

Chapter 1

CEREAL GENOMICS: AN OVERVIEW

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1. INTRODUCTION

Cereals are widely cultivated and produce annually, 1800 to 1900 million tonnes of food grains worldwide (see Table 1; FAO website <http://apps.fao.org>). Cereals also represent 60% of the calories and proteins consumed by human beings. They include a variety of crops including rice, maize, wheat, oats, barley, rye, etc., but excluding millets like pearl millet and other minor millets. In the past, cereals have been a subject of intensive cytogenetic investigations that are now extended further in the genomics era using powerful tools of molecular biology. The progress in cereal genomics research during the last two decades, involving the use of molecular markers for a variety of purposes, and the whole genome sequencing in rice has been remarkable indeed. The results of genomics research resolved many aspects, which the conventional cytogenetics failed to resolve. For instance, this involved initially the preparation of molecular maps, which were utilized extensively for comparative genomics and cytogenomics. Cereal genomes have also been subjected to both structural and functional genomics research, which during the last two decades covered both basic and applied aspects. As a result, not only we understand better the genomes of major cereals and the mechanisms involved in the function of different cereal genes, but we have also utilized information generated from genomics research in producing better transgenic crops, which will give higher yields, sometimes with value addition. Transgenic cereals will also be available, which will be resistant to major pests and diseases and will be adapted to changing environmental conditions. In this book, while we have tried to cover for cereal crops, the areas involving molecular markers, whole genome sequencing (WGS) and

Table 1. Some details about important cereals, discussed in the book

Cereal species	Biological Name	FAO data (2002) ¹		Chromosome number	Genome size (Mbp) ²	Availability of resources	Number of ESTs available in public domain ³
		Yield (Tonnes/Hectare)	Production (Million Tonnes)				
Barley	<i>Hordeum vulgare</i>	2.5	132	$2n=2x=14$	5,000	Both genetic and physical maps (based on translocation breakpoints) available	356,848
Maize	<i>Zea mays</i>	4.3	603	$2n=2x=20$	2,500	Extensive genetic (including transcript map) and BAC-based physical maps available	393,719
Oats	<i>Avena sativa</i>	1.9	27	$2n=6x=42$	11,400	Genetic maps (but not saturated) available	574
Rice	<i>Oryza sativa</i>	3.9	580	$2n=2x=24$	430	Extensive genetic (including transcript) and YAC/BAC-based physical maps, as well as 4 drafts of complete genome sequences available	283,935
Rye	<i>Secale cereale</i>	2.2	21	$2n=2x=14$	8,400	Genetic maps (but not saturated) available	9,194
Sorghum	<i>Sorghum bicolor</i>	1.3	55	$2n=2x=20$	750	Integrated cytogenetic, genetic and physical maps available	161,813
Wheat	<i>Triticum aestivum</i>	2.7	568	$2n=6x=42$	16,000	Extensive genetic as well as deletion lines-based physical maps available	549,926

¹As per FAO website <http://apps.fao.org>; ²As per Bennett and Leitch (1995); ³As per dbEST release 030504- http://www.ncbi.nlm.nih.gov/dbEST/dbEST_summary.html

the functional genomics, by choice we have not included the transgenics, which involve only an application of genomics research and do not make a part of genomics research itself. We realize that cereal genomics has been the subject of several special issues or sections of journals like PNAS, USA (Volume 95 issue no.5, March 1998), Plant Molecular Biology (Volume 48 issue no. 1-2, January 2002), Plant Physiology (Volume 125 issue no. 4, March 2001; Volume 130 issue no. 4, December 2002), Functional & Integrative Genomics (Volume 3 issue no. 1-2, March 2003; Volume 4 issue no.1, March 2004), etc. Several review articles also adequately cover the present status of research on this important subject (Gale and Devos, 1998; Goff, 1999; Bennetzen, 2000; Devos and Gale, 2000; Wise, 2000; Edwards and Stevenson, 2001; Lagudah *et al.*, 2001; Feuillet and Keller, 2002; Rafalski, 2002; Appels *et al.*, 2003; Bennetzen and Ma, 2003; Paterson *et al.*, 2003, etc). However, the subject has not been presented elsewhere in the form of a book that may be used for teaching and research, and hence the present effort of this book on cereal genomics.

2. MOLECULAR MARKERS: DEVELOPMENT AND USE IN GENOMICS RESEARCH

2.1. Construction of Molecular Maps

A variety of molecular markers is now known and their development and use has been a subject of intensive research in all cereals. The subject has been adequately covered in several recent reviews (Kumar, 1999; Koebner *et al.*, 2001; Gupta *et al.*, 2002), but none of these reviews adequately covers all aspects. In the present book, 12 of the 20 chapters are devoted to the discussions on different types of molecular markers and their uses. The availability of molecular marker maps of cereal genomes, with varying density and resolution, has also facilitated comparative genomics studies. The group led by Mike Gale at John Innes Center (JIC), Norwich (UK), is regularly updating these results. Availability of a number of marker assays provides ample opportunity for exercising choice of a suitable marker system based on intended objective, convenience and costs. In this book, the different molecular marker systems and their evaluation in cereal genomics is being discussed in Chapter 2 by Daryl Somers from Winipeg (Canada). Rajeev Varshney and Andreas Boerner from Gatersleben and Viktor Korzun from Bergen have covered the methods for the preparation of molecular maps and the progress made so far in preparation of these maps in Chapter 3. It will be noticed that while significant progress has been made in the preparation of molecular maps in cereals, most of these maps are based on

RFLPs, the first molecular marker system that became available in early 1980s (for details see Philips and Vasil, 1994, 2001). Progress has also been made in the preparation of microsatellite maps. Although in the past it has been expensive and cumbersome to generate microsatellites, they have now been generated in almost all cereal species (Gupta and Varshney, 2000). For instance, a microsatellite map of maize genome with 900 SSR markers became available recently (Sharopova *et al.*, 2002; total ~1800 SSR mapped loci available as on October 2001; <http://www.agron.missouri.edu/ssr.html>), and another integrated microsatellite map with ~1000 SSR loci is now available in bread wheat (D. Somers, Canada, personal communication). Moreover, in recent years a large amount of sequence data has been/is being generated in many cereals from several genome sequencing and EST sequencing projects (see Table 1). Therefore the available sequence data is also being exploited for development of microsatellite markers (Kantety *et al.*, 2002; Varshney *et al.*, 2002; Gao *et al.*, 2003). In this direction, more than 2000 SSR loci have already been mapped in rice (McCouch *et al.*, 2002) and work is in progress in other cereals like barley (Varshney *et al.*, unpublished) and wheat (M. Sorrells, USA, personal communication). Availability of sequence data also provided the next generation of markers, i.e. single nucleotide polymorphism (SNP, popularly pronounced as snip). However, SNP discovery is costly, so that the construction of SNP maps in cereals will take time. This is in sharp contrast to the situation in human genome, where a large number of microsatellites and at least two million SNPs have already been mapped. A programme for the preparation of a HapMap for the human genome, utilizing haplotypes, based on SNPs, was also initiated in late 2002 under the SNP Consortium (<http://snp.cshl.org/>; The International HapMap Consortium, 2003). Among cereals, SNPs are now being discovered and will be extensively used in future for genotyping in crops like barley, rice, maize and wheat. EST-based SSRs, SNPs, or RFLPs, are also being used for construction of 'functional or transcript maps' in many cereals like rice (Kurata *et al.*, 1994; Harushima *et al.*, 1998; Wu *et al.*, 2002), maize (Davis *et al.*, 1999), barley (A. Graner, Germany, personal communication). EST-based markers are also being used, *firstly*, to assess functional diversity, and *secondly*, to anchor genic regions in BAC/YAC-based physical maps, etc. Physical maps have also been prepared in some cereals like rice (Tao *et al.*, 2001; Chen *et al.*, 2002), maize (Yim *et al.*, 2002; <http://www.agron.missouri.edu/maps.html>), sorghum (Klein *et al.*, 2000; Childs *et al.*, 2001; <http://sorghumgenome.tamu.edu/>), etc. However, construction of BAC/YAC-based physical maps is difficult in large and complex genomes like those of wheat and barley. Therefore, for physical mapping, translocation breakpoints (aneuploid stocks) were used in barley (Künzel *et al.*, 2002) while deletion lines (another aneuploid stocks)- are being used in wheat (B.S. Gill, USA, personal communication;

http://wheat.pw.usda.gov/NSF/progress_mapping.html). At SCRI in UK, efforts are underway for preparation of local physical maps in barley by using radiation hybrids (RH) or HAPPY mapping (Waugh *et al.*, 2002; Thangavelu *et al.*, 2003).

Physical maps are important for chromosome walking in map-based cloning projects (see later) and have also facilitated identification of gene rich regions in large genomes, which are too big to be used for whole genome sequencing. These gene rich regions will be the target for genome sequencing in these crops e.g. wheat (see later) where BAC libraries are already available. This aspect of gene distribution, gene density and gene islands has been discussed by Kulvinder Gill, Washington (USA) in Chapter 12. It has been shown that cereal genomes possess gene-rich and gene-poor regions (Akhunov *et al.*, 2003). Moreover physical location, structural organization and gene densities of the gene-rich regions are similar across the cereal genomes (Feuillet and Keller, 1999; Sandhu and Gill, 2002). Despite this, cereal genomes greatly vary in their size, which is attributed to the presence of varying amounts of repetitive sequences in these genomes (Heslop-Harrison, 2000). Repetitive sequences can be found in the genome either in tandem arrays or in a dispersed fashion. Therefore repetitive sequences can be classified into 3 categories: (i) transposable including retrotransposon elements, which are mobile genetic elements; (ii) microsatellite sequences, which are tandemly repeated DNA sequences (also called simple sequence repeats, SSRs); and (iii) special classes such as telomeric/ centromeric sequences or rDNA units, etc. First two classes constitute a major proportion of the repetitive sequences, present in the genome. During the last decade, a number of studies have been carried out to study physical organization of retrotransposons in several plant genomes including cereals (for references see Kumar and Bennetzen, 1999; Wicker *et al.*, 2002). The fraction of the genome contributed by retrotransposons increases with genome size from rice, the smallest cereal genome (430 Mb, ~14% LTR retrotransposons, Tarchini *et al.*, 2000), through maize (2500 Mb, 50-80% LTR retrotransposons, SanMiguel *et al.*, 1996) to barley (5000 Mb, >70% LTR retrotransposons, Vicient *et al.*, 1999). Contribution and organization of retrotransposons and microsatellites in cereal genomes has been discussed by Alan Schulman from Helsinki (Finland) and the editors of this book in Chapter 4.

2.2. Comparative Genomics

The availability of molecular maps for all major cereal genomes facilitated studies on comparative mapping, where rice genome was used as the anchor

genome and all cereal genomes could be expressed in the form of ~30 odd genomic blocks derived from the rice genome (Moore *et al.*, 1995; Gale and Devos, 1998). These studies also led to the conclusion that maize genome really consists of two genomes of five chromosomes each and is therefore an archaic tetraploid (Devos and Gale, 2000). Comparative studies revealed a good conservation of markers within large chromosomal segments of the cereal genomes. However, mapping of resistance gene analogs (RGAs) isolated from rice, barley and foxtail millet showed limited orthology (Leister *et al.*, 1999). In recent years, isolation and sequencing of large genomic DNA fragments (100-500 kb) from many cereals provided further insights about the conservation of gene order between different cereal genomes at the sub-megabase level i.e. micro-colinearity (Chen *et al.*, 1997, 1998; Dubcovsky *et al.*, 2001), although evidence for disruption of this collinearity is also available in some cases (Tikhonov *et al.*, 1999; Tarachini *et al.*, 2000; Li and Gill, 2002). The comparative genomic studies also resolved a large number of duplications, translocations, and inversions that accompanied the evolution of these cereal genomes and could not be earlier resolved by conventional tools of cytogenetics research (Paterson *et al.*, 2000; Benntezen, 2000; Bennetzen and Ma, 2003). Thus, the detailed studies on comparative genomics of cereals facilitated researchers to utilize information generated from one cereal genome for that of the other (see Bellgard *et al.*, 2004). These aspects related to comparative mapping and genomics have been covered by Andrew Paterson from Athens (USA) in Chapter 5.

2.3. QTL Analysis: Its Use in Study of Population Structure and for Crop Improvement

Molecular markers have also been used for the study of population structures in the progenitors of our major cereals, which has been discussed by Eviatar Nevo, Haifa (Israel) in Chapter 6. Another important area of genomics research is QTL analysis (including QTL interval mapping), which has been utilized for mapping of QTL for a variety of economic traits and for developing markers that are closely associated with these QTLs in different cereal crops. One of the offshoots of this research is also the identification of traits and the associated QTL, which led to the domestication of cereals (Paterson *et al.*, 1995; Heun *et al.*, 1997; Badr *et al.*, 2000; Ozkan *et al.*, 2002; Salamini *et al.*, 2002; Peng *et al.*, 2003). This aspect has been discussed in Chapter 7 by Francesco Salamini and his colleagues from Cologne (Germany), Lodi and Milan (Italy). One of the major benefits of QTL analysis would also be to identify QTL for resistance against biotic and abiotic stresses and the associated molecular markers (e.g. Ordon *et al.*,

1998; Friedt *et al.*, 2003; Ribaut *et al.*, 2002), so that this information will be utilized in future either for the marker-aided selection or for the isolation of these QTL through map-based cloning. Exploitation of molecular markers for identification of genes/QTLs for disease resistance in barley and wheat has been discussed in Chapter 8 by Ahmed Jahoor and his colleagues from Roskilde and Horsens (Denmark). Similarly, identification of genes/QTLs conferring tolerance to abiotic stresses have been discussed in Chapter 9 by Roberto Tuberosa and Silvio Salvi from Bologna (Italy).

2.4. Marker -Assisted Selection (MAS) and Map-Based Cloning (MBC)

Marker-assisted selection (MAS) is a powerful tool for indirect selection of difficult traits at the seedling stage during plant breeding, thus speeding up the process of conventional plant breeding and facilitating the improvement of difficult traits that can not be improved upon easily by the conventional methods of plant breeding (Ribaut and Hoisington, 1998). It has been realized that despite extensive research in this area, MAS has not been put to practice in actual plant breeding, to the extent earlier anticipated (see <http://www.fao.org/biotech/logs/cl0logs.htm>). The reasons for lack of activity involving MAS, and the future possibilities of using MAS in wheat and barley breeding have recently been discussed in some reviews (Koebner *et al.*, 2001; Koebner and Summers, 2003; Thomas, 2002, 2003), etc. It has however been recognized that with the availability of a large repertoire of SSR markers in majority of cereals and with the developments of SNPs at an accelerated pace, MAS will be effectively used in future to supplement the conventional plant breeding. In Chapter 10 of this book, Robert Koebner from Norwich (UK) is dealing with the present status and future prospects of MAS in cereals.

Production of transgenic cereals requires isolation of important genes for agronomic traits (including those for resistance to diseases). Identification of closely linked markers with such genes provides the starting point for map-based cloning (MBC) of these genes. There are three major requirements for map-based gene isolation (Ordon *et al.*, 2000; Wise, 2000): (i) a high resolution genetic map spanning the gene of interest, (ii) availability of a large-insert genomic YAC or BAC library, (iii) multiple independent mutant stocks and (iv) an efficient transformation system for use in functional complementation. All these resources either have become available or their generation is in progress in almost all the cereals (Table 1). Some of the resistance genes that have been isolated include the following, i.e. *Mlo*

(Büschges *et al.*, 1997), *Mla* (Wei *et al.*, 1999), *Rar1* (Lahaye *et al.*, 1998; Shirasu *et al.*, 1999), *Rpg1* (Hovrath *et al.*, 2003) in barley; *xa-21* (Song *et al.*, 1995), *xa-1* (Yoshimura *et al.*, 1998), *PiB* (Wang *et al.*, 1999); *Pi-ta* (Bryan *et al.*, 2000) in rice; and *Lr10* (Stein *et al.*, 2000; Feuillet *et al.*, 2003), *Lr21* (Huang *et al.*, 2003) and *Pm3* (Yahiaoui *et al.*, 2003) in wheat. In rice, progress is underway to isolate *xa-5* (Blair *et al.*, 2003), genes required from rice yellow mosaic virus (RYMV movement) (Albar *et al.*, 2003). In recent years some studies have targeted cloning of QTLs also by using MBC approach (see Yano, 2001). For instance, a *fruit weight2.2* (*fw2.2*) QTL in tomato (Fraray *et al.*, 2000) and two major photoperiod sensitivity QTLs, *Hdl* (Yano *et al.*, 2000) and *Hd6* (Takahashi *et al.*, 2001) in rice have recently been isolated. As an example for QTL isolation in cereals other than rice, *Vgt1* responsible for transition from vegetative to the reproductive phase in maize is looked upon as one possible target (Salvi *et al.*, 2002). With the availability of resources and expertise, developed recently, it is expected to isolate some important QTLs in other cereals also in the near future. In Chapter 11, Nils Stein and Andreas Graner from Gatersleben (Germany) have discussed methodology and progress in the area of MBC. Gene tagging using transposon induced mutant populations together with cDNA approaches are also gaining importance in some cereals like maize (Bensen *et al.*, 1995; Das and Martienssen, 1995; for review see Osborne and Baker, 1995 and Walbot, 2000), rice (Hirochika, 1997; Izawa *et al.*, 1997; Zhu Z.G. *et al.*, 2003), barley (Scholz *et al.*, 2001), etc.

3. LARGE- SCALE GENOME/ TRANSCRIPTOME SEQUENCING AND ITS UTILIZATION

3.1. Methods and Progress of Whole Genome Sequencing (WGS) in Cereals

Among higher plants, Arabidopsis genome is the first to be fully sequenced (TAGI, 2000). However, during the last two years (2001-2003) four drafts of rice genome sequences have also become available and are being extensively utilized for a variety of purposes (Barry, 2001; Goff *et al.*, 2002; Yu *et al.*, 2002; IRGSP- <http://rgp.dna.affrc.go.jp/IRGSP/>). The high quality sequences for three rice chromosomes 1, 4 and 10 have also been completed and published (Sasaki *et al.* 2002; Feng *et al.* 2002; The Rice Chromosome 10 Sequencing Consortium, 2003). As we know, two different approaches are available for whole genome sequencing, one of them involving preparation of physical maps of BACs first, and then sequence the genome BAC-by-BAC, and the other involving whole genome shotgun (WGS) approach

pioneered by James C. Venter, Rockville (USA) for the human genome (Venter *et al.*, 1998). Both these approaches have been utilized for whole genome sequencing of rice genome. In Chapter 13, Yeisoo Yu and Rod Wing from Tucson (USA) presents a detailed account on the methodology and the progress made in this direction. After completion of sequencing of Arabidopsis and rice genomes, efforts are underway to characterize and annotate all the genes in these two genomes. Information generated from these genomes will continue to prove very useful in different aspects of genomics research in other cereals. Takuji Sasaki and Baltazar Antonio from Tsukuba (Japan) have discussed the rice genome as a model system for cereals in Chapter 18. Similarly, in Chapter 17, Klaus Mayer and his colleagues from MIPS, Neuberberg (Germany) have discussed the Arabidopsis genome and its use in cereal genomics. However, some cereals like barley have a unique property of malting, which makes it different from other cereals. This suggests that at least for this particular trait, barley genome has genes, which are absent in Arabidopsis and rice genomes. Similar unique genes for some other traits may be available in other cereals also. Therefore, several large-scale EST sequencing projects were initiated in barley, wheat, sorghum, maize, etc. and as a result large amount of data has been generated (Table 1). Due to importance of maize as a cereal crop, the Maize Genome Sequencing Project is also underway (Chandel and Brendel, 2002; <http://www.maizegenome.org/>). It is believed that the maize genome sequence will be useful for annotation of rice genome in the same manner as mouse genome proved useful for the human genomes (Gregory *et al.*, 2002). However, barley and wheat are also important cereals, but whole genome sequencing has not been planned for these two cereals due to their large genome size (Table 1). However, in an ITMI meeting (Winipeg, Canada, June 1-4, 2002) Bikram Gill and other cereal workers discussed the concept of IGROW (International Genome Research on Wheat) to lead wheat genome sequencing and improvement effort for the next 10 years. IGROW has the following objectives: (i) identification of gene-rich regions by using BAC-library and *Cot*-based procedures, and (ii) shotgun sequencing of the identified gene-rich regions of the wheat genome (<http://wheat.pw.usda.gov/ggpages/awn/48/Textfiles/IGROW.html>). In November 2003, another meeting of IGROW sponsored by the National Science Foundation and the United States Department of Agriculture was held to discuss the need and a strategy for sequencing the wheat genome consisting of 16,000 Mbp. It was argued that the wheat genome sequence would provide a model for structural and functional changes that accompany polyploidy and that model species cannot be used to study the unique traits in wheat (Gill and Appels, 2004).

3.2 Bioinformatics and its Use in Development and Use of Cereal Databases

Extensive data on all aspects of cereal genomics are now available at GrainGenes (<http://wheat.pw.usda.gov/>). An independent database Gramene (<http://www.gramene.org/>) has also been created, which has major emphasis on rice genome and its relationship with other cereal genomes. Other independent databases are also available for some individual cereal crops, like rice (Oryzabase <http://www.shigen.nig.ac.jp/rice/oryzabase/>) and maize (ZeaDB <http://www.zmdb.iastate.edu/>; MaizeDB <http://www.agron.missouri.edu/>). Similar databases have yet to be developed for other cereals like wheat, barley and oats. Tools of bioinformatics are already being used for development and use of these databases for mining useful information. Some efforts are also underway at the University of California, Berkley (USA) to create a database (CereGenDB) for coding sequences that are conserved not only between rice and other cereals, but also between cereals and Arabidopsis. These aspects have been discussed in Chapter 14 by Dave Matthews, Olin Anderson and their colleagues from Ithaca and Albany (USA).

3.3. Functional Genomics and its Utility for Crop Improvement

During the last 5 years, as mentioned above, a large amount of sequence data, has been generated from many genome/EST sequencing projects in cereals (Table 1). Available sequence data are being already utilized for a variety of purposes, including annotation of these genomic sequences. An important area of research in the field of functional genomics in cereals is the study of expression patterns in time and space (see Schena, 1999; Kehoe *et al.*, 1999). These studies are being related with the whole genome sequences with and without known functions and also with the information available about the structure and function of proteins available in the databases. In this direction, mainly cDNA clones corresponding to the ESTs, have been utilized to prepare cDNA macro/micro-arrays (Richmond and Somerville, 2000). Exploitation of microarray technology for gene expression studies in cereals is still in its infancy (see Sreenivasulu *et al.*, 2002b). Nevertheless some progress has been made in identification of genes involved in embryo/seed development, seed germination, grain filling, etc. in some cereals like maize (Lee *et al.*, 2002), barley (Sreenivasulu *et al.*, 2002a; Potokina *et al.*, 2002), rice (Zhu T. *et al.*, 2003). Studies have also been targeted towards genes that are responsible for stress tolerance (Kawasaki *et al.*, 2001; Bohnert *et al.*,

2001; Ozturk *et al.*, 2003). These aspects are discussed in two chapters; Chapter 15 by Peter Langridge and his colleagues from Adelaide (Australia); and Chapter 16 by Nese Sreenivasulu and others from Gatersleben (Germany) and Hyderabad (India). Recently, a new approach, called 'genetical genomics' has also been proposed, where expression profiling of individual genes is combined with QTL mapping in a segregating (mapping) population (Jansen and Nap, 2001; Jansen, 2003). We believe that availability of large EST collections for genome-wide expression profiling and analytical tools available for molecular marker analysis in different cereals will accelerate the use of the 'genetical genomics' approach for identification of genes for different agronomic traits to be used for crop improvement programmes.

4. GENOMICS RESEARCH IN CROP IMPROVEMENT

The current investment on cereal genomics research eventually has to give returns in the form of improved cereal crops. For this purpose, we need to achieve success, both in using molecular marker aided selection (MAS) and in the development of improved transgenic cereals, which would give not only increased yield, but will also give value added cereals with improved nutritional quality. According to most cereal workers, both these expectations of cereal genomics research should be realized in the near future. Availability of complete genome sequence of rice along with the EST-sequencing projects in other cereals provides enough resources to utilize them in the wet lab as well as for *in silico* mining, with an objective to improve crops. Utilization of sequence data in post-genomic era is being discussed in Chapter 19 by Mark Sorrells, Ithaca (USA). Wanlong Li and Bikram Gill from Manhattan (USA) discuss the future role of genomics research for cereal improvement in the concluding chapter of this book (Chapter 20).

5. SUMMARY AND OUTLOOK

Significant progress in the field of cereal genomics has already been made in almost all cereals. For instance, availability of a variety of molecular markers facilitated preparation of high-density maps in almost all cereals. This activity proved useful in identification of molecular markers linked with genes/QTLs for a variety of economic traits including those conferring tolerance to biotic and abiotic stresses. In some cases, molecular markers have also been used for MAS, and for map-based cloning (MBC) of genes. However, in cereals other than rice and maize (eg., wheat and barley), further

research at an accelerated pace is required in both areas i.e. MAS and MBC. Data on genomic and EST sequences from a variety of sources are also being analysed to understand the genomes and the transcriptomes of different cereals. For instance, in the field of functional genomics, availability of ESTs from different parts of a plant in an individual cereal crop gave a momentum to research involving identification and annotation of genes for different biological processes. The genes, identified thus, now need to be integrated to the genetic and physical maps including those based on BAC clones derived from genomic and cDNA libraries. This will then allow effective use of DNA markers in MAS as well as in MBC projects with an ultimate objective of crop improvement in cereals. Additional work however is needed in the area of association mapping and linkage disequilibrium (LD), which have proved extremely fruitful in human genetics (Jannink and Walsh, 2002). Since in this area, only a beginning has been made in cereals (Thornsberry *et al.*, 2002; Remington *et al.*, 2002; see Rafalski and Morgante, 2004), and its impact is yet to be realized, this aspect has not been covered in this book. Similarly, not much work in the area of cereal proteomics is available so far to find a place in this book. We hope that more work on cereals will be done in these areas, by the time this book becomes available to the readers. In the next decade, it will be a major challenge in each cereal crop to build integrated databases, combining information on genome and proteome sequences and their maps, mRNA and protein expression profiles, mutant phenotypes, metabolism and allelic variation. This integrated information on transcriptome(s)/genome(s) will then be accessible on-line. We believe that in future, we will be talking of a 'cereal gene' rather than of a gene for a particular cereal species in order to improve the quality as well as quantity of cereal grain worldwide, which is a major challenge indeed, to be realized in the next few years.

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