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[P14]	**Genetic diversity among Melia azaderach L. collected from Turkey** N.A. Rind[1,2], S. Dikilitas*[2], O. Aksoy[2], M.U. Dahot[1], M. Rafiq[1], B. Tutunoglu[2], [1]*Institute of Biotechnology and Genetic Engineering, University of Sindh, Pakistan,* [2]*University 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. Yusuf*, 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. Curk*[1,2], F. Ollitrault[2], A. Garcia-Lor[2], F. Luro[1], Y. Froelicher[3], L. Navarro[2], P. Ollitrault[2,3], [1]*INRA, France,* [2]*IVIA, Spain,* [3]*Cirad, France*
[P17]	**Homeologs: What are they? How to infer them? What are they useful for?** N. Glover*[1,2], A. Altenhoff[3,4], H. Redestig[1], C. Dessimoz[2,5], [1]*Bayer CropScience, Belgium,* [2]*University College London, UK,* [3]*Swiss Institute of Bioinformatics, Switzerland,* [4]*ETH Zurich, Switzerland,* [5]*European Molecular Biology Laboratory, European Bioinformatics Institute, UK*
[P18]	**The Gene Balance Hypothesis: An assessment based on Arabidopsis thaliana protein interaction data** J. Defoort*[1,2], R. De Smet[1,2], Y. Van de Peer[1,3], [1]*VIB, Belgium,* [2]*Ghent University, Belgium,* [3]*University of Pretoria, South Africa*
[P19]	**Transposable elements in selected legume species: prevalence and genome distribution** B. Piereck-Moura, J.P. Bezerra-Neto, A.C. Brasileiro-Vidal, A.M. Benko-Iseppon*, *Universidade Federal de Pernambuco, Genetics Department, Brazil*
[P20]	**Genome structure and transcriptome of allotetraploid x*Brassicoraphanus*, an intergeneric hybrid between *Brassica rapa* and *Raphanus sativus* in the Brassicaceae family** G. Yi*[1], H. Shin[1], J.S. Kim[1], J.H. Ahn[1], S. Kim[1], Y.M. Kim[1], J.E. Park[1], H. Park[1], H.Y. Soh[1], H.R. Belandres[2], [1]*Seoul National University, Republic of Korea,* [2]*Sahmyook University, Republic of Korea,* [3]*Rural Development Administration, Republic of Korea,* [4]*BioBreeding, Republic of Korea*
[P21]	**SNP-discovery by RAD-sequencing in a germplasm collection of cultivated and wild grapevine accessions.** A. Marrano*[1,2], G. Birolo[2], R. Schiavon[2], R. Targon[2], L. Marchioretto[2], A. Telatin[2], S. Lorenzi[1], G. Valle[2], M.S. Grando[1], [1]*Foundation Edmund Mach, Italy,* [2]*University od Padua, Italy*
[P22]	**Resistance genes in Eucalyptus grandis: physical clustering and expression hot-spots** P.A. Tobias*[1], N. Christie[2], S. Naidoo[2], C. Külheim[3], R.F. Park[1], D.I. Guest[1], [1]*University of Sydney, Australia,* [2]*University of Pretoria, South Africa,* [3]*Australian National University, Australia*
[P23]	**Transgenics and bioinformatics working together: the search for improved frost tolerance in spring wheat** G.E. DAGGARD*[1], J. Vickers[1], [1]*University of Southern Queensland, Australia,* [2]*Centre for Crop Health, Australia*
[P24]	**Genetic diversity of Argania spinosa L. from the Argan region using Inter-Simple Sequence Repeats (ISSR) markers** C. Yatrib*[1], B. Belkadi[1], O. Pakhrou[1], M. Alami[1], L. Medraoui[1], A. El Mousadik[2], A. Ferradous[3], C. El Modafar[4], S. Ibn Souda-Kouraichi[5], A. Filal-Maltouf[1], [1]*Faculty of Sciences Rabat, Morocco,* [2]*Faculty of Science Agadir, Morocco,* [3]*Forests and Desertification Control Marrakech, Morocco,* [4]*Faculty of Sciences and Technics Marrakech, Morocco,* [5]*Faculty of Sciences and Technics Fez, Morocco*
[P25]	**Domestication of Citrus: Edible mandarins might be originated by a Pummelo introgression** A.W. Wu[2], J. Terol*[1], V. Ibañez[1], J. Carbonell[3], R. Alonso[3], J. Dopazo[3], F. Gmitter[4], D. Rokhsar[2], M. Talon[1], [1]*Instituto Valenciano de Investigaciones Agrarias IVIA, Spain,* [2]*US Department of Energy Joint Genome Institute, USA,* [3]*Centro de Investigación Príncipe Felipe, Spain,* [4]*University of Florida, USA*
[P26]	**Impact of recurrent gene duplication on adaptation of plant genomes** I. Fischer*[5], J. Dainat[1,4], V. Ranwez[1], S. Glémin[2], J-F. Dufayard[3], A. Diévart[3], N. Chantret[5], [1]*Montpellier SupAgro, France,* [2]*Université Montpellier II, France,* [3]*CIRAD, France,* [4]*Uppsala University, Sweden,* [5]*INRA, France*
[P27]	**Homeologs of the antiviral argonaute1 show different susceptibilities to mir168-mediated control** T. Gursinski[2], P. Walter[3], G. Gambino[1], S. Friedrich[2], S.E. Behrens[2], V. Pantaleo*[1], [1]*Institute for Sustainable Plant Protection-CNR, Italy,* [2]*Martin Luther University Halle-Wittenberg, Germany,* [3]*BaseClear BV, The Netherlands*
[P28]	**Evolution of the flowering time gene *FRIGIDA* in the family Brassicaceae** O.A. Fadina*, E.E. Khavkin, *Institute of Agricultural Biotechnology, Russia*

SNP-DISCOVERY BY RAD-SEQUENCING IN A GERMPLASM COLLECTION OF CULTIVATED AND WILD GRAPEVINE ACCESSIONS.

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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. *sylvestis*). 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 Frequence 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.