High Throughput Genotypic Data Management & Collaboration with Indian NARS

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Science for Better Livelihoods in Dry Areas

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Barley

Genotyping and molecular analysis

- For genomic DNA (gDNA) extraction, barley plants were grown in a growth chamber under controlled conditions with temperature range between 22-24 °C and short-day photoperiod (12 hours light).
- Total gDNA was extracted from leaf tissue collected from three-week-old plant of each accession using the CTAB (cetyltrimethylammonium bromide) method as described in Winnepenninckx et al. [19].

Genotyping, a set of 7864 independent, high confidence and gene-based SNPs markers

- incorporated into the Illumina Infinium iSelect 9k SNP barley array were used to genotype the accessions .
- The genotyping assay was performed by the TraitsGenetics GmbH.
- Markers with allele frequency < 5% or missing data > 10% were removed from further analyses.

Cluster analysis, population structure and linkage disequilibrium

The GWAS analysis identified 98 significant markers-traits associations for multiple traits including GY with four important QTLs located at 1H, 2H, 5H and 7H, which seems important for dry environments.

Manuscript:

"A Genome Wide Association Study for Yield and Yield Components in Jordanian Barley (*Hordeum vulgare* L.) Landraces Grown under Rainfed Conditions" by M. Al-Abdallat[1,2*] , A. Karadsheh[3], N. I. Hadadd[1,2], S. Ceccarelli[4], M. Baum[2], M. Hasan[5], A. Jighly[2,6,7], J. M. Abu Elenein[1]

Wheat

Genotyping:

- **A set of 173 synthetic hexaploid wheat (SHW) characterized for resistance against fungal pathogens that cause leaf, stem and yellow rusts, yellow leaf spot, Septoria nodorum and crown rot were used in genome-wide association study (GWAS).**

- **Diversity Arrays Technology (DArT) and DArTSeq markers were employed for marker–trait association**
- **The whole set of SHW lines (320) were genotyped with DArT markers;**
- **genomic DNA was extracted from 2-week-old seedlings using pooled leaf samples from five individual plants, frozen in liquid nitrogen, and stored at -80 C before DNA extraction. DNA extraction was carried out according to Ogbonnaya et al. (2001), after which 10 ll of a 100 ng ll-1 DNA of each sample was sent to Triticarte Pty. Ltd. Australia (http://www.triticarte.com.au) as a commercial service provider for whole-genome scan using DArT markers (White et al. 2008).**

- **A subset of only 173 SHW were genotyped with DArTseq, a genotyping by sequencing (GBS) approach.**
- **The full description of the DArTseq procedure was previously given in (Sehgal et al. 2015). Only markers with minor allele frequency (MAF)[5 % and missing data\20 % were selected for further analyses. The subset with 173 SHW genotypes was used for the main association test, while the remaining 147 SHW cross-validation set genotyped with DArT markers only was used to confirm the presence of some of the detected QTL as they are related to the main set.**

RESULTS

- **74 markers associated with 35 quantitative trait loci (QTL) were found to be significantly linked with disease**
- **resistances using a unified mixed model (P = 10-3 to 10-5); Of these 15 QTL originated from D genome. Six markers on 1BL, 3BS, 4BL, 6B, and 6D conferred resistance to two diseases …… 11 QTL detected in the previous 173 SHW. …..**
- **In addition, gene–gene interactions between significantly associated loci and all loci across the genome revealed five significant interactions at FDR\0.05. + more**

Source:

Genomic regions conferring resistance to multiple fungal pathogens in synthetic hexaploid wheat

Abdulqader Jighly et al. Mol Breeding (2016) 36:127 DOI 10.1007/s11032-016-0541-4

Chickpea

- Used high throughput marker systems for GWAS in chickpea using DArTseq and GBS.
  - (found the output is much better than the classical markers used before such as AFLP and SSR.)

Future plan

- Genotyping of Barley/Wheat for GWAS

- For GBS, it is also possible to be developed not only for crops but also for different organisms such as pathogens, insects, weeds…etc. Hopefully we can have it soon in our laboratory.

- For SNP data management, we don’t have system to share these data in a public database yet.