Joint Meeting
AGI - SIBV - SIGA
Cittadella di Assisi, 19-22 September 2011

SCIENTIFIC PROGRAMME
POSTER LIST

Associazione Genetica Italiana

S.I.B.V.

Società Italiana Genetica Agraria

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SCIENTIFIC PROGRAMME

MONDAY, SEPTEMBER 19th

CONGRESS SECRETARY

13:00 – 15:30 Registration and poster display

AUDITORIUM

15:30 – 16:00 Opening ceremony

Welcome address by Academical and Local Authorities
Chairpersons: Blanco A., Cella R., Pimpinelli S.

16:00 – 18:15 Session I – Epigenetics
Chairpersons: Carputo D., Cella R., Corona D.

16:00 – 16:30 **Invited Lecture**
Orlando V.
Repetitive elements transcription and mobilization contribute to human skeletal muscle differentiation and Duchenne muscular dystrophy progression

16:30 – 16:45 Rossi V., Mainieri D., Forestan C., Mascheretti I., Farinati S., Lauria M., Varotto S.
Environmental epigenetics in maize: advances from a European initiative

16:45 – 17:00 Castelletti S., Salvi S., Tuberosa R.
Determining the correlation between methylation and gene expression at a flowering time QTL in maize

17:00 – 17:15 Tosi F., Vernarecci S., Iuliani M., Belloni C., Ballario P., Filetici P.
The epigenetic regulation of centromere and chromosome segregation

17:15 – 17:30 Giordano M., D'Aquila P., Crocco P., Pisani F., Rose G., Passarino G., Bellizzi D.
Mitochondrial DNA variability influence global DNA methylation levels

17:30 – 17:45 Cesarini E., D'Alfonso A., Camilloni G.
Epigenetic control of RNA Polymerase II transcription and DNA recombination by H4K16 acetylation, at rDNA of *Saccharomyces cerevisiae*

17:45 – 18:00 De Paola D., Cattonaro F., Fracchiolla A., Felice N., Pignone D., Sonnante G.
Isolation of microRNAs from artichoke and their involvement in the regulation of target genes

20:30 – 23:00 Welcome cocktail

TUESDAY, SEPTEMBER 20th

POSTER VISION SCHEDULE

10:30 – 11:30 All Session 1 and Session 2A posters

16:00 – 17:00 All Session 2B, 2C, 3A, 4, and 5C posters

COFFEE AND LUNCH BREAKS

10:30 – 11:30 Coffee break

13:00 – 14:30 Lunch break

16:00 – 17:00 Coffee break

SOCIAL DINNER

20:30 – 24:00 Cittadella di Assisi, Sala S. Pietro

SCIENTIFIC SESSIONS

AUDITORIUM

08:30 – 10:30 Session IIA
Genome structure, function and plasticity
Chairpersons: Rocchi M., Veronesi F.

08:30 – 09:00 **Invited Lecture**
Heslop-Harrison J.S.
Genome evolution over timescales from days to billions of years

09:00 – 09:15 Cifarelli R.A., D'Onofrio O., Grillo R., Mango T., Cellini F., Piarulli L., Simeone R., Blanco A., Gadaleta A.
Development of a new wheat microarray from a totipotent cDNA library and identification of differentially expressed genes for powdery mildew resistance

09:15 – 09:30 Iannuzzi L., Perucatti A., Genualdo V., Iannuzzi A., Rebl A., Incarnato D., Goldammer T., Di Meo G.P.
The X-chromosome evolution in domestic bovids as revealed by comparative fish-mapping of cattle, sheep, river buffalo and human X-chromosomes

09:30 – 09:45 Serone E., D'Addabbo P., Sette M., Poma A., Giambra V., Frezza D.
Genomic comparison of the sequences contributing to the 3D structure of the IgH 3' regulatory region (»30 kb) in vertebrates: conservation of a large palindromic structure with a polymorphism of the internal enhancer

09:45 – 10:00 Napoli N., Iafrate S., Testone G., Mele G., Iannelli M.A., Giannino D., Frugis G.
KNOX lost the MEINOX: alternative splicing of the *Arabidopsis KNAT1/BP* gene produces an isoform that lacks the protein-protein interaction domain

10:00 – 10:15 Dal Santo S., Fasoli M., Zenoni S., Farina L., Tornielli G.B., Guzzo F., Delledonne M., Pezzotti M.
Transcriptome characterization of phenotypic plasticity in *Vitis vinifera*

10:15 – 10:30 Vigilante A., Sangiovanni M., Frusciante L., Chiusano M.L.
Intriguing issues from a highly duplicated genome: an example from transcription factor gene paralogs

10:30 – 11:30 **Break**

11:30 – 13:00 Session IIA (Cont) – Genome structure, function and plasticity
Chairpersons: Conicella C., Rocchi M.

11:30 – 11:45 Pietrella M., Facella P., Perrotta G., Giuliano G., The Potato Genome Sequencing Consortium
Genome sequence and analysis of the tuber crop potato

11:45 – 12:00 Cacace A., Di Costanzo A., Ruopoli E., Di Iorio V., La Mantia G., Calabrò V.
ΔNPp63α and YB1: a functional interaction controlling cell proliferation and motility

12:00 – 12:15 Manzotti P., Parisi V., Consonni G.
The role of ta-siRNAs in maize plant development

12:15 – 12:30 Vendramin G.G., Grivet D., Torre S., Sebastiani F., Zabal-Aguirre M., González-Martínez S.C.
Candidate-gene research to understanding the role of genetic diversity in the adaptive response of Mediterranean pines

12:30 – 12:45 Burla R., Carcuro M., Raffa G.D., Galati A., Cacchione S., Crescenzi M., Cenci G., Ciapponi L., Gatti M., Saggio I.
AKTIP, a new lamin interacting protein is involved in telomere metabolism and DNA replication

12:45 – 13:00 Marroni F., Trebbi D., Miculan M., Di Centa E., Di Gaspero G., Morgante M.
Long range effects of selection for berry color on genetic diversity are detected in grape chromosome 2

13:00 – 14:30 **Break**

14:30 – 16:00 Session IIIA
Genetics, physiology and breeding of fruit plants
Chairpersons: Battistelli A., Terzi V.

14:30 – 15:00 **Invited Lecture**
Arùs P.
Peach genomics and breeding applications

15:00 – 15:15 Cirilli M., Colao M. C., Rugini E., Caboni E., Muleo R.
Go back from the adult phase

15:15 – 15:30 Licciardello C., Torrisi B., Tononi P., Allegra M., Sciacca F., Delledonne M., Intrigliolo F., Reforgiato Recupero G.
Expression analysis of gene involved in the iron deficiency of *Citrus* rootstocks

15:30 – 16:00 **Invited Lecture**
Leegood R.C.
Partitioning and metabolism of assimilates in developing fruits

16:00 – 17:00 **Break**

17:00 – 17:30 **Premio SIGA 2011**
Chairpersons: Blanco A., Filippone E.

17:00 – 17:15 **Premio "Gian Tommaso Scarascia Mugnozza" per la Genetica Agraria**
Zamboni A., Di Carli M.
Identification of putative stage - specific grapevine berry biomarkers and omics data integration into networks

17:15 – 17:30 **Premio "Natale Di Fonzo" per il Miglioramento Genetico**
Diretto G.
Transcriptional - metabolic networks in β-carotene-enriched potato tubers: the long and winding road to the Golden phenotype

17:30 – 19:30 SIGA General Assembly

SALA SAN GIOVANNI

08:30 – 10:30 Session IIB
Proteostasis
Chairperson: Vitale A.

08:30 – 09:00 **Invited Lecture**
Hwang I.
Unfolded plastid precursors in the cytosol: targeting vs degradation by quality control

09:00 – 09:15 Savazzini F., Ceriotti A.
Interchain disulfide bond formation in the assembly of high- and low-molecular-weight glutenin subunits

09:15 – 09:30 Ruberti C., Costa A., Zottini M., Lo Schiavo F.
An *Arabidopsis* tail-anchored protein involved in organelle fission unveils a dynamic network of endomembrane structures

09:30 – 09:45 Pedrazzini E., Rocchetti A., Martinoia E., Vitale A.
Only a minority of integral membrane proteins with complex n-glycans reside on the tonoplast

09:45 – 10:00 Vescovi M., Costa A., Zaffagnini M., Trost P., Lo Schiavo F.
Arabidopsis thaliana glyceraldehyde-3-phosphate dehydrogenase as an oxidative stress sensor

10:00 – 10:30 **Invited Lecture**
Raikhel N.
Dissecting the endomembrane network via chemical genomics

10:30 – 11:30 **Break**

11:30 – 13:00 Session IIC
Transport and assimilation: from single cells to whole plant
Chairperson: Soave C.

11:30 – 12:00 **Invited Lecture**
Mencuccini M.
Hydraulic systems and sugar transport in plants: an ecological scaling perspective

12:00 – 12:15 Zottini M., Costa A., Loro G., Drago I., Pozzan T., Lo Schiavo F.
Detection of mitochondrial Ca^{2+} dynamics in *Arabidopsis* plants expressing the FRET-based cameleon probe

12:15 – 12:30 Fiorilli V., Vietti V., Balestrini R., Lanfranco L., Bonfante P.
Expression of fungal and plant phosphate transporters in arbusculated cells: a competition for Pi uptake?

12:30 – 12:45 Manara A., Dal Corso G., Furini A.
PCP1 and ATOSA1: plastidial proteins involved in oxidative stress response and metal homeostasis in *Arabidopsis* chloroplast

12:45 – 13:00 Trono D., Soccio M., Laus M.N., Pastore D.
Effect of K^+ channel activity on the oxidative phosphorylation in durum wheat mitochondria from control and hyperosmotic-stressed seedlings

13:00 – 17:00 **Break**

17:00 – 17:30 **Premio Dottorato "Franca Rasi Caldogno"**
Chairperson: Nardini A.
Gerotto C.
Photoprotection mechanisms in the moss *Physcomitrella patens*: insights on the photosynthesis adaptation during land colonization

17:30 SIBV General Assembly

SALA MUSICA

14:30 – 16:00 Session IIIB
La diversità genetica umana e il concetto di razza
Un simposio in onore di Italo Barrai, Guido Modiano, Giorgio Morpurgo
Chairperson: Barbujani G.

14:30 – 15:00 **Invited Lecture**
Cassata F.
Eugenica, "Racial Science" e Genetica Umana

15:00 – 15:30 **Invited Lecture**
Colonna V.
Cosa ci insegna il progetto 1000 Genomes a proposito di variabilità genetica umana

15:30 – 16:00 **Invited Lecture**
Gasparini P.
Come variano i geni per il gusto, l'olfatto e l'udito lungo la Via della Seta

16:00 – 16:30 **Break**

16:30 – 18:00 Session IIIC
La storia della Genetica Italiana
Chairperson: Pimpinelli S.

16:30 – 17:00 **Invited Lecture**
Volpone A.
La genetica classica in Italia, le origini, le relazioni con le altre discipline biologiche e con gli interessi pratici (produzione agricola in particolare)

17:00 – 17:30 **Invited Lecture**
Cassata F.
La genetica italiana dopo la Seconda Guerra Mondiale, dal convegno di Bellagio all'origine del LIGB

17:30 – 18:00 **Invited Lecture**

Fantini B.

Dalla genetica classica alla biologia molecolare. Il contributo della genetica, della citologia e dell'embriologia

18:00 – 18:30 **Premio Dottorato AGI**

Chairperson: Pimpinelli S.

18:30 – 19:30 AGI General Assembly

WEDNESDAY, SEPTEMBER 21th

POSTER VISION SCHEDULE

10:30 – 11:30 All Session 6A, 6B and 7 posters

16:30 – 17:30 All Session 8 and Session 9 posters

COFFEE AND LUNCH BREAKS

10:30 – 11:30 Coffee break

13:00 – 14:30 Lunch break

16:30 – 17:30 Coffee break

SCIENTIFIC SESSIONS

AUDITORIUM

08:30 – 10:30 Session IV

Systems Biology

Chairpersons: Cavalieri D., Morandini P.

08:30 – 09:00 **Invited Lecture**

Hofmeyr J.-H.S.

Putting "systems" back into systems biology

09:00 – 09:15 Frusciante S., Giuliano G., Diretto G.

Local systems biology and analysis of transcriptional-metabolic networks in fruits of tomato (*Solanum lycopersicum* L.) carotenoid mutants reveal novel findings in the regulation of fruit carotenogenesis

09:15 – 09:30 Morelli G., Ciolfi A., Sessa G., Sassi M. Possenti M., Ruberti I.

Dynamic changes in *Arabidopsis* transcriptome during shade avoidance response

09:30 – 09:45 Ramazzotti M., Berna L., Cavalieri D.

Phylogenomics applied to *Saccharomyces cerevisiae* strains reveals genes with high evolutionary resolution

09:45 – 10:00 Cappelletti V., Stefanini I., Berna L., Lee W., Kapushesky M., Cavalieri D.

Master regulators of colony morphology switch in yeast *Saccharomyces cerevisiae*

10:00 – 10:30 **Invited Lecture**
Kishony R.
Pathogen evolution within human host

10:30 – 11:30 **Break**

11:30 – 13:00 Session VC
Green biotechnology for industrial uses
Chairpersons: Cardi T., Cellini F.

11:30 – 12:00 **Invited Lecture**
Poirier Y.
Production of renewable polymers from crop plants

12:00 – 12:15 Chiaiese P., Palomba F., Tatino F., Lanzillo C., Ruotolo G., De Biasi M.-G., Filippone E.
Green microalgae and plants expressing fungal laccases useful for environmental and industrial applications

12:15 – 12:30 Lionetti V., Francocci F., Bastianelli E., Ferrari S., Pontiggia D., Benedetti M., De Lorenzo G., Bellincampi D., Cervone F.
Improving exploitation and saccharification of biomass for bioconversion

12:30 – 12:45 Palmucci M., Giordano M.
Use of Fourier transform infrared spectroscopy for the characterization of algal composition and the selection of strains for productive processes

12:45 – 13:00 Durante M., Quarta A., Nisi R., De Paolis A., Rizzello F., Mita G., Caretto S.
Utility of beta-cyclodextrins for enhancing artemisinin production in *Artemisia annua* cells

13:00 – 14:30 **Break**

14:30 – 16:30 Session VIA
Crop productivity: physiology and genetics
Chairpersons: Morosinotto T., Valè G.

14:30 – 15:00 **Invited Lecture**
Salvi S.
Genomic approaches to dissect the genetic bases of stress tolerance in cereals

15:00 – 15:15 Sabetta W., Blanco A., Montemurro C.
Identification and characterization of induced mutations in a sunflower TILLING platform

15:15 – 15:30 Barcaccia G., Collani S., Galla G., Ghedina A., Tiozzo S., Tiozzo R.
Discovery of nuclear male-sterility in red chicory: genetic analysis and methods for the marker-assisted breeding of F1 hybrid varieties

15:30 – 15:45 Chitarra W., Balestrini R., Perrone I., Vitali M., Pagliarani C., Schubert A., Lovisolo C.
The pressure collar technique applied to grapevine shoots elucidates contribution of abscisic acid (ABA) and gene expression of vessels associated cells (VACS) during embolism formation and repair

15:45 – 16:00 Trost P., Trivelli X., Thumiger A., Marri L., Fermani S., Calvaresi M., Falini G., Zerbetto F., Pupillo P., Sparla F.
CP12: a redox switch for the regulation of the Calvin-Benson cycle

16:00 – 16:30 **Invited Lecture**
Maffei M.
Early and late events in plant-herbivore interactions

16:30 – 17:30 **Break**

17:30 – 19:30 Session VII
Biotic interactions: symbiosis and pathogenesis
Chairpersons: Bonfante P., Frugis G.

17:30 – 18:00 **Invited Lecture**
Frugier F.
Cytokinin pathways regulating *Medicago truncatula* symbiotic nodule development

18:00 – 18:15 Navarro B., Gisel A., Rodio M.E., Delgado S., Flores R., Di Serio F.
Involvement of RNA silencing in plant response to infectious non- RNAs

18:15 – 18:30 Pavan S., Schiavulli A., Appiano M., Marcotrigiano A.R., Cillo F., Visser R.G.F., Bai Y., Lotti C., Ricciardi L.
Pea powdery mildew *er1* resistance is associated to loss-of-function mutations at a *MLO* homologous locus

18:30 – 18:45 Genre A., Chabaud M., Novero M., Faccio A., Barker D., Bonfante P.
Calcium spiking in arbuscular mycorrhizas: the who and where of presymbiotic signaling

18:45 – 19:00 Locato V., Cimini S., Novo Uzal E., Levi M., Micera A., Balzamino B.O., Evidente A., De Gara L.
Ophiobolin a activates different defence responses depending on the applied dose in TBY-2 cells

19:00 – 19:30 **Invited Lecture**
Bellincampi D.
Plant cell wall in pathogenesis: how its structure can influence plant-pathogen interactions

SALA SAN GIOVANNI

11:30 – 13:00 Session VB
Starch biology and biotechnology
Chairperson: Trost P.

11:30 – 12:00 **Invited Lecture**
Zeeman S.C.
Understanding starch metabolism in plants and the potential to improve starch crops

12:00 – 12:15 Paparelli P., Parlanti S., Gonzali S., Novi G., Mariotti L., Van Dongen J.T., Perata P.
Integration of chloroplast starch metabolism with hormonal regulation of plant growth

12:15 – 12:30 Sparla F., Valerio C., Marri L., Costa A., Issakidis-Bourguet E., Pupillo P., Trost P.
Redox-regulated BAM1 and its role in diurnal starch degradation

12:30 – 12:45 Sestili F., Botticella E., Lafiandra D.
Genetic manipulation of starch composition to improve nutritional and technological properties of durum and bread wheat

12:45 – 13:00 **General discussion**

SALA MUSICA

11:30 – 13:00 Session VA
Selected talks from AGI posters
Chairpersons: Bazzicalupo M., Lodi T.

11:30 – 11:45 Dallabona C., Marsano R.M., Arzuffi P., Ghezzi D., Mancini P., Zeviani M., Ferrero I., Donnini C.
Yeast as a model system to shed light on the role of the human disease protein MPV17

11:45 – 12:00 Olivieri A., Achilli A., Lancioni H., Hooshiar Kashani B., Perego U.A., Nergadze S.G., Carossa V., Santagostino M., Capomaccio S., Felicetti M., Verini-Supplizi A., Woodward S.R., Semino O., Silvestrelli M., Giulotto E., Torroni A.
Horse mitochondrial genomes: at least 17 matrilineal lineages underwent domestication

12:00 – 12:15 Volpi S., Bongiorni S., Wakimoto B.T., Prantera G.
The nucleoporin mRNA export protein, RAE1, exerts pleiotropic effects on mitotic and meiotic cell cycle, and viability in *Drosophila melanogaster*

12:15 – 12:30 Vernì F., Cenci G.
A role for the *Drosophila* histone variant H2Av in mitotic chromosome segregation

12:30 – 12:45 Marzio A., Gatti M., Vernì F.
Vitamin B6 is required for *Drosophila* chromosome integrity

12:45 – 13:00 **General discussion**

13:00 – 14:30 **Break**

14:30 – 16:30 Session VIB
Genes and human hereditary diseases
Chairpersons: Brancati F., Calabrò V.

14:30 – 15:20 **Invited Lecture**
Van Bokhoven H.
Genetic and epigenetic networks disrupted in intellectual disability

15:20 – 15:40 **Invited Lecture**
Brancati F.
Role of cell adhesion molecules nectins 1 and 4 in the pathogenesis of Ectodermal Dysplasia Syndromes

15:40 – 16:00 **Invited Lecture**
Calabrò V.
p63 and DLX relationships: relevance in human hereditary Ectodermal Dysplasia Syndromes

16:00 – 16:15 Quartararo J., Indrieri A., Franco B., Ferrero I., Goffrini P.
Studies in yeast model of pathological mutations of the human gene *HCCS*

16:15 – 16:30 Marullo L., Mamolini E., Carrieri A., Guarnelli M.A., Annunziata M., Guida L., Romano F., Aimetti M., Scapoli C.
Gene-gene interaction among cytokine polymorphisms influence susceptibility to aggressive periodontitis

THURSDAY, SEPTEMBER 22nd

AUDITORIUM

09:00 – 11:00 Session VIII
Food nutritional value and life span
Chairpersons: de Gara L., Tonelli C.

09:00 – 09:30 **Invited Lecture**
Van den Ende W.
Fructans counteract ROS in plants, in food and in the human body

09:30 – 09:45 La Rocca N., Pasin A., Andreoli C., Rascio N., Moro I.
Canthaxanthin production by *Scenedesmus* sp., a chlorophyta from Antarctica

09:45 – 10:00 Moglia A., Lanteri S., Comino C., Butelli E., Martin C.
The silencing of a GST gene increases the content of health-promoting dicaffeoylquinic acids in tomato

10:00 – 10:15 Panzeri D., Cassani E., Doria E., Tagliabue G., Forti L., Campion B., Bollini R., Brearley C.A., Pilu R., Nielsen E., Sparvoli F.
The bean *low phytic acid 1* mutation is due to a defective MRP transporter, affecting the regulation of phytic acid pathway, seed MYO-inositol content and seed germination sensitivity to ABA, but does not impact performances under abiotic stresses

10:15 – 10:30 Lupi R., Denery D., Lafiandra D., Masci S., Larré C.
How much the transgenesis affects the allergenicity?

10:30 – 10:45 Fantini E., Falcone G., Giuliano G.
Dissecting lycopene biosynthesis in tomato fruits through virus-induced gene silencing

10:45 – 11:00 Proietti S., Moscatello S., Brugnoli E., Mattioni C., Battistelli A.
Degradative metabolism of oxalic acid and ascorbic acid in spinach (*Spinacia oleracea* L.).

11:00 – 11:30 Closing ceremony

POSTER PRESENTATIONS LIST

SESSION 1
EPIGENETICS

1.08 Forestan C., Farinati S., Becker C., Rossi V., Weigel D., Varotto S. - A multiple approach to study environmental stress-induced epiallele formation and inheritance in *Zea mays*

1.09 Pace R., Marconi G., Raggi L., Guiducci M., Falcinelli M., Benincasa P., Albertini E. - DNA methylation analysis in rapeseed (*Brassica napus* var. o*leifera* DEL.) under salt stress based on M-SAP markers

1.10 Fè D., Raggi L., Ciancaleoni S., Torricelli R., Negri V. - Methylation patterns in *Brassica oleracea* L.: changes during time and between different agroclimatic conditions

1.11 Saponari M., Loconsole G., Yokomi R.Y., Saldarelli P., Montemurro C., Leonetti P., Fanelli V., De Giovanni C. - *Citrus tristeza virus* resistance gene locus: small RNA profile and preliminary epigenetic studies

1.12 Cremona G., Aiese-Cigliano R., Paparo R., Consiglio M.F., Conicella C. - Down-regulation of a histone deacetylase affects male meiosis in *Arabidopsis*

1.13 Aiese-Cigliano R., Cremona G., Paparo R., Consiglio M.F., Conicella C. - A histone deacetylase is required for fertility, seed germination and seedling growth rate in *Arabidopsis*

1.14 Mascheretti I., Mainieri D., Varotto S., Rossi V. - The maize WD-repeat chromatin remodeling gene *nfc102* regulates the maize homolog of the *Arabidopsis* florigen *FT*

1.15 Ballottari M., Termolino P., Di Dato F., Cammareri M., Bossi S., Bassi R., Maffei M., Grandillo S. - Biochemical and physiological effects of *PsbS* gene silencing by RNAi in *Solanum lycopersicum*

1.16 Accardo M.C., Giordano E., Mariotti F.R., Damia E., Messina G., Piacentini L., Moschetti R., Caizzi R., Fanti L., Dimitri P. - The YETI gene of *Drosophila* encodes a BCNT protein required for chromosome organization

SESSION 2A
GENOME STRUCTURE, FUNCTION AND PLASTICITY

2A.13 Orrù L., Urso S., Lamontanara A., Bagnaresi P. - A comparative study of skeletal muscle transcriptional profiles in two cattle breeds

2A.14 Mercati F., Riccardi P., Longo C., Falavigna A., Leebens-Mack J., Sunseri F. - Different approaches to develop novel molecular markers for sex determination in *Asparagus officinalis*

2A.15 Rainaldi G., Panarese S., Miacola C., Lotti C. - Mitochondrial genome of *Asplenium nidus* reveals features highly similar to those of seed plant mtDNAs

2A.16 Capuzzo A., Maffei M., Gnavi G. - Molecular discrimination of the genus *Mentha* by sequencing and RFLP analysis of the 5S rRNA Non-Transcribed Spacer (NTS) region

2A.17 Mazzamurro V., Barbieri M., Garvin D.F., Marcel T.C., Niks R.E., Francia E., Pasquariello M., Pecchioni N. - QTLs for resistance to the leaf rust *Puccinia brachypodii* in the model plant *Brachypodium distachyon*

2A.18 Tartarini A., Polegri L., Perla C., Bernabeo L., Pace L., Spanò L. - Genetic diversity in *Artemisia petrosa* ssp. *eriantha*

2A.19 Fasoli M., Zenoni S., Tornielli G.B., Dal Santo S., Citterio S., Pezzotti M. - *PhEXPA1* controls cell size and the timing of axillary meristem development in *Petunia hybrida*

2A.20 Damiani F., Passeri V., Paolocci F. - Interference of *LAR* genes depletes the synthesis of proanthocyanidins in *Lotus corniculatus* leaves

2A.21 Passeri V., Damiani F., Pellegrino R.M., Paolocci F. - The transcription factor *VvMYBPA1* induces a metabolic reprogramming of flavonoids in tobacco flowers

2A.22 Riccioni C., Murat C., Belfiori B., Martin F., Paolocci F., Rubini A. - Mining microsatellites in the *Tuber melanosporum* genome for population genetic analyses

2A.23 Belfiori B., Riccioni C., Martin F., Paolocci F., Rubini A. - Identification and characterization of sex-related genes in *Tuber melanosporum* genome

2A.24 Carelli M., Biazzi E., Panara F., Tava A., Scaramelli L., Porceddu A., Graham N., Odoardi M., Piano E., Arcioni S., May S., Calderini O., Scotti C. - Characterization of *Medicago truncatula* LHA gene as multifunctional oxidase involved in the biosynthesis of haemolytic saponin

2A.25 Iannelli M.A., Di Giacomo E., Iafrate S., Rodrigues-Pousada R.A., Peng J., Chen R., Frugis G. - Role of a novel *KNOX1* transcription factor of *Medicago truncatula* in the determination of leaf morphology

2A.26 Panara F., Passeri V., Damiani F., Calderini O., Paolocci F. - Identification of a *Medicago truncatula* glutathione S-transferase gene essential for anthocyanin accumulation

2A.27 Carbone F., Placido A., Ceci L.R., Giuliano G., Gallerani R., Perrotta G. - Tomato plants overexpressing Cryptochrome 2 reveal modified expression of chloroplast genome

2A.28 Dibari B., Murat F., Pont C., Blanco A., Salse J. - A deep inside plants gene structure plasticity: PSY gene family as a case study

2A.29 Centomani I., Leonetti P., De Giovanni C., Viggiano L. - Energy biogenesis: how to coordinate two genomes

2A.30 Gregis V., Sessa A., Guerra R., Andres F., Coupland G., Pavesi G., Kater M.M. - Functional characterisation of short vegetative phase by a chromatin immuno-precipitation sequencing approach

2A.31 Borghi C., Laura M., Bobbio V., Allavena A. - *De novo* sequencing and transcriptome analysis of *Kalanchoe* to identify putative genes involved in epiphilly

2A.32 Leoni C., Volpicella M., Gallerani R., Ceci L.R. - The spinach *Lhcb1* multigene family. Why multiple genes for isofunctional proteins?

2A.33 Tononi P., Mica E., Fasoli M., Jayakumar B.K., Horner D.S., Ferrarini A., Zenoni S., Pè M.E., Delledonne M., Pezzotti M. - Development of a *Vitis vinifera* miRNA microarray platform

2A.34 Dago N., Malerba G., Ferrarini A., Tononi P., Venturini L., Xumerle L., Fasoli M., Zenoni S., Pezzotti M., Delledonne M. - Performance assessment of different microarray grape designs

2A.35 Costantini L., Malacarne G., Battilana J., Coller E., Lorenzi S., Troggio M., Vrhovsek U., Stefanini M., Velasco R., Mattivi F., Grando M.S., Moser C. - A multidisciplinary approach to identify the genetic determinants of flavonoid content in grapes

2A.36 Venturini L., Ferrarini A., Noel D., Tononi P., Buson G., Zenoni S., Bellin D., Pezzotti M., Delledonne M. - *De novo* reconstruction of the *Vitis vinifera* cv. Corvina transcriptome

2A.37 Finezzo L., Cavallini E., Zenoni S., Zamboni A., Pezzotti M., Tornielli G.B. - Exploring the MYB-bHLH-WD regulatory complex of the flavonoid pathway in *Vitis vinifera*: the bHLH side

2A.38 Malacarne G., Perazzolli M., Cestaro A., Sterck L., Fontana P., Van De Peer Y., Viola R., Velasco R., Salamini F. - Transposition mediated deconstruction of a (paleo)polyploid genome

2A.39 Busconi M., Cucurachi M., Morreale G., Zanetti A., Bavaresco L., Fogher C. - Characterization and study of *Vitis vinifera* L. sirtuin genes

2A.40 Vannozzi A., Boss P.K., Walker A.R., Dry I.B., Lucchin M. - Role of VvMYB14 and VvMYB15, two novel R2R3 MYB factors, in biotic and abiotic stress response and in the regulation of stilbene biosynthesis in grapevine

2A.41 Pugliesi C., Salvini M., Fambrini M. - In the *turf* mutant of sunflower, a transposon insertion in a *CYCLOIDEA* gene (*HaCYC2c*) changes the floral symmetry and fertility of ray flowers

2A.42 Pagnotta M.A., Rey N., Mondini L., Sonnante Ga., Morgese A., Sonnante Gi., Fernandez J.A., Gilabert C.E., Boury S., Hamon C. - Molecular characterization of the wider European *Cynara* collection by means of markers

2A.43 Sonnante G., Cattonaro F., Scalabrin S., De Paola D., Pignone D., Morgante M. - Insight into the organization of the *Cynara cardunculus* genome

2A.44 Barghini E., Cossu R.M., Giordani T., Cattonaro F., Morgante M., Natali L., Cavallini A. - Towards the construction of OLEAREP: a database of repeated sequences of *Olea europaea* L.

2A.45 Donnarumma F., Paffetti D., Fladung M., Biricolt S., Ernst D., Altosaar I., Vettori C. - Molecular analysis of gene expression levels in *Populus* spp. transgenic lines

2A.46 Giordani T., Cossu R.M., Pè M.E. - Centromeric sequences in three poplar species

2A.47 Cossu R.M., Giordani T., Barghini E., Marroni F., Pinosio S., Cattonaro F., Morgante M., Natali L., Cavallini A. - Analysis of LTR retrotransposons in the genus *Populus*

2A.48 Giacomello S., Zaina G., Vezzi F., Scalabrin S., Felice N., Cattonaro F., Morgante M. - *De novo* assembly and genome structure analysis in the *Populus* genus

2A.49 Scalabrin S., Policriti A., Nadalin F., Del Fabbro C., Miculan M., Pinosio S., Cattonaro F., Vendramin E., Aramini V., Verde I., Rossini L., Testolin R., Morgante M. - A catalog of molecular diversity within *Prunus* germplasm inferred from next-generation sequencing data: bioinformatic approaches and challenges

2A.50 Maestri E., Marmiroli M., Visioli G., Marmiroli N. - Correlation between single nucleotide polymorphism genotype and phenotypic response to cadmium exposure in *Populus* spp.

2A.51 Turchi L., Carabelli M., Sassi M., Possenti M., Ruzza V., Melatti C., Morelli G., Ruberti I. - HD-Zip II transcription factor genes control adaxial-abaxial patterning in *Arabidopsis* leaf morphogenesis

2A.52 Calafiore R., Ruocco M., Lorito M., Cascone P., Rao R. - Expression of *Trichoderma harzianumm* hydrophobin in *Solanum lycopersicum*

2A.53 Brog M., Tripodi P., Cammareri M., Osorio-Algar S., Fraser P., Fernie A., Grandillo S., Zamir D. - Phenomics of the sequenced genomes of the cultivated tomato and its wild ancestor *Solanum pimpinellifolium*

2A.54 Andolfo G., Sanseverino W., Rombauts S., Frusciante L., Ercolano M.R. - Tomato R-genes genome-wide sorting

2A.55 Antonecchia G., Viscosi V., Gerber S., Leger P., Lepais O., Scippa S., Fortini P. - Molecular characterization of genetic diversity in sympatric white oak species (*Quercus spp.*)

2A.56 Specchia V., Di Tommaso S., Berloco M., Tritto P., Piacentini L., Fanti L., Pimpinelli S., Giangrande A., Bozzetti M.P. - Genetic characterization of known and novel components of piRNA pathways in *Drosophila melanogaster* gonads

2A.57 Salemme M., Sica M., Gaudio L., Aceto S. - Identification and expression analysis of class C and D MADS-box genes in *Orchis italica* (Orchidaceae)

2A.58 Raimondi I., Ciribilli Y., Bisio A., De Sanctis V., Inga A., Campomenosi P. - Identification and validation of the response elements for the p53 family members in the gene encoding the mitochondrial tumor suppressor proline dehydrogenase

2A.59 De Pittà C., Biscontin A., Albiero A., Mazzotta G.M., Bertolucci C., Sales G., Romualdi C., Lanfranchi G., Costa R. - Gene expression profiling around the clock in the Antarctic krill (*Euphausia superba*)

2A.60 Linguiti G., Vaccarelli G., Picardi E., Antonacci R., Ciccarese S. - A first survey of the genomic organization of the T-cell receptor gamma locus in *Tursiops truncatus*

2A.61 Lancioni H., Capomaccio S., Felicetti M., Cappelli K., Silvestrelli M., Verini Supplizi A., Achilli A. - Horse mitochondrial genome analyses to define the origin of ancient human populations

2A.62 Vaccarelli G., Antonacci R., Tasco G., Hassanane M.S., Massari S., Casadio R., Ciccarese S. - The repertoire of gamma/delta TCR in dromedary is diversified by somatic mutation and CDR3 diversification

2A.63 Monti V., Mandrioli M., Rivi M., Bizzaro D., Manicardi G.C. - The stability of instability: occurrence of a functional telomerase in the holocentric chromosomes of aphids

2A.64 Marsano R.M. - Identification of novel LTR-retrotransposons in the genome of *Culex quinquefasciatus*

2A.65 Federico C., Picciotto R., Galvagno M., Tosi S., Motta S., Saccone S. - Evolutionary chromosomal rearrangements leave unchanged intranuclear position of translocated loci in primate cells

2A.66 Gerace R., Brenna A., Cagliostro A., Baciareli Falini L., Filetici P., Ballario P. - Molecular characterization of *Tuber melanosporum* responses to light

2A.67 Woodrow P., Pontecorvo G., Fuggi A., Kafantaris I., Annunziata M.G., Carillo P. - Mobility of Ttd1a retrotransposon by stress modulate resistance expression gene in durum

2A.68 Malgioglio A., Donnini S., Gavazzi G., Consonni G. - Study of a maize viviparous mutant impaired in the last step of ABA biosynthesis and in the Moco pathway

2A.69 Catellani M., Pea G., Paul Stephenraj E., Olango T.M., Porceddu E., Pè M.E. - Wheat genotyping by Illumina goldengate assay: a test case

2A.70 Giusti L., Faccioli P., Colaiacovo M., Cattivelli L., Crosatti C. - Deep sequencing-based characterization of wheat miRNome under stress condition

2A.71 Michelotti V., Lacrima K., Desiderio F., Barabaschi D., Gadaleta A., Centomani I., Giancaspro A., Giove S., Francia E., Mazzamurro V., Pecchioni N., Fricano A., Piffanelli P., Mastrangelo A.M., Valarik M., Blanco A., Stanca A.M., Cattivelli L., Valé G. - Evaluation of the synteny for 5AS chromosome in *Triticum* species with different ploidy levels

2A.72 Marè C., Havlickova L., Rizza F., Aprile A., Borrelli G.M., Panna R., Mastrangelo A.M., Perrotta C., De Bellis L., Cattivelli L. - Transcriptomic analysis of drought and heat responses in durum wheat and eQTLs mapping to identify the loci controlling the molecular response to drought

2A.73 Piccinini S., Lauria M., Viotti A. - Genomic and proteomic analyses of zeins in inbred lines and Lombard varieties of maize

2A.74 Botticella E., Sestili F., Lafiandra D. - Analysis of polymorphisms between *SBEIIa* homoeologous genes in wild and cultivated wheats

2A.75 Giancaspro A., Giove S.L., Nigro D., Zacheo S., Colasuonno P., Gadaleta A., Valè G., Cattivelli L., Stanca A.M., Blanco A. - Physical mapping of genomic and EST-derived SSR markers on the homoeologous group 5 chromosomes of wheat

2A.76 Nigro D., Gadaleta A., Gu Y., Huo N., Blanco A., Anderson O. - Structural analysis of the wheat genes encoding NADH-dependent glutamine-2-oxoglutarate amidotransferases (NADH-GOGAT) and comparison with other species

2A.77 Margiotta B., Colaprico G., Urbano M., Sestili F., Lafiandra D. - Proteomic characterization of C-type LMW-GS in durum wheat

2A.78 De Leonardis A.M., D'Orso F., Ruberti I., Cattivelli L., Papa R., Morelli G., Mastrangelo A.M. - Evolutionary conserved stress-responsive CCCH zinc finger proteins are involved in germination processes in *Arabidopsis* and durum wheat

2A.79 Laidò G., Taranto F., Marone D., Mangini G., Mastrangelo A.M., Cattivelli L., Papa R., Blanco A., De Vita P. - Linkage disequilibrium and population structure in tetraploid wheat

2A.80 Marone D., Laidò G., Gadaleta A., Colasuonno P., Giancaspro A., Giove S., De Vita P., Blanco A., Cattivelli L., Papa R., Mastrangelo A.M. - Development of a high-density consensus map in durum wheat

2A.81 Mondini L., Nachit M.M., Porceddu E., Pagnotta M.A. - New SNPs mutations of DREB genes in durum wheat identified by HRM technology

2A.82 Egidi E., Janni M., Sestili F., Ceriotti A., D'Ovidio R., Lafiandra D., Kasarda D.D., Vensel W.H., Masci S. - Characterization of wheat low-molecular-weight glutenin subunits and their maturation process

2A.83 Gombaud G., Rogniaux H., Masci S., Lafiandra D. - Identification of chromosome 5A encoded polypeptides in wheat kernels

2A.84 Coppola M., Buonomo T., Coppola V., Corrado G., Martinelli R., Rao R. - Tomato transcriptome is reprogrammed following prosystemin over-expression

2A.85 Scarano M.-T., Cristiano L., Tavano R., Frusciante L., Aversano R. - Genomic stability of androgenetic haploids derived from *Solanum tuberosum (+) S. bulbocastanum* somatic hybrids

2A.86 Miraglia V., Traini A., Bradeen J.M., Iorizzo M., Mann H., Chiusano M.L., Carputo D. - Structural genomics of wild potato species based on DArT alignments

SESSION 2B
PROTEOSTASIS

2B.07 Vitale A., Biava F., Ragni L., Klein E.M., Morandini F., Maîtrejean M., Schmidt M., Herman E.M., Pedrazzini E. - Mechanism of gamma-zein protein body formation within the endoplasmic reticulum

2B.08 De Marchis F., Pompa A., Bellucci M. - Phaseolin: a model protein for investigation on recombinant protein stability in the chloroplast

2B.09 Visioli G., Marmiroli M., Marmiroli N. - Two dimensional liquid chromatography technique coupled with mass spectrometry analysis to compare the proteomic response to cadmium stress in poplar

2B.10 Rocchetti A., Grippa A., Grassi G., Carpaneto A., Czempinski K., Vitale A., Pedrazzini E. - Biogenesis of the AtKCO3 potassium channel

2B.11 Giovanardi M., Pantaleoni L., Ferroni L., Baldisserotto C., Longoni P., Concia L., Crimaldi L., Cella R., Pancaldi S. - Nuclear transformation of two cell wall-less strains of *Chlamydomonas reinhardtii* for the overexpression of two phytoene synthase exogenous genes

SESSION 2C
TRANSPORT AND ASSIMILATION: FROM SINGLE CELLS TO WHOLE PLANT

2C.06 Pedà G., Nardini A., Salleo S. - Leaf hydraulic vulnerability correlates with drought resistance in *Acer* and *Quercus* species

2C.07 Di Masi F., Nardini A., Salleo S. - Ion-mediated regulation of xylem hydraulics in the genera *Fraxinus* and *Acer*: relationships with xylem anatomy and drought adaptation

2C.08 Salleo S., Lo Gullo M.A., Trifilò P. - Phloem cooling as a tool for inhibiting xylem refilling after cavitation in laurel

2C.09 Raimondo F., Lo Gullo M.A., Glatzel G., Devkota M., Trifilò P., Richter H. - Mistletoes and albino leaves as terminal sinks for elements normally recycled between xylem and phloem

2C.10 Criscuolo G., Valkov V., Parlati A., Alves Martins L., Chiurazzi M. - Preliminary characterization of the *Lotus japonicus* nitrate transporter gene families

2C.11 Parlati A., D'Apuzzo E., Valkov V., Criscuolo G., Alves Martins L., Vavasseur A., Chiurazzi M. - The *Lotus japonicus* PII protein is involved in a drought response signalling pathway controlling the stomata movement

2C.12 Pallucca R., Visconti S., Camoni L., Torreri P., Aducci P. - Interaction studies of different *Arabidopsis* 14-3-3 isoforms with the plasma membrane H^+-ATPase

2C.13 Marmiroli M., Pigoni V., Maestri E., Marmiroli N. - Inorganic arsenic speciation analysis in different tomato cultivars (*Solanum lycopersicum* L.) and influence of silicon (Si) exposure

2C.14 Trifilò P., Salleo S., Raimondo R., Nardini A., Lo Gullo M.A. - Has the "ionic effect" a role in plant salt tolerance?

2C.15 Zancani M., Petrussa E., Peresson C., Zanin L., Monte R., Tomasi N., Pinton R., Vianello A. - Effect of urea on gene expression and activity of enzymes involved in nitrogen metabolism in maize seedlings

SESSION 3A
GENETICS, PHYSIOLOGY AND BREEDING OF FRUIT PLANTS

3A.05 De Pace C., Catarcione G., Vittori D., Rugini E. - Modeling genetic variation for phenological events in *Corylus avellana* L.

3A.06 Catarcione G., Vittori D., Rugini E., De Pace C. - Significant levels of phenotypic and genetic variation for eriophyoid mite control is present in hazelnut (*Corylus avellana* L.) cultivated accessions and breeding populations

3A.07 Villani F., Mattioni C., Martin A. - Integrating genetic and morphological characterization of chestnut cultivars: where are we and what for?

3A.08 Caruso M., Distefano G., Merelo P., La Malfa S., Lo Piero A.R., Talon M., Gentile A., Tadeo F.R. - Identification of candidate genes involved in pollen-pistil interaction in *Citrus*

3A.09 Provenzano S., Spelt K., Brugliera F., Quattrocchio F., Koes R., Ferrandino A., Tanaka Y., Schubert A. - Genetic control of anthocyanin methylation in petunia and grapevine

3A.10 Palma D., Molesini B., Sabbadini S., Polverari A., Navacchi O., Mezzetti B., Pandolfini T. - Development of a method for conferring resistance to GFL and GLR associated viruses through post transcriptional gene silencing

3A.11 Forlani G., Giberti S., Bertazzini M. - Purification and properties of *Malus domestica* carotenoid cleavage dioxygenase 4

3A.12 Guerra D., Lamontanara A., Bagnaresi P., Baldoni L., Rizza F., Pagani D., Cattivelli L., Mazzucotelli E. - Molecular and physiological adaptation of *Olea europeae* to low temperatures

3A.13 Pirona R., Fuligni F., Peano C., Rizzi E., Lazzari B., Beleggia R., Platani C., Bassi D., De Bellis G., Stella A., Cattivelli L., Rossini L. - RNA-seq and metabolite profiling of two peach varieties

3A.14 Vannozzi A., Nicolè S., Dry I.B., Lucchin M. - Genomic characterization and expression analysis of genes belonging to a family of ABC transporters involved in response to stress in *Vitis vinifera* L.

3A.15 Montemurro C., Sabetta W., Rusek J., Blanco A. - Discovery of DNA polymorphisms in olive *fad7* gene by EcoTILLING

3A.16 Salimonti A., Vizzarri V., Lombardo L., Micali S., Perri E., Zelasco S. - High resolution melting for mutation scanning of oleate desaturase encoding gene

3A.17 Anaclerio A., Alba V., Gasparro M., Caputo A.R., Montemurro C., Blanco A., Antonacci D. - Ampelographic and molecular characterization of Aglianico accessions (*Vitis vinifera* L.) collected in Southern-Italy

3A.18 Morcia C., Carletti G., Corino L., Reggiani F., Terzi V. - Genetic structure of a grape collection and genetic traceability in wine making chain

3A.19 Cavallini E., Harris N.N., Robinson S.P., Pezzotti M., Walker A.R., Tornielli G.B. - Understanding the roles of VvMYB5a and VvMYB5b in the regulation of the flavonoid biosynthetic pathway in grape

3A.20 Dondini L., Paris R., Liang W., De Franceschi P., Venturi S., Gennari F., Tartarini S. - Genetic variability of an Italian apple germplasm collection

3A.21 Paris R., Pagliarani G., Arens P., van de Weg E., Tartarini S. - A sensitive and specific tool for the detection of *Mal d 1* allergen gene transcripts in apple

3A.22 Di Rienzo V., Böttcher C., Davies C. - Characterization of a *Vitis vinifera* GH3 gene family involved in the control of hormone levels

3A.23 D'Andrea M., Pilla F., Lima G., Scarano M.-T. - Characterization of the main olive cultivars in Molise Region by means of SSR molecular markers

3A.24 Galla G., Botton A., Baldoni L., Muleo R., Perrotta G., Ramina A., Barcaccia G. - Comparative genomics for identifying flower organ identity genes in peach and olive

3A.25 Collani S., Alagna F., Caceres M.E., Colao M.C., Galla G., Ramina A., Baldoni L., Muleo R., Perrotta G., Barcaccia G. - Cytological and molecular evidences support a sporophytic self-incompatibility system in olive

SESSION 4
SYSTEMS BIOLOGY

4.07 Sgobba A., Blanco E., Viggiano L., De Pinto M.C. - "cAMP-sponge": a new genetic tool to investigate the role of cAMP in plants

4.08 Colaiacovo M., Bernardo L., Cattaneo A.M., Centomani I., Crosatti C., Alberici R., Cattivelli L., Giusti L., Faccioli P. - Analysis of gene regulatory networks in peach: the interplay between transcription factors and microRNAs

4.09 Del Giudice L., Massardo D.R., Iacobino E., De Stefano M., Hartings H., Pignone D., Alifano P., Pontieri P. - Effects of the metalloid oxyanion tellurite on growth of the yeast *Saccharomyces cerevisiae*

4.10 Nesler A., Dal Corso G., Furini A. - Controlling heavy metal accumulation in plants

4.11 Ruotolo G., De Biasi M.G., Chiaiese P., Marino M., Di Palma A., Palomba F., Lanzillo C., Salluzzo A., Filippone E. - Ionome characterisation of *Solanum lycopersicum* cv. M82 *X S. pennellii* Introgression Lines (ILs)

4.12 Hartings H., Lazzaroni N., Motto M. - Protein, amino acid, and transcriptome analyses of the *Zea mays* mutants *Opaque-2* and *Opaque-7*

4.13 Berná L., Rizzetto L., Cavalieri D. - Friend or foe: using Systems Biology to elucidate the interaction between fungi and their hosts

4.14 Fincato P., Moschou P.N., Ahou A., Angelini R., Roubelakis-Angelakis K.A., Federico R., Tavladoraki P. - Differential gene expression of polyamine oxidases in *Arabidopsis thaliana*

4.15 Fracassetti M., Lazzaroni N., Hartings H. - Molecular characterization of the *Opaque*-6 mutation of *Zea mays* L.

SESSION 5C
GREEN BIOTECHNOLOGY FOR INDUSTRIAL USES

5C.06 Bisogno S., Nigris S., Barbi T., Purelli M., Fabbri A., Baldan B. - Plant cell cultures from *Jatropha curcas*: a possible source of renewable energy

5C.07 Bucci A., Cerino Badone F., Cassani E., Schievano A., Papa G., Adani F., Pilu R. - Preliminary studies of an Italian giant reed (*Arundo donax* L.) clones collection

5C.08 Agrimonti C., Poli F., Sacchetti G., Conforti F., Statti G., Marmiroli N. - Characterization of Calabria and Sardinia myrtle using genetic, chemical and biological markers

5C.09 Comino C., Dolzhenko Y., Lanteri S., Portis E. - Identification of *Artemisia umbelliformis* genotypes suitable for cultivation

5C.10 Borriello M., Ferriello F., D'Addio D., Caruso G., Angelino G., Frusciante L., Ercolano M.R. - A candidate gene approach for identifying quantitative trait loci affecting tomato biomass chemical composition

5C.11 Maggio C., Bartolucci A., Doria E., Longoni P., Concia L., Pantaleoni L., Cella R. - Rhizosecretion of cellulases for bioethanol production

5C.12 Acquadro A., Portis E., Scaglione D., Mauro R.P., Campion B., Falavigna A., Zaccardelli R., Ronga D., Perrone D., Mauromicale G., Lanteri S. - *Cynara cardunculus* L.: from vegetable to energy crop

5C.13 Cucurachi M., Busconi M., Marudelli M., Fogher C. - Recovery of thermostable cellulases from woodland soil by means of metagenomic approaches

5C.14 Pompa A., De Marchis F., Bellucci M. - Characterization of human alpha-mannosidase secretory pathway in tobacco plants

5C.15 Marconi G., Mari A., Sgaravizzi G., Lancioni H., Palomba A., Porceddu A., Panara F., Albertini E. - *In planta* production of *Dermatophagoides pteronyssinus* Der p 10 allergen

5C.16 Gecchele E., Merlin M., Avesani L., Pezzotti M. - Expression and purification of a mutated form of human GAD65 from transgenic tobacco leaves

5C.17 Merlin M., Gecchele E., Brozzetti A., Avesani L., Pezzotti M. - Expression of N-truncated GAD65mut forms in a plant-based platform

SESSION 6A

CROP PRODUCTIVITY: PHYSIOLOGY AND GENETICS

6A.07 Petrarulo M., Marone D., De Vita P., Sillero J.C., Ferragonio P., Giovanniello V., Papa R., Cattivelli L., Rubiales D., Mastrangelo A.M. - Mapping QTLs for root morphological traits in durum wheat

6A.08 Verlotta A., Liberatore M.T., Papa R., Trono D. - The secretory phospholipase A_2 ($sPLA_2$) gene family in durum wheat: identification, characterization and evidence for a role in adaptation to drought stress

6A.09 Yousefi Javan I., Mondini L., Nachit M., Pagnotta M.A. - Intra-specific map of durum wheat based on SSR markers

6A.10 Mangini G., Hassan M.I.M., Signorile M.A., Barbieri M., Ravaglia S., De Vita P., Blanco A. - Validation of grain protein content in durum wheat

6A.11 Maccaferri M., Van Der Vossen E.A.G., Trebbi D., De Heer P., Sørensen A., Sanguineti M.C., Tuberosa R. - SNP development and validation in durum wheat using Next Generation Sequencing (NGS) technique

6A.12 Terracciano I., Maccaferri M., Bassi F., Mantovani P., Simkova H., Massi A., Tuberosa R., Sanguineti M.C. - Fine mapping of the leaf rust resistant *Lr14* locus in durum wheat

6A.13 Francia R., Maccaferri M., Massi A., Vecchi S., Gobbo R., Sanguineti M.C. - Mapping QTLs for grain yield, yield components and quality in durum wheat

6A.14 Graziani M., Maccaferri M., Terracciano I., Paux E., Feuillet C., Sanguineti M.C., Massi A., Castelletti S., Tuberosa R. - High-resolution mapping of a major QTL for grain yield *per se* in durum wheat

6A.15 Ricci A., Maccaferri M., Stefanelli S., Colalongo C., Sanguineti M.C., Tuberosa R. - Thousand kernel weight and number of sterile spikelets in durum wheat: two sides of the same coin?

6A.16 Sanguineti M.C., Maccaferri M., Ammar K., Massi A., Talebi R., Tabib Ghaffary M., Kema G., Corneti S., Tuberosa R. - Association mapping for resistance to *Septoria tritici* blotch in durum wheat

6A.17 Colasuonno P., Incerti O., Taranto F., Mangini G., Sabetta W., Piarulli L., Gadaleta A., Blanco A. - Development of a TILLING population in durum wheat cv. Aureo

6A.18 Menzo V.M., Mastrangelo A.M., Cattivelli L., Papa R., De Vita P. - Development of a marker assisted selection program for the improvement of durum wheat (*Triticum durum* Desf.)

6A.19 Taranto F., Mangini G., Digesù A.M., Del Faro L., Delvecchio L.N., Pasqualone A., Blanco A. - Functional markers for grain polyphenol oxidase activity in a wheat collection

6A.20 Kuzmanovic L., Gennaro A., Benedettelli S., Lattanzi G., Quarrie S.A., Ceoloni C. - Positive effects on yield-related traits of different chromosomal segments of the wild *Thinopyrum ponticum* introgressed into durum wheat

6A.21 Forte P., Kuzmanovic L., Gennaro A., Bitti A., Ceoloni C. - Using wild species of *Thinopyrum* genus in breeding wheat resistant to *Fusarium* head blight

6A.22 Tavakol E., Verderio G., Fusca T., Ciannamea S., Hussien A., Close T.J., Druka A., Waugh R., Mihaela M., Mayer K., Ariyadasa R., Schulte D., Zhou R., Stein N., Muehlbauer G.J., Rossini L. - High-throughput genotyping and comparative genomics approaches for map based cloning of *Uniculme4*, a Mendelian locus controlling barley shoot architecture

6A.23 Pilu R., Bucci A., Casella L., Lago C., Cerino Badone F., Cassani E., Landoni M., Reginelli D. - *r1* gene is tightly associated to a QTL involved in maize yield

6A.24 Farinati S., Forestan C., Varotto S. - Auxin efflux transporters in maize: phylogenetic analysis and gene expression studies

6A.25 Frascaroli E., Aung H.H., Pè M.E., Landi P., Pea G. - Deep genome -wide characterization of recombinant near-isogenic lines for heterotic QTL in maize

6A.26 Lanubile A., Kladnik A., Bernardi J., Chourey P.S., Marocco A. - Seed development and IAA biosynthetic genes are regulated differentially in the defective endosperm-18 seed mutant of maize

6A.27 Casella L., Greco R., Tacconi G., Bruschi G., Albertario E., Lupotto E., Valè G., Piffanelli P. - Exploring drought resistance in temperate rice for a sustainable rice production in Italy

6A.28 Pedretti A., Greco R., Casella L., Bruschi G., Stella A., Piffanelli P., Biffani S. - A comparison of methods for association mapping in rice

6A.29 Schiavulli A., Lotti C., Marcotrigiano A.R., Pavan S., Grillo S., Iovieno P., Miacola C., Zonno V., Ricciardi L. - Identification of tomato differentially expressed genes involved in response to water deficit

6A.30 Sanampudi V.R.R., Picarella M.E., Mazzucato A. - Conditional expression of the tomato proline transporter *LeProT1* confers tolerance to heat and other abiotic stresses

6A.31 Pucci A., Ruiu F., Picarella M.E., Mazzucato A. - Advances in the characterization of tomato mutants putatively affected in class B MADS-box transcription factors

6A.32 Fasano C., Caruso I., D'Amelia V., Aversano R., Carputo D. - Preliminary analysis of *an1* MYB gene in wild and cultivated potato species

6A.33 Barchi L., Lanteri S., Portis E., Valè G., Acciarri N., Ciriaci T., Toppino L., Rotino G.L. - Development of an SNP-based genetic linkage map and QTL analysis in eggplant

6A.34 Lo Cicero L., Madesis P., Tsaftaris A., Lo Piero A.R. - First results on the overexpression of *Cs*GSTU isoenzymes in transgenic tobacco plants

6A.35 Turchi A., Tamantini I., Camussi A., Racchi M.L. - Expression of a metallothionein A1 gene of *Pisum sativum* in white poplar enhances tolerance and accumulation of zinc and copper

6A.36 Fambrini M., Mariotti L., Parlanti S., Giorgetti L., Picciarelli P., Salvini M., Ceccarelli N., Pugliesi C. - A deletion in the *ent-kaurenoic acid oxidase1* (*HaKAO1*) gene affect the *dwarf2* (*dw2*) mutant of sunflower

6A.37 Bizzarri M., Rugini E., De Pace C. - Genetic diversity for the response to external stimuli affecting physiological mechanisms in *Helianthus tuberosus* clones

6A.38 Gutierrez Pesce P., Bizzarri M., Rugini E., De Pace C. - *In vitro* microtuberization for simulating the developmental physiology of underground storage organ in *Helianthus tuberosus*

6A.39 Fabbrini F., Gaudet M., Harfouche A., Bastien C., Zaina G., Morgante M., Beritognolo I., Scarascia Mugnozza G., Sabatti M. - Phenotypic plasticity and QTL mapping of bud set process in *Populus nigra*

6A.40 Bertazzini M., Forlani G. - Differential sensitivity of Italian rice cultivars to salt stress conditions

6A.41 Petrollino D., Liboni M., Giberti S., Berlicki L., Kafarski P., Forlani G. - Phytotoxicity of pyrroline-5-carboxylate reductase inhibitors

6A.42 Cardi M., Chibani K., Rouhier N., Jacquot J.P., Esposito S. - Characterization of poplar plastidic P2-G6PDH

6A.43 Giacomelli L., Caputi L., Vrhovsek U., Moser C. - The gibberellic acid response of different *Vitis vinifera* cultivars during fruit set

6A.44 Faè M., Balestrazzi A., Macovei A., Confalonieri M., Valassi A., Carbonera D. - The *MtTdp2* (5'-Tyrosyl-DNA phosphodiesterase) gene is involved in the plant response to genotoxic stress

6A.45 Parlanti S., Giuntoli B., Droge-Laser W., Weiste C., Perata P., Licausi F. - *ERF16*, a JA-induced AP2/ERF transcription factor of *Arabidopsis thaliana*

6A.46 Contran N., Bellavite D., Kumah F.K.A., Dawoe E., Oti-Boateng C., Mulas M., Lubino M. - A promising energy crop for rural development: improvement of *Jatropha curcas* agro-practices

6A.47 Rotondi S., Tartarini A., Spanò L. - Molecular and functional characterization of amorpha-4,11-diene synthase gene in *Artemisia annua* Anamed A3

6A.48 Vasco M., De Stefano R., Di Matteo A., Punzo B., Molisso M., Lotti C., Ricciardi L., Barone A. - Candidate genes controlling fruit quality in a tomato introgression line tolerant to water deficit

SESSION 6B
GENES AND HUMAN HEREDITARY DISEASES

6B.06 Bisio A., Andreotti V., Gargiulo S., Latorre E., Del Vescovo V., Provenzani A., Quattrone A., Bianchi-Scarrà G., Denti M.A., Ghiorzo P., Inga A. - *CDKN2A*/P16^{INK4A} 5'UTR variants in melanoma predisposition: lost in translation, somewhere

6B.07 Bignami F., Pilotti E., Bertoncelli L., Ronzi P., Gullì M., Marmiroli N., Lopalco L., Ruotolo R., Galli M., Cossarizza A., Casoli C. - Striking changes of miRNAs expression in CD4+ T lymphocytes occurred even in the absence of an established HIV-1 infection

6B.08 Tosoni E., Palumbo E., Cordelli E., Pardini M.C., Russo A. - *Fra14A2*, the murine orthologue of common fragile site *FRA3B,* is unstable *in vivo* in somatic and germ cells

6B.09 Meloni F., Ghezzi D., Zeviani M., Ferrero I., Goffrini P. - *SDH6* a new gene of *Saccharomyces cerevisiae* required for assembly of complex II

SESSION 7
BIOTIC INTERACTIONS: SYMBIOSIS AND PATHOGENESIS

7.07 Panza L., Lazzaroni N., Balconi C., Berardo N., Hartings H. - Study of *Fusarium*-induced biosynthetic pathway shifts in *Zea mays* L.

7.08 Pii Y., Molesini B., Pandolfini T. - Study of *MtN5* transcriptional control and of its involvement in *Medicago truncatula* nodulation pathway

7.09 Valente M.T., Infantino A., Aragona M. - Understanding the role of an extracellular endo-1,4-β-glucanase in the *Pyrenochaeta lycopersici*-tomato pathosystem

7.10 Caranci S., Iannacone M., Cervone F., Caprari C. - Analysis of pectic enzyme activities produced by three phytopathogenic fungi grown on plant cell walls

7.11 Baccelli I., Scala A., Glave A., Pazzagli L., Cappugi G., Bernardi R. - Cerato-platanin and cerato-populin induce differential gene expression in *Platanus acerifolia*

7.12 Laura M., Lazzari B., Bobbio V., Caprera A., Borghi C., Strozzi F., Allavena A., Stella A. - *De novo* sequencing of *Anemone coronaria* transcriptome to discover putative genes involved in *Tranzechelia discolour* infection responce

7.13 Calabrese I.T., Paradiso A., Ciccarese F., De Pinto M.C. - *Oidium neolycopersici* infection induces different responses on resistant and susceptible tomato plants

7.14 Savatin D.V., Gigli Bisceglia N., Cervone F., De Lorenzo G. - Identification of early transduction elements involved in oligogalacturonide signalling

7.15 Biselli C., Martini A., Urso S., Faccini N., Tacconi G., Cattivelli L., Valè G. - Haplotype analysis of the *Rdg2a* locus in different barley varieties

7.16 Desiderio F., Como F., Mastrangelo A.M., Rubiales D., Pasquini M., Baravelli M., Simeone R., Blanco A., Cattivelli L., Valè G. - Identification and mapping of a new leaf rust resistance gene derived from *Triticum turgidum* var. *dicoccum*

7.17 Barbierato V., Tononi P., Toppino L., Delledonne M., Rotino G.L. - Microarray analysis of gene expression variation in eggplant roots subjected to inoculation with *Fusarium oxysporum* and *Verticillium dahliae*

7.18 Janni M., Volpi C., D'Ovidio R. - Production of transgenic wheat plants expressing the protein inhibitors AcPMEI and PvPGIP2 to enhance resistance to fungal diseases

7.19 Moscetti I., Kalunke R., Janni M., Rocchi V., Sella L., Favaron F., D'Ovidio R. - Isolation and characterization of xylanase inhibitors from chromosome group 5 of wheat

7.20 D'Ovidio R., Moscetti I., Janni M., Volpi C., Cervone F. - The expression of a fungal polygalacturonase causes cell wall pectin modification and alters plant growth in wheat

7.21 Volpi C., Raiola A., Janni M., O'Sullivan D.M., Gordon A., Favaron F., D'Ovidio R. - The lack of recognition of the polygalacturonases secreted by *Claviceps purpurea* by PvPGIP2 is responsible for susceptibility in wheat transgenic plants

7.22 Kalunke R., Janni M., Benedetteli S., D'Ovidio R. - Co-transformation of pectinase and xylanase inhibitors (PGIP, PMEI and XI) to enhance wheat resistance to fungal disease

7.23 Abbruscato P., Nepusz T., Mizzi L., Del Corvo M., Morandini P., Fumasoni I., Michel C., Paccanaro A., Guiderdoni E., Schaffrath U., Morel J.B., Piffanelli P., Faivre-Rampant O. - Expression profiling of the WRKY monocot-specific clade in rice

7.24 Bernardi J., Lanubile A., Maschietto V., Marocco A. - Isolating resistance genes against *Fusarium* ear rot in maize

7.25 Ferriello F., Tramparulo M., Puopolo G., Zoina A., Frusciante L., Ercolano M.R. - Towards the modeling of tomato-FORL interaction

7.26 Pontieri P., Iacobino E., Massardo D.R., Pignone D., Del Giudice L., Tredici S.M., Pizzolante G., De Caroli S., Talà A., Alifano P., Maffei M.E., Gnavi G., Atbeha Zebelo S., Cordero C., Rubiolo P., Bicchi C. - Identification of bacteria living in the *Chrysolina herbacea* gut by culture-based approaches

7.27 Baldan E., Squartini A., Zottini M., Baldan B. - Characterization and diversity of bacterial endophytes of *Vitis vinifera*

7.28 Maffei G., Miozzi L., Fiorilli V., Lanfranco L., Accotto G.P. - Tomato, arbuscular mycorrhizal fungi and geminiviruses: plant health in a tripartite interaction

7.29 Laino P., Russo M.P., Fantozzi E., Guardo M., Reforgiato-Recupero G., Valè G., Cattivelli L., Moliterni V.M.C. - CTV-induced modulation of the *Citrus* bark proteome – and phosphoproteome – during compatible and incompatible interactions

7.30 Zaugg I., Panzeri D., Daminati M.G., Bollini R., Bacher S., Sparvoli F. - A new Arcelin variant responsible for resistance of common bean seeds to bean weevils?

7.31 Lanzanova C., Berardo N., Valoti P., Hartings H., Torri A., Motto M., Balconi C. - IDIAM – Project: identification of genetic variability and genes for selection of genotypes tolerant to rootworm damage in maize

7.32 Coppa T., Pansa M.G., Ingegno B.L., Tavella L., Vaccino P. - Interactions between bugs' feeding and wheat quality

7.33 Cerana R., Crosti P., Malerba M. - Chitosan-induced cell death in sycamore cultured cells

7.34 Ferrari S., Galletti R., De Lorenzo G. - Role of MAP kinases in the activation of *Arabidopsis* defense responses triggered by elicitors

7.35 Landoni M., Bellatti S., De Francesco A., Delledonne M., Ferrarini A., Venturini L., Tonelli C. - A mutation in the FZL gene of *Arabidopsis* causes a lesion mimic phenotype

7.36 Sicilia F., Modesti V., Andreani F., Gramegna G., Cervone F., De Lorenzo G. - An interaction network mediated by the oligogalacturonide receptor WAK1 regulates *Arabidopsis* local response to wounding

7.37 Molesini B., Pii Y., Cecconi D., Bulgarini A., Pandolfini T. - A proteomic approach to study the autoregulation of nodulation in *Medicago truncatula*

7.38 Verrillo F., Lomaglio T., Lindermayr C., Durner J., Scippa G.S., Marra M., Rocco M. - Analysis of S-nitrosylated proteins *in Arabidopsis thaliana* leaves subjected to oxidative stress or wounding

7.39 Baldoni E., Mattana M., Locatelli F., Picchi V., Cagliani L.R., Consonni R., Genga A. - Metabolic and molecular responses of Italian rice cultivars to BTH treatment

7.40 Vandelle E., Sottocornola B., Bellin D., Delledonne M. - The specificity of tyrosine nitration questions the redundancy of AtMKK4 and AtMKK5 during plant defense responses

7.41 Bellin D., Hussain J., Bouneb M., Kleinfelder Fontanesi K., Pachaiappan R., Vandelle E., Delledonne M. - cGMP signaling in plant-pathogen interactions

7.42 Di Giacomo E., Iafrate S., Iannelli M.A., Peng J., Chen R., Plet J., Frugier F., Frugis G. - Role of *KNOX1* transcription factors of *Medicago truncatula* in root nodule formation and hormone signal transduction

SESSION 8
FOOD NUTRITIONAL VALUE AND *LIFE SPAN*

8.08 Marzario S., Gioia T., D'Onofrio A., D'Agrosa G., Logozzo G., Spagnoletti Zeuli P. - Evolution of the genetic structure in *Triticum durum* Desf. germplasm from Southern Italy

8.09 Alfieri M., Redaelli R. - Screening of favourable alleles forβ-carotene content in maize inbred lines

8.10 Paoletti F., Sestili F., Botticella E., Masci S., Lafiandra D. - Comparative proteomic analysis of metabolic and starch granule-associated proteins in wheat kernel of a high amylose transgenic line and its corresponding untransformed cultivar

8.11 Palombieri S., Sestili F., Paoletti F., Botticella E., Lafiandra D. - Polymorphism of starch granule protein 1 (Sgp-1) in polyploid and diploid wheat species

8.12 Rivera Ortiz L.M., Benedettelli S., Ghiselli L., Lafiandra D., Masci S. - Accumulation of CM proteins in old and new durum wheat cultivars under different nitrogen fertilization

8.13 Giberti S., Bertazzini M., Trono D., Forlani G. - Lipoxygenase activity in *Triticum durum*: differential properties of enzyme forms

8.14 Finocchiaro F., Gianinetti A., Grausgruber H., Baronchelli M., Cattivelli L., De Santis G., Platani C., Terzi V., De Vita P. - A study of biodiversity of phenolic content in the wheat caryopsis

8.15 Graziano S., Pafundo S., Gullì M., Marmiroli N. - Development of Real-Time PCR assays for the detection of allergenic species in food

8.16 Volpicella M., Panarese S., Leoni C., Fanizza I., Gallerani R., Ceci L.R. - Molecular cloning and characterization of allergenic proteins from maize

8.17 Cerino Badone F., Amelotti M., Hamad N., Schiraldi A., Fessas D., Cesari V., Toschi I., Cremona R., Delogu C., Villa D., Lucchini G., Pilu R. - Low phytic acid 1 mutation in maize, not only a phosphorous issue

8.18 Lago C., Cassani E., Petroni K., Calvenzani V., Tonelli C., Pilu R. - Study of maize genotypes rich in anthocyanins for human and animal nutrition

8.19 Doria E., Nielsen E., Glahn R., Tava A., Dani V., Sparvoli F., Perrone D., Campion B. - Nutritional quality improvement in common beans by genetic reduction of phytic acid and other antinutritional factors

8.20 Vietina M., Agrimonti C., Marmiroli M., Bonas U., Marmiroli N. - Applicability of SSR markers to the traceability of monovarietal olive oils

8.21 Menin B., Comino C., Kankar C., Portis E., Moglia A., Bouwmeester H., Beekwilder J., Lanteri S. - Investigation on a (+)-germacrene A synthase involved in sesquiterpene lactones biosynthesis in globe artichoke

8.22 Patui S., Peresson C., Clincon L., Navarini L., Del Terra L., Vianello A., Zancani M., Braidot E. - Characterization of lipase activity in green coffee beans during storage and germination

8.23 Bertolini A., Braidot E., Petrussa E., Peresson C., Patui S., Tubaro F., Wählby U., Coan M., Vianello A., Zancani M. - Lamb's lettuce (*Valerianella olitoria* [L.] Pollich) storage at low temperature is improved by partitioned light

8.24 Pistelli La., Barberini S., Raffi D., Leonardi M., Bertoli A., Pistelli Lu., Ruffoni B. - HPPR gene identification in *Salvia officinalis* cell cultures for the production of rosmarinic acid

8.25 Nacca F., Massaro G., Annunziata M.G., Iannuzzi F., Carillo P., Fuggi A. - Glutathione oxido-reductive state into *Brassica rapa* L. cv. *sylvestris* during postharvest storage

8.26 Pontecorvo G., Woodrow P., Massaro G., Carillo P., Kafantaris I., Fuggi A. - Changes ascorbate peroxidase gene expression post-harvest in *Brassica rapa* L.

8.27 Massaro G., Nacca F., Annunziata M.G., Iannuzzi F., Carillo P., Fuggi A. - Metabolites and peroxidase activities in *Brassica rapa* L. cv. *sylvestris* during postharvest storage

8.28 Santangelo E., Picarella M.E., Soressi G.P., Mazzucato A. - Novel insights and perspectives for the breeding and exploitment of high-anthocyanin tomatoes

8.29 Scarano D., Corrado G., Rao R. - DNA testing as a means to protect 'San Marzano' PDO products

8.30 Savo Sardaro M.L., Marmiroli M., Maestri E., Marmiroli N. - Molecular characterization and discrimination of Italian tomato cultivars

8.31 D'Alessandro A., Francese G., Rotino G.L., Mennella G. - Evolution of some quality parameters during fruit ripening in *Solanum melongena* L. introgression lines

8.32 Di Matteo A., Ruggieri V., Sacco A., Carriero F., Rigano M.M., Lombardi N., Barone A. - Resolving gene network that controls phenolics accumulation in tomato fruit

8.33 Orsi I., Malatrasi M., Belfanti E., Gullì M., Marmiroli N. - Determining resistance to *Pseudomonas syringae* in tomato, a comparison with different molecular markers

8.34 Minutolo M., Amalfitano C., Chiaiese P., Errico A. - Antioxidant content in tomato varieties and ecotypes

SESSION 9
GENETICS, PHYSIOLOGY AND BIOTECHNOLOGY

9.01 Milner S.G., Bovina R., Castelletti S., Terracciano I., Buonfiglioli C., Corneti S., Salvi S. - Testing High-Resolution Melting for SNP discovery and genotyping in diploid and polyploid cereals

9.02 Farina A., Gennaro A., Giorgi D., Grosso V., Lucretti S. - Improving the technology for flow sorting wheat 5A chromosome arms specific DNA

9.03 Ferradini N., Nicolia A., Gori V., Veronesi F., Rosellini D. - *Lolium perenne TERMINAL FLOWER 1* gene expression in alfalfa and tobacco does not affect floral transition

9.04 Galassi E., Gazzelloni G., Taddei F., Crespi P., Gazza L., Pogna N. - Hordoindoline composition and kernel hardness in barley (*Hordeum vulgare*)

9.05 Paolacci A.R., Giancaspro A., Gadaleta A., Pacelli A., Tanzarella O.A., Blanco A., Ciaffi M. - Cloning and characterization of three homoeologous wheat PDI-like genes located on group 5 chromosomes

9.06 Ciaffi M., Tanzarella O.A., Paolacci A.R. - Isolation and characterization of APR (adenosine 5' - phosphosulfate reductase) and APR-like genes in wheat

9.07 Rossi D., Busconi M., Lorenzoni C., Baldi G., Fogher C. - Evidence of herbicide tolerance gene flow from cultivated clearfield rice (*Oryza sativa* L.) to red rice (*Oryza sativa* f. *spontanea*)

9.08 Sciacca F., Russo M.P., Palumbo M. - Molecular techniques for the fingerprinting of durum wheat varieties

9.09 Motisi A., Catalano C., Abbate L., Lucretti S., Aracri B., Fatta Del Bosco S. - Isolation of protoplasts from mesophyll cells of *Dendrobium*

9.10 Catalano C., Motisi A., Abbate L., Carrubba A., Fatta Del Bosco S. - Biotechnological approaches to the genetic improvement of C*hrysanthemum cinerariaefolium* L.

9.11 Grosso V., Nardi L., Farina A., Aracri B., Pashkoulov D., Debora G., Lucretti S. - Polyploidy induction and protoplast isolation from protocorm like bodies in orchids

9.12 Gatto A., Danzi D., Curci P.L., Khaldi S., Morgese A., Sonnante Gi., De Paola D., Blanco E., Sonnante G. - Wild cardoon variation and the domestication of artichoke

9.13 Vischi M., Poscic F. - Identification of *Helianthus* hybrids through DNA barcodes

9.14 Falistocco E., Falcinelli M., Ranfa A. - Cytogenetic characterization of cultivated and wild species of subfamily Cichorioideae (Asteraceae)

9.15 Torricelli R., Raggi L., Ciancaleoni S., Tissi C., Negri V. - SOLIBAM: breeding barley, bean and broccoli for organic and low input management systems

9.16 Barocco R., Pacicco L., Venanzoni R., Veronesi F., Negri V. - Strategy development to identify the most appropriate areas for *in situ* conservation of plant genetic resources

9.17 Biagetti E., Bitocchi E., Bellucci E., Nanni L., Giardini A., Attene G., Papa R. - Common bean domestication in Mesoamerica and Andes highlighted by nucleotide data

9.18 Marmiroli N., Scialabba A., Agrimonti C. - Assessment of genetic variation in Sicilian *Helichrysum* (Asteraceae) and implication to germplasm conservation

9.19 Caser M., Gaino W., Scariot V. - Cultivation of evergreen azalea cuttings in neutral-alkali solutions: a way to select new ornamentals

9.20 Aversano R., Adamo P., Frusciante L., Iorizzo M., Quetel C., Zampella M.V., Carputo D. - Molecular and chemical markers to trace the genetic identity and the geographical origin of potatoes

9.21 Albertini E., Raggi L., Vagnini M., Achilli A., Marconi G., Lancioni H., Falcinelli M., Veronesi F., Miliani C., Sassolini A. - Tracing the biological origin of siccative oils used in paintings through chloroplast DNA analysis

9.22 Liu J., Visentin I., Bonfante P., Lovisolo C., Schubert A., Cardinale F. - Validation of genes involved in strigolactones biosynthetic pathway in *Lotus japonicus*

9.23 Russi L., Torricelli R., Falcinelli M. - Adaptation of vetch, field bean and lucerne to organic farming

9.24 Leonetti P., De Giovanni C., Viggiano L., Rosellini D., Veronesi F. - Epigenetics aspects of polyploidization: studies of expression pattern of DNA methylation genes in *Medicago sativa* L.

9.25 Nicolia A., Ferradini N., Veronesi F., Rosellini D. - Molecular analysis of T-DNA insertion events in alfafa

9.26 Scotti C., Carelli M., Gaudenzi P. - Managing genetic diversity in the construction of alfalfa semi-hybrids

9.27 Calistri E., Intrieri M.C., Ciofini A., Buiatti M., Bogani P. - Characterization of some *P. vulgaris* and *P. coccineus* cultivars from Garfagnana Region in Tuscany by trap molecular markers

9.28 Allegrucci S., Ferradini N., Nicolia A., Rosellini D., Veronesi F. - Chromosome pairing behaviour in newly synthesized tetraploid alfalfa

9.29 Goretti D., Bitocchi E., Bellucci E., Nanni L., Attene G., Papa R. - The effects of domestication on the structure of the nucleotide diversity in the common bean from Mesoamerica

9.30 Moubayidin L., Di Mambro R., Pacifici E., Terpstra I., Perilli S., Dello Ioio R., Heidstra R., Costantino P., Sabatini S. - Cytokinins-auxin dependent molecular mechanisms necessary for the stem cell niche maintenance in the *Arabidopsis thaliana* root meristem

9.31 Spanò L., Massa S., Paolini F., Venuti A., Franconi R. - Non-toxic mutant form of saporin for developing cancer vaccines

9.32 Barbaro M.R., Costa A., Krieger-Liszkay A., Pupillo P., Trost P. - Is the redox activity of plasma membrane cytochrome AIR12 involved in cell separation events?

9.33 Ederli L., Calderini O., Pasqualini S. - Calcium influxes and protein kinase activation mediate ozone-induced defence gene expression in tobacco plants

9.34 Pasqualini S., Ederli L. - Ozone effect on ragweed pollen viability and NAD(P)H oxidase activity

9.35 Vita F., Lucarotti V., Alpi E., Alessio M., Alpi A. - Proteomic profiling of white truffle (*Tuber magnatum* Pico) naturally grown in different Italian areas

9.36 Lucarotti V., Vita F., Alpi A. - Proteomic analysis of cold stressed *Arabidopsis thaliana* chloroplasts

9.37 Piano D., Bochtler M., Buchel C., De Sanctis D., Haniewicz P. - Crystallization of Photosystem II from *Nicotiana tabacum*

9.38 Zaffagnini M., Bedhomme M., Marchand C., Couturier J., Gao X.-H., Rouhier N., Lemaire S.D., Trost P. - Glutaredoxin S12: unique properties for redox signaling

9.39 Benucci G.M.N., Raggi L., Albertini E., Bencivenga M., Di Massimo G. - Tomentelloid fungi: among one of the most abundant and diverse ectomycorrhizal mycobionts in truffle orchard

9.40 Rigoldi M.P., Rapposelli E., Satta D., Rau D., Resta P., De Giorgio D., Porceddu A. - Genetic diversity of almond cultivars and characterization of self-incompatibility alleles

9.41 Vanetti I., Falanga V., Binelli G., Mameli G., Filigheddu R. - Genetic analysis of two rare Sardinian endemic of the *Centaurea* genus

9.42 Dattola A., Mercati F., Schneider A., Zappia R., Sunseri F. - Genetic diversity among grapevine cultivars from the Ionian coast of Reggio Calabria

9.43 Bartoli G., Bernardi R., Durante M. - Transcriptome analyses of O_3 –responsive genes in leaves of two differentially susceptible poplar genotypes

9.44 Puglisi S., Lieggi M., Lops A., Rubino L., Rainaldi G. - New results on the genetic differentiation between populations of Scots pine (*Pinus sylvestris* L.) from several geographic regions of its natural range

9.45 Ghirotto S., Tassi F., Fumagalli E., Colonna V., Lari M., Rizzi E., Caramelli D., Barbujani G. - Origins and evolution of the Etruscans' DNA

9.46 Di Meo G.P., Perucatti A., Genualdo V., Iannuzzi A., Manzone M., Peretti V., Matassino D., Iannuzzi L. - Cytogenetic survey in some endangered animal species reared in Campania Region

9.47 Dato S., Soerensen M., Montesanto A., Lagani V., Passarino G., Christensen K., Christiansen L. - *UCP3* polymorphisms, hand grip performance and survival at old age

9.48 Pisani F., Tallaro F., Crocco P., Giordano M., D'Aquila P., Bellizzi D., Passarino G., Rose G. - The gene variability of neuronal nitric oxide synthase affects cognitive functioning and survival in the elderly

9.49 Tallaro F., Campa D., Di Cianni F., Rizzato C., De Rango F., Barale R., Passarino G., Canzian F., Gemignani F., Montesanto A., Landi S., Rose G. - A multilocus analysis shows the role of genetic variability of genes involved in metabolic pathways in human longevity

9.50 Metelli A., Matmati N., Achilli A., Lancioni H., Babudri N. - The role of sphingolipid metabolism genes in the response of *Saccharomyces cerevisiae* cells to starvation for essential nutrients

9.51 Baruffini E., Serafini F., Ferrero I., Lodi T. - Overexpression of DNA polymerase zeta reduces the mitochondrial mutability caused by pathological mutations in DNA polymerase gamma in yeast

9.52 Buiatti M., Livi R., Calistri E. - Structural variability in gene promoter

9.53 Merigliano C., Piergentili R., Gatti M., Vernì F. - Protein phosphatase 2A (PP2A) is required for the maintenance of *Drosophila* chromosome integrity

9.54 Di Giorgio M.L., Morciano P., Cenci G. - The citrate lyase regulates cell division during *Drosophila* male meiosis

9.55 Morciano P., Di Giorgio M.L., Mannini L., Musio A., Giansanti F., Rong Y.S., Cenci G. - The citrate lyase plays conserved roles in the maintenance of genome stability

9.56 Grugni V., Battaglia V., Parolo S., Hooshiar Kashani B., Al-Zahery N., Torroni A., Semino O. - Unraveling genetic traces of ancient migratory middle Eastern routes: a survey of Y-chromosome variation in Iran

9.57 Bonfiglio S., Achilli A., Olivieri A., De Gaetano A., Agha S., Tesfaye K., Ajmone-Marsan P., Negrini R., Colli L., Torroni A., Ferretti L. - Mitochondrial DNA haplogroup R in modern cattle: a contribution of Italian aurochsen?