

Monday 25 August

Sessions 1 and 2: Exploring and exploiting wheat genetic resources

O10

Conserving crop diversity: navigating politics and climate change to create a global system

Cary Fowler

Global Crop Diversity Trust, Italy

Abstract not yet received

O11

Metabolic phenotyping of genetically diverged species in Gramineae

Mochida K¹, Furuta T¹, Ogihara Y², Shinozaki K¹, Kikuchi J¹

¹*Kihara Institute for Biological Research, Yokohama 244-0813, Japan,*

²*RIKEN Plant Science Center, Yokohama 230-0045, Japan*

Systematic evaluation of phenotypic variations among cereal breeds based on metabolic profiling is an effective approach to holistic discovery of metabolic markers as well as nutrition targeted breeding. Furthermore, integrated analysis of metabolo-phenotype and genotype of natural variations or cultivars should be useful to find out metabolic markers in association with genotypes. NMR method is a spectroscopy allowing us to elucidate 3D structure and dynamics of biological molecules with high repeatability. Various NMR methods make it possible to gain holistic metabolic profile data not only from solution samples but also from insoluble and/or solid state samples. We are applying NMR method to perform metabolic profiling in Gramineae plants, wheat, barley and rice, and developing a novel metabolic-phenotyping procedure by global measurement of metabolite in various samples. To monitor metabolic profile, solution samples extracted from seed grains of 21 wheat, 21 barley and 18 rice strains were conducted to measurement of metabolite using ¹H-NMR and ¹H-¹H NMR method. The metabolic fingerprint of each of 60 strains by ¹H-NMR were analysed using principal coordinate analysis (PCA) and hierarchical clustering analysis (HCA) to compare metabolic profiling among species and to screen chemical shift spectrum corresponding to metabolite specifically abundant in each strain. Profiling using ¹H-¹H NMR was applied to measure of abundance of major metabolite. In total, 22 metabolites were compared among strains. These major metabolite profiles allow us to evaluate nutritious balance in cereal grains. Furthermore, in order to compare genetic divergence and metabolo-phenotypic variations, we performed genome wide genotyping using AFLP analysis for comparison between genotype and metabolo-phenotype to discover metabolites in association with genetic polymorphisms. NMR based metabolic-phenotyping and that integration with genome wide genotyping should be mostly applicable to systematic exploration of cereal genetic resources as well as to metabolite based breeding involved in cereal productivity.

O12

Molecular diversity, structure and association mapping in a collection of synthetic hexaploid wheat

Ogbonnaya FC^{1,2}, Ye G¹, Emebiri LC¹, Trethowan R³, van Ginkel M^{1,2}

^{1,2}*Department of Primary Industries, Primary Industries Research Victoria (PIRVic), Private Bag 260, Horsham, Victoria 3401, Australia*

²*International Centre for Agricultural Research in the Dry Areas, PO Box 5466, Aleppo, Syria*

³*Plant Breeding Institute, University of Sydney, PMB 11, Camden, NSW 2570, Australia*

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Synthetic hexaploid wheats (SHWs), which were mostly developed over the last twenty years at CIMMYT based on crosses between tetraploid durum wheats (AABB genome) and representatives of the diploid wheat ancestor *Aegilops tauschii* (DD genome), are becoming increasingly popular in providing new sources of resistance/tolerance to biotic and abiotic stresses. The SHWs are potentially a rich source of novel traits, genes and alleles that can be readily transferred to elite bread wheat varieties. The objectives of this study were to analyse the molecular diversity in a collection of SHWs, and explore the use of markers developed using Diversity Arrays Technology (DArT), for association mapping of cereal cyst nematode resistance genes. The results suggest a high level of molecular diversity in SHWs and revealed the existence of genetic structure. Marker–trait associations were also readily detected. These results also provide us with a guide to the exploitation in ongoing breeding programs of this set of SHWs for other agronomically important traits for which they have been evaluated.

O13

Swimming in the genepool - a rational approach to exploiting large genetic resource collections

Ken Street
ICARDA, Syria

Abstract not yet received

O14

Allele mining and sequence diversity at the wheat powdery mildew resistance locus *Pm3*

Kaur K¹, Street K², Mackay M³, Yahiaoui N^{1,4} and Keller B¹

¹ *Institute of Plant Biology, University of Zurich, Zollikerstrasse 107, 8008 Zürich, Switzerland,* ² *ICARDA, PO Box: 5466, Aleppo, Syria,* ³ *Australian Winter Cereals Collection, 4 Marsden Park Road, CALALA NSW 2340, Australia,* ⁴ *UMR Biologie et Génétique des Interactions Plante-Parasite CIRAD TA A-54/K Campus International de Baillarguet 34398, Montpellier cedex 15, France.*

In wheat, race-specific resistance to powdery mildew is controlled by *Pm* genes. Recently, the *Pm3* allelic series *Pm3a to g*, have been cloned. The molecular tools derived from *Pm3* haplotype studies were applied to study the genetic diversity at this locus. This study is a large scale systematic allele mining, including 1320 hexaploid wheat landraces selected on the basis of eco-geographical parameters favouring growth of powdery mildew. The landraces were infected with a set of differential powdery mildew isolates, which allowed the selection of resistant lines. The newly isolated *Pm3* alleles showed sequence diversity as compared to the known *Pm3* alleles, with the differences mainly lying in the LRR domain. The multitude of the new *Pm3* allele sequences obtained in this study will shed a light on the specificity determination of *Pm3* genes. Based on transient expression assays as well as Virus Induced Gene Silencing (VIGS), we conclude that we have identified at least two new functional *Pm3* alleles. The new interesting and functional alleles can be transferred to susceptible but economically important wheat varieties as single genes or R-gene cassettes to achieve efficient control of mildew. This study contributes to targeted use of genetic diversity resources for research and breeding.

O15

Imprint of selection in pedigrees of modern bread wheat varieties

Horvath A, Charmet G, Balfourier F

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INRA, UMR 1095 Genetics, Diversity and Ecophysiology of Cereals, F-63100 Clermont-Ferrand, France

Hexaploid bread wheat (*Triticum aestivum* L.) is cultivated since Neolithic times. Until the 1800s, only landraces were cultivated, the intensive selection got started in the middle of the 19th century. In the present work we tempt to detect selection signature by tracing back haplotypes in modern French bread wheat varieties, using pedigree information. It is known that regions of the genomes showing a positive selective value present a strongly reduced allelic diversity and a longer range of local linkage disequilibrium (LD) pattern due to hitch-hiking effects. Based on these facts, we make an attempt to describe haplotypic variability within pedigrees of elite breeding lines. Pedigrees of a selected set of seven modern varieties have been reconstructed back to the landraces when it was possible. For a first approach, 3B chromosome of bread wheat was chosen as a model and was widely genotyped with microsatellite (SSR) markers, then haplotype diversity, linkage disequilibrium patterns and temporal variance of allele frequencies (Fc) were determined and compared between ancient and modern genitors. Three regions present a relative loss of haplotype diversity along the chromosome. One among them comes with a larger linkage disequilibrium pattern, thus it seems to be influenced by selection effect. High temporal variations of allele frequencies were also detected in these three regions, particularly at the distal end of the chromosome. Interestingly, haplotype diversity profiles of ancient and modern genitors were identical in this latter region, which suggest the presence of an imprint of domestication. Comparison with the B-genome ancestor, *Triticum turgidum* ssp. *dicoccoides* will be discussed. Finally, a genome-wide multilocus screen has been initiated with Diversity Array Technology (DArT) in order to identify across the whole genome other regions suspected to be under selection.