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CONTENTS

Welcome Letter	4
Member Societies	5
Committees - Secretariat	6
Session Organisers	7
Map	8
Programme Overview	9
PROGRAMME	10
ABSTRACTS	
Plenary Lecture	29
Plenary Symposium	30
PS1 - Cancer Stem Cells	30
PS2 - CRISPR/CAS: from a prokaryotic immune system to a powerful tool for biomedical and agricultural research	31
PS3 - Oxygen Sensing and Redox Signalling: common themes of aerobic life	32
PS4 - Systems Biology: from Genetic Networks to Organismal Functions	33
PS5 - New roles and molecular pathophysiology of mitochondria	34
The EMBO Keynote Lecture	35
Parallel Symposia	36
S1 - The (recent) evolution of human evolution	36
S2 - From Reverse- to Structural-Vaccinology and beyond. Current challenges against infectious diseases	37
S3 - Nitrogen: Nutritious and Noxious	38
S4 - Shaping the Cancer Genome: from pathways to mutational signatures	39
S5 - Unfolding truth: making sense of intrinsically disordered proteins	40
S6 - Plant adaptation and phenotypic plasticity to climate change	41
Poster and Selected Short Talks	42
1 - Environmental Microbiology and Biotechnology	42
2 - Genomics, Proteomics and Systems Biology	50
3 - Chromosome Biology, Cell Division and Cell Cycle	57
4 - Epigenetics and Epigenetic Therapies	60
5 - Oncogenes and Tumor suppressors	64
6 - Plant Metabolism and Environmental Stress	70
7- Genetics of Microorganisms	78
8 - Transcription Mechanisms and Networks	81
9 - DNA replication, Repair and Recombination	83
10 - Non-coding RNA	87
11 - Environmental and Molecular Mutagenesis	89
12 - Plant Nutrition	91
13 - Cellular Stress, apoptosis and autophagy	94
14 - Development, Differentiation and Aging	98
15 - Metabolism and its regulation in health and diseases	100
16 - Human Genetics and Genomic Diversity	106
17 - Neurobiology	112
18 - Immunology and Host-Pathogen Interaction	114
19 - Protein Synthesis, Degradation and Homeostasis	117
20 - Stem Cells, iPS, Cancer Stem Cells	119
21 - Nutrition Biochemistry	122
22 - Evolution	125
23 - Cell Communication, Cell Adhesion and Membrane Trafficking	127
24 - Plant Development and Disease	129
Author Index	135

12 - Plant Nutrition

P12.1

The characterization of durum wheat adaptive responses to different Fe availability highlights an optimum Fe requirement threshold

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Durum wheat, as Strategy II plant, copes with iron (Fe) deficiency by increasing the secretion of phytosiderophores (PS). Sulfate assimilatory pathway is known to be induced upon Fe deprivation in several grasses, such as maize, barley and wheat, most likely because PS are produced from nicotianamine, whose precursor is methionine. The physiological plant response - in terms of plant ionome, PS release, thiol content and S pathway-related enzymes - induced by decreasing Fe availability by degrees (from 75 to 0 μM) allowed the identification of three specific limit Fe concentrations: 75 μM , 25 μM and 0 μM Fe, i.e. the complete Fe starvation. At each limit, plants begin to induce different and specific adaptive responses to improve Fe acquisition or to reduce the damage resulting from limited Fe availability. The identification of the Fe availability level below which durum wheat plants start an expensive metabolic reorganization of S and several other elements, could be of benefit not only for an effective cultivation of the crop but also for the grain quality.

P12.2

Nitrogen assimilation, yield productivity and quality in mycorrhized tomato plants

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The effects of root colonization by arbuscular mycorrhizal (AM) of mix fungus *Glomus mosseae* and *Glomus intraradices*, on nitrogen metabolism, fruit yield and environmental sustainability were studied in field-grown tomato plants by drip irrigation and exposed to limiting P soil content 5 $\mu\text{g/gDW}$ (basal soil) with nitrate fertilization (40 $\mu\text{g/gDW}$), after greenhouse germination. At 140 days after sowing, in the harvesting fruit stage mycorrhizal plants (M) had significantly higher mineral nutrient, organic nitrogen and phosphate compounds in both roots and leaves compared to no mycorrhizal plants (NM). In this contest the enzyme activity as NR and GS involved in nitrogen metabolism was tested in root as in leaf. AM inoculation also significantly increased growth and productivity parameters. The fruit yields of M plants were higher than NM plants by 40% and containing significantly higher quantities of lycopene, carotene, mineral nutrients and total amino acids, than NM plants, suggesting that mycorrhizal colonization affects host plant nutritional status, and growth under P limitant field conditions and modified reproductive behaviour, fruit production and quality. We thank the University of Molise and the Microspore S.p.A. for their support.

P12.3

Lupinus albus (L.) plants use common mechanisms to overcome either iron (Fe) or phosphorus (P) deficiencies

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White lupin (*Lupinus albus* L.) has developed a highly efficient strategy to acquire sparingly soluble nutrients, like P and Fe, from soils. This strategy is based on modification of the root architecture with the formation of cluster roots that are able to release large amounts of exudates in a small volume of soil. The aim of this work was to unravel the mechanisms involved in these processes

via the combination of RNAseq and physiological approaches. In comparison to control roots (+Fe, +P), about 5500 or 2000 genes were modulated in cluster roots of Fe- or P-deficient plants, respectively; more than 1000 genes were commonly modulated. Most of the known genes coding for mechanisms involved in either Fe or P acquisition were upregulated by Fe as well as by P deficiency. The reciprocal activation of Fe and P acquisition systems was also confirmed by uptake and mobilization assays using labelled ⁵⁹Fe and ³²P sources. In conclusion, white lupin plants activate both P and Fe acquisition mechanisms contributing to the overall nutrient efficiency of white lupin plants; this behavior would reflect an adaptation to low pH soils, where Fe and P co-precipitate.

P12.4

Diatom response to variations in nitrogen availability

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Nutrient concentrations, in particular Nitrogen (N), in the ocean show significant temporal and spatial variability, which affects growth and distribution of phytoplankton. Diatoms are unicellular microalgae constituting one of the most important phytoplankton groups in the ocean, their adaptive capacity suggests that they have sophisticated mechanisms to perceive and respond to environmental variations. The molecular mechanisms that allow diatoms to efficiently cope with N availability remain largely unknown. Our analysis of available genomic and transcriptomic data shows that, the presence of multiple NH₄⁺(AMT) and NO₃⁻(NRT2s/NPFs) transporter genes, differentially regulated, is a conserved feature of diatom species living in different ecological niches and we refined the analysis with a phylogenetic assessment (Rogato et al. 2015). In addition, we found that N limitation influence the expression of the light-harvesting protein family LHCXs, potential markers for evaluating the effects of N deficiencies (Taddei et al. 2016). These preliminary studies provide a springboard to shed light on the evolutionary advantage of these N transporters and on the N metabolism in diatoms.

P12.5

Action of protein hydrolysates on maize seedlings roots: a genome-wide transcriptional analysis

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Protein hydrolysates are plant growth-promoting products that contain a mixture of peptides and free amino acids derived from the hydrolysis of plant and animal sources, but also from industrial and agricultural residues. Free amino acids have several beneficial effects, but the role played by short chain peptides could also be relevant. The aim of this work is to study the effects and the mechanism of action of a protein hydrolysate produced by SICIT 2000 S.P.A. on maize roots compared with the effects produced by either free amino acids mixture or inorganic nitrogen. The protein hydrolysate was highly effective in promoting root growth and increasing the concentration of micronutrients. The total surface area of the lateral roots was approximately 1.5 and 7 times higher in seedlings treated with the protein hydrolysate as compared with seedlings treated with the same total N supplied as either free amino acids or inorganic N, respectively. The genome-wide transcriptional analysis allowed to highlight global changes in gene transcription produced