Biology **2013**, *2*, 1357-1377; doi:10.3390/biology2041357

OPEN ACCESS

biology

ISSN 2079-7737

www.mdpi.com/journal/biology

Review

Next Generation Characterisation of Cereal Genomes for Marker Discovery

Paul Visendi [1,2], Jacqueline Batley [3] and David Edwards [1,*]

[1] Australian Centre for Plant Functional Genomics, School of Agriculture and Food Science, the University of Queensland, Brisbane, QLD 4072, Australia; E-Mail: paul.muhindira@uqconnect.edu.au

[2] Centre for Biotechnology and Bioinformatics, College of Biological and Physical Sciences, the University of Nairobi, P. O. Box 30197 G.P.O, Nairobi 00100, Kenya

[3] Centre for Integrative Legume Research, School of Agriculture and Food Science, the University of Queensland, Brisbane, QLD 4072, Australia; E-Mail: j.batley@uq.edu.au

* Author to whom correspondence should be addressed; E-Mail: Dave.Edwards@uq.edu.au; Tel.: +61-7-3346-7084; Fax: +61-7-3365-1176.

Received: 16 August 2013; in revised form: 29 October 2013 / Accepted: 8 November 2013 / Published: 25 November 2013

Abstract: Cereal crops form the bulk of the world's food sources, and thus their importance cannot be understated. Crop breeding programs increasingly rely on high-resolution molecular genetic markers to accelerate the breeding process. The development of these markers is hampered by the complexity of some of the major cereal crop genomes, as well as the time and cost required. In this review, we address current and future methods available for the characterisation of cereal genomes, with an emphasis on faster and more cost effective approaches for genome sequencing and the development of markers for trait association and marker assisted selection (MAS) in crop breeding programs.

Keywords: sequencing; single nucleotide polymorphisms; genotyping by sequencing; polyploidy; markers; cereals

1. Introduction

Cereals constitute over 60% of the world's food sources. In the African continent, cereals comprise 46% of the diet, roots and tubers 20% and animal products 7%, while in Western Europe these constitute

26%, 20% and 4%, respectively (www.FAOstat.fao.org). The importance of cereals can be attributed to their phenotypic plasticity, enabling them to adapt to various climatic conditions. Several of the major cereal genomes are large and complex, mainly due to an abundance of transposable elements (TEs), and polyploidy [1,2]. As a result, genetic analysis of diversity, allele and haplotype frequencies is a challenge. Traditional breeding practices rely on phenotypic selection with cycles of 5–12 years depending on the crop and breeding system, however more rapid selection systems are urgently required to develop cereal varieties that are high yielding and resilient to floods, droughts and high or low temperatures to feed the growing world population in the face of climate change. The field of genomics is accelerating through the development and application of Next Generation Sequencing (NGS) technologies coupled with advanced computational algorithms and statistics. The cheaper per base cost of NGS compared to traditional Sanger sequencing comes at a cost of shorter read lengths and reduced accuracy, but offers the potential for increased depth of coverage required for confident variant discovery [3,4]. A summary of genomic approaches for crop improvement is presented in Figure 1.

2. DNA Sequencing Technology

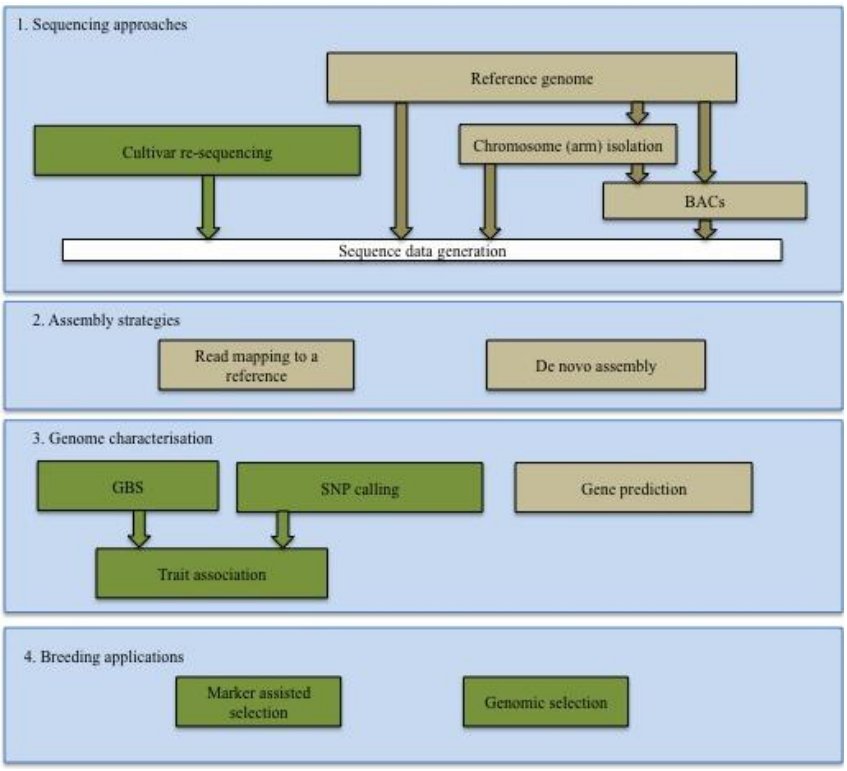
DNA sequencing technologies have evolved rapidly since the popular method developed by Sanger in the 1970s [5,6]. The initial Sanger sequencing method was automated [7] with improvements in read length and accuracy [8], resulting in error rates of as low as one in 10,000 bp, with read lengths between 800–1000 bp. Sanger sequencing is being rapidly replaced by NGS technologies. The first commercially available NGS platform was the GS20, produced by 454 Life Sciences and commercialised by Roche [9]. The latest 454 platform, the GS FLX+ model produces up to 700 Mbp per run, with read lengths of 1,000 bp. A major limitation of this pyrosequencing is the accurate determination of homopolymer regions. Illumina (www.illumina.com) have developed a range of popular NGS platforms and now dominate the NGS field. They apply a sequencing by synthesis (SBS) approach [10] and can produce read pairs where two reads are in a known orientation and approximate distance to each other, greatly facilitating genome assembly and read mapping in complex genomes. Their current platforms include the HiSeq systems which produce around 600 Gbp per run with read lengths of up to 150 bp; and the MiSeq which produces reads up to 250 bp within 24 hours, but with reduced data output of around 10 Gbp per run. The use of indexed paired read libraries, high data output and relatively low error rates makes this an increasingly popular technology for diversity studies, re-sequencing and SNP discovery [11–16].

Recent developments in third generation sequencing platforms (TGS) promise longer read lengths and eliminate bias caused by PCR amplification. Ion Torrent's non-optical DNA sequencing technology (www.iontorrent.com) is based on complementary metal-oxide semiconductors (CMOS) [17]. Read lengths of 100–200 bp have been produced on a single run using 1.2 million sensors, generating more than 10 Gbp. The reduced cost and ease of scalability makes this technology cost-effective for re-sequencing and SNP discovery, though sequence error has yet to be fully evaluated.

Pacific Biosciences (www.pacificbiosciences.com) apply a single-molecule sequencing technique called SMRT™ (Single Molecule Real Time) technology [18] in which nucleotides incorporated during synthesis are detected directly by DNA polymerase. Read lengths of 2,500–10,000 bp have

been reported [19]. A drawback of these longer read lengths is increased error rates. Attempts have been made to correct these errors by using Illumina reads which are shorter but more accurate [20].

Figure 1. A schematic representation of cereal crop improvement using Next Generation Sequencing (NGS) technologies. Blue denotes main steps in the characterization of cereal genomes, brown denotes reference specific approaches while green represents applications to several cultivars or populations for variation discovery. (1) Sequencing approaches are determined by the project aims. For characterization of previously un-sequenced genomes without a closely related species, generation of a reference genome is undertaken. This may involve direct whole genome shotgun (WGS), chromosome (arm) isolation or BAC-by-BAC approaches or a combination of these. For GWAS, where a suitable reference genome is available, a large number of cultivars or populations are sequenced at low coverage. (2) Assembly strategies depend on the nature of the genome to be assembled, reads available (length, read types *i.e.*, paired end (PE) or mate pair (MP)), coverage depth, and whether there is a high quality draft genome of a closely related species of which if absent, de-novo assembly is undertaken. (3) Characterization then follows which involves gene prediction based on orthologous genes in related species or *ab-initio*. (4) Variation discovery through SNPs discovery and GBS within cultivars or populations enables trait associations and the generation of molecular markers for applications in crop breeding programs.



Oxford Nanopore (www.nanoporetech.com) exploits a synthetic protein with an ion channel at its core, embedded into a lipid bilayer membrane. Chauffer enzymes are utilised to either direct DNA strands into the protein nanopore (strand sequencing) or attach the DNA followed by cleaving one base at a time (exo-nuclease sequencing). In both cases, as nucleotides pass through the nanopore, specific

disruptions to the current applied to the lipid bilayer are detected, enabling the determination of the DNA sequence of a strand [21,22]. While this technology is actively under development with little publicly available data on error profiles, Oxford Nanopore have reported error rates of about 4%.

2.1. Sequencing of Cereal Genomes

Rice was the first cereal to be sequenced [23], which paved the way for NGS characterization of more complex cereals. Bread wheat has a hexaploid genome (2n = 6x = 42) that contains three closely related ancestral diploid genomes (AABBDD), each with a set of seven chromosomes. The genome of bread wheat is also very large, around 17 Gbp and is predominantly composed of repeats [24,25]. Maize is an allotetraploid consisting of ~ 85% repeat sequence [26,27]. This compares to a repeat content of 35% in rice [23] and 55% in sorghum [28]. Due to the size and complex nature of most cereal genomes, sequencing, assembly and characterisation has been a daunting task. These challenges have led to the application of diverse approaches and sequencing platforms, such as BAC-by-BAC approaches, and the use of isolated chromosome arms [29].

Several attempts are currently underway to sequence the bread wheat genome. A recent whole genome shotgun (WGS) approach applied 454 sequencing technology, building an assembly of genic regions based on orthologous relationships to barley, sorghum, rice and Brachypodium [25,30]. With a WGS approach, the differentiation of homoeologous chromosome sequences is challenging. This complexity can be resolved by using flow cytometry to isolate individual chromosome arms [31] enabling a detailed study of homoeologous genes and translocations within wheat chromosome arms [32–36]. A BAC-by-BAC approach has also been applied to sequence isolated wheat chromosomes, with recent success for chromosome 3B.

Both WGS and BAC-by-BAC approaches have also been combined to sequence other cereal genomes (Table 1). Rice, *Oryza sativa* ssp. *japonica* cv. Nipponbare, was sequenced by the International Rice Genome Sequencing Project (IRGSP) using a BAC-by-BAC approach based on genetic maps, BAC and YAC physical maps [23]. The resultant assembly included two earlier draft genome assemblies of rice from Monsanto [37] and Syngenta [38] that were sequenced using a WGS approach. The US Department of Energy (DOE) and the Joint Genome Institute (JGI) have sequenced the *Sorghum bicolor* genome using a WGS approach and validated the resultant assembly with 27 individually sequenced BACs [28]. The integration of physical and genetic maps with a BAC-by-BAC approach has also been used to sequence maize using a minimum tilling path (MTP) of 16,848 BACs and 63 fosmids [27]. A similar physical map has also been generated for barley [39].

Several factors impact the outcome of a genome assembly. These include; sequence coverage, data quality, repeats in the target genome and sequence read lengths. Sequence coverage and data quality are addressed by current sequencing platforms which produce large volumes of data cost effectively with high read accuracy, though there is a potential bias in base calling [40]. Different sequencing technologies have different error profiles, with 454 sequencing tending to exhibit homopolymer length errors, while Illumina base calling errors tend to occur towards the end of reads. Furthermore, different assembly methods result in different impacts of errors, with de Brujin graph methods handling sequence errors in Illumina short read data well, due to the relatively high k-mer coverage, compared to overlap layout consensus approaches frequently used for longer 454 and Sanger reads.

Table 1. Current sequenced cereal genomes. All assemblies are usually shorter than the predicted genome size.

Crop	Assembly/Genome Size (Mb)	Year	Sequencing strategy	Reference
Oryza sativa ssp. japonica (Nipponbare)	370/389	2005	Sanger, BAC-by-BAC	[23]
Oryza sativa ssp. japonica (Nipponbare)	389/420	2002	Sanger, WGS	[38]
Oryza sativa ssp. indica	362/466	2002	Sanger, WGS	[191]
Setaria italica (Foxtail Millet)	423/515	2012	Illumina, WGS	[192]
Sorghum bicolor (L.) Moench	679/730	2009	Sanger, WGS	[28]
Zea mays (Palomero Toluqueno) (popcorn)	177/2100	2009	Sanger, WGS	[193]
Zea mays (B73)	2000/2300	2009	Sanger, BAC-by-BAC	[27]
Triticum aestivum (Bread wheat)	*/17000	2012	454, WGS	[25]
Hordeum vulgare (Barley)	4900/5100	2012	454, BAC-by-BAC	[194]
Aegilops tauschii	4491/4630	2013	Illumina, 454, WGS	[195]
Triticum urartu	3920/4940	2013	Illumina, WGS	[196]

* The *Triticum aestivum* assembly was that of orthologous genic sequences.

Repeats, either due to transposons, centromeric regions, ribosomal genes or polyploidy affect the quality of sequence assembly, and their impact is also dependent on the assembly algorithm applied. For many genomes, and especially highly repetitive cereal genomes, repeats pose the greatest challenge to attaining accurate assemblies. Long read lengths that span repeats would be desirable, but the current main NGS sequencing platforms have read length limits of 1 kbp. Greater read lengths can be obtained with some third generation sequencing technologies, but with these, sequence quality is compromised and they still would not span the extensive repetitive regions observed in many cereals. As such, a significant shortfall of current sequencing and assembly methods is the poor resolution of repeats, often resulting in collapsed repeats [40,41] within assemblies. The application of mate pair (MP) sequence data, where reads are several kbp apart, improves the resolution of repeats, and this has greatly expanded the scope of WGS genome assembly projects. It is expected that read lengths and MP technology improvements will continue to enhance the application of NGS technologies for sequencing complex cereal crop genomes.

3. Genome Characterization

3.1. Orthology and Synteny Based Characterisation

Marker development is greatly dependent on access to well characterised reference genomes from which gene prediction, annotation and trait association follows. For cereal genomes without well-characterised reference genomes, gene orthology to closely related species can be used to assist in gene prediction and annotation. Gene orthology is a generally accepted approach to infer gene function for genes of newly sequenced genomes sharing an ancestor with a well-characterised reference. However, recent studies have showed that orthologous relationships do not necessarily imply functional equivalence, specifically in the context of complex evolutionary history, as reviewed in [42].

Cereal genomes exhibit complex evolutionary histories, and as such, orthology based synteny is currently the preferred approach to functional annotation of novel cereal genomes. Such approaches in

wheat using isolated chromosomes and chromosome arms 3B, 4A, 4BS, 4D, 5A, 5D, 7BS, 7DS [32,33,35,43–53] are based on synteny conservation with multiple closely related grasses such as rice (*Oryza sativa*) [23], sorghum (Sorghum bicolor) [28] and Brachypodium [54]. Rice and Brachypodium have ~80% of their genes in conserved syntenic positions, Brachypodium being the closest relative to the *Triticeae,* having diverged around 25–30 million years ago (MYA), while ~40 MYA, divergence between rice and Brachypodium occurred, and sorghum diverged earlier at ~50 MYA [54–56]. As such, wheat and Brachypodium have more than 80% of their genes being syntenic [32]. Despite the success in the use of synteny for annotation of genes, the identification of non-syntenic genes remains a challenge. Exploiting multiple synteny observed among the *Triticeae* and leveraging on previous genomic studies still remains useful as it gives greater confidence in functional inference and trait association and continues to be applied to cereal genomes.

3.2. Single Nucleotide Polymorphisms (SNPs)

Traditional marker systems such as restriction fragment length polymorphism (RFLPs) [57] have been applied in wheat [58–61], rice [62–65], barley [66–69], sorghum [70–73] and maize [74–76]. RFLPs were replaced by amplified fragment length polymorphisms (AFLPs) [77] and simple sequence repeats (SSRs) [78], which in turn have mostly been replaced by single nucleotide polymorphisms (SNPs) [79–81]. AFLPs have been widely applied to cereals including maize [82–89], sorghum [90–92], barley [93–97] and wheat [98–102], while SSRs have been exploited for diversity studies in sorghum [103,104], rice [105–108], wheat [104,107–110], maize [90,111], soybean [112] and millet [113]. SSRs have also been successfully used for genetic mapping studies in several cereals such as Tef (*Eragrotis tef*) [114], sorghum [115], soybean [116–118], maize [117], rice [119], wheat [120–127], rice and wheat [128] and millet [129,130]. Additionally, SSRs have been used for mapping of complex traits, for example in wheat [53,131–133]. SSRs have also been mined from ESTs [134–138], though EST based SSRs have been shown to have lower polymorphism when compared to genomic SSRs [104,109]. Despite this, EST SSRs have been applied across cereals [128,139].

SNPs are now the most common form of marker for genetic analysis [140–142]. They are abundant in plant genomes and their abundance provides very high resolution compared to other markers [104,109]. SNPs can be categorised as transitions or transversions [143,144]. Transitions are where the differing nucleotides are both purines (A/G) or both pyrimidines (C/T). When the SNP is between a purine and a pyrimidine, (C/G, A/T, C/A, or T/G) the SNPs are categorised as transversions. While indels are not true SNPs, they are sometimes considered as SNP markers, as they can be assayed in the same way as SNP markers.

Given the prevalence of genome duplication in plants [145,146], and specifically cereals [147], SNP identification is often confounded due to homoeologous and paralogous genes. This genome complexity makes SNP discovery a significant challenge. For example, about 40% of SNPs predicted in maize have been attributed to paralogous genes [27,148]. In addition to genome complexity, the high rate of sequence error in NGS data generates a further challenge for SNP discovery. Several approaches have been used to assess and improve SNP calling accuracy, these include a SNP redundancy score, which is a count of how frequently a SNP is observed at a particular locus [149],

and the transition/transversion ratio can also be used to provide an indication of the overall SNP prediction accuracy. This is as a result of higher mutation rates observed in methylated C nucleotides [150], although other mechanisms such as UV radiation are also thought to contribute [151].

The large data volumes produced by Illumina sequencing enables the identification of high-density SNP markers, potentially driving genomics assisted crop improvement in complex crops, such as wheat, in the future [152,153] and further revolutionising genotyping by sequencing (GBS) approaches. This is evident in wheat where more than 900,000 SNPs have been identified on the group 7 chromosomes with 93% validation accuracy [154,155], and 14,078 SNPs identified from 6,255 distinct wheat reference sequences with a 65% validation rate [156]. Similar approaches to SNP discovery using Illumina data have also been successful in rice, with the identification of 3.6 million SNPs from 517 rice landraces, providing a model for complex trait association [157], and more than 1 million SNPs identified between six inbred maize lines [158].

Several tools have been developed for the discovery of SNPs from plant NGS data [159–163]. These include AutoSNPdb, which determines SNPs from 454 transcriptome data [164–166] (http://www.autosnpdb.appliedbioinformatics.com.au/) storing results in a relational database for web based querying. AutoSNPdb is based on autoSNP software which scores SNPs based on redundancy score and co-segregation [149,167]. Second-Generation Sequencing autoSNP (SGSautoSNP) has been applied to identify more than 1.5 million SNPs in canola, with accuracy greater than 95% (D. Edwards, unpublished data) with similar success in wheat with an accuracy of greater than 93% of SNPs being between wheat cultivars [154]. Other approaches involve targeted genomic SNP identification [168], and AGSNP, which has been applied to identify 497,118 candidate SNPs in *Ae. tauschii* [169]. Some of the identified SNPs have been applied for the development of high throughput Illumina Infinium assays, for example in barley [170], wheat [171], canola and maize [172] .

3.3. Genotyping by Sequencing (GBS)

Genotyping by sequencing (GBS) extends traditional approaches to genotyping by exploiting NGS technologies to calling genotypes. The first published GBS approach [148] involved the use of 27 inbred maize lines, reducing the complexity of the genome with methylation sensitive restriction enzymes followed by sequencing and mapping the reads to the B73 maize reference genome [173]. Polymorphic sites among the inbred lines were then determined which showed evidence for specific regions involved in domestication and the geographic adaptation of maize. Similar approaches have recently been applied to 50 rice accessions [174]. This study identified candidate domestication genes that had low diversity in the cultivated rice accessions compared to wild type accessions. Two well-known rice domestication genes, *prog1* [175,176] and *sh4* [177], associated with erect growth and pod shattering, respectively, were identified. The main advantage with this approach over other genotyping methods is that no predetermined markers are required to study a particular population, as the markers are developed during the genotyping. Such approaches have been successfully demonstrated in rice, both with parental lines [178,179] and without the use of parental lines [180], as well as more recently in durum wheat [181].

The high marker density associated with GBS makes it a suitable platform for genome wide association studies (GWAS). A recent study in *Arabidopsis arenosa* [182] in which 12 *A. arenosa*

individuals selected from Austria and Germany were sequenced, identified selective sweeps within the genome and indicated genes associated with housekeeping processes such as chromosome segregation, cohesion, transcription regulation and homologous recombination which were active as a result of genome duplication. In particular, a non-synonymous mutation in the meiosis gene *ASYNAPSIS1* was identified as a rare variant in diploid *A. arenosa,* highlighting ongoing mutations in the diploid genome. A larger study in rice [157] in which 517 rice landraces of *Oryza sativa indica* subspecies were sequenced with subsequent GWAS analysis of 14 agronomic traits, showed approximately 36% of the identified loci explained phenotypic differences.

The advent of NGS technologies and associated reduction in sequencing costs has made skim based genotyping by sequencing, without complexity reduction, feasible. Skim GBS offers advantages over other genotyping by sequencing methods in that it is genome wide with flexible density determined by the quantity of data generated. Other GBS approaches rely on targeting specific regions on the genome. Such approaches include the use of complexity reduction of polymorphic sequences (CRoPS) methods as shown in maize [183,184] and wheat [185], the use of restriction enzymes followed by sequencing in mapping populations in wheat, maize and barley [146,186,187].

As GBS approaches offer quicker and more accurate recombination breakpoint determination, with higher accuracy and resolution due to high density, more individuals can be analysed at a relatively lower cost. As DNA sequencing costs continue to decline, it is expected that GBS without the bias of complexity reduction will become increasingly popular for cereal genome analysis.

3. Conclusions

As more cereal genomes are sequenced, storage and analysis of this vast amount of data has been an increasing challenge, though this challenge has been met with advances in bioinformatics [188]. With further improvements to sequencing platforms resulting in longer reads, combined with the expansion of third generation single molecule sequencing technologies, genome sequencing GBS and GWAS are likely to increase in popularity. As an increasing number of cereal crop genomes are sequenced, there will be a move away from the generation of genome references and a greater focus on trait association, leading to a greater understanding of the function of these genomes on a population scale and bridging the genotype to phenotype divide [189] with insights into the emerging concept of the 'Pangenome' [190] in the context of crop breeding and improvement.

Acknowledgments

This work was supported by the Australian Research Council Projects LP110100200, LP0989200 and DP0985953. Support from the Queensland Cyber Infrastructure Foundation (QCIF), the Australian Genome Research Facility (AGRF), Australia Awards and the Australian Partnership for Advanced Computing (APAC) is gratefully acknowledged.

Conflicts of Interest

The authors declare no conflict of interest.

References

1. Meyers, L.A.; Levin, D.A. On the abundance of polyploids in flowering plants. *Evolution* **2006**, *60*, 1198–1206.
2. Leitch, A.R.; Leitch, I.J. Genomic plasticity and the diversity of polyploid plants. *Science* **2008**, *320*, 481–483.
3. Li, H. A statistical framework for SNP calling, mutation discovery, association mapping and population genetical parameter estimation from sequencing data. *Bioinformatics* **2011**, *27*, 2987–2993.
4. Kim, S.Y.; Lohmueller, K.E.; Albrechtsen, A.; Li, Y.; Korneliussen, T.; Tian, G.; Grarup, N.; Jiang, T.; Andersen, G.; Witte, D.; *et al.* Estimation of allele frequency and association mapping using next-generation sequencing data. *BMC Bioinformatics* **2011**, *12*, 231.
5. Sanger, F.; Nicklen, S.; Coulson, A.R. DNA sequencing with chain-terminating inhibitors. *Proc. Natl. Acad. Sci. USA* **1977**, *74*, 5463–5467.
6. Sanger, F. The Croonian Lecture, 1975. Nucleotide sequences in DNA. *Proc. R. Soc. Lond. B Biol. Sci.* **1975**, *191*, 317–333.
7. Zimmermann, J.; Voss, H.; Schwager, C.; Stegemann, J.; Ansorge, W. Automated Sanger dideoxy sequencing reaction protocol. *FEBS Lett.* **1988**, *233*, 432–436.
8. Shendure, J.; Ji, H. Next-generation DNA sequencing. *Nat. Biotechnol.* **2008**, *26*, 1135–1145.
9. Margulies, M.; Egholm, M.; Altman, W.E.; Attiya, S.; Bader, J.S.; Bemben, L.A.; Berka, J.; Braverman, M.S.; Chen, Y.-J.; Chen, Z.; Dewell, S.B.; *et al.* Genome sequencing in microfabricated high-density picolitre reactors. *Nature* **2005**, *437*, 376–380.
10. Bentley, D.R.; Balasubramanian, S.; Swerdlow, H.P.; Smith, G.P.; Milton, J.; Brown, C.G.; Hall, K.P.; Evers, D.J.; Barnes, C.L.; Bignell, H.R.; *et al.* Accurate whole human genome sequencing using reversible terminator chemistry. *Nature* **2008**, *456*, 53–59.
11. Edwards, D.; Wilcox, S.; Barrero, R.A.; Fleury, D.; Cavanagh, C.R.; Forrest, K.L.; Hayden, M.J.; Moolhuijzen, P.; Keeble-Gagnère, G.;*et al*. Bread matters: A national initiative to profile the genetic diversity of Australian wheat. *Plant Biotechnol. J.* **2012**, *10*, 703–708.
12. Shulaev, V.; Sargent, D.J.; Crowhurst, R.N.; Mockler, T.C.; Folkerts, O.; Delcher, A.L.; Jaiswal, P.; Mockaitis, K.; Liston, A.; Mane, S.P.; *et al.* The genome of woodland strawberry (*Fragaria vesca*). *Nat. Genet.* **2011**, *43*, 109–116.
13. Dong, C.-H.; Li, C.; Yan, X.-H.; Huang, S.-M.; Huang, J.-Y.; Wang, L.-J.; Guo, R.-X.; Lu, G.-Y.; Zhang, X.-K.; Fang, X.-P.; *et al.* Gene expression profiling of *Sinapis alba* leaves under drought stress and rewatering growth conditions with Illumina deep sequencing. *Mol. Biol. Rep.* **2012**, *39*, 5851–5857.
14. Williams-Carrier, R.; Stiffler, N.; Belcher, S.; Kroeger, T.; Stern, D.B.; Monde, R.-A.; Coalter, R.; Barkan, A. Use of Illumina sequencing to identify transposon insertions underlying mutant phenotypes in high-copy mutator lines of maize. *Plant J.* **2010**, *63*, 167–177.
15. Imelfort, M.; Edwards, D. De novo sequencing of plant genomes using second-generation technologies. *Brief. Bioinformatics* **2009**, *10*, 609–618.
16. Edwards, D.; Batley, J.; Snowdon, R.J. Accessing complex crop genomes with next-generation sequencing. *Theor. Appl. Genet.* **2013**, *126*, 1–11.

17. Rothberg, J.M.; Hinz, W.; Rearick, T.M.; Schultz, J.; Mileski, W.; Davey, M.; Leamon, J.H.; Johnson, K.; Milgrew, M.J.; Edwards, M.; *et al.* An integrated semiconductor device enabling non-optical genome sequencing. *Nature* **2011**, *475*, 348–352.
18. Eid, J.; Fehr, A.; Gray, J.; Luong, K.; Lyle, J.; Otto, G.; Peluso, P.; Rank, D.; Baybayan, P.; Bettman, B.; Bibillo, A.; *et al.* Real-time DNA sequencing from single polymerase molecules. *Science* **2009**, *323*, 133–138.
19. Mason, C.E.; Elemento, O. Faster sequencers, larger datasets, new challenges. *Genome Biol.* **2012**, *13*, 314.
20. Au, K.F.; Underwood, J.G.; Lee, L.; Wong, W.H. Improving PacBio long read accuracy by short read alignment. *PLoS ONE* **2012**, *7*, e46679.
21. Kasianowicz, J.J.; Brandin, E.; Branton, D.; Deamer, D.W. Characterization of individual polynucleotide molecules using a membrane channel. *Proc. Natl. Acad. Sci. U.S.A.* **1996**, *93*, 13770–13773.
22. Stoddart, D.; Heron, A.J.; Mikhailova, E.; Maglia, G.; Bayley, H. Single-nucleotide discrimination in immobilized DNA oligonucleotides with a biological nanopore. *Proc. Natl. Acad. Sci. U.S.A.* **2009**, *106*, 7702–7707.
23. International Rice Genome Sequencing Project. The map-based sequence of the rice genome. *Nature* **2005**, *436*, 793–800.
24. Flavell, R.B.; Rimpau, J.R.; Smith, D.B. Repeated sequence DNA relationships in four cereal genomes. *Chromosoma* **1977**, *63*, 205–222.
25. Brenchley, R.; Spannagl, M.; Pfeifer, M.; Barker, G.L.A.; D'Amore, R.; Allen, A.M.; McKenzie, N.; Kramer, M.; Kerhornou, A.; Bolser, D.; *et al.* Analysis of the bread wheat genome using whole-genome shotgun sequencing. *Nature* **2012**, *491*, 705–710.
26. SanMiguel, P.; Gaut, B.S.; Tikhonov, A.; Nakajima, Y.; Bennetzen, J.L. The paleontology of intergene retrotransposons of maize. *Nat. Genet.* **1998**, *20*, 43–45.
27. Schnable, P.S.; Ware, D.; Fulton, R.S.; Stein, J.C.; Wei, F.; Pasternak, S.; Liang, C.; Zhang, J.; Fulton, L.; Graves, T.A.; *et al.* The B73 maize genome: complexity, diversity, and dynamics. *Science* **2009**, *326*, 1112–1115.
28. Paterson, A.H.; Bowers, J.E.; Bruggmann, R.; Dubchak, I.; Grimwood, J.; Gundlach, H.; Haberer, G.; Hellsten, U.; Mitros, T.; Poliakov, A.; *et al.* The *Sorghum bicolor* genome and the diversification of grasses. *Nature* **2009**, *457*, 551–556.
29. Doležel, J.; Kubaláková, M.; Paux, E.; Bartos, J.; Feuillet, C. Chromosome-based genomics in the cereals. *Chromosome Res.* **2007**, *15*, 51–66.
30. Duran, C.; Edwards, D.; Batley, J. Genetic Maps and the Use of Synteny. In *Plant Genomics*; Gustafson, J.P., Langridge, P., Somers, D.J., Eds.; Humana Press: New York, NY, USA, 2009; Volume 513, pp. 41–55.
31. Doležel, J.; Kubaláková, M.; Bartos, J.; Macas, J. Flow cytogenetics and plant genome mapping. *Chromosome Res.* **2004**, *12*, 77–91.
32. Berkman, P.J.; Visendi, P.; Lee, H.C.; Stiller, J.; Manoli, S.; Lorenc, M.T.; Lai, K.; Batley, J.; Fleury, D.; Simková, H.; *et al.* Dispersion and domestication shaped the genome of bread wheat. *Plant Biotechnol. J.* **2013**, *11*, 564–571.

33. Berkman, P.J.; Skarshewski, A.; Manoli, S.; Lorenc, M.T.; Stiller, J.; Smits, L.; Lai, K.; Campbell, E.; Kubaláková, M.; Simková, H.; *et al.* Sequencing wheat chromosome arm 7BS delimits the 7BS/4AL translocation and reveals homoeologous gene conservation. *Theor. Appl. Genet.* **2011**, *124*, 423–432.
34. Berkman, P.J.; Skarshewski, A.; Lorenc, M.T.; Lai, K.; Duran, C.; Ling, E.Y.S.; Stiller, J.; Smits, L.; Imelfort, M.; Manoli, S.; *et al.* Sequencing and assembly of low copy and genic regions of isolated *Triticum aestivum* chromosome arm 7DS. *Plant Biotechnol. J.* **2011**, *9*, 768–775.
35. Hernandez, P.; Martis, M.; Dorado, G.; Pfeifer, M.; Gálvez, S.; Schaaf, S.; Jouve, N.; Simková, H.; Valárik, M.; Doležel, J.; *et al.* Next-generation sequencing and syntenic integration of flow-sorted arms of wheat chromosome 4A exposes the chromosome structure and gene content. *Plant J.* **2012**, *69*, 377–386.
36. Nie, X.; Li, B.; Wang, L.; Liu, P.; Biradar, S.S.; Li, T.; Doležel, J.; Edwards, D.; Luo, M.; Weining, S. Development of chromosome-arm-specific microsatellite markers in *Triticum aestivum* (Poaceae) using NGS technology. *Am. J. Bot.* **2012**, *99*, e369–e371.
37. Barry, G.F. The use of the Monsanto draft rice genome sequence in research. *Plant Physiol.* **2001**, *125*, 1164–1165.
38. Goff, S.A.; Ricke, D.; Lan, T.-H.; Presting, G.; Wang, R.; Dunn, M.; Glazebrook, J.; Sessions, A.; Oeller, P.; Varma, H.; *et al.* A draft sequence of the rice genome (*Oryza sativa* L. ssp. *japonica*). *Sci. New Ser.* **2002**, *296*, 92–100.
39. Mayer, K.F.X.; Waugh, R.; Brown, J.W.S.; Schulman, A.; Langridge, P.; Platzer, M.; Fincher, G.B.; Muehlbauer, G.J.; Sato, K.; Close, T.J.; *et al.* International Barley Genome Sequencing Consortium, A physical; genetic and functional sequence assembly of the barley genome. *Nature* **2012**, *491*, 711–716.
40. Dohm, J.C.; Lottaz, C.; Borodina, T.; Himmelbauer, H. Substantial biases in ultra-short read data sets from high-throughput DNA sequencing. *Nucleic Acids Res.* **2008**, *36*, e105.
41. Salzberg, S.L.; Phillippy, A.M.; Zimin, A.; Puiu, D.; Magoc, T.; Koren, S.; Treangen, T.J.; Schatz, M.C.; Delcher, A.L.; Roberts, M.; *et al.* A critical evaluation of genome assemblies and assembly algorithms. *Genome Res.* **2012**, *22*, 557–567.
42. Gabaldón, T.; Koonin, E.V. Functional and evolutionary implications of gene orthology. *Nat. Rev. Genet.* **2013**, *14*, 360–366.
43. Carter, A.H.; Garland-Campbell, K.; Morris, C.F.; Kidwell, K.K. Chromosomes 3B and 4D are associated with several milling and baking quality traits in a soft white spring wheat (*Triticum aestivum* L.) population. *Theor. Appl. Genet.* **2012**, *124*, 1079–1096.
44. Vitulo, N.; Albiero, A.; Forcato, C.; Campagna, D.; Dal Pero, F.; Bagnaresi, P.; Colaiacovo, M.; Faccioli, P.; Lamontanara, A.; Simková, H.; *et al.* First survey of the wheat chromosome 5A composition through a next generation sequencing approach. *PLoS One* **2011**, *6*, e26421.
45. Rustenholz, C.; Choulet, F.; Laugier, C.; Safár, J.; Simková, H.; Doležel, J.; Magni, F.; Scalabrin, S.; Cattonaro, F.; Vautrin, S.; *et al.* A 3,000-loci transcription map of chromosome 3B unravels the structural and functional features of gene islands in hexaploid wheat. *Plant Physiol.* **2011**, *157*, 1596–1608.

46. Cseh, A.; Kruppa, K.; Molnár, I.; Rakszegi, M.; Doležel, J.; Molnár-Láng, M. Characterization of a new 4BS.7HL wheat-barley translocation line using GISH, FISH, and SSR markers and its effect on the β-glucan content of wheat. *Genome* **2011**, *54*, 795–804.
47. Yoshida, T.; Nishida, H.; Zhu, J.; Nitcher, R.; Distelfeld, A.; Akashi, Y.; Kato, K.; Dubcovsky, J. *Vrn-D4* is a vernalization gene located on the centromeric region of chromosome 5D in hexaploid wheat. *Theor. Appl. Genet.* **2010**, *120*, 543–552.
48. Breen, J.; Wicker, T.; Kong, X.; Zhang, J.; Ma, W.; Paux, E.; Feuillet, C.; Appels, R.; Bellgard, M. A highly conserved gene island of three genes on chromosome 3B of hexaploid wheat: diverse gene function and genomic structure maintained in a tightly linked block. *BMC Plant Biol.* **2010**, *10*, 98.
49. Saintenac, C.; Falque, M.; Martin, O.C.; Paux, E.; Feuillet, C.; Sourdille, P. Detailed recombination studies along chromosome 3B provide new insights on crossover distribution in wheat (*Triticum aestivum* L.). *Genetics* **2009**, *181*, 393–403.
50. Alfares, W.; Bouguennec, A.; Balfourier, F.; Gay, G.; Bergès, H.; Vautrin, S.; Sourdille, P.; Bernard, M.; Feuillet, C. Fine mapping and marker development for the crossability gene *SKr* on chromosome 5BS of hexaploid wheat (*Triticum aestivum* L.). *Genetics* **2009**, *183*, 469–481.
51. Ren, X.-B.; Lan, X.-J.; Liu, D.-C.; Wang, J.-L.; Zheng, Y.-L. Mapping QTLs for pre-harvest sprouting tolerance on chromosome 2D in a synthetic hexaploid wheat x common wheat cross. *J. Appl. Genet.* **2008**, *49*, 333–341.
52. Paux, E.; Sourdille, P.; Salse, J.; Saintenac, C.; Choulet, F.; Leroy, P.; Korol, A.; Michalak, M.; Kianian, S.; Spielmeyer, W.; *et al.* A physical map of the 1-gigabase bread wheat chromosome 3B. *Science* **2008**, *322*, 101–104.
53. Maccaferri, M.; Mantovani, P.; Tuberosa, R.; Deambrogio, E.; Giuliani, S.; Demontis, A.; Massi, A.; Sanguineti, M.C. A major QTL for durable leaf rust resistance widely exploited in durum wheat breeding programs maps on the distal region of chromosome arm 7BL. *Theor. Appl. Genet.* **2008**, *117*, 1225–1240.
54. International Brachypodium Initiative. Genome sequencing and analysis of the model grass *Brachypodium distachyon*. *Nature* **2010**, *463*, 763–768.
55. Wicker, T.; Mayer, K.F.X.; Gundlach, H.; Martis, M.; Steuernagel, B.; Scholz, U.; Simková, H.; Kubaláková, M.; Choulet, F.; Taudien, S.; *et al.* Frequent gene movement and pseudogene evolution is common to the large and complex genomes of wheat, barley, and their relatives. *Plant Cell* **2011**, *23*, 1706–1718.
56. Bossolini, E.; Wicker, T.; Knobel, P.A.; Keller, B. Comparison of orthologous loci from small grass genomes Brachypodium and rice: Implications for wheat genomics and grass genome annotation. *Plant J.* **2007**, *49*, 704–717.
57. Botstein, D.; White, R.L.; Skolnick, M.; Davis, R.W. Construction of a genetic linkage map in man using restriction fragment length polymorphisms. *Am. J. Hum. Genet.* **1980**, *32*, 314–331.
58. Asakura, N.; Mori, N.; Nakamura, C.; Ohtsuka, I. Genotyping of the Q locus in wheat by a simple PCR-RFLP method. *Genes Genet. Syst.* **2009**, *84*, 233–237.
59. Han, F.P.; Fedak, G.; Benabdelmouna, A.; Armstrong, K.; Ouellet, T. Characterization of six wheat x *Thinopyrum intermedium* derivatives by GISH, RFLP, and multicolor GISH. *Genome* **2003**, *46*, 490–495.

60. Ma, X.F.; Ross, K.; Gustafson, J.P. Physical mapping of restriction fragment length polymorphism (RFLP) markers in homoeologous groups 1 and 3 chromosomes of wheat by *in situ* hybridization. *Genome* **2001**, *44*, 401–412.
61. Sim, S.; Chang, T.; Curley, J.; Warnke, S.E.; Barker, R.E.; Jung, G. Chromosomal rearrangements differentiating the ryegrass genome from the Triticeae, oat, and rice genomes using common heterologous RFLP probes. *Theor. Appl. Genet.* **2005**, *110*, 1011–1019.
62. Singh, R.K.; Mishra, R.P.N.; Jaiswal, H.K.; Kumar, V.; Pandey, S.P.; Rao, S.B.; Annapurna, K. Isolation and identification of natural endophytic rhizobia from rice (*Oryza sativa* L.) through rDNA PCR-RFLP and sequence analysis. *Curr. Microbiol.* **2006**, *52*, 345–349.
63. Huang, W.; Wang, L.; Yi, P.; Tan, X.-L.; Zhang, X.-M.; Zhang, Z.-J.; Li, Y.-S.; Zhu, Y.-G. RFLP analysis for mitochondrial genome of CMS-rice. *Yi Chuan Xue Bao* **2006**, *33*, 330–338.
64. Xu, X.F.; Mei, H.W.; Luo, L.J.; Cheng, X.N.; Li, Z.K. RFLP-facilitated investigation of the quantitative resistance of rice to brown planthopper (*Nilaparvata lugens*). *Theor. Appl. Genet.* **2002**, *104*, 248–253.
65. Lu, B.-R.; Zheng, K.L.; Qian, H.R.; Zhuang, J.Y. Genetic differentiation of wild relatives of rice as assessed by RFLP analysis. *Theor. Appl. Genet.* **2002**, *106*, 101–106.
66. Maestri, E.; Malcevschi, A.; Massari, A.; Marmiroli, N. Genomic analysis of cultivated barley (*Hordeum vulgare*) using sequence-tagged molecular markers. Estimates of divergence based on RFLP and PCR markers derived from stress-responsive genes, and simple-sequence repeats (SSRs). *Mol. Genet. Genomics* **2002**, *267*, 186–201.
67. Künzel, G.; Waugh, R. Integration of microsatellite markers into the translocation-based physical RFLP map of barley chromosome 3H. *Theor. Appl. Genet.* **2002**, *105*, 660–665.
68. Saeki, K.; Miyazaki, C.; Hirota, N.; Saito, A.; Ito, K.; Konishi, T. RFLP mapping of BaYMV resistance gene *rym3* in barley (*Hordeum vulgare*). *Theor. Appl. Genet.* **1999**, *99*, 727–732.
69. Michalek, W.; Künzel, G.; Graner, A. Sequence analysis and gene identification in a set of mapped RFLP markers in barley (*Hordeum vulgare*). *Genome* **1999**, *42*, 849–853.
70. Jordan, D.R.; Tao, Y.; Godwin, I.D.; Henzell, R.G.; Cooper, M.; McIntyre, C.L. Prediction of hybrid performance in grain sorghum using RFLP markers. *Theor. Appl. Genet.* **2003**, *106*, 559–567.
71. Schloss, J.; Mitchell, E.; White, M.; Kukatla, R.; Bowers, E.; Paterson, H.; Kresovich, S. Characterization of RFLP probe sequences for gene discovery and SSR development in *Sorghum bicolor* (L.) Moench. *Theor. Appl. Genet.* **2002**, *105*, 912–920.
72. Haussmann, G.; Hess, E.; Seetharama, N.; Welz, G.; Geiger, H. Construction of a combined sorghum linkage map from two recombinant inbred populations using AFLP, SSR, RFLP, and RAPD markers, and comparison with other sorghum maps. *Theor. Appl. Genet.* **2002**, *105*, 629–637.
73. Subudhi, P.K.; Nguyen, H.T. Linkage group alignment of sorghum RFLP maps using a RIL mapping population. *Genome* **2000**, *43*, 240–249.
74. Gauthier, P.; Gouesnard, B.; Dallard, J.; Redaelli, R.; Rebourg, C.; Charcosset, A.; Boyat, A. RFLP diversity and relationships among traditional European maize populations. *Theor. Appl. Genet.* **2002**, *105*, 91–99.

75. Dubreuil, P.; Charcosset, A. Relationships among maize inbred lines and populations from European and North-American origins as estimated using RFLP markers. *Theor. Appl. Genet.* **1999**, *99*, 473–480.
76. Lin, B.Y.; Peng, S.F.; Chen, Y.J.; Chen, H.S.; Kao, C.F. Physical mapping of RFLP markers on four chromosome arms in maize using terminal deficiencies. *Mol. Gen. Genet.* **1997**, *256*, 509–516.
77. Vos, P.; Hogers, R.; Bleeker, M.; Reijans, M.; van de Lee, T.; Hornes, M.; Frijters, A.; Pot, J.; Peleman, J.; Kuiper, M. AFLP: a new technique for DNA fingerprinting. *Nucleic Acids Res.* **1995**, *23*, 4407–4414.
78. Tautz, D.; Schlötterer, C. Simple sequences. *Curr. Opin. Genet. Dev.* **1994**.
79. Batley, J.; Jewell, E.; Edwards, D. Automated Discovery of Single Nucleotide Polymorphism and Simple Sequence Repeat Molecular Genetic Markers. In *Methods in Molecular Biology*; Edwards, D., Ed.; Humana Press: New York, NY, USA, 2007; Volume 406, pp. 473–494.
80. Batley, J.; Edwards, D. Mining for Single Nucleotide Polymorphism (SNP) and Simple Sequence Repeat (SSR) Molecular Genetic Markers. In *Bioinformatics for DNA Sequence Analysis*; Posada, D., Ed.; Humana Press: New York, NY, USA, 2009; pp. 303–322.
81. Duran, C.; Edwards, D.; Batley, J. Molecular marker discovery and genetic map visualisation. *Bioinformatics* **2009**, *4*, 165–189.
82. Hartings, H.; Berardo, N.; Mazzinelli, G.F.; Valoti, P.; Verderio, A.; Motto, M. Assessment of genetic diversity and relationships among maize (*Zea mays* L.) Italian landraces by morphological traits and AFLP profiling. *Theor. Appl. Genet.* **2008**, *117*, 831–842.
83. Zhang, Z.F.; Wang, Y.; Zheng, Y.L. AFLP and PCR-based markers linked to *Rf3*, a fertility restorer gene for S cytoplasmic male sterility in maize. *Mol. Genet. Genomics* **2006**, *276*, 162–169.
84. Zhang, F.; Wan, X.-Q.; Pan, G.-T. QTL mapping of *Fusarium moniliforme* ear rot resistance in maize. 1. Map construction with microsatellite and AFLP markers. *J. Appl. Genet.* **2006**, *47*, 9–15.
85. Schrag, T.A.; Melchinger, A.E.; Sørensen, A.P.; Frisch, M. Prediction of single-cross hybrid performance for grain yield and grain dry matter content in maize using AFLP markers associated with QTL. *Theor. Appl. Genet.* **2006**, *113*, 1037–1047.
86. Peng, S.-F.; Lin, Y.-P.; Lin, B.-Y. Characterization of AFLP sequences from regions of maize B chromosome defined by 12 B-10L translocations. *Genetics* **2005**, *169*, 375–388.
87. Miranda Oliveira, K.; Rios Laborda, P.; Augusto F Garcia, A.; Zagatto Paterniani, M.E. A.G.; de Souza, A.P. Evaluating genetic relationships between tropical maize inbred lines by means of AFLP profiling. *Hereditas* **2004**, *140*, 24–33.
88. Cai, H.-W.; Gao, Z.-S.; Yuyama, N.; Ogawa, N. Identification of AFLP markers closely linked to the *rhm* gene for resistance to southern corn leaf blight in maize by using bulked segregant analysis. *Mol. Genet. Genomics* **2003**, *269*, 299–303.
89. Agrama, H.A.; Houssin, S.F.; Tarek, M.A. Cloning of AFLP markers linked to resistance to *Peronosclerospora sorghi* in maize. *Mol. Genet. Genomics* **2002**, *267*, 814–819.
90. Legesse, B.W.; Myburg, A.A.; Pixley, K.V.; Botha, A.M. Genetic diversity of African maize inbred lines revealed by SSR markers. *Hereditas* **2007**, *144*, 10–17.
91. Wen, L.; Tang, H.V.; Chen, W.; Chang, R.; Pring, D.R.; Klein, P.E.; Childs, K.L.; Klein, R.R. Development and mapping of AFLP markers linked to the sorghum fertility restorer gene *rf4*. *Theor. Appl. Genet.* **2002**, *104*, 577–585.

92. Klein, P.E.; Klein, R.R.; Cartinhour, S.W.; Ulanch, P.E.; Dong, J.; Obert, J.A.; Morishige, D.T.; Schlueter, S.D.; Childs, K.L.; Ale, M.; *et al.* A high-throughput AFLP-based method for constructing integrated genetic and physical maps: progress toward a sorghum genome map. *Genome Res.* **2000**, *10*, 789–807.
93. Zhang, D.; Ding, Y. Genetic diversity of wild close relatives of barley in Tibet of China revealed by AFLP. *Yi Chuan* **2007**, *29*, 725–730.
94. Takahashi, H.; Akagi, H.; Mori, K.; Sato, K.; Takeda, K. Genomic distribution of MITEs in barley determined by MITE-AFLP mapping. *Genome* **2006**, *49*, 1616–1620.
95. Komatsuda, T.; Maxim, P.; Senthil, N.; Mano, Y. High-density AFLP map of nonbrittle rachis 1 (*btr1*) and 2 (*btr2*) genes in barley (*Hordeum vulgare* L.). *Theor. Appl. Genet.* **2004**, *109*, 986–995.
96. He, C.; Sayed-Tabatabaei, B.E.; Komatsuda, T. AFLP targeting of the 1-cM region conferring the *vrs1* gene for six-rowed spike in barley, *Hordeum vulgare* L. *Genome* **2004**, *47*, 1122–1129.
97. Turpeinen, T.; Vanhala, T.; Nevo, E.; Nissilä, E. AFLP genetic polymorphism in wild barley (*Hordeum spontaneum*) populations in Israel. *Theor. Appl. Genet.* **2003**, *106*, 1333–1339.
98. Wang, Y.; Zhu, J.; Zhao, H.M.; Lei, D.H.; Wang, Z.Y.; Peng, Y.K.; Xie, C.J.; Sun, Q.X.; Liu, Z.Y.; Yang, Z.M. Screening and identification of the AFLP markers linked to a new powdery mildew resistance gene in wheat cultivar Brock. *Fen Zi Xi Bao Sheng Wu Xue Bao* **2008**, *41*, 294–300.
99. Ozbek, O.; Millet, E.; Anikster, Y.; Arslan, O.; Feldman, M. Spatio-temporal genetic variation in populations of wild emmer wheat, *Triticum turgidum* ssp. *dicoccoides*, as revealed by AFLP analysis. *Theor. Appl. Genet.* **2007**, *115*, 19–26.
100. Xu, D.H.; Ban, T. Conversion of AFLP markers associated with FHB resistance in wheat into STS markers with an extension-AFLP method. *Genome* **2004**, *47*, 660–665.
101. Tyrka, M. Fingerprinting of common wheat cultivars with an Alw44I-based AFLP method. *J. Appl. Genet.* **2004**, *45*, 405–410.
102. Zhou, W.; Kolb, F.L.; Bai, G.; Shaner, G.; Domier, L.L. Genetic analysis of scab resistance QTL in wheat with microsatellite and AFLP markers. *Genome* **2002**, *45*, 719–727.
103. Ng'uni, D.; Geleta, M.; Bryngelsson, T. Genetic diversity in sorghum (*Sorghum bicolor* (L.) Moench) accessions of Zambia as revealed by simple sequence repeats (SSR). *Hereditas* **2011**, *148*, 52–62.
104. Balfourier, F.; Roussel, V.; Strelchenko, P.; Exbrayat-Vinson, F.; Sourdille, P.; Boutet, G.; Koenig, J.; Ravel, C.; Mitrofanova, O.; Beckert, M.; Charmet, G. A worldwide bread wheat core collection arrayed in a 384-well plate. *Theor. Appl. Genet.* **2007**, *114*, 1265–1275.
105. Ashfaq, M.; Khan, A.S. Genetic diversity in basmati rice (*Oryza sativa L.*) germplasm as revealed by microsatellite (SSR) markers. *Genetika* **2012**, *48*, 62–71.
106. Zhang, P.; Li, J.; Li, X.; Liu, X.; Zhao, X.; Lu, Y. Population structure and genetic diversity in a rice core collection (*Oryza sativa* L.) investigated with SSR markers. *PLoS One* **2011**, *6*, e27565.
107. Hao, C.; Wang, L.; Ge, H.; Dong, Y.; Zhang, X. Genetic diversity and linkage disequilibrium in Chinese bread wheat (*Triticum aestivum* L.) revealed by SSR markers. *PLoS One* **2011**, *6*, e17279.
108. Achtar, S.; Moualla, M.Y.; Kalhout, A.; Röder, M.S.; MirAli, N. Assessment of genetic diversity among Syrian durum (*Triticum turgidum* ssp. *durum*) and bread wheat (*Triticum aestivum* L.) using SSR markers. *Genetika* **2010**, *46*, 1500–1506.

109. Roussel, V.; Leisova, L.; Exbrayat, F.; Stehno, Z.; Balfourier, F. SSR allelic diversity changes in 480 European bread wheat varieties released from 1840 to 2000. *Theor. Appl. Genet.* **2005**, *111*, 162–170.
110. Wang, H.; Wang, X.; Chen, P.; Liu, D. Assessment of genetic diversity of Yunnan, Tibetan, and Xinjiang wheat using SSR markers. *J. Genet. Genomics* **2007**, *34*, 623–633.
111. Yao, Q.; Yang, K.; Pan, G.; Rong, T. Genetic diversity of maize (*Zea mays* L.) landraces from southwest China based on SSR data. *J. Genet. Genomics* **2007**, *34*, 851–859.
112. Singh, R.K.; Bhatia, V.S.; Bhat, K.V.; Mohapatra, T.; Singh, N.K.; Bansal, K.C.; Koundal, K.R. SSR and AFLP based genetic diversity of soybean germplasm differing in photoperiod sensitivity. *Genet. Mol. Biol.* **2010**, *33*, 319–324.
113. Hu, X.; Wang, J.; Lu, P.; Zhang, H. Assessment of genetic diversity in broomcorn millet (*Panicum miliaceum* L.) using SSR markers. *J. Genet. Genomics* **2009**, *36*, 491–500.
114. Zeid, M.; Belay, G.; Mulkey, S.; Poland, J.; Sorrells, M.E. QTL mapping for yield and lodging resistance in an enhanced SSR-based map for tef. *Theor. Appl. Genet.* **2011**, *122*, 77–93.
115. Apotikar, D.B.; Venkateswarlu, D.; Ghorade, R.B.; Wadaskar, R.M.; Patil, J.V.; Kulwal, P.L. Mapping of shoot fly tolerance loci in sorghum using SSR markers. *J. Genet.* **2011**, *90*, 59–66.
116. Fu, S.; Zhan, Y.; Zhi, H.; Gai, J.; Yu, D. Mapping of SMV resistance gene *Rsc-7* by SSR markers in soybean. *Genetica* **2006**, *128*, 63–69.
117. Liu, J.-C.; Chu, Q.; Cai, H.-G.; Mi, G.-H.; Chen, F.-J. SSR linkage map construction and QTL mapping for leaf area in maize. *Yi Chuan* **2010**, *32*, 625–631.
118. Ha, B.-K.; Robbins, R.T.; Han, F.; Hussey, R.S.; Soper, J.F.; Boerma, H.R. SSR mapping and confirmation of soybean QTL from PI 437654 conditioning resistance to reniform nematode. *Crop Sci.* **2007**, *47*, 1336.
119. Su, C.-C.; Zhai, H.-Q.; Wang, C.-M.; Sun, L.-H.; Wan, J.-M. SSR mapping of brown planthopper resistance gene *Bph9* in kaharamana, an indica rice (*Oryza sativa* L.). *Yi Chuan Xue Bao* **2006**, *33*, 262–268.
120. Maccaferri, M.; Sanguineti, M.C.; Demontis, A.; El-Ahmed, A.; Garcia del Moral, L.; Maalouf, F.; Nachit, M.; Nserallah, N.; Ouabbou, H.; Rhouma, S.; *et al.* Association mapping in durum wheat grown across a broad range of water regimes. *J. Exp. Bot.* **2011**, *62*, 409–438.
121. Gupta, K.; Balyan, S.; Edwards, J.; Isaac, P.; Korzun, V.; Röder, M.; Gautier, M.F.; Joudrier, P.; Schlatter, R.; Dubcovsky, J.; *et al.* Genetic mapping of 66 new microsatellite (SSR) loci in bread wheat. *Theor. Appl. Genet.* **2002**, *105*, 413–422.
122. Röder, M.S.; Korzun, V.; Wendehake, K.; Plaschke, J.; Tixier, M.H.; Leroy, P.; Ganal, M.W. A microsatellite map of wheat. *Genetics* **1998**, *149*, 2007–2023.
123. Somers, D.J.; Isaac, P.; Edwards, K. A high-density microsatellite consensus map for bread wheat (*Triticum aestivum* L.). *Theor. Appl. Genet.* **2004**, *109*, 1105–1114.
124. Guyomarc'h, H.; Sourdille, P.; Charmet, G.; Edwards, J.; Bernard, M. Characterisation of polymorphic microsatellite markers from *Aegilops tauschii* and transferability to the D-genome of bread wheat. *Theor. Appl. Genet.* **2002**, *104*, 1164–1172.
125. Song, Q.J.; Fickus, E.W.; Cregan, P.B. Characterization of trinucleotide SSR motifs in wheat. *Theor. Appl. Genet.* **2002**, *104*, 286–293.

126. Song, Q.J.; Shi, J.R.; Singh, S.; Fickus, E.W.; Costa, J.M.; Lewis, J.; Gill, B.S.; Ward, R.; Cregan, P.B. Development and mapping of microsatellite (SSR) markers in wheat. *Theor. Appl. Genet.* **2005**, *110*, 550–560.
127. Stephenson, P.; Bryan, G.; Kirby, J.; Collins, A.; Devos, K.; Busso, C.; Gale, M. Fifty new microsatellite loci for the wheat genetic map. *Theor. Appl. Genet.* **1998**, *97*, 946–949.
128. Yu, J.-K.; La Rota, M.; Kantety, R.V.; Sorrells, M.E. EST derived SSR markers for comparative mapping in wheat and rice. *Mol. Genet. Genomics* **2004**, *271*, 742–751.
129. Jia, X.; Zhang, Z.; Liu, Y.; Zhang, C.; Shi, Y.; Song, Y.; Wang, T.; Li, Y. Development and genetic mapping of SSR markers in foxtail millet (*Setaria italica* (L.) P. Beauv.). *Theor. Appl. Genet.* **2009**, *118*, 821–829.
130. Lin, H.-S.; Chiang, C.-Y.; Chang, S.-B.; Kuoh, C.-S. Development of simple sequence repeats (SSR) markers in *Setaria italica* (Poaceae) and cross-amplification in related species. *Int. J. Mol. Sci.* **2011**, *12*, 7835–7845.
131. Maccaferri, M.; Sanguineti, M.C.; Corneti, S.; Ortega, J.L.A.; Salem, M.B.; Bort, J.; DeAmbrogio, E.; del Moral, L.F.G.; Demontis, A.; El-Ahmed, A.; Maalouf, F.; *et al.* Quantitative trait loci for grain yield and adaptation of durum wheat (*Triticum durum* Desf.) across a wide range of water availability. *Genetics* **2008**, *178*, 489–511.
132. Breseghello, F.; Sorrells, M.E. Association mapping of kernel size and milling quality in wheat (*Triticum aestivum* L.) cultivars. *Genetics* **2006**, *172*, 1165–1177.
133. Li, S.; Jia, J.; Wei, X.; Zhang, X.; Li, L.; Chen, H.; Fan, Y.; Sun, H.; Zhao, X.; Lei, T.; *et al.* A intervarietal genetic map and QTL analysis for yield traits in wheat. *Mol Breeding* **2007**, *20*, 167–178.
134. Emebiri, L.C. EST-SSR markers derived from an elite barley cultivar (*Hordeum vulgare* L. "Morex"): Polymorphism and genetic marker potential. *Genome* **2013**, *52*, 665–676.
135. Dong, P.; Wei, Y.-M.; Chen, G.-Y.; Li, W.; Wang, J.-R.; Nevo, E.; Zheng, Y.-L. EST-SSR diversity correlated with ecological and genetic factors of wild emmer wheat in Israel. *Hereditas* **2009**, *146*, 1–10.
136. Wang, H.-Y.; Wei, Y.-M.; Yan, Z.-H.; Zheng, Y.-L. EST-SSR DNA polymorphism in durum wheat (*Triticum durum* L.) collections. *J. Appl. Genet.* **2007**, *48*, 35–42.
137. Mullan, D.J.; Platteter, A.; Teakle, N.L.; Appels, R.; Colmer, T.D.; Anderson, J.M.; Francki, M.G. EST-derived SSR markers from defined regions of the wheat genome to identify *Lophopyrum elongatum* specific loci. *Genome* **2005**, *48*, 811–822.
138. Duran, C.; Singhania, R.; Raman, H.; Batley, J.; Edwards, D. Predicting polymorphic EST-SSRs in silico. *Mol. Ecol. Resour.* **2013**, *13*, 538–545.
139. Sim, S.-C.; Yu, J.-K.; Jo, Y.-K.; Sorrells, M.E.; Jung, G. Transferability of cereal EST-SSR markers to ryegrass. *Genome* **2009**, *52*, 431–437.
140. Appleby, N.; Edwards, D.; Batley, J. New Technologies for Ultra-high Throughput Genotyping in Plants. In *Plant Genomics*; Gustafson, J.P., Langridge, P., Somers, D.J., Eds.; Humana press: New York, NY, USA, 2009; Volume 513, pp. 19–39.
141. Edwards, D.; Forster, J.W.; Cogan, N.O.I.; Batley, J.; Chagné, D. Single Nucleotide Polymorphism Discovery. In *Association Mapping in Plants*; Oraguzie, N.C., Rikkerink, E.H.A., Gardiner, S.E., De Silva, D.H.N., Eds. Springer: New York, NY, USA, 2007; pp. 53–76.

142. Batley, J.; Edwards, D. SNP Applications in Plants. In *Association Mapping in Plants*; Oraguzie, D.N.C., Rikkerink, D.E.H.A., Gardiner, D.S.E., De Silva, D.H.N., Eds.; Springer: New York, NY, USA, 2007; pp. 95–102.
143. Edwards, D.; Forster, J.W.; Chagné, D.; Batley, J. What are SNPs? In *Association Mapping in Plants*; Oraguzie, D.N.C., Rikkerink, D.E.H.A., Gardiner, D.S.E., De Silva, D.H.N., Eds.; Springer: New York, NY, USA, 2007; pp. 41–52.
144. Hao, Z.; Li, X.; Xie, C.; Weng, J.; Li, M.; Zhang, D.; Liang, X.; Liu, L.; Liu, S.; Zhang, S. Identification of functional genetic variations underlying drought tolerance in maize using SNP markers. *J. Integr. Plant. Biol.* **2011**, *53*, 641–652.
145. Bowers, J.E.; Chapman, B.A.; Rong, J.; Paterson, A.H. Unravelling angiosperm genome evolution by phylogenetic analysis of chromosomal duplication events. *Nature* **2003**, *422*, 433–438.
146. Simillion, C.; Vandepoele, K.; Van Montagu, M.C.E.; Zabeau, M.; Van de Peer, Y. The hidden duplication past of *Arabidopsis thaliana*. *Proc. Natl. Acad. Sci. U.S.A.* **2002**, *99*, 13627–13632.
147. Vandepoele, K.; Simillion, C.; Van de Peer, Y. Evidence that rice and other cereals are ancient aneuploids. *Plant Cell* **2003**, *15*, 2192–2202.
148. Gore, M.A.; Chia, J.-M.; Elshire, R.J.; Sun, Q.; Ersoz, E.S.; Hurwitz, B.L.; Peiffer, J.A.; McMullen, M.D.; Grills, G.S.; Ross-Ibarra, J.; *et al.* A first-generation haplotype map of maize. *Science* **2009**, *326*, 1115–1117.
149. Barker, G.; Batley, J.; O' Sullivan, H.; Edwards, K.J.; Edwards, D. Redundancy based detection of sequence polymorphisms in expressed sequence tag data using autoSNP. *Bioinformatics* **2003**, *19*, 421–422.
150. Coulondre, C.; Miller, J.H.; Farabaugh, P.J.; Gilbert, W. Molecular basis of base substitution hotspots in *Escherichia coli*. *Nature* **1978**, *274*, 775–780.
151. Ossowski, S.; Schneeberger, K.; Lucas-Lledó, J.I.; Warthmann, N.; Clark, R.M.; Shaw, R.G.; Weigel, D.; Lynch, M. The rate and molecular spectrum of spontaneous mutations in *Arabidopsis thaliana*. *Science* **2010**, *327*, 92–94.
152. Berkman, P.J.; Lai, K.; Lorenc, M.T.; Edwards, D. Next-generation sequencing applications for wheat crop improvement. *Am. J. Bot.* **2012**, *99*, 365–371.
153. Lai, K.; Lorenc, M.T.; Edwards, D. Genomic databases for crop improvement. *Agronomy* **2012**, *2*, 62–73.
154. Lorenc, M.T.; Hayashi, S.; Stiller, J.; Lee, H.; Manoli, S.; Ruperao, P.; Visendi, P.; Berkman, P.J.; Lai, K.; Batley, J.; *et al.* Discovery of single nucleotide polymorphisms in complex genomes using SGSautoSNP. *Biology* **2012**, *1*, 370–382.
155. Lai, K.; Berkman, P.J.; Lorenc, M.T.; Duran, C.; Smits, L.; Manoli, S.; Stiller, J.; Edwards, D. WheatGenome.info: An integrated database and portal for wheat genome information. *Plant Cell Physiol.* **2012**, *53*, e2.
156. Allen, A.M.; Barker, G.L.A.; Berry, S.T.; Coghill, J.A.; Gwilliam, R.; Kirby, S.; Robinson, P.; Brenchley, R.C.; D'Amore, R.; McKenzie, N.; Waite, D.; *et al.* Transcript-specific, single-nucleotide polymorphism discovery and linkage analysis in hexaploid bread wheat (*Triticum aestivum* L.). *Plant Biotechnol. J.* **2011**, *9*, 1086–1099.

157. Huang, X.; Wei, X.; Sang, T.; Zhao, Q.; Feng, Q.; Zhao, Y.; Li, C.; Zhu, C.; Lu, T.; Zhang, Z.; *et al.* Genome-wide association studies of 14 agronomic traits in rice landraces. *Nat. Genet.* **2010**, *42*, 961–967.
158. Lai, J.; Li, R.; Xu, X.; Jin, W.; Xu, M.; Zhao, H.; Xiang, Z.; Song, W.; Ying, K.; Zhang, M.; *et al.* Genome-wide patterns of genetic variation among elite maize inbred lines. *Nat. Genet.* **2010**, *42*, 1027–1030.
159. Lee, H.C.; Lai, K.; Lorenc, M.T.; Imelfort, M.; Duran, C.; Edwards, D. Bioinformatics tools and databases for analysis of next-generation sequence data. *Brief. Funct. Genomics* **2012**, *11*, 12–24.
160. Duran, C.; Eales, D.; Marshall, D.; Imelfort, M.; Stiller, J.; Berkman, P.J.; Clark, T.; McKenzie, M.; Appleby, N.; Batley, J.; *et al.* Future tools for association mapping in crop plants. *Genome* **2010**, *53*, 1017–1023.
161. Marshall, D.J.; Hayward, A.; Eales, D.; Imelfort, M.; Stiller, J.; Berkman, P.J.; Clark, T.; McKenzie, M.; Lai, K.; Duran, C.; *et al.* Targeted identification of genomic regions using TAGdb. *Plant Methods* **2010**, *6*, 19.
162. Imelfort, M.; Duran, C.; Batley, J.; Edwards, D. Discovering genetic polymorphisms in next-generation sequencing data. *Plant Biotechnol. J.* **2009**, *7*, 312–317.
163. Duran, C.; Appleby, N.; Edwards, D.; Batley, J. Molecular genetic markers: discovery, applications, data storage and visualisation. *Current Bioinformatics* 2009, *4*, 16–27.
164. Lai, K.; Duran, C.; Berkman, P.J.; Lorenc, M.T.; Stiller, J.; Manoli, S.; Hayden, M.J.; Forrest, K.L.; Fleury, D.; Baumann, U.; *et al.* Single nucleotide polymorphism discovery from wheat next-generation sequence data. *Plant Biotechnol. J.* **2012**, *10*, 743–749.
165. Duran, C.; Appleby, N.; Clark, T.; Wood, D.; Imelfort, M.; Batley, J.; Edwards, D. AutoSNPdb: an annotated single nucleotide polymorphism database for crop plants. *Nucleic Acids Res.* **2009**, *37*, D951–D953.
166. Duran, C.; Appleby, N.; Vardy, M.; Imelfort, M.; Edwards, D.; Batley, J. Single nucleotide polymorphism discovery in barley using autoSNPdb. *Plant Biotechnol. J.* **2009**, *7*, 326–333.
167. Batley, J.; Barker, G.; O'Sullivan, H.; Edwards, K.J.; Edwards, D. Mining for single nucleotide polymorphisms and insertions/deletions in maize expressed sequence tag data. *Plant Physiol.* **2003**, *132*, 84–91.
168. Bundock, P.C.; Eliott, F.G.; Ablett, G.; Benson, A.D.; Casu, R.E.; Aitken, K.S.; Henry, R.J. Targeted single nucleotide polymorphism (SNP) discovery in a highly polyploid plant species using 454 sequencing. *Plant Biotechnol. J.* **2009**, *7*, 347–354.
169. You, F.M.; Huo, N.; Deal, K.R.; Gu, Y.Q.; Luo, M.-C.; McGuire, P.E.; Dvorak, J.; Anderson, O.D. Annotation-based genome-wide SNP discovery in the large and complex *Aegilops tauschii* genome using next-generation sequencing without a reference genome sequence. *BMC Genomics* **2011**, *12*, 59.
170. Close, T.J.; Bhat, P.R.; Lonardi, S.; Wu, Y.; Rostoks, N.; Ramsay, L.; Druka, A.; Stein, N.; Svensson, J.T.; Wanamaker, S.; *et al.* Development and implementation of high-throughput SNP genotyping in barley. *BMC Genomics* **2009**, *10*, 582.
171. Cavanagh, C.R.; Chao, S.; Wang, S.; Huang, B.E.; Stephen, S.; Kiani, S.; Forrest, K.; Saintenac, C.; Brown-Guedira, G.L.; Akhunova, A.; *et al.* Genome-wide comparative diversity uncovers

multiple targets of selection for improvement in hexaploid wheat landraces and cultivars. *Proc. Natl. Acad. Sci. U.S.A.* **2013**, *110*, 8057–8062.

172. Ganal, M.W.; Durstewitz, G.; Polley, A.; Bérard, A.; Buckler, E.S.; Charcosset, A.; Clarke, J.D.; Graner, E.-M.; Hansen, M.; Joets, J.; *et al.* A large maize (*Zea mays* L.) SNP genotyping array: Development and germplasm genotyping, and genetic mapping to compare with the B73 reference genome. *PLoS One* **2011**, *6*, e28334.
173. Seeb, J.E.; Carvalho, G.; Hauser, L.; Naish, K.; Roberts, S.; Seeb, L.W. Single-nucleotide polymorphism (SNP) discovery and applications of SNP genotyping in nonmodel organisms. *Mol Ecol Resour* **2011**, *11*, 1–8.
174. Xu, X.; Liu, X.; Ge, S.; Jensen, J.D.; Hu, F.; Li, X.; Dong, Y.; Gutenkunst, R.N.; Fang, L.; Huang, L.; *et al.* Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. *Nat. Biotechnol* **2012**, *30*, 105–111.
175. Jin, J.; Huang, W.; Gao, J.-P.; Yang, J.; Shi, M.; Zhu, M.-Z.; Luo, D.; Lin, H.-X. Genetic control of rice plant architecture under domestication. *Nat. Genet.* **2008**, *40*, 1365–1369.
176. Tan, L.; Li, X.; Liu, F.; Sun, X.; Li, C.; Zhu, Z.; Fu, Y.; Cai, H.; Wang, X.; Xie, D.; *et al.* Control of a key transition from prostrate to erect growth in rice domestication. *Nat. Genet.* **2008**, *40*, 1360–1364.
177. Li, C.; Zhou, A.; Sang, T. Rice domestication by reducing shattering. *Science* **2006**, *311*, 1936–1939.
178. Huang, X.; Feng, Q.; Qian, Q.; Zhao, Q.; Wang, L.; Wang, A.; Guan, J.; Fan, D.; Weng, Q.; Huang, T.; *et al.* High-throughput genotyping by whole-genome resequencing. *Genome Res.* **2009**, *19*, 1068–1076.
179. Yu, H.; Xie, W.; Wang, J.; Xing, Y.; Xu, C.; Li, X.; Xiao, J. Gains in QTL detection using an ultra-high density SNP map based on population sequencing relative to traditional RFLP/SSR markers. *PLoS One* **2011**, *6*, e17595.
180. Xie, W.; Feng, Q.; Yu, H.; Huang, X.; Zhao, Q.; Xing, Y.; Yu, S.; Han, B.; Zhang, Q. Parent-independent genotyping for constructing an ultrahigh-density linkage map based on population sequencing. *Proc. Natl. Acad. Sci. U.S.A.* **2010**, *107*, 10578–10583.
181. van Poecke, R.M.P.; Maccaferri, M.; Tang, J.; Truong, H.T.; Janssen, A.; van Orsouw, N.J.; Salvi, S.; Sanguineti, M.C.; Tuberosa, R.; van der Vossen, E.A.G. Sequence-based SNP genotyping in durum wheat. *Plant Biotechnol. J.* **2013**, *11*, 809–817.
182. Hollister, J.D.; Arnold, B.J.; Svedin, E.; Xue, K.S.; Dilkes, B.P.; Bomblies, K. Genetic adaptation associated with genome-doubling in autotetraploid *Arabidopsis arenosa*. *PLoS Genet.* **2012**, *8*, e1003093.
183. Mammadov, J.A.; Chen, W.; Ren, R.; Pai, R.; Marchione, W.; Yalçin, F.; Witsenboer, H.; Greene, T.W.; Thompson, S.A.; Kumpatla, S.P. Development of highly polymorphic SNP markers from the complexity reduced portion of maize (*Zea mays* L.) genome for use in marker-assisted breeding. *Theor. Appl. Genet.* **2010**, *121*, 577–588.
184. van Orsouw, N.J.; Hogers, R.C.J.; Janssen, A.; Yalçin, F.; Snoeijers, S.; Verstege, E.; Schneiders, H.; van der Poel, H.; van Oeveren, J.; Verstegen, H.; *et al.* Complexity reduction of polymorphic sequences (CRoPS): A novel approach for large-scale polymorphism discovery in complex genomes. *PLoS One* **2007**, *2*, e1172.

185. Trebbi, D.; Maccaferri, M.; de Heer, P.; Sørensen, A.; Giuliani, S.; Salvi, S.; Sanguineti, M.C.; Massi, A.; van der Vossen, E.A.G.; Tuberosa, R. High-throughput SNP discovery and genotyping in durum wheat (*Triticum durum* Desf.). *Theor. Appl. Genet.* **2011**, *123*, 555–569.
186. Elshire, R.J.; Glaubitz, J.C.; Sun, Q.; Poland, J.A.; Kawamoto, K.; Buckler, E.S.; Mitchell, S.E. A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. *PLoS One* **2011**, *6*, e19379.
187. Chutimanitsakun, Y.; Nipper, R.W.; Cuesta-Marcos, A.; Cistué, L.; Corey, A.; Filichkina, T.; Johnson, E.A.; Hayes, P.M. Construction and application for QTL analysis of a restriction site associated DNA (RAD) linkage map in barley. *BMC Genomics* **2011**, *12*, 4.
188. Batley, J.; Edwards, D. Genome sequence data: management, storage, and visualization. *BioTechniques* **2009**, *46*, 333–336.
189. Edwards, D.; Batley, J. Plant bioinformatics: from genome to phenome. *Trends in Biotechniques* **2004**, *22*, 232–237.
190. Tetz, V.V. The pangenome concept: a unifying view of genetic information. *Med. Sci. Monit.* **2005**, *11*, HY24–HY29.
191. Yu, J.; Hu, S.; Wang, J.; Wong, G.K.-S.; Li, S.; Liu, B.; Deng, Y.; Dai, L.; Zhou, Y.; Zhang, X.; *et al*. A draft sequence of the rice genome (*Oryza sativa* L. ssp. *indica*). *Science* **2002**, *296*, 79–92.
192. Zhang, G.; Liu, X.; Quan, Z.; Cheng, S.; Xu, X.; Pan, S.; Xie, M.; Zeng, P.; Yue, Z.; Wang, W.; *et al.* Genome sequence of foxtail millet (*Setaria italica*) provides insights into grass evolution and biofuel potential. *Nat. Biotechnol.* **2012**, *30*, 549–554.
193. Vielle-Calzada, J.-P.; Martínez de la Vega, O.; Hernández-Guzmán, G.; Ibarra-Laclette, E.; Alvarez-Mejía, C.; Vega-Arreguín, J.C.; Jiménez-Moraila, B.; Fernández-Cortés, A.; Corona-Armenta, G.; Herrera-Estrella, L.; *et al.* The Palomero genome suggests metal effects on domestication. *Science* **2009**, *326*, 1078–1078.
194. International Barley Genome Sequencing Consortium. Mayer, K.F.X.; Waugh, R.; Brown, J.W.S.; Schulman, A.; Langridge, P.; Platzer, M.; Fincher, G.B.; Muehlbauer, G.J.; Sato, K.; *et al.* A physical, genetic and functional sequence assembly of the barley genome. *Nature* **2012**, *491*, 711–716.
195. Jia, J.; Zhao, S.; Kong, X.; Li, Y.; Zhao, G.; He, W.; Appels, R.; Pfeifer, M.; Tao, Y.; Zhang, X.; *et al. Aegilops tauschii* draft genome sequence reveals a gene repertoire for wheat adaptation. *Nature* **2013**, *496*, 91–95.
196. Ling, H.-Q.; Zhao, S.; Liu, D.; Wang, J.; Sun, H.; Zhang, C.; Fan, H.; Li, D.; Dong, L.; Tao, Y.; *et al.* Draft genome of the wheat A-genome progenitor *Triticum urartu*. *Nature* **2013**, *496*, 87–90.