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Universal Molecular Markers for Plant Breeding and Genetics Analysis

Shirish A Ranade* and Hemant Yadav

Genetics and Molecular Biology Division, CSIR-National Botanical Research Institute (CSIR-NBRI), India

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Plant breeding, like several other classical fields of R&D in plant sciences has also been substantially influenced by the development and use of molecular markers. These markers have been found to be powerful tools for wide ranging applications in many plant breeding areas, notably, identification and analysis of quantitative/qualitative trait loci (QTLs) and their positioning on linkage maps; cloning of genes for desirable traits based on the molecular linkage maps; gene pyramiding and Marker-assisted selection (MAS), the determination and analysis of genetic diversity within germplasms and other plant collections and analysis of genome structures for several crop plants [1-4]. As applied in breeding programs, the molecular markers help to accelerate the incorporation of genes that control or contribute to the variation of the target traits and also provide reliable information of kinship and phylogeny between species. Considerable progress and achievements in the area of molecular marker research have been reported for more than three decades now, ever since the first molecular marker application as a RFLP was reported by Botstein et al. [5]. Increasing applications of molecular markers and progressive improvements to the various technologies involved have also ensured that the molecular markers continue to be deployed for plant breeding work regularly [1-3,6-8]. Since the proposition of the concept in 1980, various types of molecular markers such as RFLP, RAPD, AFLP, SSR, SNP among others have been developed [5,9-15]. These markers vary in their resolution power, genome coverage and linkage or otherwise to loci controlling traits of relevance to the breeder. Likewise, these markers have also varying levels of complexities of experimental designs, ease of field level application and the need for advanced skill sets and resources for successful application in breeding strategies. Successful applications of these markers have depended on their deployment as markers of choice based on exhaustive studies over a large time period (more than 3 decades) and across a large number of crop plants. These markers have been developed as general markers while at the same time we also now have specific sets of molecular for specific crops that can be deployed with ease and high efficiency anywhere in the world.

In the recent years, with an increasing availability of completely sequenced genomes, the single nucleotide polymorphism and structural variations in sequenced genomes have been used to develop highly reliable molecular markers [12]. The development of a high density of molecular markers as well as the determination of entire genomic nucleotide sequences of many closely related plants has generated an interesting spin-off that enables a comparative study of these markers, genome sequences and organization of the markers along the genomes. Such comparative studies have revealed surprisingly high levels of conservation of numbers or orders or locations of the loci and markers in these related plants. This has opened out new vistas for species that have not yet been sequenced, but can still be tested for marker co-linearity or synteny relative to those of the known genomes [16,17]. As revealed through the comparison of genomes between different plants, orthologous genes to a certain extent conserve synteny and co-linearity in the chromosomes [16]. The establishment of the co-linearity or synteny of the order and numbers of loci along the chromosomes immediately suggests the possibility of exploiting these co-linear or synteny states of one or more known genomes to derive corresponding information from an unknown but related genome. Indeed, Wu and co-workers have developed universal primers in *solanaceous* species with single-copy orthologs (COSII), and successfully applied COSII to the study of syntenic relationships among tomato, eggplant, pepper, and *Nicotiana* [18-21]. These results have a great significance for the analysis of those genomes where marker and sequence density is scarce or lacking but is available in case of a related taxon [22-24]. Thus, if one were to consider a crop plant for molecular breeding work, say for instance, the cluster bean (*Cyamopsis tetragonoloba*) or any other leguminous crops, where such data are scanty or altogether lacking, it is now possible to deploy markers and genome sequence derived orthologs from the sequenced *leguminous* taxon closest in relation to these crops with no or little genome sequence data to achieve an unprecedented level of rich marker density in a much shorter period of time than that it would otherwise have taken to develop *de novo* the entire set of marker data. This possibility of developing markers universally based on markers and sequences of orthologs of a related sequenced genome is exciting in its potential application to even trees which have always been less studied for molecular breeding on account of their long generation times. Several papers have highlighted the existence of gene and marker synteny across taxa. The important rationale here is the derivation of present day genomes from an ancestral one during the course of evolution. That this has happened is the basis for the several phylogenetic and phylogenomic studies reported so far in plants. Tracing the evolutionary history of the genome is in fact based on the synteny / co linearity of genes and gene orders. It is because of the expectation of a synteny that it also becomes easy to identify deviations from the synteny that occasionally occurs due to transposition, mutations recombination events so that certain portions of the genome or even single gens may be a mosaic or chimera of elements with more than one ancestral lineage. Such regions become the landmarks relative to which rest of the genome can be aligned and assessed for co linearity. This is another R&D area where advancement has been enabled by the deployment of molecular markers. Thus not just specific traits alone, but also for larger parts of the genome, the molecular markers have important roles to play, often as specific landmarks within a genome.

The advancement in next generation genome sequencing (NGS) technologies have made it a realistic and viable proposition to develop new molecular markers based on the genome sequence data [25-29]. As is evident from the several excellent reviews about the NGS technologies, the extent of throughput, volume of data and cost per sequencing are related with increasingly favorable trends such that

***Corresponding author:** Shirish A Ranade, Genetics and Molecular Biology Division, CSIR-National Botanical Research Institute (CSIR-NBRI), India, Tel: 91-522-2297-949; E-mail: shirishranade@gmail.com

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the costs are decreasing while at the same time generated data is increasing qualitatively as well as quantitatively. It thus a realistic scenario to envisage the age of "universal markers" [30] rather than that of individual taxon markers that the next few years promise to unfold. Surely any and all technological advancements that make this scenario that much more realizable are welcome.

References

1. Mohan M, Nair S, Bhagwat A, Krishna TG, Yano M, et al. (1997) Genome mapping, molecular markers and marker-assisted selection in crop plants. Mol Breed 3:87-103
2. Bagge M, Xia X, Lübberstedt T (2007) Functional markers in wheat. CurrOpin Plant Biol 10: 211-216.
3. Peleman JD, van der Voort JR (2003) Breeding by design. Trends Plant Sci 8: 330-334.
4. Deschamps S, Llaca V, May GD (2012) Genotyping-by-Sequencing in Plants. Biology 1:460-483
5. Botstein D, White RL, Skolnick M, Davis RW (1980) Construction of a genetic linkage map in man using restriction fragment length polymorphisms. Am J Hum Genet 32: 314-331.
6. Kowalski SP, Lan TH, Feldmann KA, Paterson AH (1994) Comparative mapping of Arabidopsis thaliana and Brassica oleracea chromosomes reveals islands of conserved organization. Genetics 138: 499-510.
7. Lin L, Tang H, Compton RO, Lemke C, Rainville LK, et al. (2011) Comparative analysis of Gossypium and Vitis genomes indicates genome duplication specific to the Gossypium lineage. Genomics 97: 313-320.
8. Liu HL, Lin YA, Chen GB, Shen YO, Liu J, et al. (2012) Genome-scale identification of resistance gene analogs and the development of their intron length polymorphism markers in maize. Mol Breed 29:437-447
9. Williams JG, Kubelik AR, Livak KJ, Rafalski JA, Tingey SV (1990) DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. Nucleic Acids Res 18: 6531-6535.
10. Vos P, Hogers R, Bleeker M, Reijans M, van de Lee T, et al. (1995) AFLP: a new technique for DNA fingerprinting. Nucleic Acids Res 23: 4407-4414.
11. Becker J, Heun M (1995) Barley microsatellites: allele variation and mapping. Plant MolBiol 27: 835-845.
12. Ganal MW, Altmann T, Röder MS (2009) SNP identification in crop plants. CurrOpin Plant Biol 12: 211-217.
13. Wang X, Zhao X, Zhu J, Wu W (2005) Genome-wide investigation of intron length polymorphisms and their potential as molecular markers in rice (Oryza sativa L.). DNA Res 12: 417-427.
14. Yang L, Jin G, Zhao X, Zheng Y, Xu Z, et al. (2007) PIP: a database of potential intron polymorphism markers. Bioinformatics 23: 2174-2177.
15. Tang DQ, Lu JJ, Fang W, Zhang S, Zhou MB (2010) Development, characterization and utilization of GenBank microsatellite markers in Phyllostachyspubescens and related species. Mol Breed 25:299-311
16. Tang H, Bowers JE, Wang X, Ming R, Alam M, et al. (2008) Synteny and collinearity in plant genomes. Science 320: 486-488.
17. Chen SY, Lin YT, Lin CW, Chen WY, Yang CH, et al. (2010) Transferability of rice SSR markers to bamboo. Euphytica 175:23-33
18. Wu FN, Muller LA, Crouzillat D, Petiard V, Tanksley SD (2006) Combining bioinformatics and phylogenetics to identify large sets of single-copy orthologous genes (COSII) for comparative, evolutionary and systematic studies: a test case in the euasterid plant clade. Genetics 174:1407–1420.
19. Wu FN, Eannetta NT, Xu YM, Durrett R, Mazourek M, et al.(2009) A COSII genetic map of the pepper genome provides a detailed picture of synteny with tomato and new insights into recent chromosome evolution in the genus Capsicum. Theor Appl Genet 118:1279–1293
20. Wu F, Eannetta NT, Xu Y, Tanksley SD (2009) A detailed synteny map of the eggplant genome based on conserved ortholog set II (COSII) markers. Theor Appl Genet 118: 927-935.
21. Wu F, Eannetta NT, Xu Y, Plieske J, Ganal M, et al. (2010) COSII genetic maps of two diploid Nicotiana species provide a detailed picture of synteny with tomato and insights into chromosome evolution in tetraploid N. tabacum. TheorAppl Genet 120: 809-827.
22. Quraishi UM, Abrouk M, Bolot S, Pont C, Throude M, et al. (2009) Genomics in cereals: from genome-wide conserved orthologous set (COS) sequences to candidate genes for trait dissection. FunctIntegr Genomics 9: 473-484.
23. Liu L, Li Y, Li S, Hu N, He Y, et al. (2012) Comparison of next-generation sequencing systems. J Biomed Biotechnol 2012: 251364.
24. Liu H, Guo X, Wu J, Chen GB, Ying Y (2013) Development of universal genetic markers based on single-copy orthologous (COSII) genes in Poaceae. Plant Cell Rep 32: 379-388.
25. Zhou X, Ren L, Meng Q, Li Y, Yu Y, et al. (2010) The next-generation sequencing technology and application. Protein Cell 1: 520-536.
26. Suzuki S, Ono N, Furusawa C, Ying BW, Yomo T (2011) Comparison of sequence reads obtained from three next-generation sequencing platforms. PLoS One 6: e19534.
27. Henry RJ, Edwards M, Waters DL, Gopala Krishnan S, Bundock P, et al. (2012) Application of large-scale sequencing to marker discovery in plants. J Biosci 37: 829-841.
28. Quail MA, Smith M, Coupland P, Otto TD, Harris SR, et al. (2012) A tale of three next generation sequencing platforms: comparison of Ion Torrent, Pacific Biosciences and Illumina Mi Seq sequencers. BMC Genomics 13: 341.
29. Zalapa JE, Cuevas H, Zhu H, Steffan S, Senalik D, et al. (2012) Using next-generation sequencing approaches to isolate simple sequence repeat (SSR) loci in the plant sciences. Am J Bot 99: 193-208.
30. Chapman MA, Chang J, Weisman D, Kesseli RV, Burke JM (2007) Universal markers for comparative mapping and phylogenetic analysis in the Asteraceae (Compositae). Theor Appl Genet 115: 747-755.