



COST Action FA1306:
The quest for tolerant varieties –
Phenotyping at plant and cellular level



COST WG1 / EPPN2020 workshop 29th - 30th of September 2017

Novi Sad

Abstract book

Organizers:



Sponsors:



Scientific Committee:

Sebastien Carpentier

Roland Pieruschka

Diego Rubiales

Ankica Kondić-Špika

The Local organizers:

Ankica Kondić-Špika

Sanja Vasiljević

Ana Marjanović-Jeromela

Dragana Trkulja

Sanja Mikić

Milka Brdar-Jokanović

Marijana Ačanski

Kristian Pastor

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Scientific Programme

Friday, September 29th

8:00 – 9:00	Registration
9:00 – 9:05	Welcome
9:05 – 9:20	IFVCNS movie
9:20 – 9:45	Roland Pieruschka: <i>Integrating plant phenotyping community in Europe: EPPN2020: access to phenotyping facilities EMPHASIS: long term operation of pan European phenotyping infrastructure</i>
9:45 – 10:30	Key lecture: Hendrik Poorter: <i>Pampered inside, pestered outside? Ways to bridge the gap between lab and field experiments</i>
10:30 – 10:45	Coffee Break
Session 1: Phenotyping/Breeding for biomass improvement Chair: Roland Pieruschka	
10:45 – 11:00	Koller: <i>Non-invasive phenotyping technologies enable investigating plant responses to antibiotic and biotic interactions</i>
11:00 – 11:15	van Rooijen et al.: <i>High throughout phenotyping of photosynthesis and growth to identify relevant genetic loci in Arabidopsis</i>
11:15 – 11:30	Onno Muller: <i>BreedFACE: phenotyping for plants under elevated CO2 concentrations</i>
11:30 – 11:45	Sciara et al.: <i>High-throughput phenotyping of vegetative growth and water-use efficiency of durum wheat near isogenic lines for QYLD.IDW-3B, a major QTL for yield per se</i>
11:45 – 11:55	Ljubičić et al.: <i>Normalized Difference Vegetation Index (NDVI) as a tool for wheat yield traits estimation</i>
11:55 – 12:05	Hernandez et al.: <i>Quantization of Harvested Tomatoes from RGBD Images</i>
12:05 – 12:15	Herrera et al.: <i>How can drones and modern phenotyping methods contribute to the understanding of Genotype × Environment interactions (G × E)?</i>
12:15 – 12:25	Szabados et al.: <i>A non-destructive method to monitor plant growth and development in vitro</i>
12:25 – 12:35	Sekmen et al.: <i>The Role of Hydrogen Peroxide in Elongation Dynamics of the First Internode of a Wheat Cultivar Tolerant to Deep-Sowing Condition</i>
12:35 – 13:30	Lunch
13:30 – 14:30	Poster session
Session 2: Phenotyping/Breeding for nutrient efficiency Chair: Astrid Junker	
14:30 – 14:45	Junker et al.: <i>Integrated analysis of plant growth and development using high throughput multi-sensor platforms at IPK</i>

14:45 – 15:00	Salon et al.: <i>High throughput root phenotyping using the “Rhizo” suite</i>
15:00 – 15:15	Pastor et al.: <i>Relationship between liposoluble fingerprints and botanical origin of various agricultural crops</i>
15:15 – 15:30	Lillemo et al.: <i>Reliable and efficient high-throughput phenotyping to accelerate genetic gains in Norwegian plant breeding</i>
15:30 – 15:45	Vasconcelos et al.: <i>Phenotyping soybean and common bean for better growth and nutrition under elevated CO²</i>
15:45 – 16:15	Coffee Break
Session 3: Phenotyping/Breeding of perennial crops	
Chair: Rick Van de Zedde	
16:15– 16:30	Gonçalves & Martins: <i>An efficient phenotyping for selection in ancient grapevine varieties</i>
16:30– 16:45	Svensgaard et al.: <i>Phenotyping of perennial ryegrass by physiological fingerprinting and UAV remote sensing using RGB-, thermo- and multi-reflectance imaging</i>
16:45– 17:00	Corke et al.: <i>Breeding perennial species to enhance the sustainability of grassland based agriculture</i>
17:00– 17:15	He et al.: <i>Novel 3D Imaging System for Strawberry Phenotyping</i>
17:15– 17:30	Paudel et al.: <i>Heavy soil and treated waste water result in reduced hydraulics and reduced levels of plasma membrane aquaporin (PIP) mRNA in citrus trees</i>
17:30– 17:45	Costa et al.: <i>Dynamics of canopy and soil temperature variation in a Mediterranean vineyard</i>
20:00 – 23:00	Gala Dinner

Saturday, September 30th

8:30 – 9:00	Papa: <i>The impact of domestication on the phenotypic architecture of durum wheat under contrasting nitrogen fertilisation</i>
Session 4: Phenotyping/Breeding for biotic stress tolerance	
Chair: Diego Rubiales	
9:00 – 9:15	Boureau et al.: <i>Quantification of biotic stresses on aerial parts of plants using Chlorophyll Fluorescence Imaging and Image Analysis</i>
9:15 – 9:30	Rubiales: <i>Resistance to rusts: can we predict durability by complementation of field and growth chamber studies with histology?</i>
9:30 – 9:45	Costa et al.: <i>Phenotyping Castanea hybrids from controlled crosses for resistance to Phytophthora cinnamomi</i>
9:45 – 10:00	Aznar-Fernández & Rubiales: <i>Phenotyping Pisum sativum germplasm for resistance to aphid (Acyrtosiphon pisum) and weevil (Bruchus pisorum) under field and controlled conditions</i>
10:00 – 10:15	Svara et al.: <i>Polyploidy influences Malus x domestica / Venturia inaequalis interactions</i>

10:15 – 11:00	Coffee Break
Session 5: Phenotyping/Breeding for abiotic stress tolerance	
Chair: Sebastien Carpentier	
11:00 – 11:30	Pauk et al.: <i>Phenotyping for drought tolerance in wheat using complex stress diagnostic system</i>
11.30 – 11.45	Welcker_ et al.: <i>A genome-wide approach combining field and platform phenotyping to investigate plant responses to drought and high temperature</i>
11:45 – 12:00	Rakosy-Tican et al.: <i>Phenotyping preselected somatic hybrids of potato with the wild species <i>Solanum chacoense</i> and <i>S. bulbocastanum</i> for drought tolerance</i>
12:00 – 12:15	Carpentier et al.: <i>High throughput growtainer phenotyping combined with on line transpiration monitoring to select water efficient cultivars: a proof of principle in the banana bio(di)versity collection.</i>
12:15 – 12:30	Paul et al.: <i>Synergistic effects of salt and drought stress in wheat responses studied by high throughput phenotyping</i>
12:30 – 12:45	Sundgren et al.: <i>Root growth and anatomy of spring wheat in response to waterlogging</i>
12:45 – 13:00	Nazemi et al.: <i>Molecular mapping of root traits in durum wheat in environments with lower water availability</i>
13:00 – 13:15	Aliferis: <i>Functional genomics and phenomics: focusing on plant protection products' R&D</i>
13:15 – 13:30	Baytar et al.: <i>Association mapping for fiber traits and drought tolerance in elite cotton (<i>Gossypium hirsutum</i> L.) germplasm</i>
13:30 – 13:45	Ottosen et al.: <i>Phenotyping for heat tolerance - from lab to field</i>
13:45 – 14:00	Moshelion & Dalal: <i>Whole-plant stress performance analysis: a new tool for functional phenotyping</i>
14:00 – 14:30	Lunch
15:00 – 18:00	Excursion

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Phenotypic evaluation of variability among dry bean cultivars landraces from breeding collections of Institute of Field and Vegetable Crops Novi Sad

Aleksandra D. Savić¹, Mirjana Vasić¹, Miodrag Dimitrijević², Milka Brdar-Jokanović¹, Dario Danojević¹, Sofija Petrović², Milan Zdravković³

¹*Institute of Field and Vegetable Crops Novi Sad, Serbia*

²*Faculty of Agriculture, University of Novi Sad, Serbia*

³*Institute of Soil Sciences, Belgrade, Serbia*

Dry bean (*Phaseolus vulgaris* L.) is one of the most important food legumes and source of proteins and dietary fibers. Two major gene pools exist in cultivated dry bean, one being Middle American, and second Andean. Dry bean accessions and cultivars belonging to each of these two gene pools are distinguished based of phenotypic traits, as well as on molecular and biochemical level. Most of the dry bean germplasm is maintained *ex situ* in gene banks and collections of the research institutes around the world which is characterized with high level of genetic diversity. Possibility to identify this genetic variation is of greatest importance for conservation and utilization of dry bean germplasm. Phenotypic evaluation is the first step in discrimination and classification of these accessions.

The aim of this work was to assess phenotypic diversity of 37 dry bean genotypes (domestic and foreign cultivars and landraces) held at dry bean breeding collection of Institute of Field and Vegetable Crops, Novi Sad. We analyzed eight qualitative traits (growth type, color of flower standard, color of flower wings, pod color, seed pattern, color of seed coat, seed brilliance, seed shape) following the Bioversity International Key descriptor for common bean and six quantitative traits (number of pods per plant, number of seeds per plant, seed weight per plant, 1000 seed mass, number of days to flowering, number of days to maturity). Multivariate analyses, consisting of principal component analysis and cluster analysis were applied. In a principal component analysis first two axis explained 46.9% of variation, and the most important traits in discriminating between genotypes were separated. The genotypes differed mostly for number of pods per plant, number of seeds per plant, color of flower standard, color of flower wings, seed coat color and 1000 seed mass. Positive correlations were observed between number of pods per plant, number of seeds per plant, seed weight per plant and growth habit, as well as between growth habit and number of day to flowering and number of days to maturity. Negative correlation was observed between 1000 seed mass and other yield components and growth habit. Both principal component analysis (PCA) and cluster analysis clustered the genotypes into two major groups presenting Mesoamerican and Andean gene pools. Only two foreign cultivars (KP-12 and KP-13) were distinguished as third, separate group. Possible hybrids between these two genepools were identified, meaning genotypes with a combination of traits representing Andean or Mesoamerican gene pool.

Key words: *Phaseolus vulgaris*, phenotypic variation, gene pool