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# Single nucleotide polymorphism genotyping in polyploid wheat with the Illumina GoldenGate assay

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**Abstract** Single nucleotide polymorphisms (SNPs) are indispensable in such applications as association mapping and construction of high-density genetic maps. These applications usually require genotyping of thousands of SNPs in a large number of individuals. Although a number of SNP genotyping assays are available, most of them are designed for SNP genotyping in diploid individuals. Here, we demonstrate that the Illumina GoldenGate assay could be used for SNP genotyping of homozygous tetraploid and hexaploid wheat lines. Genotyping reactions could be carried out directly on genomic DNA without the necessity of preliminary PCR amplification. A total of 53 tetraploid and 38 hexaploid homozygous wheat lines were genotyped at 96 SNP loci. The genotyping error rate estimated after removal of low-quality data was 0 and 1% for tetraploid and hexaploid wheat, respectively. Developed SNP genotyping assays were shown to be useful for genotyping wheat cultivars.

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This study demonstrated that the GoldenGate assay is a very efficient tool for high-throughput genotyping of polyploid wheat, opening new possibilities for the analysis of genetic variation in wheat and dissection of genetic basis of complex traits using association mapping approach.

## Introduction

Single nucleotide polymorphism (SNP) is a ubiquitous type of genetic variation in eukaryotic genomes. SNPs are ideally suited for the construction of high-resolution genetic maps, investigation of population evolutionary history and discovery of marker–trait associations in association mapping experiments (International HapMap Consortium 2007; Zhao et al. 2007; Aranzana et al. 2005). In association mapping, a dense set of SNP markers covering the entire genome is needed for finding a casual mutation or an SNP that is in linkage disequilibrium with the casual mutation (Aranzana et al. 2005; Flint-Garcia et al. 2005). Inclusion of a large number of individuals in an association mapping study is critical to have sufficient power of association test (Aranzana et al. 2005; Flint-Garcia et al. 2005). Construction of high-density genetic maps requires genotyping large progeny at a large number of loci (Troggio et al. 2007; International HapMap Consortium 2007). These applications, therefore, require genotyping platforms capable of producing multi-locus genotypes in a large panel of individuals. A number of genotyping technologies are currently available that satisfy these requirements. The recently developed genotyping platform Illumina BeadArray combined with the GoldenGate assay is able to genotype up to 1,536 polymorphic sites in 384 individuals in a single reaction (Oliphant et al. 2002). Molecular Inversion Probe (MIP) technology offers 12,000-plex SNP genotyping assay

for genotyping of a limited number of individuals (Hardenbol et al. 2005). An open-source, medium throughput SNP genotyping platform has recently been developed for genotyping thousands of individuals at tens to hundreds of SNP loci (Macdonald et al. 2005). All these technologies are based on oligo ligation assay (OLA) (Oliphant et al. 2002).

The Illumina GoldenGate assay utilizes two allele-specific oligonucleotides (ASOs) to discriminate between the allelic states at an SNP locus (Fan et al. 2003). The discriminating nucleotides are located at the 3' ends of the pair of ASOs. The third primer, referred to as the locus specific oligonucleotide (LSO), anneals downstream of ASO. This primer contains an address sequence (IllumiCode) unique for each SNP site. After annealing, the ASO with a 3'-end base complementary to the base at the SNP site is extended by polymerase and ligated to the corresponding LSO forming a PCR template. The extension and ligation reaction is performed at multiple (up to 1,536) SNP loci simultaneously. The templates are then PCR amplified using a set of three primers common to all SNP sites. Two of them are labeled with either Cy3 or Cy5 fluorescent dye and each anneals to one of the two ASO sequences. The third primer anneals to a common sequence in the LSOs. PCR products are annealed to an array composed of beads carrying oligonucleotides complementary to the IllumiCode sequences in the LSOs that are used for recognition of each SNP site. The ratio of the intensity of Cy3 and Cy5 fluorescence is used to determine the allelic state at an SNP site. Equal intensity of Cy3/Cy5 signal (ratio 1:1) corresponds to the heterozygous state; 1:0 or 0:1 signal ratios correspond to one of the alternative homozygous states at an SNP site. The actual genotype calling is performed after clustering of fluorescence intensity values taking into account variation in data collected from individual beads and averaging and removing outliers. Up to three genotype clusters could be obtained for each SNP site in a diploid organism.

Most of the high-throughput SNP genotyping platforms and the SNP data analysis algorithms were developed for generating and analyzing diploid genotype data. Genotyping of polyploid organisms, mostly represented by plant species, is complicated by the presence of two or more gene copies in the nucleus. A frequently used strategy to overcome this complication is selective PCR amplification using primers specific to one or another copy of the duplicated locus (Caldwell et al. 2004). However, this approach could not be easily scaled up and used for developing high-throughput genotyping assays.

Recently, the Illumina GoldenGate genotyping assays, also referred to as oligonucleotide pool assays (OPAs), were designed for complex plant genomes such as soybean and barley (Hyten et al. 2008; Rostoks et al. 2006). In both OPAs, approximately 90% of the SNP assays produced high-quality genotype calls (Rostoks et al. 2006; Hyten

et al. 2008). However, even though barley and soybean genomes contain significant proportions of duplicated genes (Blanc and Wolfe 2004), the level of gene duplication and homology of the duplicated copies is far less than those in recently evolved polyploids, such as wheat.

Wheat species form a classical polyploid series of diploid, tetraploid and hexaploid species that evolved as follows. Tetraploid wheat *Triticum turgidum* (genome formula AABB) evolved via hybridization of two diploid species closely related to *T. urartu* (genome formula AA) and *Aegilops speltoides* (genome formula SS, where S is similar to B) (Sarkar and Stebbins 1956; Dvorak and Zhang 1990; Dvorak et al. 1993). Hybridization of *T. turgidum* with diploid *Ae. tauschii* (genome formula DD) resulted in the evolution of hexaploid wheat, *T. aestivum* (genome formula AABBDD) (Kihara 1944; McFadden and Sears 1946). Polyploid wheat genotyping currently relies on RFLP, AFLP, SSR, DArT or genome-specific STS markers (Gill et al. 1991; Lotti et al. 2000; Song et al. 2005; Akbari et al. 2006). However, none of these markers is easily amenable to high-throughput genotyping. Here we demonstrate that the Illumina BeadArray platform and GoldenGate SNP assay provide a fast, reliable and cost-effective method for the large-scale acquisition of SNP genotype data in polyploid wheat. Along with the recently developed resource of nearly 2,000 wheat loci harboring SNPs (<http://wheat.pw.usda.gov/SNP/new/index.shtml>) and advances in sequencing technologies making high-throughput SNP discovery a feasible task (Barbazuk et al. 2007; Margulies et al. 2005; Shendure et al. 2005), the Illumina BeadArray platform opens new possibilities for the genome-wide analysis of genetic variation in wheat.

## Materials and methods

### Plant material

A total of 91 polyploid wheat lines including 53 lines of wild tetraploid emmer wheat *Triticum turgidum* ssp. *dicoccoides* (henceforth *T. dicoccoides*), 29 lines of hexaploid *T. aestivum* (16 varieties and 13 landraces) and 9 lines of synthetic wheat derived from the hybridization of various tetraploid wheats with *Ae. tauschii* were genotyped at 96 SNP loci. The identity of these lines is summarized in supplementary Table S1. Plants were grown in a greenhouse and DNA was extracted from leaves of 3–4-week-old seedlings according to a described protocol (Dvorak et al. 1988).

### Genotyping and data analysis

A set of 135 SNPs discovered in a panel of 32 lines of tetraploid and hexaploid wheat by sequencing of 92 gene

fragments was downloaded from the Wheat SNP Database (<http://wheat.pw.usda.gov/SNP/new/index.shtml>). The total length of sequenced regions was 51,493 bp. The discovery panel included 10 accessions of wild emmer, 13 accessions of hexaploid wheat represented by landraces and 9 accessions of synthetic wheats (<http://wheat.pw.usda.gov/SNP/new/index.shtml> and Supplementary Table S1). The list of SNPs is provided in the Supplementary materials. Repetitive elements in the sequences detected by comparing them with the TREP (<http://wheat.pw.usda.gov/ITMI/Repeats/>) and GIRI ([www.girinst.org](http://www.girinst.org)) databases were masked. The SNP-harboring sequences were then submitted to Illumina for processing by Illumina® Assay Design Tool (ADT). ADT generates scores for each SNP that could vary from 0 to 1; SNPs with the scores above 0.6 have a high probability to be converted into a successful genotyping assay. In a set of 135 submitted SNPs, the ADT score varied from 0.18 to 0.99 with mean 0.85 (Table S2). A total of 96 SNP sites that were present at the frequency above 2 in the discovery panel and having ADT scores above 0.6 were selected for OPA design (Tables S2, S3). Out of 96 SNPs, 26 were in the wheat D-genome and 70 SNPs were in the A-genome.

A total of 150 ng of genomic DNA per plant was used for Illumina SNP genotyping at the UC Davis Genome center ([www.genomecenter.ucdavis.edu/dna\\_technologies](http://www.genomecenter.ucdavis.edu/dna_technologies)) using the Illumina BeadArray platform and GoldenGate Assay following the manufacturer's protocol. The fluorescence images of an array matrix carrying Cy3- and Cy5-labeled beads were generated with the two-channel scanner. Raw hybridization intensity data processing, clustering and genotype calling were performed using the genotyping module in the BeadStudio package (Illumina, San Diego, CA, USA). Illumina developed a self-normalization algorithm that relies on information contained in each array. This algorithm adjusts for channel-dependent intensity variations, differences in the background between the channels, and possible crosstalk between the dyes. The normalization procedure implemented in the BeadStudio genotyping module includes outlier removal and background correction and scaling (details of this proprietary normalization algorithm could be obtained from Illumina, San Diego, CA). Before genotype calling, the trimmed mean intensities were calculated from the normalized intensity values obtained for each bead type on the array by rejecting outliers to ensure high quality of genotype data. Genotype calls were generated using the GenCall software incorporated into the BeadStudio package. This algorithm uses a Bayesian model to assign normalized intensity values to one of the three possible homozygous and heterozygous genotype clusters. In the presence of only two homozygous clusters, GenCall computes the location of a missing heterozygous cluster by simulating data using the artificial neural network (Shen et al. 2005). Since only two

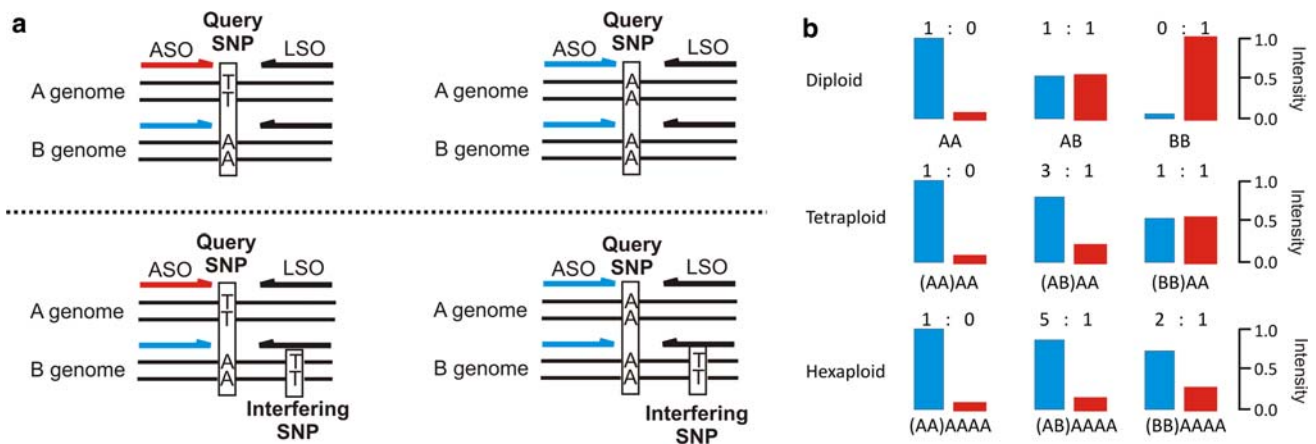
clusters were expected for homozygous polyploid wheat lines (see "Discussion" for details), the genotype clusters generated for each SNP locus by GenCall were edited manually after visual inspection of Cy3 and Cy5 fluorescence intensity clustering on two-dimensional Cartesian plots. SNPs that failed to show two-group clustering were excluded from the analysis.

Genotyping error rate was assessed by comparing SNP genotypes determined with the GoldenGate assay with those determined by Sanger sequencing. Trace files for 56 SNP-harboring gene loci were downloaded from the Wheat SNP project database (<http://wheat.pw.usda.gov/SNP/new/index.shtml>). Base calling and sequence assembly were performed using the phred/phrap and consed programs (Ewing and Green 1998; Ewing et al. 1998; Gordon et al. 1998). SNP discovery was performed with the polyphred program using the default settings (Stephens et al. 2006) followed by visual inspection of sequence trace files and manual verification of each discovered SNP. Genetic diversity, defined as the probability that two randomly chosen alleles from the population are different (Weir 1996, p. 150, 151), was calculated using the PowerMarker program (Liu and Muse 2005).

## Results

### Genotyping with the Illumina GoldenGate assay

The GoldenGate assay ASOs and LSOs may anneal to targets in two or three genomes in wheat, depending on ploidy. GoldenGate genotyping reaction performed on polyploid wheat genomic DNA is therefore expected to produce Cy3/Cy5 fluorescence ratios that differ from those expected for a diploid. Consider the origin of a new haplotype in the A-genome of tetraploid wheat (Fig. 1a, top panel). Mutation (A>T) in the A-genome creates a derived T base and an A/T SNP. In the B-genome, the ancestral A base remains unchanged. Hence, the SNP results in two homozygous genotypes, AAAA and TTAA (Fig. 1a). The ratio of A:T bases in these two genotypes are 1:0 and 1:1 (Fig. 1b). Since Cy3/Cy5 labeled ASOs anneal to the targets in both A- and B-genomes, the Cy3/Cy5 ratios will also be 1:0 and 1:1 (Fig. 1b). Following a similar reasoning, the genotypes will be AAAAAA and TTAAAA in hexaploid wheat, resulting in the 1:0 and 1:2 Cy3/Cy5 ratios (Fig. 1b). In both examples, the presence of the target sequence on homeologous chromosomes shifts the Cy3/Cy5 fluorescence ratio toward that of the ancestral allele of the SNP and affects genotype clustering. The SNP genotyping of heterozygous tetraploid and hexaploid plants would produce 3:1 and 5:1 Cy3/Cy5 ratios, respectively (Fig. 1b).



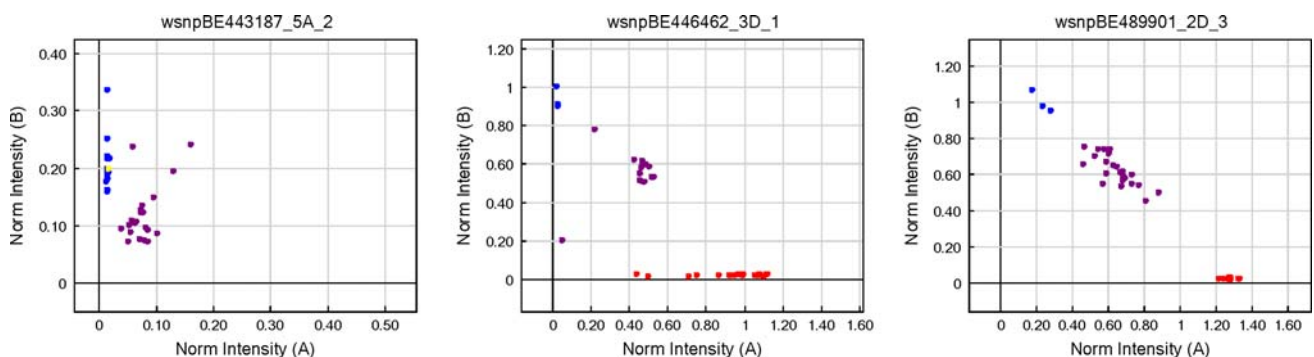
**Fig. 1** GoldenGate SNP genotyping in polyploid wheat. **a** Principles of GoldenGate SNP genotyping in tetraploid wheat. The *top panel* shows two genotypes of *T. dicoccoides* polymorphic for A/T SNP in the A-genome and monomorphic for the T base at the orthologous site in the B-genome. The *bottom panel* shows the same two genotypes except for the LSO annealing site in the B-genome showing a secondary

mutation resulting in imperfect match. Upstream ASOs are *blue* and *red* and downstream LSO is *black*. **b** The expected Cy3/Cy5 fluorescence ratios for homozygous (AA, TT) and heterozygous (AT) diploid, tetraploid and hexaploid plants. The genotypes of the polymorphic sites are shown in *parentheses*

A 96-plex OPA included 70 A-genome SNPs and 26 D-genome SNPs that were discovered by sequencing gene fragments in the SNP discovery panel consisting of 32 lines of tetraploid and hexaploid wheat. For an SNP to be selected for this study, the minor allele count had to be  $\geq 2$  (6.3%) in the screening population. A total of 91 polyploid wheat lines including 53 lines of *T. dicoccoides*, 29 lines of hexaploid *T. aestivum* (16 cultivars and 13 landraces) and 9 lines of synthetic wheat were genotyped using GoldenGate assay. Clustering of Cy3 and Cy5 normalized intensities in a Cartesian plot was used to infer the SNP genotypes. A total of 8 (12%) SNPs in tetraploid wheat and 15 (15.6%) in hexaploid wheat that failed to generate the two-group clustering expected for homozygous lines were excluded from further analyses (Fig. 2). Genotype calls for the remaining 62 A-genome SNPs in tetraploid wheat and 81 A- and B-genome SNPs in hexaploid wheat could be grouped into one or two clusters depending on whether an SNP site was monomorphic or polymorphic (Fig. 3a, b). In the panel of

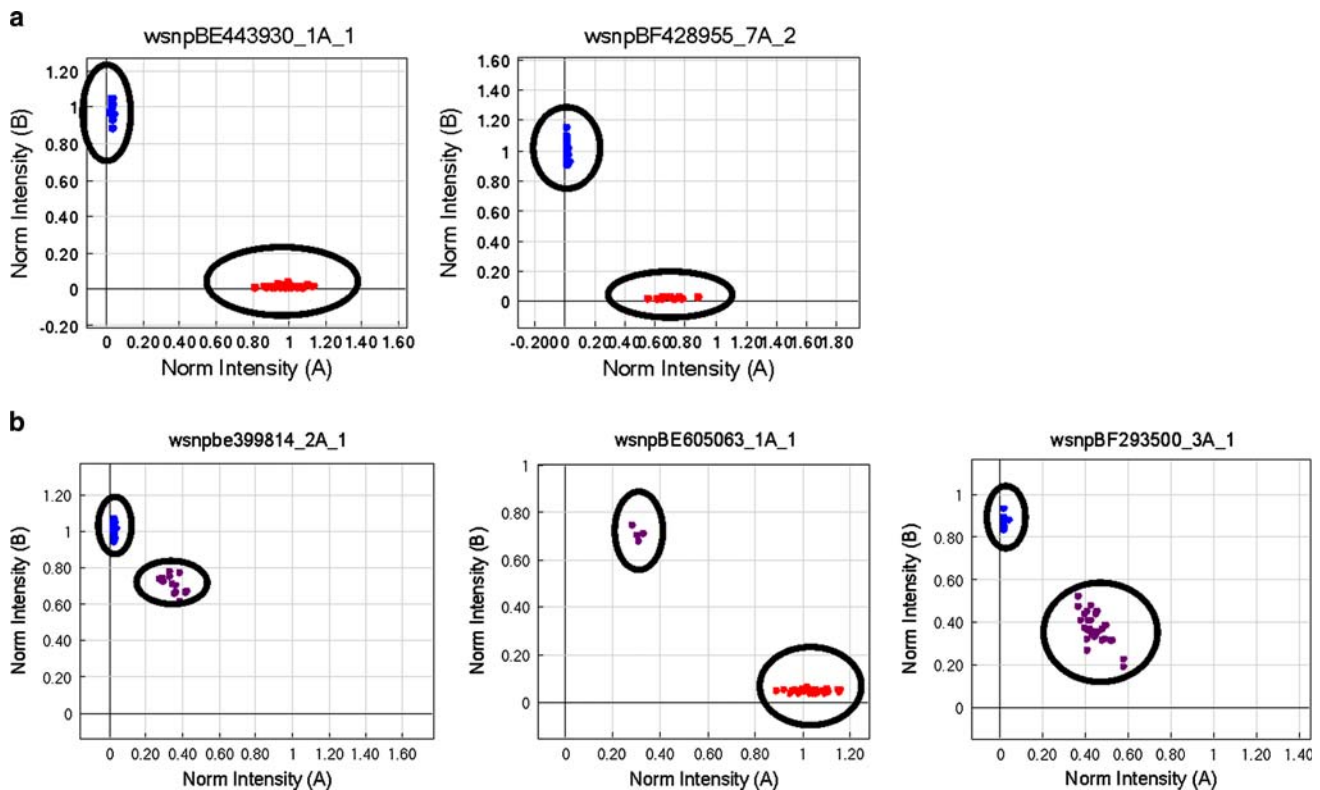
hexaploid wheat lines, 8 SNP sites were monomorphic (all in the A-genome) and 73 were polymorphic (52 SNPs in the A-genome and 21 SNPs in the D-genome). In tetraploid wheat, 2 SNP sites were monomorphic and 60 SNP sites were polymorphic. As expected, there were more monomorphic SNP sites in cultivated wheat (25/81) than in the panel of 13 wheat landraces (9/81).

Concordance between the SNP genotypes determined with the GoldenGate assay and those determined with a standard Sanger sequencing approach was used to assess the accuracy of genotyping (Table 1). These comparisons were made for 56 SNP sites in 10 accessions of *T. dicoccoides* and 22 accessions of hexaploid wheat, although not all accessions could be compared for some SNPs because of low-quality sequence reads (Table 1). Out of 1,304 SNP genotype calls generated by GoldenGate assay (403 SNP genotypes in tetraploid wheat and 901 SNP genotypes in hexaploid wheat) 1,292 were identical with the genotypes obtained by Sanger sequencing. This results in genotyping



**Fig. 2** SNP sites failing to produce a two-cluster pattern. Genotyping plots were generated by graphing normalized Cy3 and Cy5 fluorescence intensities





**Fig. 3** Genotype calls in a sample of 53 accessions of tetraploid *T. dicoccoides* (a) and 38 accessions of hexaploid *T. aestivum* (b). The accession numbers of mapped EST unigenes are shown on the top of each panel. Genotyping plots were generated by plotting Cy3 and Cy5

normalized fluorescence intensities. **a** SNP sites polymorphic in the A-genome of *T. dicoccoides*. **b** SNP sites that were polymorphic in the hexaploid wheat A- or D-genomes

accuracy rate of 100% in tetraploid wheat (data not shown) and 99% in hexaploid wheat (Table 1).

Clustering of Illumina genotype calls may fail in an allopolyploid for the same reasons as in a diploid and also for allopolyploidy-specific reasons. Oligonucleotide probes designed for SNP detection (ASO and LSO) anneal to short regions flanking the query SNPs. Since there are three nearly identical homeologous sets of chromosomes present in the polyploid wheat genome, genotyping oligos have up to three homeologous targets to bind to. If sequences of these targets are identical, genotyping oligos will bind with equal efficiency to each of the homeologs. However, divergence of the annealing sites in homeologous chromosomes could change oligonucleotide binding efficiency and interfere with genotyping assay resulting in its failure (Fig. 1a, bottom panel). To assess if the divergence of homeologous sequences at the genotyping oligonucleotide binding sites could be the cause of genotyping assay failures or inadequate clustering, regions flanking the two SNPs (wsnpBE443187\_5A\_2 and wsnpBE489901\_2D\_3) excluded from the analyses were investigated (Fig. 2). For both SNPs sequences from homeologous chromosomes were available. Sequences flanking the SNP site in the wsnpBE443187\_5A\_2 locus, which is located in the A-genome were

compared with the orthologous sequences from both the B- and D-genomes of polyploid wheat. Similarly, sequences flanking the SNP site in the wsnpBE489901\_2D\_3 locus, which is located in the D-genome were compared with the B-genome orthologous sequence. In both cases, divergence found at the oligonucleotide annealing sites could be associated with the failure to generate defined clusters on the Cartesian plots (Fig. 2). At the wsnpBE443187\_5A\_2 SNP site, both ASOs and LSO A-genome annealing sites differed by one nucleotide either in the B- or D-genome. At the wsnpBE489901\_2D\_3 SNP site, the A-genome ASOs annealing site differed from that in the B-genome by a dinucleotide indel.

#### Diversity estimation with the Illumina GoldenGate assay

Genetic diversity of the A- and D-genomes of hexaploid wheat was 0.31 and 0.34, respectively. Diverse panel of 13 wheat landraces demonstrated a higher level of genetic diversity (A-genome 0.32; D-genome 0.35) than the panel of 16 wheat cultivars (A-genome 0.23; D-genome 0.31). The observed 28 and 11% reduction in the levels of genetic diversity in the A- and D-genomes, respectively, most likely results from the bottleneck caused by selection

**Table 1** Accuracy of SNP genotype calls in hexaploid wheat

SNP	Chrom.	Genome	No. of SNPs genotyped with GoldenGate and Sanger sequencing	Successful genotypes <sup>a</sup>	Call rate (%)
wsnpBE399936_2A_1	2	A	17	17	100
wsnpBE403506_2D_1	2	D	14	14	100
wsnpBE403597_2A_1	2	A	18	17	94
wsnpBE403597_2A_2	2	A	18	17	94
wsnpBE403956_1A_1	1	A	14	14	100
wsnpBE405518_1D_1	1	D	22	21	95
wsnpBE405518_1D_2	1	D	22	22	100
wsnpBE406351_2A_1	2	A	17	17	100
wsnpBE406351_2A_2	2	A	17	17	100
wsnpBE406877_5A_1	5	A	14	14	100
wsnpBE406943_7A_1	7	A	18	18	100
wsnpBE425879_1A_1	1	A	14	14	100
wsnpBE443187_5A_1	5	A	15	15	100
wsnpBE443568_3A_1	3	A	22	21	96
wsnpBE443588_1A_1	1	A	7	7	100
wsnpBE443588_1A_2	1	A	6	6	100
wsnpBE443588_1A_3	1	A	7	7	100
wsnpBE443930_1A_1	1	A	14	14	100
wsnpBE443948_2A_1	2	A	17	16	94
wsnpBE444144_2D_1	2	D	22	22	100
wsnpBE445121_1D_1	1	D	21	21	100
wsnpBE445121_1D_2	1	D	21	21	100
wsnpBE446462_3D_2	3	D	10	10	100
wsnpBE471022_1A_1	1	A	13	13	100
wsnpBE471272_7A_2	7	A	17	17	100
wsnpBE489901_2D_1	2	D	10	10	100
wsnpBE489901_2D_2	2	D	12	12	100
wsnpBE490219_7A_1	7	A	18	18	100
wsnpBE490643_7A_1	7	A	18	17	94
wsnpBE490643_7D_1	7	D	21	21	100
wsnpBE497177_1A_1	1	A	17	17	100
wsnpBE497177_1A_2	1	A	12	12	100
wsnpBE498566_2A_1	2	A	16	14	88
wsnpBE499309_3D_1	3	D	20	20	100
wsnpBE499309_3D_2	3	D	20	20	100
wsnpBE517627_2A_1	2	A	18	18	100
wsnpBE518435_1A_1	1	A	12	12	100
wsnpBE585780_1A_1	1	A	14	14	100
wsnpBE585797_3D_1	3	D	14	14	100
wsnpBE586140_1D_1	1	D	22	22	100
wsnpBE586140_1D_2	1	D	21	21	100
wsnpBE590634_1A_1	1	A	14	13	93
wsnpBE605063_1A_1	1	A	15	15	100
wsnpBF145580_2A_1	2	A	17	17	100
wsnpBF145580_2A_2	2	A	17	17	100
wsnpBF200742_1A_1	1	A	11	11	100
wsnpBF201102_5A_1	5	A	15	15	100

**Table 1** continued

SNP	Chrom.	Genome	No. of SNPs genotyped with GoldenGate and Sanger sequencing	Successful genotypes <sup>a</sup>	Call rate (%)
w SNPBF201102_5A_2	5	A	15	15	100
w SNPBF293016_5A_1	5	A	13	13	100
w SNPBF293500_3A_1	3	A	21	20	95
w SNPBF473056_1D_1	1	D	23	22	96
w SNPBF474966_7A_1	7	A	18	18	100
w SNPBF475149_1A_1	1	A	14	14	100
w SNPBF484028_5A_1	5	A	17	17	100
w SNPBF485305_1D_1	1	D	17	17	100
w SNPBG263358_1A_3	1	A	12	11	92

<sup>a</sup> Number of genotype calls based on GoldenGate assay that were identical to calls based on Sanger sequencing

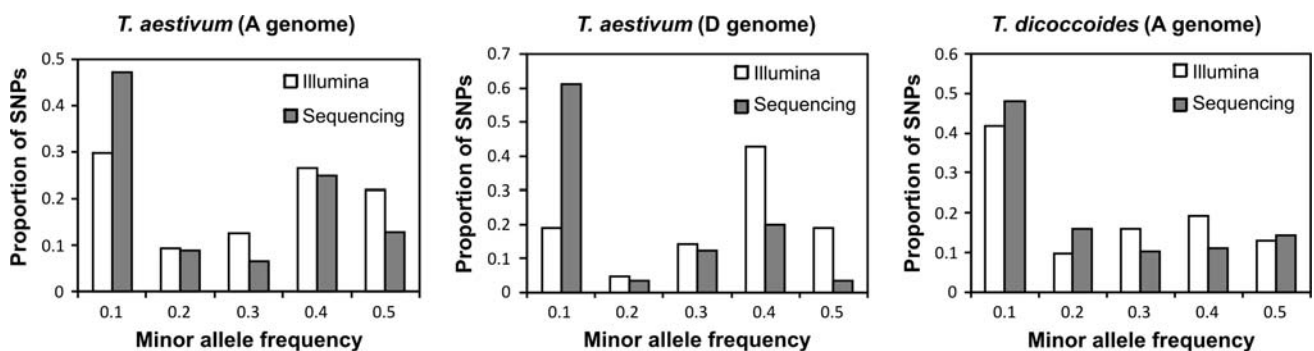
of only limited number of accessions for the development of adapted cultivars. Genetic diversity of the A-genome of tetraploid wild emmer (0.25) was very close to that of the A-genome of cultivated wheat (0.23). However, when only shared set of SNP loci (55) was compared, the level of genetic diversity in the A-genome of polyploid wheat (0.3) was higher than that in the A-genome of tetraploid wild emmer (0.26). It should be noted, however, that provided estimates of diversity need to be treated cautiously. Since only common SNP variants were used for genotyping assay design, obtained diversity statistic is different from the one that can be obtained using all SNPs. This type of bias, known also as an ascertainment bias, is hard to control and should be avoided if the purpose of study is the inference of population history (Clark et al. 2005; Brumfield et al. 2003).

Mean genetic diversity was also computed for a subset of data for which both genotype calls and nucleotide sequences were available. Mean genetic diversity was 0.33 and 0.36 in the A- and D-genomes of *T. aestivum*, respectively, and 0.26 in the A-genome of *T. dicoccoides*. This simple descriptive statistic obtained by Illumina GoldenGate genotyping was compared with that calculated for all SNPs detected by sequencing (<http://wheat.pw.usda.gov/SNP/new/index.shtml>) (Fig. 4). Estimates of genetic diver-

sity based on nucleotide sequences were 0.26 and 0.23 for the A- and D-genomes of *T. aestivum*, respectively, and 0.18 for the A-genome of *T. dicoccoides*. Mean genetic diversity calculated using SNPs derived from DNA sequences was lower than that calculated using SNPs obtained with the Illumina GoldenGate assay. The observed discrepancy between the Illumina GoldenGate data and nucleotide sequence data could be attributed to a bias introduced during selection of SNPs for the Illumina OPA design. Only those SNPs that present at frequency 2 and higher in the discovery population were selected for assay design. It could be clearly seen in Fig. 4 that the frequency spectrum of SNPs in OPA is shifted toward the high-frequency variants compared to that in Sanger sequence data.

## Discussion

All analyses of SNP genotyping results in this study assumed that the genotypes have been obtained from homozygous plants. Due to high rates of self-pollination, this assumption holds for most of wheat landraces, wheat breeding lines and plants collected from wild populations. Genotyping of a mixture of homozygous and heterozygous plants, a situation prevailing in mapping populations



**Fig. 4** Distribution of minor allele frequencies of SNPs in the A- and D-genomes of *T. aestivum* and the A-genome of *T. dicoccoides* detected with the GoldenGate assay and sequencing in the SNP discovery panel



generated from bi-parental crosses, would probably be more challenging due to the tight clustering of fluorescence intensity ratio values on genotyping plots. Apparently, it will be problematic to generate reliable genotype calls from such data. This limitation needs to be considered if the Illumina GoldenGate assay is planned to be used in gene mapping projects using bi-parental cross populations and can be overcome by using homozygous plants produced either by several generations of self-pollination or doubled-haploid technique.

The proportion of SNPs that could be converted into working assays is a very important factor that influences the cost of genotyping assay development. The presence of repetitive elements, palindromes and neighboring polymorphisms around a query SNP is known to affect the conversion rate (Fan et al. 2003). Homology search using two databases of repetitive elements was performed here during the selection of SNPs for OPA design to increase this rate. All sequences showing similarity to known repeats were masked before submitting them to Illumina for assay design. In addition, Illumina used its own proprietary bioinformatical screening procedures implemented in ADT to increase the assay conversion rate.

In polyploid species devoid of genome sequence data, such as wheat, the task of SNP selection with high “designability scores” is additionally complicated by the presence of multiple targets within the nucleus. Since GoldenGate assay relies on annealing of genotyping oligonucleotides to regions flanking a query SNP, the divergence of orthologous sequences in homeologous chromosomes or undetected polymorphisms could interfere with annealing of genotyping oligonucleotides and genotyping reactions. For example, the nucleotide sequence of the B-genome annealing sites might have diverged from the A-genome sequence and harbor mutations (Fig. 1a, bottom panel). Such mutations will reduce oligonucleotide annealing efficiency with the B-genome target, which will negatively affect clustering and reduce genotype calling rate. Interference of secondary SNPs at oligonucleotide annealing sites with genotyping accuracy has been demonstrated in *Drosophila* (Macdonald et al. 2005). In the present study, poor genotype call clustering (more than two clusters) was encountered at 8 SNP sites in tetraploid wheat (12%) and 15 sites in hexaploid wheat (15.6%). Homology of the orthologous annealing sequences was investigated at two of these sites. Divergent mutations were encountered at both sites suggesting that this may be an important source of clustering failure in genotyping of polyploids. To minimize the effect of divergent mutations on performance of genotyping assays, all copies of orthologous sequences in the wheat nucleus should be analyzed. However, this analysis could be performed only for a limited number of SNP loci until a complete wheat genome sequence is produced.

The presence of paralogous genes within genome can also have negative impact on genotyping. High incidence (27.7%) of recently duplicated genes in the wheat genome (Akhunov et al. 2003) increases the chance of designing genotyping assays targeting paralogous duplications. This could be avoided by additional analysis of genomic regions prior to genotyping assay design. Paralogs can be identified by sequence analysis of PCR amplicons or Southern hybridization analysis. For example, wheat EST database is an excellent resource for selecting non-repetitive targets in the wheat genome (<http://wheat.pw.usda.gov/wEST/>).

Despite the complexities intrinsic to polyploidy and large sizes of the wheat genomes, a high level of genotyping accuracy, 99–100% after removal of SNPs failed to produce two clusters on Cartesian plots, was achieved. This accuracy level is comparable to that achieved with the Illumina GoldenGate assays in human populations (99.7–99.9%) after applying quality cutoffs (Fan et al. 2003; Steemers and Gunderson 2007). A conversion rate of 89 and 84% achieved in tetraploid and hexaploid wheat, respectively, for SNPs selected from the wheat SNP database was also comparable to a conversion rate for human SNPs. Only SNPs that had a minor allele frequency of 6.3% or higher (two or more hits in the screening population) were used for wheat OPA design. Fan et al. (2003) reported a conversion rate of 81% for randomly selected SNPs from dbSNP (<http://www.ncbi.nlm.nih.gov/SNP/>) and 94–96% for “double-hit” SNPs (SNPs encountered in database two or more times). Enhanced conversion rates for double hit SNPs in both studies argues for selection of SNPs based on their frequency in the screening population to minimize conversion failures. This procedure also increases the chance that the selected SNP will be polymorphic in genotyped populations.

Another potential source of genotyping errors in wheat is the presence of identical polymorphisms at orthologous loci in homeologous chromosomes (shared polymorphisms). Shared polymorphisms could be either inherited from the diploid ancestors or, less likely, evolved independently in polyploid wheat. The presence of a shared polymorphism A/T in the two genomes of tetraploid wheat would result in four possible genotypes: AAAA, TTAA, AATT and TTTT. The TTAA and AATT genotypes would likely appear identical in the Cy3/Cy5 plot. Three clusters would therefore be expected. If the TTAA and AATT genotypes would not appear identical in the plot, four clusters would be possible. To assess the significance of shared polymorphism for genotyping in polyploid wheat, 82 inter-genomic sequence alignments (total length of aligned sequence is 35,715 bp; data not shown) were compared. No shared polymorphism was found, indicating that shared polymorphisms are of negligible significance for Illumina genotyping in polyploid wheat.

A source of genotyping errors that was not considered in our study is the presence of SNP sites with three or four alleles in polyploid wheat. These SNP sites are inherently very rare in populations because their origin requires two or more independent mutations at the same site. The probability of such mutations is extremely low given spontaneous mutation rates of  $10^{-8}$ – $10^{-9}$  mutations at site<sup>-1</sup> year<sup>-1</sup> in eukaryotic genomes. We therefore expect that this class of SNPs has a negligible effect on genotyping error rate in wheat.

Our study calls for caution in using a limited number of SNPs, particularly if preselected on the basis of their polymorphism and allele frequencies in the screening population, in making inferences about diversity and evolutionary history of populations. First of all, since only polymorphic sites are investigated, the estimates of genetic diversity are expected to be biased upward. For instance, genetic diversity of the wheat D-genome estimated in this study using OPA was higher than the genetic diversity of the wheat A-genome. Genetic diversity based on the Sanger sequence data showed that the A-genome is more diverse than the D-genome (see “Results”). A survey of a larger number of gene loci by sequencing also demonstrated that the genetic diversity of the wheat D-genome is significantly lower than genetic diversity of the wheat A-genome (unpublished data). The observed discrepancy results from the bias introduced by the selection of high-frequency SNPs for OPA design (Fig. 4). Preferential use of SNPs that are present at intermediate frequencies in a population will affect the population statistics relying on the frequency spectrum of SNPs, such as genetic diversity, population differentiation and linkage disequilibrium (Clark et al. 2005; Brumfield et al. 2003). For example, medium frequency SNPs will most likely be shared between populations and, therefore, the extent of population differentiation will be underestimated. It has also been suggested that focusing on common SNPs might have an effect on the power of detecting association between genetic variants and causal mutations. The deficit of rare SNPs could result in reduced power of association analysis when causal variants are rare in a population (Clark et al. 2005).

The distribution of SNPs in cultivated wheat gene pool defines their utility for breeding and marker-assisted selection applications. Our results suggest that the panel of wheat lines used for SNP discovery captured significant proportion of genetic variation present in modern cultivated wheat. About 70% of SNPs preselected on the basis of their polymorphisms in the discovery panel were also polymorphic in a set of 16 wheat cultivars (Table S1). This is consistent with the conclusion based on the analysis of 359 SNPs derived from the same database (Chao et al. 2009). Selection of SNPs with the frequency above 2 in the discovery panel might have also increased the probability of

finding polymorphic SNP sites in the cultivated gene pool. High-frequency SNPs had a higher chance to pass through the population bottleneck that apparently accompanied the development of adapted cultivars. This is evident from the comparison of the genetic diversity of landraces and cultivars. The latter lost 28 and 11% of their genetic diversity in the A- and D-genomes, respectively, compared to that in landraces (see “Results”). Loss of genetic diversity in wheat varieties compared to that in the populations of landraces has also been reported by Chao et al. (2009).

## Conclusion

It is demonstrated that SNPs can be genotyped in polyploid wheat pure lines with the Illumina BeadArray technology coupled with GoldenGate assay without the need of a prior PCR amplification step. About 89 and 84% of SNPs in tetraploid and hexaploid wheat, respectively, could be converted into successful genotyping assays. After eliminating SNPs showing low-quality clustering, the accuracy of genotyping was 100 and 99% for tetraploid and hexaploid wheat, respectively. The utility of SNPs selected from the wheat SNP database for genotyping of wheat varieties was demonstrated. The Illumina BeadArray platform, therefore, can offer a cost- and time-effective approach to genotyping of thousands of polyploid wheat lines at thousands of polymorphic sites. This technology represents an excellent tool for studying genetic architecture of complex traits, association mapping and, with proper safeguards, evolutionary forces that shaped the genetic diversity of polyploid wheat and its wild relatives.

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