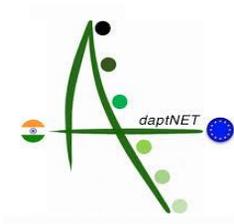# Erasmus+ AdaptNET

Workshop

27 th – 31 st January 2020

Polytechnic University of Marche (UNIVPM)
Department of agricultural, food and environmental sciences (D3A)

"GENETIC RESOURCES AND GENE DISCOVERY FOR CLIMATE CHANGE MITIGATION"

Advanced **GENOMIC** techniques will be addressed in association with **STATISTICAL** and **BIOINFORMATICAL TOOLS**, combined with **ARTIFICIAL INTELLIGENCE** techniques for the analysis of plant genetic resources in relation to climate change.

The lectures will range from **population genetics**, to **GWAS** (Genome Wide Association Studies) analysis to **functional genomics**. For this purpose, various softwares and analysis tools will be used such as R, SeqGen, Xcalibur (and others).

Speakers:

Roberto Papa	UNIVPM	**Marina Paolanti**	UNIVPM
Elena Bitocchi	UNIVPM	**Maud Tenallion**	CNRS Le Moulon
Matteo Dell'Acqua	S. Sant'Anna di Pisa	**Olivier Tenallion**	Universitè de Paris
Jacques David	Montpellier SupAgro	**Carlo Pozzi**	University of Milan
Emma Forst	INRA Paris	**Alseekh Saleh**	Max Planck Golm
Monica Rodriguez	University of Sassari	**Massimo Delle Donne**	University of Verona
Emanuele Frontoni	UNIVPM		

Speaker	Short Bio	Picture
Roberto Papa UNIVPM r.papa@univpm.it	PhD in Plant Breeding and Plant Genetics (Università degli Studi di Sassari, IT), currently Full Professor in Plant Genetics at the Department for Agricultural, Food and Environmental Sciences (D3A, UNIVPM). From 2014 to 2016, he was a guest researcher at the Forschungszentrum Jülich, Germany. From 2010 to 2014, he was Director of the Cereal Research Centre-Agricultural Research Council (CREA-CER), Foggia, Italy. His research interest and publications are focused on evolution of crop plants (wide expertise in population genomics), plant breeding, biodiversity conservation and plant genetics resources, ecology, with particular focus on legume species (Phaseolus vulgaris, P. coccineus, Vicia faba) and cereals (wheat and barley).	
Elena Bitocchi UNIVPM ebitocch@mta01.univpm.it	PhD in 'Crop and Environmental Sciences' and Researcher at UNIVPM. Her expertise is mainly in population genomics, crop evolution and biodiversity conservation, with particular focus on P. vulgaris, P. coccineus, barley and maize species. She was Project Leader of FIRB 2013 Project 'NextBEAN: Comparative evolutionary genomics of Phaseolus domestication investigated through next-generation sequencing technologies, to identify the domestication genes in the common bean (Phaseolus vulgaris L.): towards the development of genomic resources for future challenges relating to climate change, population increase, sustainable agriculture, and food quality and security.', funded by the Italian Government (MIUR)	
Matteo Dell'Acqua Scuola Sup. S.Anna di Pisa matteo.dellacqua@santannapisa.it	Matteo Dell'Acqua is Assistant Professor in agricultural genetics at Scuola Superiore Sant'Anna (SSSA) in Pisa, Italy. His research focuses on forward genetics approaches to unravel the molecular basis of complex traits in crops. After a MSc in Evolutionary Biology at the University of Milan he moved on to a PhD in Agrobiodiversity in SSSA that he defended in 2014. During his graduate studies he visited the Jackson Laboratory in Bar Harbor ME, USA, to apply quantitative methods developed in mice multiparental populations to maize. His current research focuses on multiparental populations development and analysis as well as on the exploration of plant genetic resources of emerging countries. Matteo's research taps into social sciences approaches to extract the traditional knowledge of smallholder farmers and combine it with genomics and climate sciences to support breeding for local adaptation in Africa. He is involved in several European projects exploring these methods to improve food security and adaptation in different cropping systems.	

Speaker	Short Bio	Picture
Jacques David Montpellier SupAgro Jacques.David@supagro.fr	Genetic population education, quantitative genetics, plant breeding at Montpellier SupAgro Project leader: Junior Research Lab, ARCAD (Agropolis Resource Centre for Crop Conservation, Adaptation and Diversity) "Preferential helping to relatives: A potential mechanism responsible for lower yield of crop variety mixtures?" " Pervasive hybridizations in the history of wheat relatives" " Evolutionary forces affecting synonymous variations in plant genomes"	
Emma Forst INRA Paris Emma.Forst@moulon.inra.fr	Emma Forst is currently a postdoctoral research fellow at the research unit « Quantitative Genetics and Evolution – Le Moulon » near Paris (France). She is a quantitative geneticist working in the team « Diversity, Evolution and Adaptation of Populations » lead by Jérôme Enjalbert. She carried out her PhD thesis, under his supervision together with Isabelle Goldringer, on breeding methods and participatory design of wheat variety mixtures. She is interested in statistical models for plant-plant interactions, especially for estimating mixing ability for intra- and inter-specific mixtures, and their use in plant breeding programs. Emma is also an agronomist focusing on genetics and agroecology in crop diversification using variety mixtures or heterogeneous populations. She has been working with organic farmers on designing improved mixtures based on key traits to consider for plant interactions, and more recently on an analysis of the management and selection of agrobiodiversity in participatory plant breeding	
Monica Rodriguez University of Sassari mrodrig@uniss.it	My research activity has started in 2001 at UNISS, where I've achieved my PhD in 2005 with a thesis on "Genotype by Environment Interaction in Barley (Hordeum vulgare L.) grown in Mediterranean Environments". As a Marie Curie Fellow, I've conducted part of the PhD research at NIAB (National Institute of Agricultural Botany, Cambridge UK). Until 2019, I've continued as a Post-Doc research fellow at UNISS (at the Biodiversity Centre and the Agricultural Department), with a few shorter collaborations with Bioversity International and FAO/ESA (2006), NIAB (2010) and Università Politecnica delle Marche (2018). I've worked on biodiversity conservation and populations genetics with insights into genetic mapping; linkage disequilibrium; genetic diversity, structure and its spatial distribution in different populations of different species (e.g. barley, common bean, tomato). At present, I'm mainly working on GWA in tomato, common bean and wheat.	

Speaker	Short Bio	Picture

Marina Paolanti
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Marina Paolanti received the Ph.D. degree in Information Engineering the Department of Information Engineering (DII), Università Politecnica delle Marche, in 2018. Her Ph.D. thesis was on "Pattern Recognition for Challenging Computer Vision Applications". She currently has a post doc position with DII. Her research focuses on Deep Learning, Machine Learning, image processing, and Computer Vision.

Emanuele Frontoni
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Emanuele Frontoni joined the Dept. of Information Engineering (DII) at the Università Politecnica delle Marche, as a Ph.D. student in Intelligent Artificial Systems. He obtained his PhD in 2006 discussing a thesis on Vision Based Robotics. He is currently an Associate Professor of Computer Science in the same department. His research focuses on applying artificial intelligence and computer vision techniques to mobile robots, intelligent retail environments; senseable spaces, digital cultural heritage and precision farming. He is a member of IEEE, MESA, GIRPR and AI*IA.

Maud Tenallion
CNRS Le Moulon
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Maud Tenaillon is a CNRS researcher, working in the Department of Quantitative Genetics and Evolution (Université Paris-Saclay). Her research group focuses on evolutionary genomics and adaptation in crops. She uses maize and its closest wild relatives as model systems. She has studied the impact of demographic bottlenecks and admixture during domestication, breeding, and the geographic expansion of maize. She has been working on questions related to variation in genome size and transposable element content. Finally, she has investigated adaptive processes and their genetic determinants both at a long-time scale investigating patterns of local adaptation in teosintes; and at a shorter time scale, conducting experimental evolution for flowering time in maize.

Olivier Tenallion
Universitè de Paris
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Olivier Tenaillon is an associate Professor at Ecole Polytechnique and an INSERM researcher, working in the Department of Infection, Antimicrobials, Modelling, Evolution (Université de Paris). His research group focuses on quantitative evolutionary microbiology. He combines experimental evolution in bacteria (E. Coli), comparative genomics, epidemiological observations and population genetics to study the tempo and mechanisms underlying microbial adaptation. He also uses integrated models to describe phenotypic complexity, predict the evolvability of traits, and connect abstract adaptive landscapes to experimental data gathered at the protein, network or genome level.

Speaker	Short Bio	Picture

Carlo Pozzi
University
of Milan
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imi.it

Carlo Pozzi is associate professor in Plant Genetics, at the Dept. of Agricultural and Environmental Sciences (DISAA), at Milan State University. C.M.P. teaches advanced molecular breeding and plant biotechnologies. His research interests span from plant development (mainly in barley), to plant quality and production (in peach fruits), to plant pharming (in tobacco) and plant abiotic stress coping (in tobacco). He has extensive experience in public and private sectors in plant molecular breeding. He has and H index =18. He co-authored 5 international patents. He holds a professional Project Management Institute certificate.

Alseekh Saleh
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Saleh Alseekh is a senior research scientist and project leader at Max-Planck-Institute of Molecular Plant Physiology, Germany. Saleh is expertise in metabolic profiling, QTL mapping and data integration analysis. Saleh Alseekh holds a PhD from Potsdam University and Max Planck Institute of Molecular Plant Physiology in 2015. In the last few years Saleh Alseekh conducted metabolic QTL mapping in tomato, maize and common bean. He has over 60 research articles in pre-reviewed journals, teaching experience and co-supervised MSc and PhD students.

Massimo Delle Donne
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Massimo Delledonne received his Ph.D. from Università Cattolica del S. C. in 1994. During 1995-1998 he visited Chris Lamb at the Salk Institute for Biological Studiesin California, discovering the function of nitric oxide in plant disease resistance. In 2001, he joined the University of Verona as Associate Professor of Plant Genetics (SSD Agr/07) and a few year later he joined the genomic revolution by adopting the new technologies that Next Generation Sequencing was offering to microbial, plant, animal and human biologists.
Massimo Delledonne is currently Full Professor of Genetics (SSD Bio/18). He manages a vigorous research program that emphasizes interdisciplinary approaches to understanding plant and human biology. His own expertise is in the areas of genetics, molecular biology and genomics, and collaborates with researchers in diverse fields, including bioinformatics, microbiology and plant genomics, and medicine.