

## **Genomics Interventions in Crop Breeding for Sustainable Agriculture**

Pawan L Kulwal, Mahendar Thudi, Rajeev K Varshney

\*Author for correspondence:

[r.k.varshney@cgiar.org](mailto:r.k.varshney@cgiar.org)

## **Genomics Interventions in Crop Breeding for Sustainable Agriculture**

**In: Encyclopedia of Sustainability Science and Technology**

**This is author version postprint archived in the official open access repository of ICRISAT [www.icrisat.org](http://www.icrisat.org)**

# Genomics Interventions in Crop Breeding for Sustainable Agriculture

Pawan L Kulwal<sup>1</sup>, Mahendar Thudi<sup>2</sup>, Rajeev K Varshney<sup>2,3,4,\*</sup>

<sup>1</sup>State Level Biotechnology Centre, Mahatma Phule Agricultural University, Rahuri-413722, District- Ahmednagar (MS), India

<sup>2</sup>Centre of Excellence in Genomics (CEG), International Crops Research Institute for the Semi-Arid Tropics, Patancheru- 502324, Hyderabad (AP), India

<sup>3</sup>Genomics Towards Gene Discovery Subprogramme, Generation Challenge Programme (GCP), CIMMYT, Int APDO Postal 6-641, 06600 Mexico DF, Mexico

<sup>4</sup>School of Plant Biology (M084), Faculty of Natural and Agricultural Sciences, The University of Western Australia, 35 Stirling Highway, Crawley, WA 6009, Australia

\* Author for correspondence: r.k.varshney@cgiar.org

Article outline (Table of contents)

Glossary

Introduction and importance of sustainable agriculture

Contribution of plant genomics technology to agricultural sustainability

Some modern breeding approaches

Challenges in adoption of genomics technologies

Future directions

Bibliography

## **Glossary**

*Association mapping* — is a high-resolution method for mapping quantitative trait loci (QTLs) or gene(s) for traits of interest based on linkage disequilibrium (LD) and holds great promise for the dissection of complex genetic traits.

*Back cross (BC)* — is a cross of the  $F_1$  with either of the parental genotype and the resultant progeny is called  $BC_1$ . The progeny of the cross between  $BC_1$  and the recurrent parent is called as  $BC_2$ .

*Gene pyramiding* — is a process of accumulating the favorable genes/alleles from different genotypes into an elite/ commercial cultivar. Gene pyramiding is often performed through marker-assisted selection (MAS).

*Genome-wide selection or genomic selection (GS)* — is a concept for accelerating genetic gain especially for complex traits in elite genotypes by utilizing genomic information and estimating their breeding values in breeding strategies. GS is becoming very popular over marker-assisted selection that was focused on few individual genes or few QTLs to improve genotypes especially when recent advances in genomic technologies have drastically reduced the cost on marker genotyping.

*Genomics-assisted breeding (GAB)* —is a holistic approach, where genomics technologies including molecular markers, transcriptomics, metabolomics, proteomics, bioinformatics and phenomics are integrated with conventional breeding strategies for

breeding crop plants resistant/ tolerant to biotic and abiotic stresses or improved for quality and yield.

*Haplotype* —is a set of alleles of closely linked loci on a chromosome that tend to be inherited together.

*Linkage disequilibrium (LD)* —is a non-random association of alleles at different loci, describing the condition with non-equal (increased or reduced) frequency of the haplotypes in a population at random combination of alleles at different loci. LD is not the same as linkage, although tight linkage may generate high levels of LD between alleles.

*Marker-assisted selection (MAS)* — is a process of indirect selection for improving the traits of interest by employing morphological, biochemical or DNA-based markers. DNA based markers/ molecular markers, in the recent past were proven to be the markers of choice for MAS.

*Narrow genetic base* — does frequently exists in modern crop cultivars or breeding lines due to the continuous use of small number of elite genotypes in breeding programs. In fact, it is a serious obstacle to sustain and improve crop productivity due to rapid vulnerability of genetically uniform cultivars to emerging biotic and abiotic stresses.

*Next generation sequencing (NGS)* technologies — include various novel sequencing technologies for example 454/FLX (Roche Inc.), ABI SOLiD (Applied Biosystems), Solexa (Illumina Inc.) etc. that have surpassed traditional Sanger sequencing in throughput and in cost-effectiveness for generating large-scale sequence data.

*Polygenes* —are a group of non-allelic genes, each having a small quantitative effect, that together produce a wide range of phenotypic variation.

*Quantitative trait loci (QTLs)* —are the loci or regions in the genome that contribute towards conferring tolerance to abiotic stresses (e.g. drought, salinity) or resistance to biotic stresses (e.g. fungal, bacterial, viral diseases) or improving agronomic traits (e.g. yield, quality) which are generally controlled by polygenes and greatly depend on gene  $\times$  environmental ( $G \times E$ ) interactions.

*Sustainable agriculture* —refers to efficient agricultural production while maintaining the environment, farm profitability and prosperity of farming communities.

*Sustainable development* —is defined as balancing the fulfillment of human needs with the protection of the environment so that these needs can be met not only at the present time, but also in the future.

## **1. Definition of the subject**

There has been significant improvement in production and productivity of important cereal crops globally as a consequence of the “Green Revolution” and other initiatives (1). However, today the stage has reached that the available traditional methods of crop improvement are not sufficient to provide enough and staple food grains to the constantly growing world population (2). This situation is projected to be worse by the year 2050 especially in context of climate change (3). In other words, the conventional plant breeding practices may not be able to achieve the sustainability in today’s agriculture.

It is under such circumstances, that advances in plant genomics research are opening up a new era in plant breeding where the linkage of genes to specific traits will lead to more efficient and predictable breeding programmes in future. Several initiatives have been started towards use of genomics technologies in number of crop plants to ensure the sustainable production of healthy and safe crops and the results are encouraging. It is therefore expected that the genomics will be the integral part of the agricultural/ plant breeding practices in future for improving crop productivity leading to achieve food security and sustainable production.

## **2. Introduction and importance of sustainable agriculture**

The goal of agricultural science is to increase crop productivity coupled with the quality of the products, and maintain the environment (1). Food security is a growing concern worldwide and more than 1 billion people are estimated to lack sufficient dietary energy

availability (2). The issue of “food security” has become so important that prominent scientific journals including Science have also published a special issue on this subject recently (February 12, 2010 issue). With the current rate of growth, the global population is likely to plateau at some 9 billion people by roughly the middle of this century (3). With this ever-increasing human population and amidst the fear of shrinking resources in terms of cultivable area, irrigation resources, newly emerging insect pests, stagnated yields, etc., it has become difficult to maintain agricultural sustainability. In order to make today’s agriculture sustainable it is necessary that plant breeders adopt innovative technologies that can increase the efficiency of selection with more precision (4). Under such circumstances molecular approaches including modern genomics and genetic engineering technologies have emerged as powerful tools to assure rapid and precise selection for the trait(s) of interest. Maintaining effective and environmentally friendly agricultural practices is a necessary prerequisite for maintaining sustainability.

Plant genomics is a rapidly developing field, which is radically improving our understanding of plant biology by making available novel tools for the improvement of plant properties relevant to sustainable agricultural production. Recent advances in high-throughput genomics technologies including that of next generation sequencing and high-throughput genotyping have helped immensely in understanding the functions and regulation of genes in crop plants (5). The ever-increasing availability of genome sequences in crop plants have facilitated greatly the development of genomic resources that will allow us to address biological functions and a number of basic processes relevant to crop production leading to sustainable agriculture.

One of the myths linked to sustainable agriculture means going back to past techniques/ farm practices, which were followed by our ancestors. In fact, sustainable agriculture can be achieved by combining some of the wisdom of past practices, with careful use of current technology, including the vast array of information technologies now available. Sustainable agriculture is a key element of sustainable development and is essential to the future well-being of the human race and the planet. A compelling need exists for restorative and sustainable agriculture to help address the pressing trends of population, climate, energy, water, soil and food. Sustainable agriculture needs to be economically viable, environmentally sound and socially acceptable. In other words, it is a system of agricultural production that, over the long term, will: i) satisfy human food, feed and fibre needs; ii) enhance the environmental quality and the natural resource base upon which the agricultural economy depends; iii) make the most efficient use of available technologies, non-renewable resources and on-farm resources, and integrate, where appropriate, natural biological cycles and controls; iv) sustain the economic viability of farm operations; and v) enhance the quality of life for farmers and society as a whole.

There are various components of sustainable agriculture, which include technological interventions, environmental and socio-economic factors. As the factors related to socio-economics and environments have been discussed in a number of reviews earlier, in this article, we focus on the interventions of plant genomics technologies in crop breeding.



### **3. Contribution of plant genomics technology to agricultural sustainability**

Plant genomics technologies have contributed immensely in today's agriculture which has led to better understanding of how plants function, and how they respond to the environment. This has also helped in achieving targeted objectives in breeding programs to improve the performance and productivity of crops. The DNA based molecular markers has facilitated smarter and knowledge based breeding, by enabling early generation selection for key traits, thus reducing the need for extensive field selection. Besides this, the molecular tools can effectively be used for the characterization, conservation and use of genetic resources.

Recent advances made in the area of molecular biology and bioinformatics offer substantial opportunities for enhancing the effectiveness of classical plant breeding programs. These tools can be integrated into breeding work in order to analyze efficiently high numbers of crosses at the early seedling stage. This approach is known as 'genomics-assisted breeding' (6). Through this approach, both the phenotype and the genotype of new varieties can be analyzed and the performance of new specific introgressed traits can be predicted. The goals of the integration of these technologies in classical breeding are to create genotype-to-phenotype trait knowledge for breeding objectives and to use this knowledge in product development and deployment for the resource poor farmer.

For successful utilization of genomics-assisted breeding approach in a crop, availability of basic molecular tools such as molecular markers, genetic maps, etc. is a pre-requisite.

Among molecular markers, though a variety of molecular markers such as restriction fragment length polymorphism (RFLP), randomly amplified polymorphic DNA (RAPD), microsatellite or simple sequence repeat (SSR), amplified fragment length polymorphism (AFLP), single nucleotide polymorphism (SNP) markers have been developed in a range of crops, SSR and SNP markers have emerged as the markers of choice (7-8). Because of advent of NGS technologies (5) and high-throughput genotyping platforms, SNP marker system and array-based genotyping platforms are becoming more popular (9-10). An overview on availability of genomic resources in some selected important crop species is shown in Table 1. It is evident that cereal crops especially rice, maize, wheat, barley etc. are on top in terms of availability of genomic resources (see 11). Genome sequences have already become available for several crop species including rice (<http://rgp.dna.affrc.go.jp/IRGSP/>), sorghum (12) and maize (<http://gbrowse.maizegdb.org/cgi-bin/gbrowse/maize/>). Recent investments coupled with advances in genomics technologies have contributed towards developing a good resource of genomic tools in legumes as well (13, 14).

#### **4. Some modern breeding approaches**

The availability of genomic resources in almost all important crops combined with information on pedigrees as well as optimized methods of precise phenotyping make it possible to undertake genomics-assisted breeding approaches for crop improvement. In fact, some molecular breeding approaches like Advanced-Backcross QTL (AB-QTL) analysis, marker-assisted selection (MAS) have been successfully employed in several crops leading to improved cultivars, some other approaches such as marker-assisted

**Table 1: Genomic resources among selected cereals and legumes**

Crop plant	Molecular markers (SSRs and SNPs)	Molecular maps (Genetic/ QTL map/ comparative/ physical maps)	Transcript data and expression profiling	Genome sequence data
Rice	++++ <sup>1</sup>	++++ <sup>2,3</sup>	++++ <sup>4</sup>	++++ <sup>5</sup>
Maize	++++ <sup>6</sup>	++++ <sup>2,7,8</sup>	++++ <sup>4</sup>	++++ <sup>9</sup>
Wheat	+++ <sup>10</sup>	+++ <sup>2,11,12</sup>	+++ <sup>4</sup>	++ <sup>14</sup>
Sorghum	+++ <sup>15</sup>	++++ <sup>2,16</sup>	+++ <sup>4</sup>	++++ <sup>17</sup>
Barley	+++ <sup>18</sup>	+++ <sup>19</sup>	+++ <sup>4,20</sup>	+++ <sup>21</sup>
Soybean	++++ <sup>22,23</sup>	+++ <sup>24,25,26</sup>	+++ <sup>27</sup>	++++ <sup>28</sup>
Groundnut	++ <sup>29</sup>	+ <sup>30</sup>	+ <sup>27</sup>	-
Cowpea	+++ <sup>29</sup>	++ <sup>30</sup>	+ <sup>27</sup>	-
Common bean	++ <sup>29</sup>	++ <sup>30</sup>	+ <sup>27</sup>	-
Chickpea	+++ <sup>29</sup>	++ <sup>30</sup>	+ <sup>27</sup>	-
Pigeonpea	+++ <sup>29</sup>	-	-	-

+ = Very few

+ + = Few

+ + + = Moderate

+ + + + = Abundant

<sup>1</sup> <http://www.gramene.org/markers/index.html>

<sup>2</sup> <http://www.gramene.org/cmap/>

<sup>3</sup> [http://www.gramene.org/db/qtl/qtl\\_display?query=&search\\_field=&species=Oryza+sativa&submit=Submit](http://www.gramene.org/db/qtl/qtl_display?query=&search_field=&species=Oryza+sativa&submit=Submit)

<sup>4</sup> [http://www.ncbi.nlm.nih.gov/dbEST/dbEST\\_summary.html](http://www.ncbi.nlm.nih.gov/dbEST/dbEST_summary.html) ; <http://compbio.dfci.harvard.edu/tgi/plant.html>

<sup>5</sup> [http://www.gramene.org/Oryza\\_sativa/Info/Index](http://www.gramene.org/Oryza_sativa/Info/Index)

<sup>6</sup> <http://www.maizegdb.org/probe.php>

<sup>7</sup> <http://www.maizegdb.org/map.php>

<sup>8</sup> [http://www.gramene.org/db/qtl/qtl\\_display?query=\\*&search\\_field=trait\\_name&species=Zea+mays+subsp.+mays&submit=Submit](http://www.gramene.org/db/qtl/qtl_display?query=*&search_field=trait_name&species=Zea+mays+subsp.+mays&submit=Submit)

<sup>9</sup> [http://www.maizesequence.org/Zea\\_mays/Info/Index](http://www.maizesequence.org/Zea_mays/Info/Index)

<sup>10</sup> <http://wheat.pw.usda.gov/cgi-bin/graingenes/browse.cgi?class=marker>

- <sup>11</sup><http://wheat.pw.usda.gov/GG2/maps.shtml#wheat>
- <sup>12</sup>[http://wheat.pw.usda.gov/cgi-bin/graingenes/quickquery.cgi?query=qtls&arg1=\\*](http://wheat.pw.usda.gov/cgi-bin/graingenes/quickquery.cgi?query=qtls&arg1=*)
- <sup>14</sup><http://wheat.pw.usda.gov/cgi-bin/graingenes/search.cgi?class=sequence>
- <sup>15</sup>[http://www.gramene.org/db/markers/marker\\_view?marker\\_name=&marker\\_type\\_id=&taxonomy=sorghum&action=marker\\_search&x=0&y=0](http://www.gramene.org/db/markers/marker_view?marker_name=&marker_type_id=&taxonomy=sorghum&action=marker_search&x=0&y=0)
- <sup>16</sup>[http://www.gramene.org/db/cmap/map\\_set\\_info?species\\_acc=sorghum&map\\_type\\_acc=-1](http://www.gramene.org/db/cmap/map_set_info?species_acc=sorghum&map_type_acc=-1)
- <sup>17</sup>Paterson et al. 2009, Nature 457, 551-556
- <sup>18</sup><http://wheat.pw.usda.gov/GG2/Barley/>
- <sup>19</sup><http://wheat.pw.usda.gov/GG2/maps.shtml#barley>
- <sup>20</sup>[http://wheat.pw.usda.gov/cgi-bin/graingenes/browse.cgi?class=sequence&query=barley1\\_\\*](http://wheat.pw.usda.gov/cgi-bin/graingenes/browse.cgi?class=sequence&query=barley1_*)
- <sup>21</sup><http://www.public.iastate.edu/~imagefpc/IBSC%20Webpage/IBSC%20Template-home.html>
- <sup>22</sup><http://soybeanbreederstoolbox.org/>
- <sup>23</sup><http://soybase.org/BARCSOYSSR/index.php>
- <sup>24</sup><http://lis.comparative-legumes.org/cgi-bin/cmap/viewer?changeMenu=1>
- <sup>25</sup>[http://soybeanbreederstoolbox.org/search/search\\_results.php?category=QTLName&search\\_term=](http://soybeanbreederstoolbox.org/search/search_results.php?category=QTLName&search_term=)
- <sup>26</sup><http://soybeanphysicalmap.org/>
- <sup>27</sup>[http://lis.comparative-legumes.org/lis/lis\\_summary.html?page\\_type=transcript](http://lis.comparative-legumes.org/lis/lis_summary.html?page_type=transcript)
- <sup>28</sup><http://www.phytozome.net/cgi-bin/gbrowse/soybean/?name=Gm09>
- <sup>29</sup>see Varshney et al. 2009, Curr Opin Plant Biol 12: 202–210
- <sup>30</sup>see Varshney et al. 2010, Plant Breed Rev 33: 257-304

recurrent selection (MARS) or genomic selection (GS) are being used in several crops (15, 16).

#### ***4.1 Marker-assisted selection (MAS)***

There are three major steps involved in MAS: (i) identification of molecular marker(s) associated with trait(s) of interest to breeders; (ii) validation of identified marker(s) in the genetic background of the targeted genotypes to be improved; and (iii) marker-assisted backcrossing (MABC) to transfer the QTL/gene from the donor genotype into the targeted genotype. In context of marker-trait association, linkage mapping has been extensively used for identifying the markers associated with a trait of interest in a range of crops including cereals, legumes, horticultural crops, etc. These studies have been reviewed in detail in several reviews (14, 17) and books (18). Although hundreds of studies have been undertaken, only a few studies were taken further to marker validation and MABC. This may be attributed to: i) identification of few markers associated with small-effect QTLs; ii) non-validation of markers in elite genotypes; and iii) slow adoption of markers by breeders in their breeding programs. Recent advances in association genetics, however, offer opportunities to overcome the first two constraints.

Association mapping (AM) is considered an alternative strategy to linkage mapping for identifying marker-trait associations and has been used extensively in human and animal systems. AM has a number of advantages over linkage mapping including the potential for increased QTL resolution, and an increased sampling of molecular variation (for reviews see 19, 20). AM involves studying a natural population rather than the offspring

of crosses, and associations in natural populations are typically on a much finer scale because they reflect historical recombination events. Several examples on marker-trait association using AM are available (21); however, there is a need for optimization of more advanced analytical tools in the area of association genetics (22). It is anticipated that because of reduction in costs on marker genotyping (10), AM will be extensively used for trait mapping in the future.

Once the markers associated with a trait of interest are identified through linkage mapping or AM, the next step is to use these markers in the breeding programs. In this context, the selection of one or a few genes (QTLs) through molecular markers using backcrossing is a very efficient technique (23, 24). Important advantages of MAS are that, it can be effectively utilized for traits with low heritability, for gene pyramiding, selection can be made at seedling stage and above all there are no issues involving GE crops (25). Although use of markers in breeding programs through MABC is a common practice in the private sector (26), MAS is in routine use in wheat and barley breeding programs in Australia (8, 27-29) and USA ([www.maswheat.ucdavis.edu](http://www.maswheat.ucdavis.edu); <http://barleycap.cfans.umn.edu/>). Nevertheless, there are several success stories in many crops including wheat, rice, barley, maize, soybean, etc. where MAS has successfully been utilized to develop superior lines/ varieties/ hybrids for improving quality, resistance to diseases or tolerance to abiotic stresses. For example, Gupta et al. (17) has recently summarized success stories of molecular breeding in wheat.

A widely discussed success story of molecular breeding is the introgression of the FR13A *Sub1* locus conferring resistance against submergence in an Asian rice cultivar, Swarna (30, 31) that can confer tolerance up to two weeks of complete submergence. This has offered big relief to the large number of Asian farmers where rice land is located in deltas and low-lying areas that are at risk from flooding during the monsoon season every year. Some selected examples of molecular breeding in rice and wheat (adopted from 16) are summarized in Table 2.

**Table 2: Some examples of improved cultivars or varieties developed through marker assisted introgression of important genes/QTLs in rice and wheat**

<b>Crop</b>	<b>Genes/QTL introgressed</b>	<b>Function</b>	<b>Variety developed/ released</b>	<b>Reference</b>
Rice	<i>GBSS</i>	Unique cooking and processing quality traits including amylose content	Cadet and Jacinto	33
	<i>Xa33t</i>	Bacterial blight resistance	BC <sub>3</sub> F <sub>2</sub>	34
	<i>Xa21</i>	Bacterial blight resistance	Zhongyou 6 and Zhongyou 1176	35
	<i>Sub1</i>	Submergence tolerance	BC <sub>3</sub> F <sub>2</sub>	30
	<i>Sub1</i>	Submergence tolerance	Samba Mashuri-Sub1 IR64-Sub1 TDK1-Sub1 CR1009-Sub1 BR11--Sub1	36
	<i>SUB1QTL</i>	Submergence tolerance	Sub1 introgression lines	37
	<i>Piz-5 + Xa21</i>	Blast and bacterial blight resistance	BC <sub>4</sub> F <sub>2</sub>	38
	<i>Xa4+xa5</i> and <i>Xa4+Xa7</i>	Bacterial blight resistance	Angke and Conde	39



	<i>xa7</i> and <i>Xa21</i>	Bacterial blight resistance	Zhenshan 97 × Minghui 63	40
	<i>xa13</i> and <i>xa21</i>	Bacterial blight resistance, strong aroma	Pusa 1460, IET 18990	41
	<i>xa13</i> and <i>Xa21</i>	Bacterial blight resistance	Improved Pusa RH1	42
	<i>xa5</i> , <i>xa13</i> and <i>Xa21</i>	Bacterial blight resistance	Improved PR106	43
	<i>Xa5</i> , <i>xa13</i> and <i>xa21</i>	Bacterial blight resistance	BC <sub>3</sub> F <sub>2</sub>	44
	<i>Xa5</i> , <i>Xa13</i> and <i>Xa 21</i>	Bacterial blight resistance	IET 19046	<a href="http://www.drricar.org/four_varieties.htm">http://www.drricar.org/four_varieties.htm</a>
	<i>Xa4</i> , <i>xa8</i> , <i>xa13</i> and <i>Xa21</i>	Bacterial blight resistance	BC <sub>1</sub> F <sub>3</sub>	45
	<i>Xa4</i> , <i>Xa5</i> , <i>Xa13</i> and <i>Xa21</i>	Improved bacterial blight resistance	Pusa 1526-04-25	<a href="http://www.iari.res.in/?q=node/233">http://www.iari.res.in/?q=node/233</a>
	-	Bacterial blight resistance	Xieyou 218	46
	QTL	Drought-tolerant aerobic rice	MAS 946-1	<a href="http://www.hindu.com/2007/11/17/stories/2007111752560500.htm">www.hindu.com/2007/11/17/stories/2007111752560500.htm</a>
	qSALTOL and qSUB1	Enhanced salt and submergence tolerance	F <sub>6</sub>	<a href="http://open.irri.org/sabrao/images/stories/conference/site/papers/apb09final00098.pdf">http://open.irri.org/sabrao/images/stories/conference/site/papers/apb09final00098.pdf</a>
	QTL	Improved	Birsa Vikas Dhan 111 (PY 84)	<a href="http://claria13.securesites.net/New">http://claria13.securesites.net/New</a>

		performance under drought		<a href="http://www.wheatworld.org/pdf/du/s/releases/2009/may/26018.htm">s/releases/2009/may/26018.htm</a>
Wheat	<i>QPhs.ccsu-3A.1</i> and <i>Lr24 + Lr28</i>	Pre-harvest sprouting tolerance and leaf rust resistance	BC <sub>3</sub> F <sub>3</sub>	47
	<i>Lr47</i>	Resistance to leaf rust	BIOINTA 2004	48
	<i>Gpc-B1</i>	High grain protein content	Lillian	49
	<i>Qfhs.ndsu-3AS</i>	Resistance to fusarium head blight	Bena	50
	<i>Sm1</i>	Resistance to the insect orange blossom wheat midge	Goodeve	51
	<i>Stb4</i>	Resistance to <i>Septoria</i>	Kern	<i>cited from 17</i>
	<i>Wsm-1</i>	Resistance to wheat streak mosaic virus (WSMV)	Mace	52
	<i>Yr15</i>	Seedling stripe rust	BC <sub>3</sub> F <sub>2:3</sub>	53
	<i>Qss.msub-3BL</i>	Resistance to wheat stem sawfly	McNeal, Reeder, Hank	<a href="http://www.wheatworld.org/pdf/du/bcovsky.pdf">http://www.wheatworld.org/pdf/du/bcovsky.pdf</a>
	<i>Bdv2</i>	Resistance to	Above, Avalanche, Ankor	<a href="http://www.wheatworld.org/pdf/du">http://www.wheatworld.org/pdf/du</a>

		yellow dwarf virus		<a href="#">bcovsky.pdf</a>
	<i>Yr17 and Lr37</i>	Stripe rust and leaf rust resistance	Patwin	54
	<i>CreX and CreY</i>	Cyst nematode resistance	F <sub>3</sub> progenies	55
	<i>Yr36 and Gpc-B1</i>	Resistant to stripe rust and high grain protein content	Westmore	56
	<i>Yr17 and Yr36</i>	Resistance to stripe rust	Lassik	<i>cited from 17</i>
	<i>Lr19 and Sr25</i>	Resistant to stem rust race UG99	UC1113 (PI638741)	57
	<i>Yr36 and Gpc-B1</i>	Resistance to stripe rust, high grain protein content	Farnum (WA7975)	<a href="http://www.ars-grin.gov/cgi-bin/npgs/acc/display.pl?1671746">http://www.ars-grin.gov/cgi-bin/npgs/acc/display.pl?1671746</a>
	<i>Yr15 and Gpc-B1</i>	Resistance to stripe rust and high grain protein content	Scarlet (WA7994)	<a href="http://css.wsu.edu/Proceedings/2005/2005_Proceedings.pdf">http://css.wsu.edu/Proceedings/2005/2005_Proceedings.pdf</a>
	<i>Lr1, Lr9, Lr24, Lr47</i>	Leaf rust resistance	BC <sub>1</sub> F <sub>2</sub>	58

#### ***4.2 Advanced-backcross (AB-QTL) analysis***

Although MAS has been quite successful, it has always been a difficult task to tackle linkage drag especially when a QTL or a gene is to be introgressed from wild/ exotic species. Furthermore, in MAS, QTL/gene discovery and variety development are two separate processes. To deal with this problem and to harness the potential of the wild/unadapted germplasm in breeding programs, a new approach referred as advanced backcross QTL (AB-QTL) analysis was proposed by Tanksley and Nelson (32). AB-QTL aims at simultaneous detection and transfer of useful QTLs from the wild/unadapted relatives to a popular cultivar for improvement of a trait. In this context, a superior cultivar / variety is crossed with a wild species leading to the production of a backcross population (BC<sub>2</sub>, BC<sub>3</sub>) and molecular markers are used to monitor the transfer of QTLs by conventional backcrossing. The advanced backcross approach has already been successfully utilized in different crops including tomato (59), rice (60, 61), barley (62) and wheat (63). It is anticipated that the use of AB-QTL will be accelerated in a range of crops for improving important traits such as disease resistance as well as yield traits.

#### ***4.3 Marker-assisted recurrent selection (MARS)***

In the majority of traits of interest quantitative variation is controlled by many QTLs each with minor effect. Moreover, minor QTLs show an inconsistent QTL effect in different environments and over different seasons. Even when the effect of these minor QTLs is consistent, their introgression into the desired genotype through MABC becomes extremely difficult as a larger number of progenies are required to select appropriate

lines. In such cases, MARS has been proposed for pyramiding of superior alleles at different loci/QTLs in a single genotype (64, 65).

It was demonstrated in recent studies that the response of MARS is larger when prior knowledge of the QTLs exist and the response decreases as the knowledge of the number of minor QTL associated with the trait decreases (66). In sweet corn, MARS was employed to fix six marker loci in two different F<sub>2</sub> populations which showed an increase in the frequency of marker allele from 0.50 to 0.80 (64). Similarly in a separate study, enrichment of rust resistance gene (*Lr34/ Yr18*) with an increase in frequency from 0.25 to 0.60 was reported in wheat BC<sub>1</sub> through MARS (28). MARS can be utilized effectively for selection of traits associated with multiple QTLs by increasing the frequency of favorable QTLs or marker alleles. Several companies are using MARS in their maize, soybean etc., breeding programs (66, 67). Recently, some institutes International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), the French Centre for International Agricultural Research (CIRAD) and the University of California- Riverside, USA have also initiated MARS programs in chickpea (PM Gaur, pers. commun.), sorghum (J-F Rami, pers. commun.), cowpea (J Ehlers, pers. commun.), etc. for pyramiding favorable drought tolerant alleles.

#### ***4.4 Genome-wide or Genomic Selection (GS)***

Although MAS has been practiced for the improvement of quantitative traits, it has its own limitations. Therefore in addition to MARS, Genomic Selection can be used to pyramid favourable alleles for minor effect QTLs at the whole genome level (68, 69).

Genomic selection predicts the breeding values of lines in a population by analyzing their phenotypes and high-density marker scores. A key to the success of GS is that, unlike MABC or MARS, it calculates the marker effects across the entire genome that explains the entire phenotypic variation. In simple terms genome-wide selection refers to marker based selection without significance testing and without identifying of a subset of markers associated with the trait (68). The genome wide marker data (marker loci or haplotypes) available or generated on the progeny lines, therefore, are used to calculate genomic estimated breeding values (GEBV) as the sum of the effects of all QTLs across the genome, thereby potentially exploiting all the genetic variance for a trait (68, 69). The GEBVs are calculated for every individual of the progeny based on genotyping data using a model that was 'trained' from the individuals of another training populations having both phenotyping and genotyping data. These GEBVs are then used to select the progeny lines for advancement in the breeding cycle. Thus GS provides a strategy for selection of an individual without phenotypic data by using a model to predict the individual's breeding value (69).

Recently, Wong and Bernardo (70) simulated, the comparative responses of phenotypic selection (PS), MARS, and GS with small population sizes in oil palm, and assessed the efficiency of each method in terms of years and cost per unit gain (i.e. the time and cost saved by these different methods over each other for making selection). They used markers significantly associated with the trait to calculate the marker scores in MARS, whereas all markers (without significance tests) to calculate the marker scores in GS. Responses to PS and GS were consistently greater than the response to MARS.

Furthermore, with population sizes of  $N = 50$  or  $70$ , responses to GS were 4–25% larger than the corresponding responses to PS, depending on the heritability and number of QTLs. In terms of economics, cost per unit gain was 26–57% lower with GS than with PS when markers cost US \$1.50 per data point, and 35–65% lower when markers cost \$0.15 per data point. Reduction in costs in sequencing and high-throughput marker genotyping may enhance uptake of GS for crop improvement in the future.

## **5. Challenges in adoption of genomic technologies**

Developing sustainable approaches to agriculture is one of the most difficult challenges facing growers and scientists today. Agricultural sustainability involves successful management of resources for agriculture to satisfy changing human needs, while maintaining or enhancing the quality of the environment and conserving natural resources (71). However, sustainable production is hampered by the decline in land and soil productivity as a result of inappropriate soil and water management and other agricultural practices, as well as misguided policies and frequent opposition to technological advances that have the potential to improve the quality of life of billions of people worldwide. This is in addition to the postulated challenges of climate change, the number of hazardous chemicals (pesticides and fungicides) which are constantly being released into the environment, and are becoming increasingly toxic to human and animal life (71). In recent years the use of promising biotechnology tools like genetic engineering (GE) has offered potential solutions to the above problems. However, the adoption of any new technique, particularly related to genetic engineering remains a policy matter and as mentioned above faces stiff opposition many a times. In a recent review, Farre et al. (25)

addressed several of these issues and advocated to overcome on the major barriers to adoption, which are political rather than technical, for realization of the potential of GE crops in developing countries.

It is thus obvious that the challenges facing agriculture are massive, particularly with the controversies over GE crops world over. It is clear that current methods of food production, in both the developing as well as the developed countries, are neither sufficient nor sustainable (72). Under these circumstances, genomics interventions have great role to contribute to sustainable agriculture. As mentioned in this article, genomics approaches are very powerful to predict the phenotype, with higher precision and efficiency, based on the genotype. A variety of approaches ranging from MAS to GS are available to become integral part of plant breeding. While in past, plant breeders were hesitant to use genetic variation existing in wild relatives of crop species in commercial breeding programs due to the long time it takes to recover desired phenotypes because of linkage drag, approaches like AB-QTL, in addition to MAS, can be successfully utilized. Availability of NGS technologies, associated with low costs and high-throughput, offers the opportunity to sequence either entire or major proportion of the germplasm collection for a species present in the genebanks around the world to understand genome variation. In case, the genome variation can be associated with the phenotype, which is not trivial, it will be possible to develop the ideotype, based on haplotype, of the variety to be developed.



## **6. Future directions**

While success stories of genomics-assisted breeding are available in several crops, it must also be recognized that much of the genome information generated is not being routinely used by plant breeders, especially in public breeding programs (26). This may be due to shortage of trained personnel, inadequate access to genotyping, inappropriate phenotyping infrastructure, unaffordable bioinformatics systems and a lack of experience of integrating these new technologies with traditional breeding (4, 26). However recently, several international initiatives such as the Integrated Breeding Platform (formerly Molecular Breeding Platform, [www.mbp.genetaioncp.org](http://www.mbp.genetaioncp.org)), a joint initiative of The Bill and Melinda Gates Foundation and The Generation Challenge Program have been started so that plant breeders especially from developing countries can have access to many genotyping, phenotyping as well as information technologies to integrate their breeding programs with modern genomics approaches.

We believe that integration of modern genomics in combination with other cutting edge technologies in breeding programs is invaluable for crop improvement (Fig. 1) and will lead to sustainable agriculture for food security especially in developing countries.

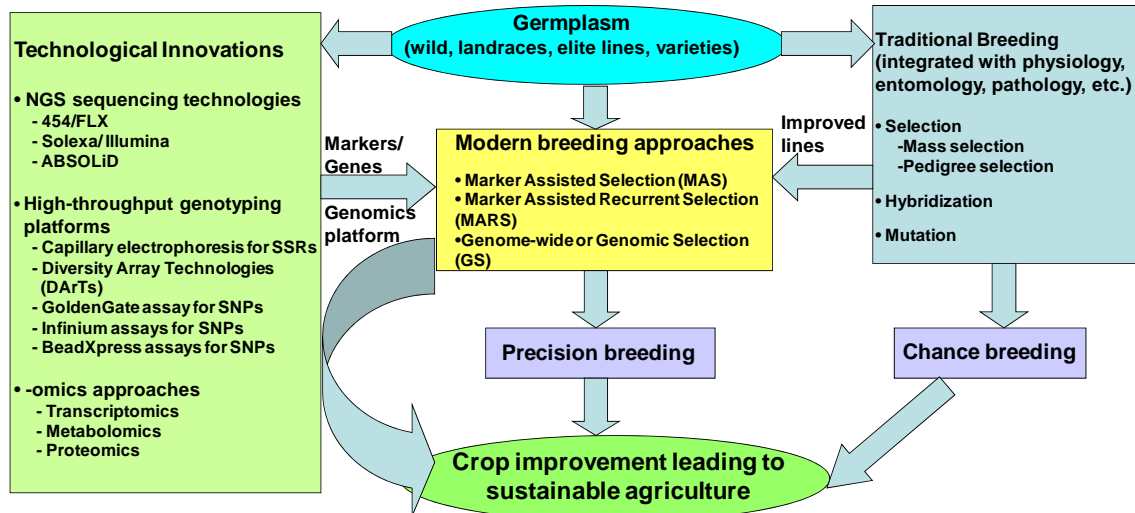


Figure 1: Schematic representation of genomics technologies for crop improvement and sustainable agriculture.

In general, traditional crop improvement programs (shown in the box on the right hand side) employ different breeding strategies integrated with physiology, pathology, entomology, etc. and generate superior lines or improved crop varieties. These approaches, however, take more time and sometimes such breeding is referred as ‘chance breeding’ due to uncertainty in successes predicted in these approaches. On the other hand, genomics technologies (shown in the box on the left hand side) such as a number of next generation sequencing (NGS) technologies, availability of high-throughput genotyping such as capillary electrophoresis for large scale SSR genotyping, microarray based DArTs, GoldenGate/Infinium/ BeadXpress assays for large scale SNP genotyping and a range of –omics technologies provide candidate markers, gene(s), QTLs to be integrated into the breeding programs by using high-throughput genomics platforms. Integrated breeding approaches (shown in the box in the middle) such as marker-assisted selection (MAS), marker-assisted recurrent selection (MARS) and genome-wide selection (GS) offer ‘precision breeding’ with a great potential, versus ‘chance breeding’ to contribute to sustainable crop improvement.

A vital task facing the plant breeding community today is to enhance food security in an environmentally friendly and sustainable manner. Though genomics interventions will not solve all the problems associated with agricultural production leading to sustainability, they have the potential, especially when are used in integrated manner as described in Fig.1, to improve the breeding efficiency to address specific problems. These include increasing crop productivity; diversification of crops; enhancing nutritional

value of food (biofortification); and reducing environmental impacts of agricultural production. However, only through judicious, rational, and science- and need-based exploitation of genetic resources through genomic technologies coupled with conventional plant breeding and genetic engineering will lead to sustainable agriculture.

**Acknowledgements:** We thank the Generation Challenge Programme ([www.generationcp.org](http://www.generationcp.org)), the Indian Council of Agriculture Research (ICAR) and the Department of Biotechnology (DBT) of Government of India for funding various research projects (RKV) on genomics applications in breeding.

## **Bibliography**

### **Primary literature**

1. Briggs SP (1998) Plant genomics: More than food for thought. *Proc Natl Acad Sci USA* 95: 1986–1988.
2. Barrett CB (2010) Measuring food insecurity. *Science* 327: 8525-828.
3. Godfray HCJ, Beddington JR, Crute IR, Haddad L, Lawrence D, Muir JF, Pretty J, Robinson S, Thomas SM, Toulmin C (2010) Food security: The challenge of feeding 9 billion people. *Science* 327: 812-818.
4. Tester M, Langridge P (2010) Breeding technologies to increase crop production in a changing world. *Science* 327: 818-22.
5. Varshney RK, Nayak SN, May GD, Jackson SA (2009c) Next generation sequencing technologies and their application for crop genetics and breeding. *Trends Biotechnol* 27: 522-530.

6. Varshney RK, Graner A, Sorrells ME (2005) Genomics-assisted breeding for crop improvement. *Trends Plant Sci* 10: 621-630.
7. Gupta PK, Varshney RK (2000) The development and use of microsatellite markers for genetics and plant breeding with emphasis on bread wheat. *Euphytica* 113: 163-185.
8. Varshney RK, Langridge P and Graner A (2007) Application of genomics to molecular breeding of wheat and barley. *Advances Genet* 58: 121-155.
9. Gupta PK, Rustgi S, Mir RR (2008) Array-based high-throughput DNA markers for crop improvement. *Heredity* 101: 5–18.
10. Varshney RK (2009) Gene-based marker systems in plants: high throughput approaches for discovery and genotyping. In: Jain SM, Brar, DS (Eds.), *Molecular Techniques in Crop Improvement, Vol II*, Springer, The Netherlands, pp. 119-140.
11. Varshney RK, Hoisington DA, Tyagi AK (2006) Advances in cereal genomics and applications in crop breeding. *Trends Biotechnol* 24: 490-499.
12. Paterson AH, Bowers JE, Bruggmann R, Dubchak I, Grimwood J, Gundlach H, Haberer G, Hellsten U, Mitros T, Poliakov AI, et al. (2009) The *Sorghum bicolor* genome and the diversification of grasses. *Nature* 457: 551-556.
13. Varshney RK, Close TJ, Singh NK, Hoisington DA, Cook DR (2009a) Orphan legume crops enter the genomics era! *Curr Opin Plant Biol* 12: 202–210.
14. Varshney RK, Thudi M, May GD, Jackson SA (2010) Legume genomics and breeding. *Plant Breed Rev* 33: 257-304.

15. Varshney RK, Dubey A (2009) Novel genomic tools and modern genetic and breeding approaches for crop improvement. *J Plant Biochem Biotechnol* 18: 127-138.
16. Phillips RL (2010) Mobilizing science to break yield barriers. *Crop Sci* 50:S99-S108.
17. Gupta PK, Kumar J, Mir RR, Kumar A (2009) Marker-assisted selection as a component of conventional plant breeding. *Plant Breed Rev* 33: 145–217.
18. Kole C (2007) *Genome Mapping and Molecular Breeding in Plants*, a series of seven volumes: cereals and millets; oilseeds; pulses, sugar and tuber crops; fruits and nuts; vegetables; technical crops; and forest trees. Springer-Verlag Berlin Heidelberg, Germany.
19. Flint-Garcia SA, Thornsberry JM, Buckler IV ES (2003) Structure of linkage disequilibrium in plants. *Ann Rev Plant Biol* 54: 357-374.
20. Gupta PK, Rustgi S, Kulwal, PL (2005) Linkage disequilibrium and association studies in higher plants: Present status and future prospects. *Plant Mol Biol* 57: 461-485.
21. Buckler IV ES, Ersoz E, Yu J (2007) Applications of linkage disequilibrium and association mapping in crop plants. In: Varshney RK and Ruberosa R (Eds). *Genomics assisted crop improvement Vol. I: Genomics approaches and platforms*, Springer, Dordrecht, The Netherlands, pp. 97-119.
22. Rafalski JA (2010) Association genetics in crop improvement. *Curr Opin Plant Biol*, doi:10.1016/j.pbi.2009.12.004

23. Collard BCY, Mackill DJ (2008) Marker-assisted selection: An approach for precision plant breeding in the twenty-first century. *Phil Trans R Soc B* 363: 557-572.
24. Varshney RK, Hoisington DA, Nayak SN, Graner A (2009b) Molecular plant breeding: methodology and achievements. In: Somers D, Langridge P, Gustafson PJ (Eds.), *Methods in Molecular Biology: Plant Genomics*, The Humana Press, Totowa, NJ, USA, pp. 283-304.
25. Farre G, Ramessar K, Twyman RM, Capell T, Christou P (2010) The humanitarian impact of plant biotechnology: recent breakthroughs vs bottlenecks for adoption. *Curr Opin Plant Biol*, doi:10.1016/j.pbi.2009.11.002
26. Ribaut J-M, de Vicente M C, Delannay X (2010) Molecular breeding in developing countries *Curr Opin Plant Biol*, doi:10.1016/j.pbi.2009.12.011
27. Langridge (2003) Molecular breeding of wheat and barley In: Tuberosa R, Phillips RL, Gale M (Eds.), *Proceedings of the International Congress "In the Wake of the Double Helix: From the Green Revolution to the Gene Revolution"*, May 27-31 2003, Bologna, Italy, pp. 279-286.
28. Kuchel H, Fox R, Reinheimer J, Mosionek L, Willey N, Bariana H, and Jefferies S (2007) The successful application of a marker-assisted wheat breeding strategy. *Mol Breed* 20: 295–308.
29. Cakir M, McLean R, Wilson R, Barclay I, Moore C, Loughman R, Haley S, Kidwell K, James Anderson J, Sorrells M, Manes Y, Hayden M, Feuille C, William M, In: *XV International Plant and Animal Genome Conference*, January

- 13-17, 2007. San Diego, CA, USA ([http://www.intl-pag.org/15/abstracts/PAG15\\_W40\\_265.html](http://www.intl-pag.org/15/abstracts/PAG15_W40_265.html))
30. Neeraja CN, Maghirang-Rodriguez R, Pamplona A, Heuer S, Collard BCY, Septiningsih EM, Vergara G, Sanchez D, Xu K, Ismail AM, Mackill DJ (2007) A marker-assisted backcross approach for developing submergence-tolerant rice cultivars. *Theor Appl Genet* 115: 767–776.
  31. Xu K, Xu X, Fukao T, Canlas P, Maghirang-Rodriguez R, Heuer S, Ismail AM, et al. (2006) *Nature* 442: 705-708.
  32. Tanksley SD, Nelson JC (1996) Advanced backcross QTL analysis: a method for simultaneous discovery and transfer of valuable QTL from unadapted germplasm into elite breeding lines. *Theor Appl Genet* 92: 191–203.
  33. Hardin B (2000) Rice breeding gets marker assists. *Agricultural Research Magazine* 48: 12, USDA-ARS, USA ([www.ars.usda.gov/is/AR/archive/dec00/rice1200.pdf](http://www.ars.usda.gov/is/AR/archive/dec00/rice1200.pdf))
  34. Natarajkumar P, Sujatha K, Laha GS, Viraktamath BC, Reddy CS, Mishra B, Balachandran SM, Ram T, Srinivasarao K, Hari Y, Sundaram RM (2010) Identification of a dominant bacterial blight resistance gene from *Oryza nivara* and its molecular mapping. *Rice Genetics Newsletters (in press)*
  35. Cao L, Zhuang J, Zhan X, Zeng K, Cheng S, Cao LY, Zhuang JY, Zhan D, Zheng KL, and Cheng SH (2003) Hybrid rice resistance to bacterial blight developed by marker assisted selection. *Chinese J Rice Sci.* 17: 184-186.

36. Septiningsih EM, Pamplona AM, Sanchez DL, Neeraja CN, Vergara GV, Heuer S, Ismail AM, Mackill DJ (2009) Development of submergence-tolerant rice cultivars: the Sub1 locus and beyond. *Annals of Botany* 103: 151–160.
37. Singh S, Mackill DJ, Ismail AM (2009) Responses of *SUB1* rice introgression lines to submergence in the field: Yield and grain quality. *Field Crops Res* 113: 12-23
38. Narayanan NN, Baisakh N, Vera Cruz CM, Gnanamanickam SS, Datta K, Datta SK (2002) Molecular breeding for the development of blast and bacterial blight resistance in rice cv. IR50. *Crop Sci* 42: 2072–2079.
39. Toennissen GH, Toole JCO, DeVries J (2003) Advances in plant biotechnology and its adoption in developing countries. *Curr Opin Plant Biol* 6: 191-198.
40. He Y, Li X, Zhang J, Jiang G, Liu S, Chen S, Tu J, Xu C and Zhang Q (2004) Gene pyramiding to improve hybrid rice by molecular-marker techniques. In new directions for a diverse planet: Proc. 4<sup>th</sup> Intern Crop Sci Cong, Brisbane, Australia (<http://www.cropscience.org.au/icsc2004/>)
41. Gopalakrishnan S, Sharma RK, Anand Rajkumar K, Joseph M, Singh VP, Singh AK, Bhat KV, Singh NK, Mohapatra T (2008) Integrating marker assisted background analysis with foreground selection for identification of superior bacterial blight resistant recombinants in Basmati rice. *Plant Breed* 127: 131–139.
42. Basavaraj SH, Singh VK, Singh A, Singh A, Singh A, Anand D, Yadav S, Ellur RK, Singh D, Gopalakrishnan S, Nagarajan M, Mohapatra T, Prabhu KV and Singh AK (2010) Marker-assisted improvement of bacterial blight resistance in



- parental lines of Pusa RH10, a superfine grain aromatic rice hybrid. *Mol Breed*, doi:10.1007/s11032-010-9407-3.
43. Singh S, Sidhu S, Huang N, Vikal Y, Li Z, Brar DS, Dhaliwal HS, Khush GS (2001) Pyramiding three bacterial blight resistance genes (*xa5*, *xa13* and *Xa21*) using marker assisted selection into *indica* rice cultivar PR106. *Theor Appl Genet* 102: 1011–1015.
  44. Sundaram RM, Vishnupriya MR, Laha GS, Rani NS, Rao PS, Balachandran SM, Reddy, GA, Sarma NP, Sonti RV (2009) Introduction of bacterial blight resistance into Triguna a high yielding, mid-early duration rice variety. *Biotechnology Journal* 4: 400–407.
  45. Joseph M, Gopalakrishnan S, Sharma RK, Singh VP, Singh AK, Singh NK, Mohapatra T (2004) Combining bacterial blight resistance and Basmati quality characteristics by phenotypic and molecular-marker assisted selection in rice. *Mol Breed* 13: 377–387.
  46. Cheng S-H, Zhuang J-Y, Cao L-Y, Chen S-G, Peng Y-C, Fan Y-Y, Zhan XD, Zheng KL (2004) Molecular breeding for super rice. *Chinese J Rice Sci* 18: 377–383.
  47. Kumar J, Mir RR, Kumar N, Kumar A, Mohan A, Prabhu KV, Balyan HS and Gupta PK (2009) Marker assisted selection for pre-harvest sprouting tolerance and leaf rust resistance in bread wheat. *Plant Breed* doi:10.1111/j.1439-0523.2009.01758.x
  48. Bainotti C, Frascina J, Salines JH, Nisi JE, Dubcovsky J, Lewis SM, Bullrich L, Vanzetti L, Cuniberti M, Campos P, Formica MB, Masiero B, Alberione E,

- Helguera M (2009) Registration of 'BIOINTA 2004' wheat. *J Plant Registr* 3: 165–169.
49. DePauw RM, Townley-Smith TF, Humphreys G, Knox RE, Clarke FR, Clarke JM (2005) Lillian hard red spring wheat. *Can J Plant Sci* 85: 397–401.
50. Elias EM (2005) Fusarium resistant tetraploid wheat. United States Patent Application 20050273875
51. DePauw RM, Knox RE, Thomas JB, Smith M, Clarke JM, Clarke FR, McCaig TN, Fernandez MR (2009) Goodeve hard red spring wheat. *Can J Plant Sci* 89: 937–944.
52. Graybosch RA, Peterson CJ, Baenziger PS, Baltensperger DD, Nelson LA, Jin Y, Kolmer J, Seabourn B, French R, Hein G, Martin TJ, Beecher B, Schwarzacher T, Heslop-Harrison P (2009) Registration of 'Mace' hard red winter wheat. *J Plant Registr* 3: 51–56.
53. Randhawa HS, Mutti JS, Kidwell K, Morris CF, Chen X, Gill KS (2009) Rapid and targeted introgression of genes into popular wheat cultivars using marker-assisted background selection. *PLoS ONE* 4: e5752.
54. Helguera M, Khan IA, Kolmer J, Lijavetzky D, Zhong-Qi L, Dubcovsky J (2003) PCR assays for the *Lr37-Yr17-Sr38* cluster of rust resistance genes and their use to develop isogenic hard red spring wheat lines. *Crop Sci* 43: 1839–1847.
55. Barloy D, Lemoine J, Abelard P, Tanguy AM, Rivoal R, Jahier J (2007) Marker-assisted pyramiding of two cereal cyst nematode resistance genes from *Aegilops variabilis* in wheat. *Mol Breed* 20: 31–40.

56. Brevis JC, Dubcovsky J (2008) Effect of the Gpc-B1 region from *Triticum turgidum* ssp. *dicoccoides* on grain yield, thousand grain weight and protein yield. In: Appels R, Eastwood R, Lagudah E, Langridge P, Mackay M, McIntyre L, Sharp P (Eds.), In: Proceedings of 11<sup>th</sup> International Wheat Genet Symposium, Brisbane, Australia, August 24–29, 2008. Sydney University Press, pp. 1–3. (<http://hdl.handle.net/2123/3179>)
57. Yu L-X, Abate Z, Anderson JA, Bansal UK, Bariana HS, Bhavani S, Dubcovsky J, Lagudah ES, Liu S, Sambasivam PK, Singh RP, Sorrells ME (2009) Developing and optimizing markers for stem rust resistance in wheat. The Borlaug Global Rust Initiative 2009 Technical Workshop, March 17–20, 2009, Ciudad Obregon, Mexico.
58. Nocente F, Gazza L, Pasquini M (2007) Evaluation of leaf rust resistance genes *Lr1*, *Lr9*, *Lr24*, *Lr47* and their introgression into common wheat cultivars by marker-assisted selection. *Euphytica* 155: 329–336.
59. Tanksley SD, Grandillo S, Fulton TM, Zamir D, Eshed Y, Petiard V, Lopez J, Beck-Bunn T (1996) Advanced backcross QTL analysis in a cross between an elite processing line of tomato and its wild relative *L. pimpinellifolium*. *Theor Appl Genet* 92: 213-224.
60. Xiao J, Li J, Grandillo S, Ahn S, Yuan L, Tanksley SD, McCouch SR (1998) Identification of trait-improving quantitative trait loci alleles from a wild rice relative, *Oryza rufipogon*. *Genetics* 150: 899-909.
61. Moncada P, Martínez CP, Borrero J, Chatel M, Gauch Jr H, Guimaraes E, Tohme J, McCouch SR (2001) Quantitative trait loci for yield and yield components in an

- Oryza sativa* × *O. rufipogon* BC<sub>2</sub>F<sub>2</sub> population evaluated in an upland environment. *Theor Appl Genet* 102: 41-52.
62. Pillen K, Zacharias A, Léon J (2003) Advanced backcross QTL analysis in barley (*Hordeum vulgare* L.). *Theor Appl Genet* 107: 340-352.
63. Huang XQ, Cöster H, Ganai MW, Röder MS (2003) Advanced backcross QTL analysis for the identification of quantitative trait loci alleles from wild relatives of wheat (*Triticum aestivum* L.). *Theor Appl Genet* 106: 1379-1389.
64. Edwards M, Johnson L (1994) RFLPs for rapid recurrent selection. In: Analysis of Molecular Marker Data. Joint Plant Breeding Symposia Series, ASA, Madison, WI, USA, pp. 33–40.
65. Bernardo R, Charcosset A (2006) Usefulness of gene information in marker-assisted recurrent selection: A simulation appraisal. *Crop Sci* 46: 614–621.
66. Ragot M, Gay G, Muller J-P, Durovray J (2000) Efficient selection for the adaptation to the environment through QTL mapping and manipulation in maize. In: Ribaut J-M and Poland D (Eds.), *Molecular Approaches for the Genetic Improvement of Cereals for Stable Production in Water-limited Environments*. CIMMYT, México DF, Mexico, pp. 128–130.
67. Ribaut JM, Ragot M (2007) Marker-assisted selection to improve drought adaptation in maize: the backcross approach, perspectives, limitations, and alternative. *J Exp Bot* 58: 351–360.
68. Meuwissen THE, Hayes BJ, Goddard ME (2001) Prediction of total genetic value using dense marker maps. *Genetics* 157: 1819–1829.

69. Heffner EL, Sorrells ME, Jannink J-L (2009) Genomic selection for crop improvement. *Crop Sci* 49: 1-12.
70. Wong CK, Bernardo R (2008) Genome-wide selection in oil palm: increasing selection gain per unit time and cost with small populations. *Theor Appl Genet* 116: 815-824.
71. Gregory P (1989) Sustainability and CIP's research. *CIP Circular* 17, 2: 8-11, CIP, Lima, Peru.
72. Charlafti I (2003) Science and sustainability. *EMBO reports* 4: 454-456.

### **Books and reviews**

- Bradford KJ, Van Deynze A, Gutterson N, Parrott W, Strauss SH (2005) Regulating transgenic crops sensibly: lessons from plant breeding, biotechnology and genomics. *Nature Biotech* 23: 439-444.
- Gupta PK and Varshney RK (2004) *Cereal Genomics*. Kluwer Academic Publishers, The Netherlands.
- Hall D, Tegström C, Ingvarsson PK (2010) Using association mapping to dissect the genetic basis of complex traits in plants. *Brief Funct Genom Pro* doi:10.1093/bfgp/elp048
- Innes NL (2008) A plant breeding contribution to sustainable agriculture. *Ann Appl Biol* 126: 1-18.
- Moose SP, Mumm RH (2008) Molecular plant breeding as the foundation for 21st century crop improvement. *Plant Physiol* 147: 969-977.

Persley GJ, Peacock J, van Montagu M (2002) Biotechnology and sustainable agriculture.

ICSU series on science for sustainable development No. 6

Reganold JP, Papendick RI, Parr JF (1990) Sustainable agriculture. *Scientific American* 262: 112-120.

Ribaut J-M (2007) Drought adaptation in cereals. Food Products Press, Binghamton, New York, USA.

Salmeron J, Herrera-Estrella LR (2006) Plant biotechnology: Fast-forward genomics for improved crop production. *Curr Opin Plant Biol* 9:177-179.

Serageldin I (1999) Biotechnology and food security in the 21st century. *Science* 285: 387-389.

Varshney RK and Tuberosa R (2007) Genomics-assisted crop improvement. Vol I: Genomics Approaches and Platforms. Springer, The Netherlands.

Varshney RK and Tuberosa R (2007) Genomics-assisted crop improvement. Vol II: Genomics Applications in Crops. Springer, The Netherlands.