Advances in Crop Science and Technology

Beyrouthy, Adv Crop Sci Tech 2014, 2:1
http://dx.doi.org/10.4172/2329-8863.1000e110

Editorial Open Access

Genomic Approaches of Crops Genetic Diversity

Marc El Beyrouthy*, Alain Abi-Rizk and Lara Hanna Wakim

Faculty of Agricultural and Food Sciences, University of the Holy Spirit of Kaslik, Lebanon

Way before the advances of crops genomic biotechnologies, pedigree and geographical distribution analyses of plants were used for the evaluation of genetic diversities [1] and crops were profiled using only morphology and phenotypic aspects [2].

For thousands of years, crop genetic diversity (the variation of the genes within a crop species), was the only result of domestication and practices of crop production with relatively few and genetically similar high-yielding cultivars [3]. Nowadays, and since food security and availability are threatened by the incapability of crops to quickly adapt to changing environmental conditions and increasing food demand [4], many efforts were made to enhance the genetic diversity of elite breeding pools using mutants, landraces, and/or wild species closely related to the cultivated crop.

The development of the molecular marker techniques has been useful for genotyping analysis [5], determination of phylogenetic relationships, population structure, map-based cloning, QTL (Quantitative Trait Loci) mapping and MAS (Marker Assisted Selection). But these techniques do not seem very suitable for measuring the adaptive genetic diversity of crops [6]. Therefore, diversity analysis should be based on functional genes or whole-genome sequences.

From the early 90's and till today, only few plants and crops genomes have been sequenced [7] and are presented in genome-based databases that incorporate many levels and types of information such as the QTLs, mutants, physical maps, expression data, markers, and genetic diversity. In fact, the decreasing quality of genome sequences makes the organization of the data very difficult. The more fragmented is the genome; the more difficult is the creation of a useful database with exploitable information.

In the last decade, the application of NGS (Next-Generation Sequencing) technologies started to be widely applied for the re-sequencing of crop species that have a complete reference genome sequence. It was mainly used for finding SNPs suitable as DNA markers [8], examination of selection patterns either in advanced populations or during domestication [9,10], or finding functional alleles [11]. In fact, the objective for re-sequencing genomes within a species is to understand the molecular basis for "phenotype–genotype" relationships.

However, *de novo assembly* (not requiring a reference genome) using NGS with short-read lengths seems not very suitable for crops genome sequencing due to the high complexity of most plant genomes as a result of extensive duplication and the presence of repeat sequences [12].

While Genome-wide SNP genotyping is a powerful tool for evolutionary studies and association mapping [13], community-developed SNP panels present limited utility in wider sets of germ plasm. But, genotyping by sequencing will overcome these limitations and afford many more polymorphic markers [14].

Diversity panels of genotypes presented in a particular species with reference genome sequences using NGS technologies will provide a platform for understanding existing genetic diversity, phenotypes with their related genes and exploiting natural genetic diversity to help develop greater genotypes. In order to do this effectively, extensive phenotypic data must be collected for the diversity panels and combined with re-sequencing data [15].

It is important to know that collecting phenotypic data remains the most complicated task for effective use of genomics technologies in advanced plant improvement. Phenotypic traits need an experienced eye and a skilled hand to score them effectively and consistently. Therefore, phenomics (mass collection of phenotypes) has not kept pace as in genomics and nowadays few people are being trained to collect relevant phenotypes [16].

Engineers and plant scientists must create new platforms to rapidly and accurately collect phenotypes on thousands of plants at a time before combining it to genomic approaches.

Improvements are being made, but equal advances in phenomics and genomics are needed in order to meet the world challenges on food security and availability.

References

1. Hammer K (2003) A paradigm shift in the discipline of plant genetic resources. Genetic Resources and Crop Evolution 50: 3–10.
2. Gilbert JE, Lewis RV, Wilkinson MJ, Caligari PDS (1999) Developing an appropriate strategy to assess genetic variability in plant germplasm collections. Theoretical and Applied Genetics 98: 1125–1131.
3. Hyten DL, Song Q, Zhu Y, Choi I-Y, Nelson RL, Costa et al. (2006) Impacts of genetic bottlenecks on soybean genome diversity. Proceedings of the National Academy of Sciences, USA 103: 16666–16671.
4. Turner WR, Oppenheimer M, Wilcove DS (2009) A force to fight global warming. Nature 462: 278–279.
5. Tanksley SD, McCouch SR (1997) Seed banks and molecular maps: unlocking genetic potential from the wild. Science 227:1063–1066.
6. Moose SP, Mumm RH (2008) Molecular plant breeding as the foundation for 21st century crop improvement. Plant Physiology 147: 969–977.
7. Michael TP, Jackson S (2013) The first 50 plant genomes. The Plant Genome 6.
8. You FM, Huo N, Deal KR, Gu YQ, Luo MC, McGuire, et al. (2011) Annotation-based genome-wide SNP discovery in the large and complex Aegilopstauschii genome using next-generation sequencing without a reference genome sequence. BMC Genomics 12: 59.
9. Gore MA, Chia JM, Elshire RJ, Sun Q, Ersoz ES, et al. (2009) A first-generation haplotype map of maize. Science 326: 1115–1117.

***Corresponding author:** Marc El Beyrouthy, Faculty of Agricultural and Food Sciences, University of the Holy Spirit of Kaslik, Lebanon, Tel: +961 9 600878; E-mail: marcelbeyrouthy@usek.edu.lb

Received Januar 09, 2014; **Accepted** Januar 11, 2014, 2014; **Published**Januar 13, 2014

Citation: Beyrouthy MEl, Abi-Rizk A, Wakim LH (2014) Genomic Approaches of Crops Genetic Diversity. Adv Crop Sci Tech 1: e110. doi:10.4172/2329-8863.1000e110

10. McMullen MD, Kresovich S, Villeda HS, Bradbury P, Li H, et al. (2009) Genetic properties of the maize nested association mapping population. Science 325: 737–740.
11. Yan J, Kandianis CB, Harjes CE, Bai L, Kim EH, et al. (2010) Rare genetic variation at Zea mays crtRB1 increases beta-carotene in maize grain. Nature Genetics 42: 322–327.
12. Varshney RK, Nayak SN, May GD, Jackson SA (2009) Next-generation sequencing technologies and their implications for crop genetics and breeding. Trends in Biotechnology 27: 522–530.
13. Akhunov E, Nicolet C, Dvorak J (2009) Single nucleotide polymorphism genotyping in polyploid wheat with the IlluminaGoldengate assay. Theoretical and Applied Genetics 119: 507–517.
14. Huang X, Wei X, Sang T, Zhao Q, Feng Q, et al. (2010) Genome-wide association studies of 14 agronomic traits in rice landraces. Nature Genetics 42: 961–967.
15. Paterson AH, Freeling M, Tang H, Wang X (2010) Insights from the comparison of plant genome sequences. Annual Review of Plant Biology 61: 349–372.
16. Jackson S A, Iwata A, Lee S H, Schmutz J, Shoemaker R (2011) Sequencing crop genomes: approaches and applications. New Phytologist, 191: 915-925.

Citation: Beyrouthy MEl, Abi-Rizk A, Wakim LH (2014) Genomic Approaches of Crops Genetic Diversity. Adv Crop Sci Tech 1: e110. doi:10.4172/2329-8863.1000e110