROLDO, **M. MORGANTE**, M.S. GRANDO, R. VELASCO 2007 A physically anchored SNP-based genetic linkage map of grapevine (Vitis vinifera L.). **Genetics**, 176:2637-2650.

P80. The French-Italian Public Consortium for Grapevine Genome Characterization 2007 The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. **Nature,** 449:463-467.

P81. T. WICKER, F. SABOT, A. HUA-VAN, J.L. BENNETZEN, P. CAPY, B. CHALHOUB, A. FLAVELL, P. LEROY, **M. MORGANTE**, O. PANAUD, E. PAUX, P. SANMIGUEL, A. SCHULMAN 2007 A unified classification system for eukaryotic transposable elements. **Nature Reviews Genetics,** 8(12):973-82.

P82. TAN X, MEYERS BC, KOZIK A, WEST MA, **MORGANTE M**, ST CLAIR DA, BENT AF, MICHELMORE RW. 2007 Global expression analysis of nucleotide binding site-leucine rich repeat-encoding and related genes in Arabidopsis. **BMC Plant Biol**. Oct 23;7(1):56.

P83. MOROLDO M, PAILLARD S, MARCONI R, FABRICE L, CANAGUIER A, CRUAUD C, DE BERARDINIS V, GUICHARD C, BRUNAUD V, LE CLAINCHE I, SCALABRIN S, TESTOLIN R, DI GASPERO G, **MORGANTE M**, ADAM-BLONDON AF. 2008 A physical map of the heterozygous grapevine 'Cabernet Sauvignon' allows mapping candidate genes for disease resistance. **BMC Plant Biol**. Jun 13;8:66.

P84. DENOEUD F, AURY JM, DA SILVA C, NOEL B, ROGIER O, DELLEDONNE M, **MORGANTE M,** VALLE G, WINCKER P, SCARPELLI C, JAILLON O, ARTIGUENAVE F. 2008 Annotating genomes with massive-scale RNA sequencing. **Genome Biol.**;9(12):R175

P85. CASTRONOVO M, RADOVIC S, GRUNWALD C, CASALIS L, **MORGANTE M**, SCOLES G. 2008 Control of Steric Hindrance on Restriction Enzyme Reactions with Surface-Bound DNA Nanostructures. **Nano Lett.** 8:4140-4145.

P86. SARRI V, MINELLI S, PANARA F, **MORGANTE M**, JURMAN I, ZUCCOLO A, CIONINI PG. 2008 Characterization and chromosomal organization of satellite DNA sequences in Picea abies. **Genome**. Sep;51(9):705-13.

P87. NATALI L, CECCARELLI M, GIORDANI T, SARRI V, ZUCCOLO A, JURMAN I, **MORGANTE M,** CAVALLINI A, CIONINI PG. 2008 Phylogenetic relationships between annual and perennial species of Helianthus: evolution of a tandem repeated DNA sequence and cytological hybridization experiments. **Genome**. Dec;51(12):1047-53.

P88. CIPRIANI G, MARRAZZO MT, DI GASPERO G, PFEIFFER A, **MORGANTE M**, TESTOLIN R. 2008 A set of microsatellite markers with long core repeat optimized for grape (Vitis spp.) genotyping. **BMC Plant Biol**. Dec 16;8:127.

P89. SCALABRIN S, **MORGANTE M**, POLICRITI A. Automated FingerPrint Background removal: FPB. **BMC Bioinformatics.** 2009 Apr 30;10(1):127.

P90. VON KORFF M, RADOVIC S, CHOUMANE W, STAMATI K, UDUPA SM, GRANDO S, CECCARELLI S, MACKAY I, POWELL W, BAUM M, **MORGANTE M.** 2009 Asymmetric allele-specific expression in relation to developmental variation and drought stress in barley hybrids. **Plant J.** Jul;59(1):14-26.

P91. FRASCAROLI E, CANÈ MA, PÈ ME, PEA G, **MORGANTE M**, LANDI P. QTL detection in maize testcross progenies as affected by related and unrelated testers. **Theor Appl Genet.** 2009 Mar;118(5):993-1004.

P92. PEA G, PAULSTEPHENRAJ P, CANÈ MA, 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 Genet Genomics**. Apr;281(4):447-57.

P93. COLEMAN C, COPETTI D, CIPRIANI G, HOFFMANN S, KOZMA P, KOVÁCS L, **MORGANTE M**, TESTOLIN R, DI GASPERO G. The powdery mildew resistance gene REN1 co-segregates with an NBS-LRR gene cluster in two Central Asian grapevines. BMC Genet. 2009 Dec 30;10:89.

P94. 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. High throughput approaches reveal splicing of primary microRNA transcripts and tissue specific expression of mature microRNAs in Vitis vinifera. BMC Genomics. 2009 Nov 25;10:558. Corrected and republished in: BMC Genomics. 2010;11:109.

P95. BUTI M, GIORDANI T, VUKICH M, GENTZBITTEL L, PISTELLI L, CATTONARO F, **MORGANTE M**, CAVALLINI A, NATALI L. HACRE1, a recently inserted copia-like retrotransposon of sunflower (Helianthus annuus L.). Genome. 2009 Nov;52(11):904-11.

P96. BELLIN D, PERESSOTTI E, MERDINOGLU D, WIEDEMANN-MERDINOGLU S, ADAM-BLONDON AF, CIPRIANI G, **MORGANTE M**, TESTOLIN R, DI GASPERO G. Resistance to Plasmopara viticola in grapevine 'Bianca' is controlled by a major dominant gene causing localised necrosis at the infection site. Theor Appl Genet. 2009 Dec;120(1):163-76.

P97. CAVALLINI A, NATALI L, ZUCCOLO A, GIORDANI T, JURMAN I, FERRILLO V, VITACOLONNA N, SARRI V, CATTONARO F, CECCARELLI M, CIONINI PG, **MORGANTE M.** Analysis of transposons and repeat composition of the sunflower (Helianthus annuus L.) genome. Theor Appl Genet. 2010 Feb;120(3):491-508.

P98. DRUKA A, FRANCKOWIAK J, LUNDQVIST U, BONAR N, ALEXANDER J, GUZY-WROBELSKA J, RAMSAY L, DRUKA I, GRANT I, MACAULAY M, VENDRAMIN V, SHAHINNIA F, RADOVIC S, HOUSTON K, HARRAP D, CARDLE L, MARSHALL D, **MORGANTE M**, STEIN N, WAUGH R. Exploiting induced variation to dissect quantitative traits in barley. Biochem Soc Trans. 2010 Apr;38(2):683-8.

P99. SCALABRIN S, TROGGIO M, MOROLDO M, PINDO M, FELICE N, COPPOLA G, PRETE G, MALACARNE G, MARCONI R, FAES G, JURMAN I, GRANDO S, JESSE T, SEGALA C, VALLE G, POLICRITI A, FONTANA P, **MORGANTE M**, VELASCO R. Physical mapping in highly heterozygous genomes: a physical contig map of the Pinot Noir grapevine cultivar. BMC Genomics. 2010 Mar 26;11:204.

P100. CIPRIANI G, SPADOTTO A, JURMAN I, DI GASPERO G, CRESPAN M, MENEGHETTI S, FRARE E, VIGNANI R, CRESTI M, **MORGANTE M**, PEZZOTTI M, PE E, POLICRITI A, TESTOLIN R. The SSR-based molecular profile of 1005 grapevine (Vitis vinifera L.) accessions uncovers new synonymy and parentages, and reveals a large admixture amongst varieties of different geographic origin. Theor Appl Genet. 2010 Nov;121(8):1569-85.

P101. FALGINELLA L, CASTELLARIN SD, TESTOLIN R, GAMBETTA GA, **MORGANTE M**, DI GASPERO G. Expansion and subfunctionalisation of flavonoid 3',5'-hydroxylases in the grapevine lineage. BMC Genomics. 2010 Oct 12;11:562.

P102. GIORDANI T, BUTI M, NATALI L, PUGLIESI C, CATTONARO F, **MORGANTE M**, CAVALLINI A. An analysis of sequence variability in eight genes putatively involved in drought response in sunflower (Helianthus annuus L.). Theor Appl Genet. 2011 Apr;122(6):1039-49

P103. DRUKA A, FRANCKOWIAK J, LUNDQVIST U, BONAR N, ALEXANDER J, HOUSTON K, RADOVIC S, SHAHINNIA F, VENDRAMIN V, **MORGANTE M**, STEIN N, WAUGH R. Genetic dissection of barley morphology and development. Plant Physiol. 2011 Feb;155(2):617-27.

P104. ROHDE A, STORME V, JORGE V, GAUDET M, VITACOLONNA N, FABBRINI F, RUTTINK T, ZAINA G, MARRON N, DILLEN S, STEENACKERS M, SABATTI M, **MORGANTE M**, BOERJAN W, BASTIEN C. Bud set in poplar--genetic dissection of a complex trait in natural and hybrid populations. New Phytol. 2011 Jan;189(1):106-21.

P105. MARRONI F, PINOSIO S, ZAINA G, FOGOLARI F, FELICE N, CATTONARO F, **MORGANTE M.** Nucleotide diversity and linkage disequilibrium in *Populus nigra* cinnamyl alcohol dehydrogenase (*CAD4*) gene. Tree Genetics and Genomes 2011 7(5): 1011-1023.

P106. MARRONI F, PINOSIO S, DI CENTA E, JURMAN I, BOERJAN W, FELICE N, CATTONARO F, **MORGANTE M.** Large scale detection of rare variants via pooled multiplexed next generation sequencing: towards next generation Ecotilling. Plant J. 2011 Aug;67(4):736-45.

P107. BUTI M, GIORDANI T, CATTONARO F, COSSU RM, PISTELLI L, VUKICH M, **MORGANTE M**, CAVALLINI A, NATALI L. Temporal dynamics in the evolution of the sunflower genome as revealed by sequencing and annotation of three large genomic regions. Theor Appl Genet. 2011 Sep;123(5):779-91.

P108. SHAHINNIA F, DRUKA A, FRANCKOWIAK J, **MORGANTE M**, WAUGH R, STEIN N. High resolution mapping of Dense spike-ar (dsp.ar) to the genetic centromere of barley chromosome 7H. Theor Appl Genet. 2012 Feb;124(2):373-84.

P109. DI GASPERO G, COPETTI D, COLEMAN C, CASTELLARIN SD, EIBACH R, KOZMA P, LACOMBE T, GAMBETTA G, ZVYAGIN A, CINDRIĆ P, KOVÁCS L, **MORGANTE M**,

TESTOLIN R. Selective sweep at the Rpv3 locus during grapevine breeding for downy mildew resistance. Theor Appl Genet. 2012 Feb;124(2):277-86.

P110. HARFOUCHE A, MEILAN R, KIRST M, **MORGANTE M**, BOERJAN W, SABATTI M, SCARASCIA MUGNOZZA G. Accelerating the domestication of forest trees in a changing world. Trends Plant Sci. 2012 Feb;17(2):64-72.

P111. HOUSTON K, DRUKA A, BONAR N, MACAULAY M, LUNDQVIST U, FRANCKOWIAK J, **MORGANTE M**, STEIN N, WAUGH R. Analysis of the barley bract suppression gene Trd1. Theor Appl Genet. 2012 Jun;125(1):33-45.

P112. Marroni F, Pinosio S, Morgante M. The quest for rare variants: pooled multiplexed next generation sequencing in plants. Front Plant Sci. 2012;3:133. Epub 2012 Jun 28.

P113. Chen J, Källman T, Ma X, Gyllenstrand N, Zaina G, Morgante M, Bousquet J, Eckert A, Wegrzyn J, Neale D, Lagercrantz U, Lascoux M. Disentangling the roles of history and local selection in shaping clinal variation of allele frequencies and gene expression in Norway spruce (Picea abies). Genetics. 2012 Jul;191(3):865-81.

P114. Verde I, Bassil N, Scalabrin S, Gilmore B, Lawley CT, Gasic K, Micheletti D, Rosyara UR, Cattonaro F, Vendramin E, Main D, Aramini V, Blas AL, Mockler TC, Bryant DW, Wilhelm L, Troggio M, Sosinski B, Aranzana MJ, Arús P, Iezzoni A, Morgante M, Peace C. Development and evaluation of a 9K SNP array for peach by internationally coordinated SNP detection and validation in breeding germplasm. PLoS One. 2012;7(4):e35668.

P115. Jung S, Cestaro A, Troggio M, Main D, Zheng P, Cho I, Folta KM, Sosinski B, Abbott A, Celton JM, Arús P, Shulaev V, Verde I, Morgante M, Rokhsar D, Velasco R, Sargent DJ. Whole genome comparisons of Fragaria, Prunus and Malus reveal different modes of evolution between Rosaceous subfamilies. BMC Genomics. 2012 Apr 4;13:129.

P116. Fabbrini F, Gaudet M, Bastien C, Zaina G, Harfouche A, Beritognolo I, Marron N, Morgante M, Scarascia-Mugnozza G, Sabatti M. Phenotypic plasticity, QTL mapping and genomic characterization of bud set in black poplar. BMC Plant Biol. 2012 Apr 3;12:47.

P117. The International Barley Genome Sequencing Consortium; Principal investigators, Mayer KF, Waugh R, Langridge P, Close TJ, Wise RP, Graner A, Matsumoto T, Sato K, Schulman A, Muehlbauer GJ, Stein N; Physical map construction and direct anchoring, Ariyadasa R, Schulte D, Poursarebani N, Zhou R, Steuernagel B, Mascher M, Scholz U, Shi B, Langridge P, Madishetty K, Svensson JT, Bhat P, Moscou M, Resnik J, Close TJ, Muehlbauer GJ, Hedley P, Liu H, Morris J, Waugh R, Frenkel Z, Korol A, Bergès H, Graner A, Stein N; Genomic sequencing and assembly, Steuernagel B, Scholz U, Taudien S, Felder M, Groth M, Platzer M, Stein N; BAC sequencing and assembly, Steuernagel B, Scholz U, Himmelbach A, Taudien S, Felder M, Platzer M, Lonardi S, Duma D, Alpert M, Cordero F, Beccuti M, Ciardo G, Ma Y, Wanamaker S, Close TJ, Stein N; BAC-end sequencing, Cattonaro F, Vendramin V, Scalabrin S, Radovic S, Wing R, Schulte D, Steuernagel B, Morgante M, Stein N, Waugh R; Integration of physical/genetic map and sequence resources, Nussbaumer T, Gundlach H, Martis M, Ariyadasa R, Poursarebani N, Steuernagel B, Scholz U, Wise RP, Poland J, Stein N, Mayer KF; Gene annotation, Spannagl M, Pfeifer M, Gundlach H, Mayer KF; Repetitive DNA analysis, Gundlach H, Moisy C, Tanskanen J, Scalabrin S, Zuccolo A, Vendramin V, Morgante M, Mayer KF, Schulman A; Transcriptome sequencing and analysis, Pfeifer M, Spannagl M, Hedley P, Morris J, Russell J, Druka A, Marshall D, Bayer M, Swarbreck D, Sampath D, Ayling S, Febrer M, Caccamo M, Matsumoto T, Tanaka T, Sato K, Wise RP, Close TJ, Wannamaker S, Muehlbauer GJ, Stein N, Mayer KF, Waugh R; Re-sequencing and diversity analysis, Steuernagel B, Schmutzer T, Mascher M, Scholz U, Taudien S, Platzer M, Sato K, Marshall D, Bayer M, Waugh R, Stein N; Writing and editing of the manuscript, Mayer KF, Waugh R, Brown JW, Schulman A, Langridge P, Platzer M, Fincher GB, Muehlbauer GJ, Sato K, Close TJ, Wise RP, Stein N. A physical, genetic and functional sequence assembly of the barley genome. Nature. 2012 Nov 29;491(7426):711-6.

P118. The International Peach Genome Initiative, Verde I, Abbott AG, Scalabrin S, Jung S, Shu S, Marroni F, Zhebentyayeva T, Dettori MT, Grimwood J, Cattonaro F,Zuccolo A, Rossini L, Jenkins J, Vendramin E, Meisel LA, Decroocq V, Sosinski B, Prochnik S, Mitros T, Policriti A, Cipriani G, Dondini L, Ficklin S, Goodstein DM, Xuan P, Fabbro CD, Aramini V, Copetti D, Gonzalez S, Horner DS, Falchi R, Lucas S, Mica E, Maldonado J, Lazzari B, Bielenberg D, Pirona R, Miculan M, Barakat A, Testolin R, Stella A, Tartarini S, Tonutti P, Arús P, Orellana A,

Wells C, Main D, Vizzotto G, Silva H, Salamini F, Schmutz J, Morgante M, Rokhsar DS. The high-quality draft genome of peach (Prunus persica) identifies unique patterns of genetic diversity, domestication and genome evolution. Nat Genet. 2013 45(5):487-94.

P119. Vanholme B, Cesarino I, Goeminne G, Kim H, Marroni F, Van Acker R, Vanholme R, Morreel K, Ivens B, Pinosio S, Morgante M, Ralph J, Bastien C, Boerjan W. Breeding with rare defective alleles (BRDA): a natural Populus nigra HCT mutant with modified lignin as a case study. New Phytol. 2013 May;198(3):765-76.

P120. Venuti S, Copetti D, Foria S, Falginella L, Hoffmann S, Bellin D, Cindrić P, Kozma P, Scalabrin S, Morgante M, Testolin R, Di Gaspero G. Historical introgression of the downy mildew resistance gene Rpv12 from the Asian species Vitis amurensis into grapevine varieties. PLoS One. 2013 Apr 12;8(4):e61228

P121. Nystedt B, Street NR, Wetterbom A, Zuccolo A, Lin YC, Scofield DG, Vezzi F, Delhomme N, Giacomello S, Alexeyenko A, Vicedomini R, Sahlin K, Sherwood E, Elfstrand M, Gramzow L, Holmberg K, Hällman J, Keech O, Klasson L, Koriabine M, Kucukoglu M, Käller M, Luthman J, Lysholm F, Niittylä T, Olson A, Rilakovic N, Ritland C, Rosselló JA, Sena J, Svensson T, Talavera-López C, Theißen G, Tuominen H, Vanneste K, Wu ZQ, Zhang B, Zerbe P, Arvestad L, Bhalerao R, Bohlmann J, Bousquet J, Garcia Gil R, Hvidsten TR, de Jong P, MacKay J, Morgante M, Ritland K, Sundberg B, Thompson SL, Van de Peer Y, Andersson B, Nilsson O, Ingvarsson PK, Lundeberg J, Jansson S. The Norway spruce genome sequence and conifer genome evolution. Nature. 2013 May 30;497(7451):579-84.

P122. Falchi R, Vendramin E, Zanon L, Scalabrin S, Cipriani G, Verde I, Vizzotto G, Morgante M. Three distinct mutational mechanisms acting on a single gene underpin the origin of yellow flesh in peach. Plant J. 2013 Oct;76(2):175-87.

P123. Natali L, Cossu RM, Barghini E, Giordani T, Buti M, Mascagni F, Morgante M, Gill N, Kane NC, Rieseberg L, Cavallini A. The repetitive component of the sunflower genome as shown by different procedures for assembling next generation sequencing reads. BMC Genomics. 2013 Oct 6;14(1):686.

P124. Larsson, H; De Paoli, E; Morgante, M; et al. The Hypomethylated Partial Restriction (HMPR) method reduces the repetitive content of genomic libraries in Norway spruce (Picea abies) TREE GENETICS & GENOMES 2013 9(2):601-612

P125. Del Fabbro C, Scalabrin S, Morgante M, Giorgi FM. An Extensive Evaluation of Read Trimming Effects on Illumina NGS Data Analysis. PLoS One. 2013 Dec 23;8(12):e85024.

P126. Marroni F, Pinosio S, Morgante M. Structural variation and genome complexity: is dispensable really dispensable? Curr Opin Plant Biol. 2014 Apr;18:31-6.

P127. Wang S, Wong D, Forrest K, Allen A, Chao S, Huang BE, Maccaferri M, Salvi S, Milner SG, Cattivelli L, Mastrangelo AM, Whan A, Stephen S, Barker G, Wieseke R, Plieske J; International Wheat Genome Sequencing Consortium, Lillemo M, Mather D, Appels R, Dolferus R, Brown-Guedira G, Korol A, Akhunova AR, Feuillet C, Salse J, Morgante M, Pozniak C, Luo MC, Dvorak J, Morell M, Dubcovsky J, Ganal M, Tuberosa R, Lawley C, Mikoulitch I, Cavanagh C, Edwards KJ, Hayden M, Akhunov E. Characterization of polyploid wheat genomic diversity using a high-density 90,000 single nucleotide polymorphism array. Plant Biotechnol J. 2014 Aug;12(6):787-96.

P128. Barghini E, Natali L, Cossu RM, Giordani T, Pindo M, Cattonaro F, Scalabrin S, Velasco R, Morgante M, Cavallini A. The peculiar landscape of repetitive sequences in the olive (Olea europaea L.) genome. Genome Biol Evol. 2014 Apr;6(4):776-91.

P129. Maccaferri M, Ricci A, Salvi S, Milner SG, Noli E, Martelli PL, Casadio R, Akhunov E, Scalabrin S, Vendramin V, Ammar K, Blanco A, Desiderio F, Distelfeld A, Dubcovsky J, Fahima T, Faris J, Korol A, Massi A, Mastrangelo AM, Morgante M, Pozniak C, N'Diaye A, Xu S, Tuberosa R. A high-density, SNP-based consensus map of tetraploid wheat as a bridge to integrate durum and bread wheat genomics and breeding. Plant Biotechnol J. 2015 Jun;13(5):648-63.

P130. Wu GA, Prochnik S, Jenkins J, Salse J, Hellsten U, Murat F, Perrier X, Ruiz M, Scalabrin S, Terol J, Takita MA, Labadie K, Poulain J, Couloux A, Jabbari K, Cattonaro F, Del Fabbro C, Pinosio S, Zuccolo A, Chapman J, Grimwood J, Tadeo FR, Estornell LH, Muñoz-Sanz JV, Ibanez V, Herrero-Ortega A, Aleza P, Pérez-Pérez J, Ramón D, Brunel D, Luro F, Chen C, Farmerie WG, Desany B, Kodira C, Mohiuddin M, Harkins T, Fredrikson K, Burns P, Lomsadze A, Borodovsky M, Reforgiato G, Freitas-Astúa J, Quetier F, Navarro L, Roose M, Wincker P,

Schmutz J, Morgante M, Machado MA, Talon M, Jaillon O, Ollitrault P, Gmitter F, Rokhsar D. Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. Nat Biotechnol. 2014 Jul;32(7):656-62.

P131. Lind M, Källman T, Chen J, Ma XF, Bousquet J, Morgante M, Zaina G, Karlsson B, Elfstrand M, Lascoux M, Stenlid J. A Picea abies linkage map based on SNP markers identifies QTLs for four aspects of resistance to Heterobasidion parviporum infection. PLoS One. 2014 Jul 18;9(7):e101049.

P132. Barghini E, Natali L, Giordani T, Cossu RM, Scalabrin S, Cattonaro F, Šimková H, Vrána J, Doležel J, Morgante M, Cavallini A. LTR retrotransposon dynamics in the evolution of the olive (Olea europaea) genome. DNA Res. 2015 Feb;22(1):91-100.

P133. Maccaferri M, Ricci A, Salvi S, Milner SG, Noli E, Martelli PL, Casadio R, Akhunov E, Scalabrin S, Vendramin V, Ammar K, Blanco A, Desiderio F, Distelfeld A, Dubcovsky J, Fahima T, Faris J, Korol A, Massi A, Mastrangelo AM, Morgante M, Pozniak C, N'Diaye A, Xu S, Tuberosa R. A high-density, SNP-based consensus map of tetraploid wheat as a bridge to integrate durum and bread wheat genomics and breeding. Plant Biotechnol J. 2015 Jun;13(5):648-63. doi: 10.1111/pbi.12288.

P134. Zuccolo A, Scofield DG, De Paoli E, Morgante M. The Ty1-copia LTR retroelement family PARTC is highly conserved in conifers over 200 MY of evolution. Gene. 2015 Aug 15;568(1):89-99.

P135. Sanseverino W, Hénaff E, Vives C, Pinosio S, Burgos-Paz W, Morgante M, Ramos-Onsins SE, Garcia-Mas J, Casacuberta JM. Transposon Insertions, Structural Variations, and SNPs Contribute to the Evolution of the Melon Genome. Mol Biol Evol. 2015 Oct;32(10):2760-74.

P136. 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. Genetic properties of the MAGIC maize population: a new platform for high definition QTL mapping in Zea mays. Genome Biol. 2015 Sep 11;16:167.

P137. Barabaschi D, Magni F, Volante A, Gadaleta A, Šimková H, Scalabrin S, Prazzoli ML, Bagnaresi P, Lacrima K, Michelotti V, Desiderio F, Orrù L, Mazzamurro V, Fricano A, Mastrangelo AM, Tononi P, Vitulo N, Jurman I, Frenkel Z, Cattonaro F, Morgante M, Blanco A, Doležel J, Delledonne M, Stanca AM, Cattivelli L, Valè G, 2015. Physical mapping of bread wheat chromosome 5A: an integrated approach. The Plant Genome, 8: doi:10.3835/plantgenome2015.03.0011

P138. Jost M, Taketa S, Mascher M, Himmelbach A, Yuo T, Shahinnia F, Rutten T, Druka A, Schmutzer T, Steuernagel B, Beier S, Taudien S, Scholz U, Morgante M, Waugh R, Stein N. A Homolog of Blade-On-Petiole 1 and 2 (BOP1/2) Controls Internode Length and Homeotic Changes of the Barley Inflorescence. Plant Physiol. 2016 Jun;171(2):1113-27.

P139. Chen J, Källman T, Ma XF, Zaina G, Morgante M, Lascoux M. Identifying Genetic Signatures of Natural Selection Using Pooled Population Sequencing in Picea abies. G3 (Bethesda). 2016 May 6. pii: g3.116.028753. doi: 10.1534/g3.116.028753.

P140. Faivre-Rampant P, Zaina G, Jorge V, Giacomello S, Segura V, Scalabrin S, Guérin V, De Paoli E, Aluome C, Viger M, Cattonaro F, Payne A, PaulStephenRaj P, Le Paslier MC, Berard A, Allwright MR, Villar M, Taylor G, Bastien C, Morgante M. New resources for genetic studies in Populus nigra: genome-wide SNP discovery and development of a 12k Infinium array. Mol Ecol Resour. 2016 Jul;16(4):1023-36.

P141. Pinosio S, Giacomello S, Faivre-Rampant P, Taylor G, Jorge V, Le Paslier MC, Zaina G, Bastien C, Cattonaro F, Marroni F, Morgante M. Characterization of the poplar pan-genome by genome-wide identification of structural variation. Mol Biol Evol. 2016 Aug 7. pii: msw161.

P142. Allwright MR, Payne A, Emiliani G, Milner S, Viger M, Rouse F, Keurentjes JJ, Bérard A, Wildhagen H, Faivre-Rampant P, Polle A, Morgante M, Taylor G. Biomass traits and candidate genes for bioenergy revealed through association genetics in coppiced European Populus nigra (L.). Biotechnol Biofuels. 2016 Sep 8;9(1):195

P143. Wales N, Madrigal JR, Cappellini E, Baez AC, Castruita JAS, Romero-Navarro JA, Carøe C, Ávila-Arcos MC, Peñaloza F, Moreno-Mayar JV. The limits and potential of paleogenomic techniques for reconstructing grapevine domestication. Journal of Archaeological Science, 72: 57-70 2016.

P144. Giordani T, Cossu RM, Mascagni F, Marroni F, Morgante M, Cavallini A, Natali L. Genome-wide analysis of LTR-retrotransposon expression in leaves of Populus. Tree Genetics & Genomes 12:1-14 2016.

P145. Evangelistella C, Valentini A, Ludovisi R, Firrincieli A, Fabbrini F, Scalabrin S, Cattonaro F, Morgante M, Mugnozza GS, Keurentjes JJB, Harfouche A. De novo assembly, functional annotation, and analysis of the giant reed (Arundodonax L.) leaf transcriptome provide tools for the development of a biofuel feedstock. Biotechnol Biofuels. 2017 May 30;10:138.

P146. Wildhagen H, Paul S, Allwright M, Smith HK, Malinowska M, Schnabel SK, Paulo MJ, Cattonaro F, Vendramin V, Scalabrin S, Janz D, Douthe C, Brendel O, Buré C, Cohen D, Hummel I, Le Thiec D, van Eeuwijk F, Keurentjes JJB, Flexas J, Morgante M, Robson P, Bogeat-Triboulot MB, Taylor G, Polle A. Genes and gene clusters related to genotype and drought-induced variation in saccharification potential, lignin content and wood anatomical traits in Populus nigra†. Tree Physiol. 2017 May 24:1-20.

P147. Marroni F, Scaglione D, Pinosio S, Policriti A, Miculan M, Di Gaspero G, Morgante M. Reduction of heterozygosity (ROH) as a method to detect mosaic structural variation. Plant Biotechnol J. 2017 Jul;15(7):791-793.

P148. Canaguier A, Grimplet J, Di Gaspero G, Scalabrin S, Duchêne E, Choisne N,Mohellibi N, Guichard C, Rombauts S, Le Clainche I, Bérard A, Chauveau A, Bounon R, Rustenholz C, Morgante M, Le Paslier MC, Brunel D, Adam-Blondon AF. A new version of the grapevine reference genome assembly (12X.v2) and of its annotation (VCost.v3). Genom Data. 2017 Sep 18;14:56-62.

P149. Hirsch T, Rothoeft T, Teig N, Bauer JW, Pellegrini G, De Rosa L, Scaglione D, Reichelt J, Klausegger A, Kneisz D, Romano O, Secone Seconetti A, Contin R, Enzo E, Jurman I, Carulli S, Jacobsen F, Luecke T, Lehnhardt M, Fischer M, Kueckelhaus M, Quaglino D, Morgante M, Bicciato S, Bondanza S, De Luca M. Regeneration of the entire human epidermis using transgenic stem cells. Nature. 2017 Nov 16;551(7680):327-332. doi: 10.1038/nature24487.

P150. Utsunomiya YT, Milanesi M, Utsunomiya ATH, Torrecilha RBP, Kim ES, Costa MS, Aguiar TS, Schroeder S, do Carmo AS, Carvalheiro R, Neves HHR, Padula RCM, Sussai TS, Zavarez LB, Cipriano RS, Caminhas MMT, Hambrecht G, Colli L, Eufemi E, Ajmone-Marsan P, Cesana D, Sannazaro M, Buora M, Morgante M, Liu G, Bickhart D, Van Tassell CP, Sölkner J, Sonstegard TS, Garcia JF. A PLAG1 mutation contributed to stature recovery in modern cattle. Sci Rep. 2017 Dec 7;7(1):17140. doi: 10.1038/s41598-017-17127-1.

P151. Dal Santo S, Zenoni S, Sandri M, De Lorenzis G, Magris G, De Paoli E, Di Gaspero G, Del Fabbro C, Morgante M, Brancadoro L, Grossi D, Fasoli M, Zuccolotto P, Tornielli GB, Pezzotti M. Grapevine field experiments reveal the contribution of genotype, the influence of environment and the effect of their interaction (G×E) on the berry transcriptome. Plant J. 2018 Mar;93(6):1143-1159.

P152. Radovic S, Dubsky De Wittenau G, Mandl N, Betto E, Curcio F, Morgante M, Lonigro IR. A versatile method for gene dosage quantification: multiplex PCR and single base extension for copy number and gene-conversion identification of SMN genes. J Biol Regul Homeost Agents. 2018 Jan-Feb;32(1):115-121.

P153. Valentinuzzi F, Venuti S, Pii Y, Marroni F, Cesco S, Hartmann F, Mimmo T,Morgante M, Pinton R, Tomasi N, Zanin L. Common and specific responses to iron and phosphorus deficiencies in roots of apple tree (Malus × domestica). Plant Mol Biol. 2019 Sep;101(1-2):129-148.

P154. Zanin L, Venuti S, Marroni F, Franco A, Morgante M, Pinton R, Tomasi N. Physiological and RNA sequencing data of white lupin plants grown under Fe and P deficiency. Data Brief. 2019 May 28;25:104069. doi: 10.1016/j.dib.2019.104069.

P155. Venuti S, Zanin L, Marroni F, Franco A, Morgante M, Pinton R, Tomasi N. Physiological and transcriptomic data highlight common features between iron and phosphorus acquisition mechanisms in white lupin roots. Plant Sci. 2019 Aug;285:110-121.

P156. Magris G, Di Gaspero G, Marroni F, Zenoni S, Tornielli GB, Celii M, De Paoli E, Pezzotti M, Conte F, Paci P, Morgante M. Genetic, epigenetic and genomic effects on variation of gene expression among grape varieties. Plant J. 2019 Sep;99(5):895-909

P157. Vendramin V, Ormanbekova D, Scalabrin S, Scaglione D, Maccaferri M, Martelli P, Salvi S, Jurman I, Casadio R, Cattonaro F, Tuberosa R, Massi A, Morgante M. Genomic tools for durum

wheat breeding: de novo assembly of Svevo transcriptome and SNP discovery in elite germplasm. BMC Genomics. 2019 Apr 10;20(1):278.

P158. Scaglione D, Pinosio S, Marroni F, Centa ED, Fornasiero A, Magris G, Scalabrin S, Cattonaro F, Taylor G, Morgante M. Single primer enrichment technology as a tool for massive genotyping: a benchmark on black poplar and maize. Ann Bot. 2019 Mar 30.