[P14] Genetic diversity among Melia azederach L. collected from Turkey
N.A. Rind1,2, S. Dikilitas3,4, O. Aksoy5,6, M.U. Dahot7,7, M. Rufe5,6, B. Turunoglu1,2, 1Institute of Biotechnology and Genetic Engineering, University of Sindh, Pakistan, 2University of Kocaeli, Turkey

[P15] Functional profiling of endogenous miR535 in loss-of-function mutant of Ananas comosus (MD2 hybrid) mediated by artificial microRNA technology
N.H.M. Yusuf1,2, M.A. Latip, S.V. Kumar, Universiti Malaysia Sabah, Malaysia

[P16] Nuclear, mitochondrial and chloroplastic SSR, InDel and SNP markers reveal the diversity and the phylogenetic origin of limes and lemons
F. Cirk4,5, F. Gillraith1, A. García-Lor1, F. Luro1, Y. Froelicher1, L. Navarro2, P. Gillraith3,1, 1INRA, France, 3INRA, France, 1INRA, France

[P17] Homoeologs: What are they? How to infer them? What are they useful for? N. Glover1,2, A. Alterhoff3,4, H. Redestig1, C. Desimone5,6, 1Bayer CropScience, Belgium, 2University College London, UK, 3Swiss Institute of Bioinformatics, Switzerland, 4ETH Zurich, Switzerland, 5European Molecular Biology Laboratory, European Bioinformatics Institute, UK

J. Defoort1,2, R. De Smet3,4, Y. Van de Peer5,6, 1VIB, Belgium, 2Ghent University, Belgium, 3University of Pretoria, South Africa

[P19] Transposable elements in selected legume species: prevalence and genome distribution
B. Pereck-Moura, J.P. Bezerra-Neto, A.C. Brasiliero-Vidal, A.M. Benko-Isteppon*, Universidade Federal de Pernambuco, Genetics Department, Brazil

[P20] Genome structure and transcriptome of allotetraploid xBrassicaraphanus, an intergeneric hybrid between Brassica rapa and Raphanus sativus in the Brassicaceae family
G. Yi1, H. Shin1, J.S. Kim1, J.H. Ahn1, S. Kim2, Y.M. Kim1, J.E. Park1, H. Park1, H.Y. Soh1, H.R. Belandres2, 1Seoul National University, Republic of Korea, 2Sahmyook University, Republic of Korea, 3Korean Development Administration, Republic of Korea, 4Brdic, Republic of Korea

[P21] SNP-discovery by RAD-sequencing in a germplasm collection of cultivated and wild grapevine accessions
K. Marrano1,2, G. Biolo1, R. Schiavon2, R. Targoni2, L. Marchiorotto2, A. Tela2, S. Lorenzo1, G. Valle1, M.S. Grandi3, 1Foundation Edmund Mach, Italy, 2University of Padua, Italy

[P22] Resistance genes in Eucalyptus grandis: physical clustering and expression hot-spots
P.A. Tobias1, N. Christie1, S. Nalapoo1, C. Süllem1, R.F. Park1, D.L. Guest1, 1University of Sydney, Australia, 2University of Pretoria, South Africa, 3Australasian National University, Australia

[P23] Transgenesis and bioinformatics working together: the search for improved frost tolerance in spring wheat
G.E. Duggard1,2, J. Vickers1, 1University of Southern Queensland, Australia, 2Centre for Crop Health, Australia

[P24] Genetic diversity of Argania spinosa L. from the Argan region using Inter-Simple Sequence Repeat (ISSR) markers
C. Yassib1, B. Belkadi1, O. Pkhorou1, M. Alami1, L. Medraoui1, A. El Moussadik1, A. Ferrogous2, C. El Medaouf1, S. Ibn Souid-Kourachi1, A. Filal-Maltaou1, 1Faculty of Sciences Rabat, Morocco, 2Faculty of Science Agadir, Morocco, 3Forests and Desertification Control Marrakech, Morocco, 4Faculty of Sciences and Technologies Marrakech, Morocco, 5Faculty of Sciences and Technologies Fez, Morocco

[P25] Domestication of Citrus: Edible mandarins might be originated by a Pummelo introgression
A.W. Wu1, J. Tera1, V. Ibáñez1, J. Carbonell1, R. Alonso1, J. Dopazo2, F. Gimenez2, D. Rokhsaz2, M. Talon1, 1Instituto Valenciano de Investigaciones Agrarias IVA, Spain, 2US Department of Energy Joint Genome Institute, USA, 3Centro de Investigación Príncipe Felipe, Spain, 4University of Florida, USA

[P26] Impact of recurrent gene duplication on adaptation of plant genomes
I. Fischer1,2, J. Dansat2,3, V. Ranwez1, S. Gibrone2, I.H. Dufayard3, A. Dévaux2, N. Chantret2, 1Université Montpellier II, France, 2CIRAD, France, 3UPPAULA University, Sweden, 4INRA, France

[P27] Homoeologies of the antiviral argonaute1 show different susceptibilities to mir168-mediated control
T. Guinsand2, P. Walter2, G. Gambino1, S. Friedrich2, S.E. Behrens2, V. Pantaleo1, 1Institute for Sustainable Plant Protection-DWR, Italy, 2Marin Luther University Halle-Wittenberg, Germany, 3BiosoClear BV, The Netherlands

[P28] Evolution of the flowering time gene FRIGIDA in the family Brassicaceae
O.A. Fadina1, E.E. Khavkin1, 1Institute of Agricultural Biotechnology, Russia
SNP-DISCOVERY BY RAD-SEQUENCING IN A GERMLASM COLLECTION OF CULTIVATED AND WILD GRAPEVINE ACCESSIONS.


1) Fonazione Edmondo Mach, S. Michele all'Adige (TN) - Italy. annarita.marrano@fmanch.it
2) CIRI - DEPARTMENT, UNIVERSITY OF PADUA, PADUA - ITALY.

The discovery and use of genome-wide molecular markers across many individuals is crucial for evaluation of patterns and processes in evolutionary changes. Restriction-site Associated DNA Sequencing (RAD-seq) may be a suitable approach due to its ability to identify and get genotyped several markers simultaneously. A novel protocol of RAD-seq was set-up on 5500 SOLiD™ System introducing a biotinylated adapter. Afterwards the novel RAD-seq protocol was applied to a grapevine germplasm collection of 51 cultivars (Vitis vinifera subsp. sativa) and 45 wild accessions (V. vinifera subsp. sylvestris). The resulting 561'843'350 reads were aligned on the V. vinifera 'PN40024' reference genome sequence and almost all the predicted RE sites were covered. UnifiedGenotyper of Genome Analysis Toolkit was used to identify Single Nucleotide Polymorphisms (SNP). A final dataset of 52'644 good quality SNPs was obtained, among which 32'977 SNPs revealed a Minor Allele Frequency higher than 0.05. Based on the new grapevine gene prediction v2.1, 27'902 SNPs were intergenic, 5'649 missense, 240 nonsense and 3'106 synonymous. The genetic diversity analysis revealed how the RAD-seq markers are able to collect and show some undisclosed differences among wild and cultivated grapevine accessions. Therefore, the RAD-seq is a candidate approach to disclose the relationship between ancestor and domesticated species, helping to clarify the process of domestication.