

Maud Tenailon (maiden name : Le Thierry d'Ennequin)
CNRS researcher
Plant Evolutionary Genomics: Domestication and Adaptation

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EDUCATION AND RESEARCH EXPERIENCE

- Since 2020 **Director of Research CNRS** (DR1) at the Dept. GQE – Le Moulon. Head of the team 'Evolutionary Genomics and Adaptation of Domesticated plants' (GEvAD). Vice chair of the Dept. (2020-2021).
- 2013-2019 Director of Research CNRS (DR2) at the Dept. GQE – Le Moulon. Head of the team 'Genome Dynamics and Adaptation of cultivated Plants' (DyGAP)
- 2002-2013 CNRS Researcher Associate (CR) at 'Ferme du Moulon', Dept. of Plant Genetics (Gif-sur-Yvette, France). Head of the team 'Evolutionary Genetics: Adaptation and Redundancy' (GEAR) in 2012, 2013
- 2011 Awarded CNRS bronze medal
- 2009-2011 Sabbatical leave at University of California Irvine (California, USA) with Brandon Gaut
- 2009 HDR defence at the University Paris XI (Orsay)
- 1999-2002 Postdoc with Brandon Gaut at the University of California Irvine (California, USA)
- 1995-1999 PhD student in evolutionary genetics at the University Paris XI (Orsay)
- 1994-1995 Master degree in Genetic resources and plant breeding at the Institut National d'Agronomie (Paris-Grignon)
- 1990-1994 Undergraduate studies in Biology at the University of Paris VII (Jussieu) and VI (Pierre et Marie Currie)

SELECTED EXPERTISE ACTIVITIES

- President of the Scientific committee, Plant Biology Europe (FESPB, Federation of European Societies of Plant Biology), July 2023 (Marseille, France).
- Associate Editor (2019-) and Genome Reports Editor (2021-2022) of Genome Biology and Evolution.
- Local host of the Maize Genetics Conference, ~500 participants, march 2018 (St Malo, France).
- Invited researcher at the KAVLI Institute for Theoretical Physics (KITP, Université of California, Santa Barbara), Summer school 2017 « Eco-Evolutionary dynamics in Nature and the lab » (6 weeks).
- Elected member of the Society of Molecular Biology and Evolution council – SMBE councillor (2016-2018).
- Nominated member of the CNRS evaluation and recruitment panel "Integrative Plant Biology", section 23 (2012-2016).
- Associate Editor of Genetica (2005-2009)

MENTORING

2022 **Clémentine Tocco**, M1 (co-advice with E. Burban, 2 months).

2022 **Augustin Desprez**, M2 (co-advice with E. Burban, 6 months).

2021-2024 **Noa Vazeux-Blumental**, PhD student (Labex SPS doctoral fellowship, co-advice with D. Manicacci).

2021 **Noa Vazeux-Blumental**, M2 (co-advice with D. Manicacci, 6 months).

2020-2023 **Ewen Burban**, PhD Student (ANR doctoral fellowship, co-advice with PhD director S. Glémin).

2020 **Laura Mathieu**, M1 (co-advice with D. Manicacci, 2 months).

2020 **Jeanne Liger**, M2 (co-advice with P. Deschamps, ESE, 6 months).

2019 **Ewen Burban**, M1 (co-advice with A. Le Rouzic, 5 months).

2019 **Lydia Inès Maset**, DUT (co-advice with D. Manicacci, 2 months).

2017-2020 **Arnaud Desbiez-Piat**, PhD student (Doctoral school fellowship, co-advice with PhD director C. Dillmann,).

2017 **Juliette Aubert**, Undergraduate student (co-advice with D. Manicacci).

2015-2018 **Anne Lorant**, PhD student (Principal advisor J. Ross-Ibarra, NSF funding, 3 months at GQE-Le Moulon).

2015-2018 **Natalia Martínez-Ainsworth**, PhD student (CONACYT fellowship, co-advice with D. Manicacci).

2015 **Khawla Seddiki**, Master student (co-advice with C. Dillmann, 12 months).

2014 **Jason Lapeyronnie**, Master student (co-advice with S. Boitard, MNHN Paris, 6 months).

2014 **Maéva Mollion**, Master student (co-advice with C. Dillmann, 6 months).

2014 **Jessica Melique**, Undergraduate student (co-advice with J. de Meaux, Univ. Münster, Germany, 3 months in Münster, 3 months at GQE-Le Moulon).

2013 **Coraline Linguat**, Undergraduate student (3 months).

2012-2016 **Jonas Aguirre**, PhD student (Principal advisor and PhD Director Luis Eguiarte, Mexican fellowship from Conabio, 3 months at GQE-Le Moulon).

2013-2016 **Jean-Tristan Brandenburg**, Postdoc.

2012-2016 **Margaux-Alison Fustier**, PhD student (ANR fellowship, co-advice with D. Manicacci).

2012 **Betty Leitte**, Undergraduate student (4 months).

2012 **Alix Marchandin**, Undergraduate student (2 months).

2011 **Odrade Nougé**, Master student (co-advice with D. Manicacci, 6 months).

2010-2012 **Concepción Muñoz Díez**, Postdoc (co-advice with B. Gaut).

2007-2011 **Eléonore Durand**, PhD student (joint INRA-CNRS fellowship, co-advice with PhD director C. Dillmann).

2007 **Cyril Michel**, Undergraduate student (3 months).

2007 **Letizia Camus-Kulandaivelu**. Postdoc.

2006-2008 **Tatiana Zerjal**. Postdoc.

2006-2010 **Jonathan Corbi**, PhD student (CNRS fellowship, co-advice with D. Manicacci).

2006 **Letizia Camus-Kulandaivelu**, PhD student (Principal advisor and PhD Director A. Charcosset, co-advice 10 months).

2005 **Maryline Debieu**, Master student (co-advice with D. Manicacci, 6 months).

2005 **Estelle Bonleu**, Master student (6 months).

2005 **Pierre Garrabos**, Undergraduate student (co-advice with D. Manicacci, 3 months).

2004 **Milouda Sehabi**, Master student (co-advice with D. Manicacci, 6 months).

2004 **Caroline Esnault**, Undergraduate student (3 months).

FELLOWSHIPS AND GRANTS

2022 Partner of Graduate School Biosphera project 'IntercropRNAseq' (5 keuros).

2020-2026	Partner of H2020 project, Topic SFS-28-01-2019: 'GenRes and pre-breeding communities' (INCREASE), coordinator of Workpackage 'Data analysis and knowledge exploitation' (400 keuros).
2020-2026	Coordinator of an ANR grant 'Domestication as a step towards reproductive isolation' (600 keuros).
2019	Coordinator of an IDEEV grant 'Impact on life-cycle shifts on the rhizosphere microbiome in maize' (8 keuros).
2017-2018	Coordinator of a BASC grant 'Understanding the determinants of maize-bean coculture (19.000 €).
2016-2019	Partner of a labex BASC grant 'Patterns of response to selection and genotype-phenotype relationships', PI of a Task (280.000 € total for the project).
2015-2016	Partner of an INRA BAP grant 'Mesures of expression and determinism of maize floral' (23.000 €).
2015-2016	Partner of a BASC grant 'FloSeq: genotype-phenotype relationship and determinants of flowering transition in maize' (10.000 €).
2012-2016	Co-coordinator of an Ecos-Nord exchange program with Mexico 'Populations Genomics: Investigation of maize progenitors (<i>Zea mays ssp. parviglumis</i> et <i>Zea mays ssp. mexicana</i>)'
2012-2016	Coordinator of an ANR Bioadapt grant 'Identifying adaptive variation in wild relatives of two cereal crops, maize and pearl millet' (515.000 €).
2012-2013	Co-coordinator of the France-Berkeley Fund (FDF) 'Does domestication affect recombination: a pilot study in maize' (8.000 USD).
2012-2013	Partner of IDEEV grant 'Evolution of gene networks in the course of adaptation: a pilot study in two model species, drosophila and corn' (10.000 €).
2012-2013	Coordinator of an IFR87 grant 'Diversity of expression in the gene network encoding flowering transition in maize' (5.200 €)
2011-2019	Partner of a Investissements d'avenir project, Biotechnologies and bioressources ANR Grant (Amaizing), PI of the task 'Population genomics of European maize' (300.000 €).
2010-2011	Collaborator of a UC-Mexus grant 'Genome variation and transposable element content in wild subspecies of maize along altitudinal gradients' (25.000 USD)
2010-2011	Partner of an IDEEV grant 'Tracing back the history of the cultivated apple' (6.000 €)
2005-2008	Coordinator of Young researchers ANR grant 'Impact of domestication on plant genomes: empirical and theoretical evidence' (150.000 €)
2005-2007	Partner of a BRG grant 'Diversity and evolution of a multigene family involved in starch biosynthesis in grasses' (39.000 €)
2005-2007	Coordinator of a BRG Grant 'Transposable element contribution to diversity and adaptation in maize: consequences for genetic resources management' (16.500 €)
1998-1999	Doctoral fellowship from the foundation 'Amis des sciences'
1995-1998	Doctoral fellowship from the French ministry of research

INVITED RESEARCH SEMINARS

- Shift in beneficial interactions during crop evolution, Virtual seminar, Plant Comm meeting. Sept. 2022.
- Shift in beneficial interactions during crop evolution, Virtual seminar, AGAP Institute, Montpellier. June 2022.
- Genetic mechanisms underlying crop evolutionary success, Centre for Plant Biotechnology and Genomics, Madrid (Spain). May 2022.
- Crop evolution: from wild to domesticate and vice versa, Virtual seminar Iowa State University (USA). Sept. 2021.
- Crop evolution: from wild to domesticate and vice versa, Virtual seminar UC Berkeley (USA), July 2021.

- Crop evolution: from wild to domesticate and vice versa, Virtual seminar INRAE Avignon (France), June 2021.
- Crop evolution: from wild to domesticate and back. Virtual Plant Biology Seminar HHU Düsseldorf (Germany), Janv. 2021.
- Crop evolution: from wild to domesticate and back. Virtual seminar, Labex SPS, Univ. Paris-Saclay (France), Sept. 2020.
- Common gardens in teosintes reveal the establishment of a syndrome of adaptation to altitude. Virtual seminar, Department of Plant and Microbial Biology, University of Zurich (Switzerland), May 2020.
- Linking genomic footprints of selection and phenotypic variation in teosintes, Institute of Biological Research, Cluj-Napoca (Romania), October 2018.
- Drivers of maize phenotypic evolution, Max Planck Institute, Tuebingen (Germany), September 2017.
- Local adaptation of teosintes along altitudinal gradients. Institute of Ecology, UNAM, Mexico city (Mexico), January 2016.
- Local adaptation of teosintes along altitudinal gradients. Langebio, Irapuato (Mexico), January 2016.
- What drives genome variation in *Zea*, Department of Animal and Plant Sciences, Univ. Sheffield (UK), December 2013.
- What drives genome variation in *Zea*, Institut for Evolution and Biodiversity, Univ. Münster (Germany), October 2013.
- Evolution of genome size and adaptation in *Zea*, INRA, Clermont-Ferrand (France), October 2013.
- Evolution of genome size and adaptation in *Zea*. Langebio, Irapuato (Mexico), June 2013.
- A Glimpse on maize evolutionary genomics, Workshop Aquagenet, Sète (France), May 2013.
- A Glimpse on maize evolutionary genomics, INRA, Avignon (France), May 2013.
- Genome size evolution and adaptation in the genus *Zea*. Laboratoire Evolution, Génomes et Spéciation, CNRS, Gif-sur-Yvette (France), January 2013.
- Genome size evolution and adaptation in the genus *Zea*. UMR Evolution et Diversité Biologique, Univ. P. Sabatier, Toulouse (France), December 2012.
- Evolution in *Zea*: genome size, transposable elements and response to selection. Genome Dynamic and Speciation, Univ. Neuchâtel (Switzerland), December 2012.
- Evolution of genome size and adaptation in *Zea*. Institute of Ecology, UNAM, Mexico city (Mexico), October 2012.
- Contribution of transposable elements to the evolution of genome size in *Zea* and to recent adaptation in maize. Dept of Plant Biology, Univ. of Minnesota (USA), April 2011.
- Contribution of transposable elements to the evolution of genome size in *Zea* and to recent adaptation in maize. Dept of Plant Sciences, Univ. of California Davis (USA), October 2010.
- Tracking adaptive changes in maize. Dept of Ecology and Evolutionary Biology, Univ. of California Irvine (USA), October 2009.
- Genomic signatures of adaptive evolution in plants. Network of Excellence, Evoltree, Baden (Austria), January 2009.
- Domestication and patterns of selection in maize: outcomes and perspectives. LECA, Grenoble (France), November 2008.
- Genome-wide and local patterns of selection in maize. Department of Genetics, Univ. of Barcelona (Spain), November 2008.
- Domestication and associated patterns of selection. Trinity College, Univ. of Dublin (Ireland), November 2007.
- Detecting selection during maize domestication. Max Planck Institute, Koeln (Germany), July 2006.
- Speciation and gene flow in the *Zea* genus. GDR, Banyuls (France), March 2006.









- A multilocus investigation of selective and demographic processes associated with maize domestication. Dept. of Plant Genetics and Evolution, Lille (France), April 2004.
- A multilocus investigation of the domestication process in maize. Institute of Ecology, Mexico city (Mexico), March 2004.
- Selection versus demography: a multilocus investigation of the domestication process in maize. Institute of Ecology, Lausanne (Switzerland), January 2004.
- Selection versus demography: a multilocus investigation of the domestication process in maize. University of Montpellier (France), November 2003.
- Recombination and diversity in maize: selection versus demography. GDR, Lille (France), April 2003.
- Recombination and diversity in maize: selection versus demography. Dept of Ecology, Jussieu (France), March 2003.

PUBLICATIONS

52. Fréville H., Montazeaud G., Forst E., David J., Papa R., **Tenaillon M.I.** 2022. Shift in beneficial interactions during crop evolution. *Evolutionary Applications*. DOI: 10.1111/eva.13390. co-✉
51. Burban E., **Tenaillon M.I.**, Le Rouzic A. 2022. Gene network simulations provide testable predictions for the molecular domestication syndrome. *Genetics*. DOI: 10.1101/2021.03.19.436202.
50. Bellucci E., Aguilar M., Alseekh S., ... , **Tenaillon M.I.**, Papa R. 2021. The INCREASE project: Intelligent Collections of Food-Legume Genetic Resources for European Agrofood Systems. *The Plant Journal*. DOI: 10.1111/tpj.15472.
49. Desbiez-Piat A., Le Rouzic A., **Tenaillon M.I.**, Dillmann C. 2021. Interplay between extreme drift and selection intensities favors the fixation of beneficial mutations in selfing maize populations. *Genetics*. DOI: 10.1093/genetics/iyab123. co-✉
48. Barrera-Redondo J., Sanchez-de la Vega G., Aguirre-Liguori J.A., Castellanos-Morales G., Gutierrez-Guerrero Y.T., Aguirre-Dugua X., Montes-Hernandez S., Aguirre-Planter E., **Tenaillon M.I.**, Lira-Saade R., Eguiarte L.E. 2021. The domestication of *Cucurbita argyrosperma* as revealed by the genome of its wild relative. *Horticulture Research* 8, 109.
47. Le Corre V., Siol M., Vigouroux Y., **Tenaillon M.I.**, Délye C. 2020. Adaptive introgression from maize has facilitated the establishment of a teosinte as a noxious weed in Europe. *Proc. Natl. Acad. Sci. U.S.A.* 117(41): 25618-25627.
46. Fustier M-A., Martinez-Ainsworth N.E., Aguirre-Liguori J.A., Venon A., Corti H., Rousselet A., Dumas F., Dittberner H., Camarena-Hernandez M.G., Grimanelli D., Falque M., Moreau L., de Meaux J., Montes-Hernandez S., Eguiarte L.E., Vigouroux Y., Manicacci D., **Tenaillon M.I.** 2019. Genomic footprints of local adaptation along elevation gradients associate with present phenotypic variation in teosintes. *Plos Genetics*. 15(12):e1008512. co-✉
45. **Tenaillon M.I.**, Sedikki K., Mollion M., Le Guilloux M., Marchadier E., Ressayre A., Dillmann C. 2019. Transcriptomic response to divergent selection for flowering time in maize reveals convergence and key players of the underlying gene regulatory network. *BioRxiv*, 461947, ver. 5 peer-reviewed and recommended by *PCI Evolutionary Biology*. ✉
44. Aguirre-Liguori, J.A., Gaut B.S., Jaramillo-Correa J.P., **Tenaillon M.I.**, Montes-Hernández S., García-Oliva F., Hearne S., Eguiarte L.E. 2019. Divergence with gene flow is driven by local adaptation to temperature and soil phosphorus concentration in teosinte subspecies (*Zea mays parviglumis* and *Zea mays mexicana*). *Molecular ecology*. 28:2814-2830
43. Odonkor S., Martinez-Bello L., Wang X., Bahri B.A., Choi S., Chakraborty D., **Tenaillon M.I.**, Panaud O., Devos K.M. 2018. QTL mapping combined with comparative analyses identified genes for non-shattering in *Setaria italica*. *Frontiers in Plant Science*. 9:918.
42. Käfer J., Betancourt A., Villain A.S., Fernandez M., Vignal C., Marais G.A.B., **Tenaillon M.I.** (2018). Progress and Prospects in gender visibility at SMBE annual meetings. *Genome Biology and Evolution*. 10(3): 901-908. co-✉

41. Aguirre-Liguori J.A., **Tenaillon M.I.**, Vázquez-Lobo A., Gaut B.S., Jaramillo-Correa J-P., Montes-Hernandez S., Souza V., Eguiarte L.E. (2017). Connecting genomic patterns of local adaptation and niche suitability in teosintes. *Molecular Ecology*. 26(16):4226-4240.
40. Brandenburg J-T., Mary-Huard T., Rigail G., Hearne S., Corti H., Joets J., Vitte C., Charcosset A., Nicolas S., **Tenaillon M.I.** (2017) Independent introductions and admixtures have contributed to adaptation of European maize and its American counterparts. *PLOS Genetics*. 13(3):e1006666. ☒
39. Fustier M-A., Brandenburg J.T., Lapeyronnie J., L.E. Eguiarte, Boitard S., Vigouroux Y., Manicacci D., **Tenaillon M.I.** (2017). Signatures of local adaptation in lowland and highland teosintes from whole genome sequencing of pooled samples. *Molecular Ecology*. 26(10):2738-2756.☒☒
38. Berthouly-Salazar C., Thuillet A-C., Rhoné B., Mariac C., Ousseini I.S., Couderc M., **Tenaillon M.I.**, Vigouroux Y (2016). Genome scan reveals selection acting on genes linked to stress response in wild pearl millet. *Molecular Ecology*. 25(21):5500-5512.
37. **Tenaillon M.I.**, Manicacci D., Nicolas S., Tardieu F., Welcker C. (2016). Testing the link between genome size and growth rate in a collection of maize inbred lines. *Peer J*. 4:e2408. ☒
- 36- Martínez-Ainsworth N.E., **Tenaillon M.I.** (2016). Superheroes and masterminds of plant domestication. *Comptes rendus de l'Académie des Sciences Biologies*. 339(7-8) :268.☒☒
- 35- Durand E. ☺, **Tenaillon M.I.** ☺, Raffoux X., Thépot S., Jamin P., Bourgeois A., Ressayre A., Dillmann C. (2015). Dearth of polymorphism associated with a sustained response to selection for flowering time in maize. *BMC Evolutionary Biology*. 15:103.
- 34- Vitte C., Fustier M-A., Alix K., **Tenaillon M.I.** (2014). The bright side of transposons in crop evolution. *Briefings in Functional Genomics*. 13(4):276-295. ☒
- 33- Nougué O., Corbi J., Ball S.G., Manicacci D., **Tenaillon M.I.** (2014). Molecular evolution accompanying functional divergence of duplicated genes along the plant starch biosynthesis pathway. *BMC Evolutionary Biology*. 14:103. co- ☒
- 32- Muñoz Diez C., Meca E., **Tenaillon M.I.**, Gaut B.S. (2014). Three groups of transposable elements with contrasting copy number dynamics and host responses in the maize (*Zea mays* ssp. *mays*) genome. *Plos Genetics*. 10(4):e1004298.
- 31- Muñoz Diez C., Gaut B.S., Meca E., Scheinvar E., Montes-Hernandez S., Eguiarte L., **Tenaillon M.I.** (2013). Genome size variation in wild and cultivated maize along altitudinal gradients. *New Phytologist*. 199:264-276.
- 30- Hufford M., Martinez-Meyer E., Gaut B.S., Eguiarte L.E., **Tenaillon M.I.** (2012). Inferences from the historical distribution of wild and domesticated maize provide ecological and evolutionary insights. *PlosOne*. 7: e47659. ☒
- 29- Cornille A, Gladieux P., Smulders M.J.M., Roldán-Ruiz I., Laurens F., Le Cam B., Nersesyan A., Clavel J., Olonova M., Feugey L., Gabrielyan I., Zhang X.-G., **Tenaillon M.I.**, Giraud T. (2012). New insights into the history of domesticated apple: secondary contribution by several wild species to the genome of cultivated varieties. *Plos Genetics*. 8 : e1002703.
- 28- Chia J-M., Song C., Bradbury P.J., Costich D.,... **Tenaillon M.I.**, ... Buckler E.S., Zhang G., Xu Y., Ware D. (2012). Maize HapMap2 identifies extant variation from a genome in flux. *Nature Genetics*. 44 : 803-807.
- 27- Zerjal T., Rousselet A., Mhiri C., Combes V., Madur D., Grandbastien M-A., Charcosset A., **Tenaillon M.I.** (2012). Maize genetic diversity and association mapping using transposable element insertion polymorphisms. *Theoretical and Applied Genetics*. 124: 1521-1537.
- 26- Durand E., Bouchet S., Bertin P., Ressayre A., Jamin P., Charcosset A., Dillmann C., **Tenaillon M.I.** (2012). Flowering time in maize: linkage and epistasis at a major effect locus. *Genetics*. 190:1547-1562.

- 25- Corbi J., Dutheil J., Damerval C., **Tenaillon M.I.**, Manicacci D. (2012) Accelerated evolution and coevolution drove the evolutionary history of AGPase subunits during Angiosperm radiation. *Annals of Botany*. 109:693-708.
- 24- **Tenaillon M.I.**, Hufford M., Gaut B.S., Ross-Ibarra J. (2011). Genome size and transposable element content as determined by high-throughput sequencing in maize and *Zea luxurians*. *Genome Biology and Evolution*. 3:219-229.
- 23- **Tenaillon M.I.**, Charcosset A. (2011). A European perspective on maize history. *Comptes rendus de l'Académie des Sciences Biologies* 334 : 221-228. ☒
- 22- Corbi J., Debieu M., Rousselet A., Montalent P., Le Guilloux M., Manicacci D., **Tenaillon M.I.** (2011). Contrasted patterns of selection since maize domestication on duplicated genes encoding a starch pathway enzyme. *Theoretical and Applied Genetics*. 122:705-722. ☒
- 21- **Tenaillon M.I.**, Hollister J., Gaut B.S. (2010). A triptych of the evolution of plant transposable elements. *Trends in Plant Science*. 15(8) : 471-478.
- 20- Durand E., **Tenaillon M.I.**, Ridet C., Coubriche D., Jamin P., Jouanne S., Charcosset A., Dillmann C. (2010). Standing variation and new mutations both contribute to a fast response to selection for flowering time in maize inbreds. *BMC Evolutionary Biology*. 10:2.
- 19- Parisod C., Salmon A., Zerjal T., **Tenaillon M.**, Grandbastien M-A., Ainouche M. (2009). Rapid structural and epigenetic reorganization near transposable elements in hybrid and allopolyploid genomes in *Spartina*. *New Phytologist*. 184(4) : 1003-1015.
- 18- Zerjal T., Joets J., Alix K., Grandbastien M-A., **Tenaillon M.I.** (2009). Contrasting evolutionary patterns and target specificities among three *Tourist*-like MITE families in the maize genome. *Plant Molecular Biology*. 71:99-114.
- 17- Legrand D., **Tenaillon M.I.**, Matyot P., Gerlach J., Lachaise D., Cariou M-L. (2009). Species-wide genetic variation and demographic history of *Drosophila sechellia*, a species lacking population structure. *Genetics*. 182:1197-1206.
- 16- Ross-Ibarra J., **Tenaillon M.**, Gaut B.S. (2009). Historical divergence and gene flow in the genus *Zea*. *Genetics*. 181 :1399-1413.
- 15- Camus-Kulandaivelu L., Chevin L-M., Tollon C., Charcosset A., Manicacci D., **Tenaillon M.I.** (2008). Patterns of variation of the *Tb1-D8* region shed light into early maize evolutionary history. *Genetics*. 180:1107-1121. ☒
- 14- **Tenaillon M.I.** and Tiffin P.L. (2008). The quest for adaptive evolution: a theoretical challenge in a maze of data. *Current Opinion in Plant Biology* 11(2):110-115. ☒
- 13- **Tenaillon M.I.**, Austerlitz F. and Tenaillon O. (2008). Apparent mutational hotspots and long distance LD resulting from a bottleneck. *Journal of Evolutionary Biology* 21(2):541-550. ☒
- 12- Thuillet A-C., **Tenaillon M.I.**, Anderson L.K., Mitchell S.E., Kresovich S., Stack S.M., Gaut B.S. and Doebley J (2008). A weak effect of background selection on trinucleotide microsatellites in maize. *Journal of Heredity*. 99(1): 45-55.
- 11- Moeller D.A., **Tenaillon M.I.** and Tiffin P. (2007). Population structure and its effects on patterns of nucleotide polymorphism in the teosinte (*Zea mays ssp. parviglumis*). *Genetics* 176(3):1799-1809.
- 10- Masanori Y., **Tenaillon M.I.**, Vroh Bi I., Schroeder S.G., Sanchez-Villeda H., Doebley J.F., Gaut B.S., and McMullen M. (2005). A large-scale screen for artificial selection in maize identifies candidate agronomic loci for domestication and crop improvement. *Plant Cell* 17(11): 2859-2872.
- 9- **Tenaillon M.I.**, U'Ren J., Tenaillon O. and Gaut B.S. (2004). Selection versus demography: a multilocus investigation of the domestication process in maize. *Molecular Biology and Evolution* 21(7): 1214-1225. ☒
- 8- **Tenaillon M. I.**, Sawkins M. C., Anderson L. K., Stack S. M., Doebley J., and Gaut B.S. (2002). Patterns of diversity and recombination along chromosome 1 of maize (*Zea mays ssp. mays* L.). *Genetics* 162: 1401-1413.

- 7- Whitt S. R., Wilson L. M., **Tenaillon M. I.**, Gaut B. S., and Buckler E. S. (2002). Genetic diversity and selection in the maize starch pathway. *Proc. Natl. Acad. Sci. U.S.A.* 99: 12959-12962.
- 6- **Tenaillon M. I.** , Sawkins M. C. , Long A. D., Gaut R. L., Doebley J. F., and Gaut B. S. (2001). Patterns of DNA sequence polymorphism along chromosome 1 of maize (*Zea mays ssp. mays* L.). *Proc. Natl. Acad. Sci. U.S.A.* 98: 9161-9166.
- 5- Gaut B. S., **Le Thierry d'Ennequin M.**, Peek A. S., and Sawkins M. C. (2000). Maize as a model for the evolution of plant nuclear genomes. *Proc. Natl. Acad. Sci. U.S.A.* 97: 7008-7015.
- 4- **Le Thierry d'Ennequin M.**, Panaud O., Toupan B., and Sarr A. (2000). Assessment of genetic relationships between *Setaria italica* and its wild progenitor, *S. viridis* using AFLP markers to elucidate the origin of foxtail millet domestication. *Theoretical and Applied Genetics* 100: 1061-1066. 
- 3- **Le Thierry d'Ennequin M.** , Toupan B. , Robert T., Godelle B., and Gouyon P.-H. (1999). Plant domestication: a model for studying the evolution of linkage. *Journal of Evolutionary Biology* 12: 1138-1147. 
- 2- **Le Thierry d'Ennequin M.**, Panaud O., Brown S., Siljak-Yakovlev S., and Sarr A. (1998). First evaluation of nuclear DNA content by flow cytometry in *Setaria* gene pool. *Journal of Heredity* 89: 556-559. 
- 1- **Le Thierry d'Ennequin M.**, Panaud O., Robert T., and Ricoch A. (1997). Assessment of genetic relationships among sexual and asexual forms of *Allium cepa* using morphological traits and RAPD markers. *Heredity* 78 : 403-409. 

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INTERNATIONAL CONFERENCE PRESENTATIONS (AS PRESENTING AUTHOR)

- M.I. Tenaillon. **Cross-talks between wild and domesticates in Zea.** Invited talk at *Genetic admixture: inference and evolutionary consequences*, 2022 (Paris, France).
- M.I. Tenaillon. **Adaptive introgression from maize has facilitated the establishment of a noxious weed in Europe.** Invited talk at the *Ecology and coevolution: from data to models and back*, 2021 (Paris, France).
- N. Martinez-Ainsworth, Fustier M-A., de Meaux J., Dittberner H., Aguirre-Liguori J., Moreau L., Vigouroux Y., Manicacci D., Tenaillon M.I. **Linking genomic footprints of selection and phenotypic variation in teosintes.** Invited talk at *Plant genomes in a changing environment*, 2019 (Cambridge, UK).
- N. Martinez-Ainsworth, Fustier M-A., de Meaux J., Dittberner H., Aguirre-Liguori J., Moreau L., Vigouroux Y., Manicacci D., Tenaillon M.I. **Linking genomic footprints of selection and phenotypic variation in teosintes.** Contributed talk at the *Harlan International Symposium III*, 2019 (Montpellier, France).
- M.I. Tenaillon, Sedikki K., Mollion M., Le Guilloux M., Marchadier E., Ressayre A., Dillmann C **Transcriptomic response to divergent selection for flowering time reveals convergence and key players of the underlying gene regulatory network.** Poster at the *Maize Genetics Conference*, 2019 (Saint Louis, Missouri, USA).
- M.I. Tenaillon. **Linking genomic footprints of selection and phenotypic variation in teosintes.** Invited talk at the *Rapid evolutionary adaptation International meeting*, 2018 (Kiel, Germany).
- M.I. Tenaillon. **How do the evolutionary forces shape genetic variation of domestic plant genomes?** Invited talk at the *II Joint Congress on Evolutionary Biology*, Montpellier 2018 (France).
- Martinez-Ainsworth N., Fustier M-A., Corti H., Rousselet A., Falque M., Venon A., Dumas F., de Meaux J., Dittberner H., Aguirre-Liguori J., Camarena M.G., Montes S., Eguiarte L.E., Vigouroux T., Manicacci D., Tenaillon M.I. **Genomic footprints of past selection at a local scale associate with present phenotypic variation in teosintes.** Contributed talk at the *Society for Molecular Biology and Evolution meeting*, 2018 (Yokohama, Japan).

- Brandenburg J-T., Mary-Huard T., Charcosset A., Nicolas S., Tenaillon M.I. **Evolutionary genomics of European maize and its American counterparts.** Contributed talk at the *Society for Molecular Biology and Evolution meeting, 2017* (Austin, Texas, USA).
- M.I. Tenaillon, Ressayre A., Bourgaïs A., Corti H., Le Guilloux M., Marchadier E., Dillmann C. **Exploring the many facets of phenotypic changes after 13 years of divergent selection for flowering time in maize.** Poster at the *Society for Molecular Biology and Evolution meeting, 2017* (Austin, Texas, USA).
- Brandenburg J-T., Mary-Huard T., Rigaill G., Hearne S., Corti H., Joets J., Vitte C., Charcosset A., Nicolas S., Tenaillon M.I. **Independent introductions and admixtures have contributed to adaptation of European maize and its American counterparts.** Contributed talk at the *Maize Genetics Conference 59th, 2017* (Saint Louis, Missouri, USA).
- M.I. Tenaillon, M-A. Fustier, J-T. Brandenburg, J. Lapeyronnie, L.E. Eguiarte, S. Boitard, Y. Vigouroux, D. Manicacci. **Local adaptation of teosintes along altitudinal gradients.** Invited talk at the *Conférence Jacques Monod, 2016* (Roscoff, France).
- M.I. Tenaillon. **Local adaptation in teosintes,** Invited talk at the *European Meeting of PhD Students in Evolutionary Biology 22, 2016* (Gotland, Sweden).
- M-A. Fustier, J-T. Brandenburg, J. Lapeyronnie, L.E. Eguiarte, S. Boitard, Y. Vigouroux, D. Manicacci, M.I. Tenaillon. **Using whole genome sequencing of pooled samples to detect local adaptation of teosintes along two altitudinal gradients.** Poster at the *Society for Molecular Biology and Evolution meeting, 2016* (Gold Coast, Australia).
- M.I. Tenaillon. **An evolutionary perspective on European maize genomics,** Invited talk at the *XXIII Eucarpia Maize and Sorghum Conference, 2015* (Montpellier, France).
- M.I. Tenaillon. **Response to divergent selection for flowering time in maize, from phenotypes to gene network.** Invited talk at the *Workshop Evolution of Plant phenotypes, from genomes to traits, 2015* (Barcelona, Spain).
- M.I. Tenaillon. **European maize genomics: demography, adaptation and selection.** Invited talk at the *Synbreed Colloquium, 2015* (München, Germany).
- M.I. Tenaillon, E. Durand, M. Mollion, A. Ressayre, C. Dillmann. **Characterizing the response to selection of a complex trait: from phenotypes to gene network.** Contributed talk at the *Society for Molecular Biology and Evolution meeting, 2014* (Puerto Rico, USA).
- M.I. Tenaillon. **Is maize genome flexibility an important contributor of its evolutionary history?** Invited talk at the *International symposium Genome-enabled approaches towards molecular functions in ecology and evolution, 2014* (Bad Neuenahr, Germany).
- M.I. Tenaillon. **What drives genome variation in Zea?** Invited talk at the *Genomics and systems biology IV symposium, 2014* (Abu Dhabi, United Arab Emirates).
- M.I. Tenaillon, E. Durand, X. Raffoux, M. Le Guilloux, C. Charon, A. Ressayre, C. Dillmann. **Dissecting the determinants of flowering time variation in maize using an experimental evolution setting.** Poster presentation at the *Plant Genome Evolution, 2013* (Amsterdam, Pays-bas).
- M.I. Tenaillon, M.B. Hufford, J.M. Chia, M. Gore, D. Costich, E.S. Buckler, B.S. Gaut, D. Ware, J. Ross-Ibarra. **Investigating genome size variation and transposable element content in Zea by whole genome sequencing.** Invited talk at the *First international symposium on epigenetics and developmental biology, 2012* (Xalapa, Mexico).
- M.I. Tenaillon, M.B. Hufford, J-M. Chia, M. Gore, D. Costich, E.S. Buckler, B.S. Gaut, D. Ware, J. Ross-Ibarra. **Whole genome sequencing to investigate genome size variation and transposable element content within and among species in Zea.** Poster presentation at the *International Congress on Transposable Elements, 2012* (St Malo, France).
- M.I. Tenaillon, E. Durand, A. Ressayre, A. Charcosset, C. Dillmann. **Dissecting the determinants of complex traits combining experimental evolution and mapping approaches.** Contributed talk at the *Conférence Jacques Monod, 2012* (Roscoff, France).
- M.I. Tenaillon, M.B. Hufford, J-M. Chia, M. Gore, D. Costich, E.S. Buckler, B.S. Gaut, D. Ware, J. Ross-Ibarra. **Whole genome sequencing to evaluate the contribution of transposable**

- elements to the evolution of genome size in Zea.** Invited talk at the *Society for Molecular Biology and Evolution meeting, 2011* (Kyoto, Japan).
- M.I. Tenaillon. **Tracking adaptive changes, application for the management of genetic resources.** Invited talk at the *Plant genetic Resources for Food and Agriculture international workshop* held by the European Science Advisory Council, 2009 (Rome, Italy).
- M.I. Tenaillon, J. Corbi, J. Duthiel, C. Damerval and D. Manicacci. **Functional divergence and selection acting at different evolutionary timescales on duplicates in the AGPase multigene family.** Invited talk at the *International conference on Plant Molecular Biology, 2009* (St Louis, Missouri, USA).
- M.I. Tenaillon, Charcosset A. and Dillmann. **Six years of divergent selection for flowering time within inbred lines of maize.** Contributed talk at the *Society for Molecular Biology and Evolution meeting, 2007* (Halifax, Canada).
- M.I. Tenaillon. **Patterns of selection associated with maize domestication.** Invited talk at the *Conférence Jacques Monod, 2007* (Roscoff, France).
- M.I. Tenaillon, Debieu M., Rousselet A., Le Guilloux M. Damerval C. and Manicacci D. **Evolutionary fate of duplicated genes during plant speciation and maize domestication.** Poster presentation at the *Genetics of speciation, 2006* (Vancouver, Canada).
- M. I. Tenaillon. **A multilocus investigation of the domestication process in maize.** Invited talk at the *Maize Genetics Conference 47th, 2004* (Mexico city, Mexico).
- M. I. Tenaillon, U'Ren J., Tenaillon O. and Gaut B. S. **Selection versus demography: the impact of the domestication process on diversity and recombination in maize.** Contributed talk at the *Society for Molecular Biology and Evolution meeting, 2003* (Newport Beach, California, USA).
- M. I. Tenaillon, Sawkins M. C., Anderson L. K., Doebley J., Stack S. M. and Gaut B. S. **Diversity and recombination along chromosome 1 of maize.** Poster presentation at the *Maize Genetics Conference 44th, 2002* (Orlando, Florida, USA).
- M. I. Tenaillon, Sawkins M. C., Anderson L. K., Doebley J., Stack S. M. and Gaut B. S. **Patterns of diversity and recombination in maize.** Contributed talk at the *Society for Molecular Biology and Evolution meeting, 2001* (Athens, Georgia, USA).
- M. Le Thierry d'Ennequin, O. Panaud, T. Robert and A. Sarr. **AFLP mapping in foxtail millet in the context of comparative mapping of domestication genes in cereals.** Poster presentation at the *Plant genome conference VII, 1999* (San Diego, California, USA).
- M. Le Thierry d'Ennequin. **Comparative mapping of domestication genes: theoretical and experimental approaches.** Invited talk at the *Conference Jacques Monod: Towards a New Synthesis: the Evolutionary Theory at the Dawn of the Millenium, 1998* (Roscoff, France).
- M. Le Thierry d'Ennequin, O. Panaud and A. Sarr. **Evolutionary organization within Setaria species complex.** Poster presentation at the *Plant evolution in man-made habitats, 1998* (Amsterdam, The Netherlands).
- M. Le Thierry d'Ennequin, O. Panaud, T. Robert and A. Sarr. **Foxtail millet domestication: genetic diversity structure as revealed by AFLP markers.** Poster presentation at the *Plant genome conference VI, 1998* (San Diego, California, USA).
- M. Le Thierry d'Ennequin and B. Toupance. **Plant domestication: a stochastic model for understanding the influence of the reproduction mode, gene flow and drift on gene organization.** Contributed talk at the *VIth congress of the ESEB, 1997* (Arnhem, The Netherlands).
- M. Le Thierry d'Ennequin, O. Panaud, S. Siljak-Yakovlev, A. Sarr. **First evaluation of DNA content by flow cytometry in Setaria gene pool.** Poster presentation at the *Plant genome conference V, 1997* (San Diego, USA).