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# DOUBLING DOWN ON GENOMES: POLYPLOIDY AND CROP PLANTS[1]

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Polyploidy, or whole genome multiplication, is ubiquitous among angiosperms. Many crop species are relatively recent allopolyploids, resulting from interspecific hybridization and polyploidy. Thus, an appreciation of the evolutionary consequences of (allo)polyploidy is central to our understanding of crop plant domestication, agricultural improvement, and the evolution of angiosperms in general. Indeed, many recent insights into plant biology have been gleaned from polyploid crops, including, but not limited to wheat, tobacco, sugarcane, apple, and cotton. A multitude of evolutionary processes affect polyploid genomes, including rapid and substantial genome reorganization, transgressive gene expression alterations, gene fractionation, gene conversion, genome downsizing, and sub- and neofunctionalization of duplicate genes. Often these genomic changes are accompanied by heterosis, robustness, and the improvement of crop yield, relative to closely related diploids. Historically, however, the genome-wide analysis of polyploid crops has lagged behind those of diploid crops and other model organisms. This lag is partly due to the difficulties in genome assembly, resulting from the genomic complexities induced by combining two or more evolutionarily diverged genomes into a single nucleus and by the significant size of polyploid genomes. In this review, we explore the role of polyploidy in angiosperm evolution, the domestication process and crop improvement. We focus on the potential of modern technologies, particularly next-generation sequencing, to inform us on the patterns and processes governing polyploid crop improvement and phenotypic change subsequent to domestication.

**Key words:** crop improvement; domestication; epigenetics; gene duplication; genomic shock; next-generation sequencing; polyploidy; whole-genome duplication.

It is now widely accepted that domestication of wild plants was the key innovation leading to human population expansion since the dawn of the agricultural era approximately 10 000 yr ago. Tracing, in most cases, to long-lost cultures thousands of years ago, plant domestication and continued crop improvement via artificial selection generated the novel phenotypes that sustain human populations. These phenotypes often constitute a *domestication syndrome* (Hammer, 1984; Meyer et al., 2012), a suite of traits in the domesticated crop that distinguish it from its wild ancestors. Typically, such traits include, but are not limited to, a shift from the perennial to annual life cycle, the loss of dormancy and development of a nonshattering phenotype in seeds, increases in yield, improved palatability, and a wider geographical range (see Zeven and Zhukovsky, 1975). Once humans transitioned from a hunting and gathering lifestyle to an agrarian one, civilization became wholly dependent on domesticated crops, including the main cultivated grasses and legumes as well as many other species (see list in Meyer et al., 2012). Importantly, with respect to the present review, many of these crop plants are nascent polyploids identifiable via chromosomal counts (Leitch and Leitch, 2008).

Whole genome duplication (WGD) or polyploidy, where an organism possesses more than a diploid complement of chromosomes, has long been recognized as an important feature of plant genomes (Stebbins, 1950, 1971) and is thought to drive phenotypic diversification (Soltis et al., 2009). Polyploidy has been broadly classified into two types, one involving interspecific hybridization, known as allopolyploidy, and another in the absence of interspecific hybridization, known as autopolyploidy (for a review on terminology, see Wendel and Doyle, 2005). Thus, allopolyploids typically have two or more distinct subgenomes at the time of their origin, are fixed heterozygotes at many loci and typically have chromosomes that do not form multivalents at meiosis. On the other hand, autopolyploids have at least three copies of the same (or near identical) genome and regularly exhibit multivalent, or random bivalent pairing, between homologous chromosomes. While the auto- and allopolyploid designations may seem convenient at first, they do not reflect the reality of a continuum of divergence between genomes united in a polyploid nucleus (reviewed by Wendel and Doyle, 2005).

Historically, polyploid plants were identified by cytological examination of chromosome number, but advances during the present "genomics era" (Soltis et al., 2009) have revealed scores of more ancient and cryptic cases of polyploidy. For example, large-scale analysis of the age distribution of duplicate genes revealed previously unknown cases of paleopolyploidy in crops and other model plants (Blanc and Wolfe, 2004). Using synonymous substitutions to estimate divergence times between duplicate genes Blanc and Wolfe (2004) were able to identify peaks corresponding to contemporaneous bursts of duplication, inferred to be the result of ancestral WGD. Interestingly, many of the plants used in this analysis were crops, including wheat, maize, cotton, and potato.

Other cases of WGD have been inferred by observing that some sections of the genome are in multiple copies (as much as

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58% in the case of *Arabidopsis*) and sets of genes share high levels of colinearity (synteny) with their duplicated counterparts (Blanc et al., 2000; The Arabidopsis Genome Initiative, 2000). Genome-wide signatures of colinearity suggest a process of WGD, rather than local tandem or segmental duplication. Since the initial identification of ancient WGD, further evidence indicated a series of nested WGD events in the *Arabidopsis* lineage (Blanc et al., 2003). Subsequent evidence from multiple plant groups from throughout the angiosperms demonstrated a multitude of WGD events across the flowering plant phylogeny (reviewed by Soltis et al., 2009). Phylogenetic analysis of expressed sequence tags (ESTs) from seed and flowering plants, with lycophytes and bryophytes as outgroups, revealed ancestral WGD at the base of the seed plants and a separate nested event at the origin of angiosperms (Jiao et al., 2011).

So it is now clear that *all* seed plants and angiosperms have genomes that have experienced multiple rounds of WGD and that they are thus rightly considered to have a paloepolyploid ancestry. This feature of modern plant genomes may be considered one of the most significant realizations to emerge from the genomics era. Although for over 50 yr the various forms of polyploidy have been identified as vital in plant speciation and diversification, it is only over this past decade that the ubiquity and scope of WGD has truly come to light. The old and now obsolete question has changed from "is this species polyploid?" to "how many rounds of WGD occurred in the ancestral lineage of this taxon, and when was the most recent polyploidy?" (Fig. 1, Table 1). Given this ubiquity, understanding WGD and its various modes and consequences is of vital importance for a full appreciation of not only angiosperm natural history in general, but also the history and potential of the crop plants that sustain civilization. Here we review the role of crop species in shedding light on polyploidy as a general feature of plant genomes, as well as some of the features of polyploids that both complicate and facilitate crop plant improvement. In addition, we explore the role of modern high-throughput technologies in further enhancing our understanding of WGD in plant improvement efforts.

## CROP PLANTS AS MODELS OF POLYPLOID EVOLUTION

Much of our current knowledge regarding the consequences of WGD arises from research involving crop species and their

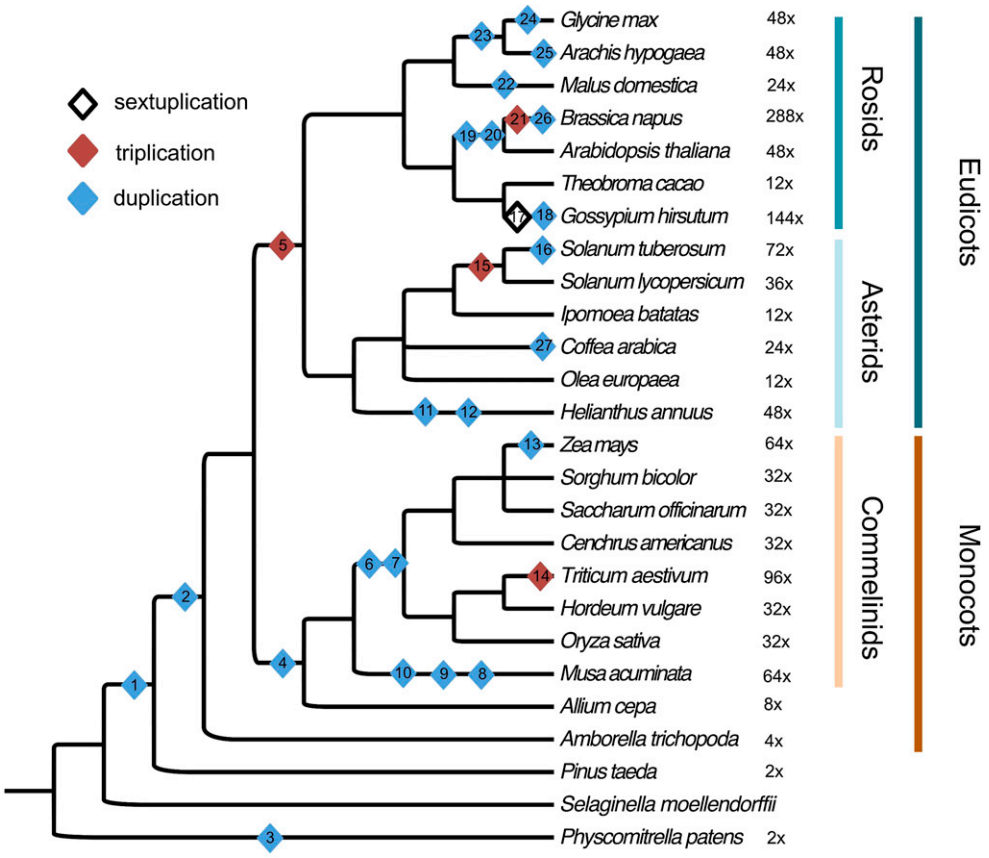


Fig. 1. A representative phylogeny of land plants with emphasis on crop species. Colored diamonds are used to indicate the placement of whole genome duplications (some WGDs, depicted as single instances, may be several sequential events, e.g., cotton sextuplication), with each having a corresponding entry in Table 1, where appropriate references are supplied. Diamonds near the terminals indicate recent WGD events (inferred through chromosome counting, for example), whereas phylogenetically deeper events are inferred through EST or synteny analysis. The estimated ploidy per haploid gametic nucleus is based on the number (and multiplication factor) of events leading to each of the terminals, and is indicated following the species name. The tree was made using the NCBI taxonomy browser with information modified from Albert et al. (2013) and the CoGe webpage (http://genomevolution.org/wiki/index.php/Plant_paleopolyploidy; accessed 5/6/14).

TABLE 1. References and details of the WGD events depicted in Fig. 1.

| Event | Name | Reference(s) | Multiplication | Data type |
|---|---|---|---|---|
| 1. | Seed plant tetraploidy | Jiao et al., 2011 | x2 | EST |
| 2. | Flowering plant tetraploidy | Jiao et al., 2011 | x2 | EST |
| 3. | Moss tetraploidy | Rensing et al., 2007 | x2 | EST |
| 4. | Monocot tetraploidy | Tang et al., 2010 | x2 | |
| 5. | Gamma | Bowers et al., 2003; Jaillon et al., 2007; Cenci et al., 2010 | x3 | EST; synteny |
| 6. | Sigma | Tang et al., 2010; D'Hont et al., 2012 | x2 | synteny |
| 7. | Rho | Paterson, Bowers, and Chapman, 2004 | x2 | |
| 8. | Banana alpha | Lescot et al., 2008; D'Hont et al., 2012 | x2 | synteny |
| 9. | Banana beta | D'Hont et al., 2012 | x2 | synteny |
| 10. | Banana gamma | D'Hont et al., 2012 | x2 | synteny |
| 11. | Sunflower | Baldwin et al., 2002; Barker et al., 2008 | x2 | EST |
| 12. | Sunflower | Baldwin, Wessa, and Panero, 2002; Barker et al., 2008 | x2 | EST |
| 13. | Maize tetraploidy | Wei et al., 2007; Schnable et al., 2011 | x2 | synteny |
| 14. | Bread wheat | Feldman and Levy, 2012 | x3 | chromosome counts |
| 15. | *Solanum* hexaploidy | Sato et al., 2012 | x3 | synteny |
| 16. | Potato tetraploidy | Xu et al., 2011 | x2 | |
| 17. | Cotton WGD | Paterson et al., 2012 | x6 | synteny |
| 18. | Polyploid cotton | Wendel and Cronn, 2003 | x2 | |
| 19. | Alpha | Bowers et al., 2003 | x2 | EST |
| 20. | Beta | Bowers et al., 2003 | x2 | EST |
| 21. | Brassica hexaploidy | Lagercrantz, 1998; Wang et al., 2011 | x3 | synteny |
| 22. | Apple tetraploidy | Velasco et al., 2010 | x2 | synteny |
| 23. | Papilionoid tetraploidy | Schlueter et al., 2004; Pfeil et al., 2005; Schmutz et al., 2010 | x2 | EST; synteny |
| 24. | Soybean tetraploidy | Schmutz et al., 2010 | x2 | synteny |
| 25. | Peanut tetraploidy | Husted, 1936 | x2 | chromosome counts |
| 26. | Neopolyploid *Brassica* | U, 1935 | x2 | chromosome counts |
| 27. | Coffee tetraploidy | Lashermes et al., 1999 | x2 | chromosome counts; genomic in situ hybridization |

genomic mimics, resynthesized from extant models of their progenitor diploids. The vast majority of this effort has been focused on allopolyploids; consequently, less is known regarding the short- and long-term outcomes of WGD in autopolyploids. We have partitioned the primary lessons about WGD into key themes and discuss them next.

***Genomic alterations in polyploids*—**It has become clear that the genome of relatively young allopolyploids may be highly dynamic, experiencing a variety of phenomena that collectively have been termed "genomic shock" (McClintock, 1984). Thus, allopolyploids often are not the sum of parental genotypes (Adams and Wendel, 2005). Although there are a multitude of outcomes following allopolyploidy, none of these are ubiquitous in all allopolyploids. There are, however, a number of commonalities, many of which have been illuminated by research on crop species.

In some neo-allopolyploids, translocations from one subgenome to another arise, as in the allopolyploid *Nicotiana tabacum* (tobacco), where whole chromosome segments have been transferred between subgenomes both in natural (Skalicka et al., 2003; Lim et al., 2007) and synthetic mimics (Lim et al., 2006). As with all of the phenomena described here, similar observations have also been reported in noncrop allopolyploids (Chester et al., 2012), but typically after having been first discovered in crops. Chromosomal alterations are not limited to translocations; chromosome losses and gains (aneuploidy) have also been observed in wheat allohexaploids (Xiong et al., 2011; Zhang et al., 2013b). Interestingly, while aneuploidy is common in allohexaploids, wheat allotetraploids have a much more stable karyotype (Zhang et al., 2013a). Nevertheless, such large-scale chromosomal alterations seen in crop and natural allopolyploid populations are unlikely to increase fitness, leading to the suggestion that nascent allopolyploids need to overcome an initial fitness cost associated with genomic aberrations.

Genomic plasticity in polyploidy plants is not restricted to karyotypic alterations. Another large-scale alteration common to allopolyploid genomes concerns the rRNA genes (ribosomal DNA or rDNA). The large rDNA (45S or 35S) subunit contains the 18S, 5.8S, and 26S genes and typically occurs in thousands of copies, arranged in tandem at one or more chromosomal loci. In allopolyploids, these genes, crucial for viability, are highly dynamic relative to their diploids progenitors. This dynamism involves changes in rDNA locus number (Kovarik et al., 2008) and the homogenization of rDNA types derived from the varying subgenomes (Wendel et al., 1995; Volkov et al., 1999; Kovarik et al., 2004), thought to be via recombination-based mechanisms (Matyasek et al., 2012), as well as changes in unit copy number (Renny-Byfield et al., 2011). Importantly, these alterations are known to occur rapidly, within a few generations following synthetic allopolyploidy (Skalicka et al., 2003). Similarly, other genes, present as homoeologs, also display evidence of homogenization (gene conversion), where the homoeolog from one of the parental subgenomes over-writes the homoeolog from the other subgenome (Flagel et al., 2012; Salmon et al., 2012). For example, over 6000 homoeologous gene pairs are estimated to have undergone nonreciprocal homoeologous recombination (Flagel et al., 2012). Moreover, comparisons of allopolyploid cotton with progenitor species revealed that gene conversion was biased in favor of one of the progenitor subgenomes (Paterson et al., 2012), in this case, where the agronomically inferior D-genome demonstrated a greater tendency to overwrite genes from the A-subgenome.

Using *Brassica* (cabbages) allopolyploids, a landmark study detailed the loss and gain of restriction fragments in newly synthesized allopolyploids mimicking natural *B. rapa* and *B. juncea* (Song et al., 1995). This study was important as Song and colleagues (1995) were able to use the precise progenitors of the allopolyploids, rather than close relatives, to assess the changes accompanying allopolyploidy. Thus, differences between the allopolyploids and progenitors were not due to intraspecific differences within the ancestral species, but occurred immediately subsequent to polyploid formation. Genetic alterations were observed in all five of the resulting generations, and interestingly, the number of changes observed was positively correlated with the genetic distance between progenitor genomes. This study provided the first example of small scale, local genetic aberrations in allopolyploids. Following these observations, similar accounts were reported. For example, investigation using early generation synthetic *B. napus* allopolyploids revealed homoeologous pairing of the A and C subgenomes during early meioses (Szadkowski et al., 2010). The resulting recombined chromosomes were often transmitted to the progeny (Szadkowski et al., 2010), resulting in chromosomes consisting of sections from each constituent subgenome. Similar observations were made in another set of resynthesized *B. napus* lines, where loss of restriction fragment length polymorphism (RFLP) bands occurred after a few generations (Gaeta et al., 2007). Importantly, Gaeta and colleagues (2007) were able to link epigenetic and sequence level alterations to phenotypic change in allopolyploid lines.

Much of our understanding regarding genome evolution following WGD arises from studies of allopolyploid wheat. In an important early study (Feldman et al., 1997), analysis of 16 low-copy sequences in the polyploids and relatives of their diploid progenitors revealed the elimination of low-copy sequences in natural allohexaploid wheat. Follow up investigations (Liu et al., 1998; Ozkan et al., 2001) demonstrated reproducible loss and gain of DNA fragments in various synthetic allopolyploid mimics, some of which appear to parallel changes observed in natural allopolyploids. These observations suggest some degree of reproducibility between independent allopolyploid events. Another interesting observation that emerged from studies in wheat is that low-copy number sequences present across the genomes of *all* diploid progenitors of hexaploid wheat (A-, B-, and D-subgenomes) became limited in distribution and chromosome or subgenome specific following allopolyploidy (Ozkan et al., 2001), indicating a loss of homoeologous regions following genomic merger (see also Chantret et al., 2005). Such a process may aid in the differentiation of homoeologous chromosomes and contribute to cytological diploidization (see below) and the prevention of homoeologous chromosome pairing during meiosis (Feldman and Levy, 2012).

***Genome diploidization and gene fractionation—***Given the ubiquity of WGD in angiosperms and the multiplicity of duplication events in any given flowering plant lineage, it is surprising that (1) angiosperm genomes are often small and (2) the number of identified genes in each genome is much lower than one might predict. That is, one might expect each WGD event to double both gene number and genome size each time, yet this is not what is observed. Although there is a huge range in genome size (GS) among angiosperms, the modal GS is relatively small (0.7 pg/1C; Leitch et al., 1998). How do we reconcile these seemingly conflicting observations?

The answer has emerged from analyses of crops and their relatives, which indicate that following WGD, a process of diploidization occurs in which the genome of a polyploid is pruned, often by poorly understood mechanisms, such that it returns to a diploid-like condition (Wolfe, 2001). This process has evidently been so efficient at removing obvious traces of WGD that it was not until the dawn of the modern genomics era that it became evident, at least within the seed plants, that true diploids do not exist and that all land plants are likely paleopolyploid. So, how does a genome go from chromosomally polyploid (neopolyploidy) to functionally diploid (paleopolyploidy) during the course of evolution, and how have crop plants informed us of this process?

From available genome size data, we know that following WGD, a period of "genome downsizing" tends to occur, after which the sum of nuclear DNA in the polyploid genome becomes less than one might expect based on diploid progenitors (Leitch and Bennett, 2004; Leitch et al., 2008). Examples are evident in many crop species, e.g., *Nicotiana* (tobacco; Leitch et al., 2008) and *Gossypium* (cotton; Grover et al., 2007). In wheat, reduction in genome size may occur relatively rapidly, after only a few generations in some synthetic lines (Eilam et al., 2008, 2010), serving to exemplify the "revolutionary" (Feldman and Levy, 2009) pace of genomic alterations that impact allopolyploid genomes. What, however, are the processes that remove redundant sequences within the genome and bring about downsizing?

It has long been known that variation in genome size is generally not the result of variation in gene content but the varying accumulation, or removal, of repetitive and nongenic DNA. Thus, it is perhaps not surprising that the majority of genome size decreases seen in allopolyploid genomes results from the removal of repetitive DNA sequences (Liu et al., 1998; Han et al., 2005; Lim et al., 2007; Renny-Byfield et al., 2011, 2012, 2013). This removal is often thought to be mediated by various recombinational mechanisms, some of which leave hallmarks such as solo long terminal repeats (LTRs), as observed in rice and barley (Shirasu et al., 2000; Vitte and Panaud, 2003), or by accumulation of small deletions as observed in cotton (Grover et al., 2007). Interestingly removal of DNA can be biased with respect to subgenomes. In tobacco, for example, the maternal genome is relatively intact, whereas the paternal genome exhibits evidence of genome erosion (Renny-Byfield et al., 2011, 2012).

This process of DNA elimination causes contraction of genome size, but also may lead to the divergence of homoeologous chromosomes, in that they become more diploid like (Ozkan et al., 2001). It has been speculated that this process is also important for aligning chromosome pairs before recombination during meiosis, stabilizing meiotic pairing and increasing fertility of nascent allopolyploid lineages (Feldman and Levy, 2012).

Despite the fact that homoeologous chromosomes may become more distinct with regard to their single/low-copy fraction, the remaining repeat content of allopolyploid genomes tend to become more homogeneous, with respect to their original genomic distinctions, over millions of years via translocations, sequence divergence, and exchange of repetitive DNA. Thus, subgenomes are "turned-over" and become largely indistinguishable in the long-term as indicated by genomic in situ hybridization (GISH; Lim et al., (2007) and Renny-Byfield et al., 2013). Furthermore, over many millions of years, duplicated chromosome numbers usually decrease, so polyploids move

back to a more ancestral-like chromosome number (Lim et al., 2007; Abrouk et al., 2010).

With respect to their genic content, how is it that plants vary so little in their gene number, despite the fact they all have experienced multiple, nested WGD events during their history? Initial insights into the nature of this phenomenon emerged from studies of rice and maize, for which a process of gene fractionation was described (Langham et al., 2004). Following WGD, duplicate genes are lost, so that over time many to most duplicated genes return to single copy status through various deletional processes (Thomas et al., 2006; Woodhouse et al., 2010; Freeling et al., 2012). Recent evidence has suggested that there may be, in some cases, bias in favor of removal of genes from one of the two progenitor genomes (Thomas et al., 2006; Woodhouse et al., 2010; Tang et al., 2012; Garsmeur et al., 2014) and that this bias correlates with a general overexpression of genes in the regions experiencing less gene loss (Schnable et al., 2011). Biased fractionation, however, was not observed in all paleopolyploid genomes examined, leading to suggestions of two distinct evolutionary outcomes following WGD (Garsmeur et al., 2014); one class, where bias is rife, and another, where random loss from each subgenome is observed. Perhaps, as the authors of the study suggest, these two distinct classes represent ancient allo- and autopolyploid events, respectively (Garsmeur et al., 2014), although this has not been firmly established. Moreover, the inference of biased fractionation at a subgenome level, or "genome dominance" in this sense (Schnable et al., 2011), relies upon unproven assumptions about ancestral reconstructions (i.e., the most fractionated homoeologs all belong to the same subgenome).

Notwithstanding these methodological considerations, it is unmistakable that WGD is followed by massive DNA loss, including loss of duplicate genes. Why then, are some duplicate genes both retained? We have discussed diploidization, gene loss, and DNA removal, but what about gene retention? Why are genes retained in duplicated at all and how might this impact crop plant function and improvement? Several ideas have been put forward to explain the retention of gene duplicates, and many of these have implications for the success of polyploid species as crops.

Some of the landmark work in this arena has come from plant geneticists studying crops, particularly the cotton geneticist S. G. Stephens, who published two key papers over half a century ago on divergence of gene duplicates and the acquisition of novel function (Stephens, 1951a, b). Much later came the widely known work of Ohno (1970), who described a process by which genes were maintained in duplicate by neo-functionalization. Simply put, because of the redundancy introduced by gene duplication, one of the duplicates is free to accumulate mutations and over time, via neutral evolution, acquire a new function, while the other copy maintains the original (ancestral) function. This intellectual framework has served as the backdrop for myriad studies of gene duplication over the decades. In most cases, however, evidence does not support a neutral model of neofunctionalization (Hughes, 1994; Chapman et al., 2006), but rather more nuanced processes (reviewed by Wang et al., 2012). A prominent alternative explanation for duplicate gene retention has been the concept of subfunctionalization, where the function of the ancestral gene is partitioned between its descendant duplicates (Force et al., 1999; Lynch and Conery, 2000; Lynch and Force, 2000; Prince and Pickett, 2002). Such partitioning renders both gene duplicates essential for maintaining function, so selection favors the maintenance of both. Several additional ideas for duplicate gene retention have been proposed, including: (1) dosage sensitivity, where genes are maintained as duplicates to prevent perturbation of stoichiometric balance between interacting protein products (Birchler et al., 2001; Freeling and Thomas, 2006; Birchler and Veitia, 2007, 2010, 2012), (2) escape from adaptive conflict (Des Marais and Rausher, 2008), and (3) selection for increased expression levels (Aury et al., 2006). Given that all crop plants are paleopolyploid and that many are neopolyploid, their genomes consequently contain a preponderance of gene duplicates, at least immediately following WGD. The processes described have, no doubt, played a key role in maintaining genes that have survived as duplicates and aided in generating some of the phenotypic novelty that have made crop plants so valuable to human civilization (see examples below).

***Transcriptomic alterations in polyploids—***An additional aspect of polyploid evolution that has garnered much attention is the effect of genome merger and doubling at the gene expression level, usually at the level of the transcriptome. These expression alterations accompanying polyploidy may also be important to phenotype and be responsive to selection under domestication (Hovav et al., 2008).

Early studies of gene expression in polyploid plants, including those in cotton and wheat, indicated that immediately following polyploidy one of the duplicate genes may be silenced relative to the diploid progenitors (Kashkush et al., 2002; Adams et al., 2003, 2004; He et al., 2003; Wang et al., 2004; Buggs et al., 2010b, c). Gene silencing can occur rapidly, with several examples of gene expression changes in first generation synthetic allopolyploid mimics (Kashkush et al., 2002; Adams et al., 2004; Hegarty et al., 2006). For some homoeolog pairs in cotton, silencing can be immediate and can also operate in a reciprocal manner, whereby one gene is activated in a given tissue and the other homoeolog is silenced in another tissue (Adams et al., 2003, 2004). These phenomena have also been observed in wild polyploid populations, as in *Tragopogon*, where similar patterns of gene expression changes are observed in populations of independent origin (Buggs et al., 2010b). Thus, the use of crop plants as models for genome and gene expression evolution has informed us of general principles that have since been confirmed in wild populations, highlighting the important role of crops and models in evolutionary biology.

Increasingly, RNA sequencing (RNA-seq) is being used to study gene expression in allopolyploids. This technology is powerful in that it enables genome-diagnostic single nucleotide polymorphisms (SNPs) to be inferred and then applied to quantitatively measure homoeolog expression. This approach has, perhaps, been most widely applied in cotton allopolyploids and relatives of its diploid progenitors (Flagel et al., 2012; Page et al., 2013a; Yoo et al., 2013), where the contribution of each homoeolog to overall expression on a genome-wide scale has been described in detail. One of the most common observations, both in cotton and in other species, is bias in homoeolog expression, that is, a statistical departure from equivalence (Grover et al., 2012). This phenomenon has been described in multiple polyploid crop plants to date, including cotton (Yang et al., 2006; Flagel et al., 2008; Hovav et al., 2008; Yoo et al., 2013), cabbages (Gaeta et al., 2007; Auger et al., 2009) and wheat (Mochida et al., 2003; Bottley and Koebner, 2008). Moreover, homoeolog expression bias also has been observed in natural, noncrop populations (Wang et al., 2004; Buggs et al.,

2010a, b; Chang et al., 2010; Chelaifa et al., 2010; Koh et al., 2010).

A related but more complex phenomenon is expression level dominance (Grover et al., 2012), where the level of total expression of duplicated genes in an allopolyploid is statistically equivalent to that of only one of the two progenitor species. This phenomenon, initially described in cotton (Rapp et al., 2009; Yoo et al., 2013) now has been observed in other crop plants, including wheat (Qi et al., 2012) and coffee (Bardil et al., 2011), and also has been observed in wild allopolypoloids (Chelaifa et al., 2010). Interestingly, in coffee, expression-level dominance was only evident under certain environmental conditions, i.e., when coffee plants were grown at higher temperature. These observations add another interesting environmental dimension to the balance of gene expression in polyploids. Noting that allopolyploidy entails the combining of trans-acting gene regulatory networks from two distinct evolutionary lineages, we suspect that their reunion into a single nucleus fundamentally alters the environment within which genes operate. This altered environment leads to genome-wide disruption of regulatory networks and perhaps epigenetic states, which operationally may be observed as bias or expression-level dominance. Studies in polyploid cotton revealed that in most cases expression-level dominance is caused by the up- or downregulation of the homoeolog deriving from the *nondominant* genome (Yoo and Wendel, 2014). This may reflect the operation of several different molecular mechanisms and interactions, including epigenetic release or silencing of the nondominant homoeolog, or *trans*-effects overpowering *cis*-regulatory differences. Irrespective of our lack of understanding of mechanistic underpinnings, expression-level dominance and homoeolog expression bias provide another source of diversity and novelty in polyploid plants relative to their diploid progenitors, which we speculate will be shown to have been significant in the context of crop breeding and improvement.

One promising future direction is to investigate gene coexpression networks. Rather than studying differential expression on a gene-by-gene basis, entire coexpression networks are analyzed. While research in higher plants is at the earliest stages, in this respect, some of its promise is revealed by a recent study from paleopolyploid maize, where network analysis revealed that over 1000 genes (of ~18 000 examined) were involved in transcriptomic rewiring following domestication (Swanson-Wagner et al., 2012). Genes exhibiting network rewiring were also enriched for candidates previously implicated as being under selection during maize domestication. Thus, network analysis may prove to be a valuable method for identifying genes important to domestication and/or crop plant improvement.

Accumulated data on gene expression in polyploids paint a picture of a highly perturbed transcriptomic network, the result of reuniting evolutionarily diverged chromosome sets into a common nucleus and only one of the two parental cytoplasms. Such extensive alterations to gene network architecture and gene expression patterns is thought to provide polyploids with the phenotypic novelty that was likely important in the domestication processes (Chen, 2007) and, in part, is likely responsible for the impressive success of polyploid plants (Soltis et al., 2009).

***Epigenetic alterations in polyploids*—**It now has become firmly established that heritable variation need not be based on alterations to DNA per se, but may be epigenetic (Zhang et al., 2013c; Cortijo et al., 2014). These epigenetic changes include a diverse set of chemical modifications to DNA and the associated histone proteins that do not change the underlying DNA sequence but are nonetheless heritable. These include DNA methylation at cytosine nucleotides and a complex suite of histone modifications some of which include methylation, acetylation, and ubiquitylation (Bender, 2002; Madlung and Wendel, 2013).

Some have cited the potential of epigenetics as an explanatory filler for "missing heritability" (Maher, 2008; Springer, 2013), and indeed it has recently come to light that epigenetic variation can be a driver of phenotypic novelty, even among isogenic lines of *Arabidopsis* (Cortijo et al., 2014). Furthermore, variation in epigenetic traits within plant populations increases production, when compared with epigenetically uniform populations (Latzel et al., 2013) and may induce phenotypic variation in genetically uniform, natural allopolyploid populations of *Spartina* (Baumel et al., 2002; Salmon et al., 2005; Parisod et al., 2009). These insights highlight the potential of epigenetic variation to be a key factor in determining plant phenotype and productivity. Importantly, hybridization and polyploidy can induce a multitude of epigenetic modifications, almost certainly important for both crop domestication and improvement (Springer, 2013).

Indeed, polyploidy can be followed by rapid reorganization of methylation patterns, relative to the diploid progenitors (Madlung and Wendel, 2013), as observed in cabbages (Lukens et al., 2006; Gaeta et al., 2007; Xu et al., 2009; Ksiazczyk et al., 2011), wheat (Kashkush et al., 2002), *Cucumis* (cucumber) (Chen and Chen, 2008), and *Arabidopsis* (Lee and Chen, 2001). In some instances, epigenetic modifications are associated with genomic alterations and expression changes (Kashkush et al., 2002; Gaeta et al., 2007), including transposable element activation (Madlung et al., 2005). In other examples, CG methylation patterns have been shown to be altered near retroelements and DNA transposon insertions (Parisod et al., 2009) and, interestingly, predominantly affect the maternal genome.

Allopolyploids exhibit changes both in methylation patterns and histone modifications, rather than being strictly additive with respect to their diploid counterparts. These changes have the potential to be important in the context of domestication and improvement, as histone modifications are known to influence gene regulation (Deal and Henikoff, 2011). Indeed, recent work in wheat has highlighted the link between patterns of expression divergence of homoeologs and epigenetic states (Hu et al., 2013). Studying the three A-, B-, and D-homoeologs of *Expansin* genes in wheat, the authors observed that the silencing of the three homoeologs in root tissue was associated with H3K9 dimethylation and a reduction in the levels of two other histone modifications (H3K4 trimethylation and H3K9 acetylation). Release of homoeologs A and D from repression, however, was correlated with alteration to histone modification states at their promoters.

In allopolyploids of *Arabidopsis suecica*, analysis of circadian clock rhythms, along with the histone state of important genes in the circadian clock pathway, revealed that epigenetic repression of *CIRCADIAN CLOCK ASSOCIATED* (*CCA1*) and *LATE ELONGATED HYPOCOTYL* (*LHY*) resulted in greater accumulation of starch and chlorophyll in the allopolyploids relative to the progenitors *A. arenosa* and *A. thaliana* (Ni et al., 2009). Furthermore, F1 hybrids and allopolyploids had greater biomass. These data suggest that epigenetic mechanisms may be at play in the generation of heterosis and transgressive traits in allopolyploids and point to the future potential of epigenetic modification to increase crop vigor and yield.

***Section conclusion—***Investigation of crops and their close relatives has revealed a wealth of genetic and genomic phenomena associated with polyploidy, and crop plants have been instrumental in generating this knowledge. In the context of the present review, a key question becomes what is it about gene and genome multiplicity that has helped enable past domestication of plants and may further facilitate crop plant improvement?

Perturbations to the genome, transcriptome, epigenome, and other "-omes" (e.g., proteome, metabolome, interactome), can be viewed as unavoidable "problems" that nascent polyploids need to overcome to persist. Some have suggested that it is this dynamism that provides polyploids with their utility in an agronomic setting (Leitch and Leitch, 2008; Soltis et al., 2009). For example, we know that large-scale genome perturbations have the potential to add novel genetic material to the genome, potentially useful in the context of domestication and selection. Similarly, alterations to the transcriptome that occur following WGD and hybridization may provide novel expression and phenotypic traits that can be subject to human selection, while silencing, activation, and up- or downregulation of individual genes has no doubt played a role in domestication. The potential of whole genome duplication to double the number of resident genes immensely increases the combinatorial complexity of the transcriptomic landscape, permitting vast new terrains of "gene expression space" to be evolutionarily explored. One can readily conceive how this might facilitate the forging of new network connections and the development of novel coexpression modules following duplication. Although there remain at present relatively few compelling empirical demonstrations of these processes as they pertain to economically relevant phenotypes in crop plants, initial insights are beginning to emerge; these are reviewed in the following section.

## POLYPLOIDY, GENE DUPLICATION, AND DOMESTICATION

We first provided a brief summary of the some of the key genomic, transcriptomic, and epigenetic novelties that arise with the onset of hybridization and genome doubling. Many have argued that the novel genetic combinations are variously responsible for the success of polyploids (Comai, 2005; Leitch and Leitch, 2008; Soltis et al., 2009), and some have connected this directly to domestication and improvement (Hilu, 1993; Dubcovsky and Dvorak, 2007). Following are some examples of the linkages between this fundamental process in plant evolution and a modern agricultural system that provides sustenance for over 7 billion people.

***Hybridization, polyploidy, and heterosis—***For decades, it has been known that hybrids and allopolyploids can grow larger, more quickly, and with higher yields compared with their diploid relatives, providing de facto evidence of the importance of these phenomena in crop improvement. This hybrid vigor, or heterosis, can increase biomass, fertility, and growth rates in hybrids or allopolyploids compared with their parents (Chen, 2010). One example is offered in the cotton genus, where the fiber (single-celled, epidermal, ovular trichomes) of allopolyploid cotton is vastly superior to homologous cells from its diploid relatives. Allopolyploid cotton originated around 1.5 million years ago (Ma) via the hybridization of an A-genome cotton species (closely related to *Gossypium herbaceum* and *G. arboreum*) and D-genome cotton, related to *G. raimondii* (Wendel and Cronn, 2003). Both A- and D-genome species produce fibers, but only A-genome species produce fibers suitable for spinning into yarn. Importantly, the fibers from the allopolyploids *G. hirsutum* (upland cotton) and *G. barbadense* (Egyptian cotton) are considerably longer, stronger, and whiter than are possible to obtain from any diploid (Wendel and Cronn, 2003). This fact suggests that the subgenomes of the D-genome cotton, with short fibers, and the A-genome cotton, with longer fibers, are able to combine and produce fibers of agronomic quality that are superior to those from either of the two diploid species alone. The fiber morphology of the agronomically important allotetraploid is thus transgressive, or perhaps heterotic, as pointed out by a number of authors (Jiang et al., 1998; Paterson, 2005). The biological mechanisms underlying the increased quality in allopolyploids is not well understood, although it includes the upregulation of genes involved in cell-wall biogenesis and significant changes to the transcriptomic network (Hovav et al., 2008; Rapp et al., 2010; Yoo and Wendel, 2014). Interestingly, many quantitative trait loci (QTL) associated with high-quality fibers map to the D-genome, inherited from the diploid species with vastly inferior fiber quality (Jiang et al., 1998; Rong et al., 2007; Paterson et al., 2012). Similarly, in at least some studies, the transcriptomic network seems to be biased in favor of expression of homoeologs from the D-genome (Hovav et al., 2008), demonstrating that genes, which long ago diverged after the split of the progenitor lineages, can combine in the nascent allopolyploid to produce useful and important agronomic traits in unexpected ways.

Other examples of allopolyploids and/or hybrids with increased vigor include those of rice (Cheng et al., 2007), wheat (Uddin et al., 1992), tobacco (Goodspeed, 1933; Matzinger and Wernsman, 1967), and maize (Crow, 1998; Duvick, 2001). In some instances, it appears as though crosses between highly diverged genotypes produce greater increases in biomass (East, 1936), while in other cases crosses of more closely related species produce greater increases in plant vigor (Matzinger and Wernsman, 1967).

The precise causes of heterosis remain under debate, although several ideas have been advanced. One theory, proposed shortly after the rediscovery of Mendelian inheritance, is that of dominance (Bruce, 1910; Chen, 2010). In this case, deleterious alleles at one or several loci are masked by more favorable dominant alleles from the other parent, allowing the negative effects of the deleterious alleles to be overcome in the hybrid population, resulting in heterosis. Other explanations include overdominance (reviewed by Chen, 2010) in which the combination of dominant alleles from the progenitor lines unify in the hybrid to produce superior effects, i.e., there are two doses of dominant effect (East, 1936). In rice hybrids, the impact of epistatic effects, in which the phenotypic impact of a given locus is dependent on genetic background, has been invoked (Yu et al., 1997; Birchler and Veitia, 2010). More recent work on plant height in elite rice cultivars indicated that epistasis is a major factor in contributing to heterosis operating via "additive by additive" and "additive by dominance" effects (Shen et al., 2014), and the authors concluded that dominance and epistasis are major forces at play in plant height heterosis. Others have highlighted the need to consider the phenotypic basis of heterosis in plants, including regulation of photosynthesis and distribution of resources, as a way of advancing improvement strategies (Blum, 2013).

In allopolyploids, the potential for epistatic affects is expanded and may have played in important role in the domestication of modern allopolyploid crop species. Considering only two interacting loci, it is possible for diploids to have two alleles at each locus, totaling four interacting gene copies. The situation in polyploids, however, is more complicated, often with four homeoalleles at each locus, thus totaling eight interacting gene pairs, with the number of interacting gene pairs rising with increasing ploidy. Determining how such networks and epistatic interactions merge in polyploids is an emerging goal within the field of polyploid research, as it likely is a driver of phenotypic novelty and heterosis in crops.

Not only is phenotype dictated by epistatic interactions among alternative genotypes, but recent work has highlighted the potential role of epigenetic modification and variability in the development of heterosis to improve yield in crop plants. Epigenetic states can be altered in hybrids and polyploids (Lee and Chen, 2001; Kashkush et al., 2002; Lukens et al., 2006; Gaeta et al., 2007; Chen and Chen, 2008; Xu et al., 2009; Ksiazczyk et al., 2011), resulting in epigenetic variation that can be heritable within a population (see earlier). It is also clear that epigenetic QTL (epiQTL) impact phenotype and can account for significant proportion of phenotypic variation in genetically uniform populations (Cortijo et al., 2014). Moreover, recent studies of inbred *Arabidopsis* lines have demonstrated that epigenetic variability within a population can result in increased biomass (Latzel et al., 2013). Similarly, it is likely that epigenetic variation induced by hybridization and polyploidy can contribute to heterosis and increased yield in crop species. The discovery of an epigenetic component to heterosis is an exciting new advance, and the utilization of epigenetic diversity within crop species will provide a novel avenue for crop improvement in the coming years.

***Domestication traits facilitated by polyploidy*—**Given that so many genomic, transcriptomic, and epigenetic novelties are generated via polyploidy, it is not surprising that examples have come to light of interesting phenotypic traits, important in the domestication process, that have been facilitated by WGD. One prominent example is the emergence of the free-threshing grain character in wheat allopolyploids (Zhang et al., 2011). In this case the *Q/q* alleles of the A-, B-, and D-subgenomes of allohexaploid wheat have diversified in function and expression since allopolyploidization. The *Q* transcription factors do not produce a free-threshing character in diploid wheat. Interestingly, however, *Q* alleles in allohexaploid wheat do produce a free-threshing grain. The *q* allele from the B-subgenome appears pseudogenized but is still expressed and apparently regulates the *Q* allele from the A-subgenome (the homoeoallele linked with the free-threshing character) and also the *Q* allele of the D-subgenome. Thus, the free threshing character, so important in the success of allohexaploid wheat, has been made possible by polyploid-induced duplication and diversification as well as interactions between homoeoalleles.

Polyploidy has also facilitated the development of diversity in wheat grains. The *Hardness* (*Ha*) locus controls grain hardness in polyploid wheat species; examination of the evolutionary history of this locus exemplifies the role WGD plays in crop improvement. In diploid wheat, the locus consists of several closely linked genes, the presence of which confer the soft grain phenotype. Deletion of these genes in allotetraploid wheat (subgenomes AABB; *Triticum durum*) resulted in the development of the hard grained phenotype, useful for making pasta. Following this, the unification of allotetraploid wheat with a D-genome diploid resulted in soft-grained allohexaploid bread wheat (AABBDD; *Triticum aestivum*). The introduction of an intact *Ha* locus from the D genome restored the soft grain phenotype desired for making dough (Chantret et al., 2005; Olsen and Wendel, 2013). In other words, allopolyploidization in wheat has facilitated both the loss and recovery of the soft grain characteristic, under diversifying selection and at different times in different cultural contexts. Furthermore, many of the subsequent varieties of bread wheat have resulted from various rearrangements, insertions, and deletion at the *Ha* locus, often associated with retroelements, perhaps activated by the "genomic shock" (McClintock, 1984) of allopolyploidy.

In the mustard family (Brassicaceae), a history of WGD coupled with local tandem duplications has been key in the utilization and diversification of glucosinolates, secondary metabolites that are powerful weapons in antiherbivory defense (Hofberger et al., 2013). The authors of this study noted that after WGD, ~45% of genes are retained as duplicates. When considering genes within the glucosinolate synthesis pathway, however, retention of genes occurred at a higher rate, with over 95% of genes retained in duplicate. These observations suggest preferential retention of duplicates involved in glucosinolate production. They also suggest that redundancy introduced by WGD expands the potential for gene diversification and that this capability has been co-opted to increase the diversity of glucosinolates in allopolyploids in the Brassicaceae. Increased potential for herbivore resistance is clearly a valuable trait in crop species and may have played a role in the adoption of members of the Brassicaceae as crops.

Another example from sunflowers demonstrates how gene duplication can provide the raw material on which natural and human selection can act. The *FLOWERING LOCUS T* (*FT*) induces reproductive tissue in response to specific photoperiods. Recent duplications have resulted in four paralogous genes (*HaFT1–HaFT4*), one of which (*HaFT1*) appears to operate as a negative regulator of another one of the paralogs (*HaFT4*) (Blackman et al., 2010). Furthermore, some of the paralogs exhibit alterations in expression level brought about by both *cis*- and *trans*-effects. The result of duplication and diversification of the *FLOWERING LOCUS T* (*FT*) has allowed alterations in flowering time so that domesticated sunflowers flower under longer day lengths. Importantly, several of the *FT* paralogs are located near the QTL for flowering time and exhibit evidence of having been under strong selective constraint during domestication (Blackman et al., 2011). Although not directly related to neopolyploidy, this combination of features strongly suggests a key role for paleoduplication and functional divergence during domestication in sunflower and further highlights the plethora of molecular mechanisms by which phenotypic change occurs.

***Section conclusion*—**The examples presented here demonstrate the role of WGD in the facilitation of selection for important agronomic traits. Diversification of gene expression and function often result in the development of novel traits useful in the domestication process. Moreover, hybridization introduces new genetic combinations, from which novel desirable traits may be extracted, and from which increased vigor, or heterosis may derive. Finally, the "genomic shock" of allopolyploidy has induced retroelement activity and a variety of other genomic effects that later were (and may be) used by humans in agronomic selection.

## POLYPLOIDS AND THE FUTURE OF CROP IMPROVEMENT

***Sequencing polyploid genomes—*** While investigation of polyploids has provided a rich understanding of plant genome biology, it is not without its difficulties. More so than diploid species, polyploids present experimental challenges largely arising from genome multiplicity. First, polyploids typically have larger genomes than their diploid relatives (Leitch and Bennett, 2004), notwithstanding genome downsizing (described earlier), and this alone makes them less attractive as model organisms. Larger genomes are more expensive to sequence and require greater computational finesse than the preferred inbred diploids typically used for genome assembly (Kelly et al., 2012).

For example, the first genome sequence of a flowering plant was that of *Arabidopsis thaliana*, chosen, in part, because of its small genome size. Early genome assemblies were based on Sanger chain termination sequencing methods, and sequencing cost was a major consideration when choosing potential species for analysis. Following the advent of next-generation sequencing, genome projects have rapidly expanded in number and phylogenetic breadth, to include sequencing projects in many crop plants and other plants as well. In part because of cost, but also because of the repetitive fraction that makes up the bulk of most plant genomes, genome sequencing has been largely restricted to species with relatively small genomes (Kelly et al., 2012). A second challenge in assembling allopolyploid genomes arises from their genomic complexity and high levels of sequence redundancy, although considerable progress raises hopes that these issues are being ameliorated (Page et al., 2013a, b; Berger et al., 2014; Nakasugi et al., 2014). Nonetheless, considerable challenges remain in assembling polyploid genomes and correctly diagnosing and assembling homoeologous genes and alleles.

For these reason, researchers have often turned to sequencing progenitor species as a first step in understanding crop genome evolution, improvement, and domestication. For example, the dual release of the first two tobacco genome assemblies were those of *Nicotiana sylvestris* and *N. tomentosiformis* (Sierro et al., 2013), the two progenitors of domesticated tobacco, rather than the allopolyploid itself. Similarly, the diploid *Gossypium raimondii*, the D-genome donor of allopolyploid cotton, was chosen for the initial cotton sequencing effort (Paterson et al., 2012), despite the fact that this species is of little or no agronomic importance. Using similar approaches, others have sequenced the genome of *Brassica rapa* (Wang et al., 2011) and *B. oleracea*, in preference to the genomes of the derived allopolyploids *B. napus*, *B. juncea*, and *B. carinata*. These are sensible approaches, given the cost and difficulties in assembling large genomes with multiple alleles at a given locus, and still provide room for important advances in understanding the history of selection in crop plants.

***Analyzing the genetics of domestication in polyploid crops—*** Understanding the genetic/genomic basis of domestication and improvement is a multifaceted pursuit involving several complementary approaches (reviewed in Olsen and Wendel, 2013). Due to the inherent complexity of sequencing polyploid genomes, to our knowledge only a single example of a "complete" polyploid genome exists, that of autotetraploid potato (Xu et al., 2011). Accordingly, researchers have turned to sequencing of related diploid species and other alternative techniques to investigate the diversity, evolutionary history, and genetics of domestication in polyploids.

One approach is to generate genomic data through "re-sequencing", as recently employed in upland cotton (Page et al., 2013Q1b; Rambani et al., 2014), using either RNA-seq or genomic reads and mapping these reads to a reference diploid genome and subsequently calling high quality, subgenome-diagnostic SNPs. In *Brassica*, new efforts have focused on generating a SNP database for the allopolyploid *B. napus*, following the publication of a genome assembly for the diploid A genome (*B. rapa*) and ongoing efforts to complete the C genome (*B. oleracea*) (Trick et al., 2009; Cheng et al., 2011; Huang et al., 2013). Others have developed SNP data sets using next-generation sequencing (NGS) in wheat (Trick et al., 2012), and over 350 000 SNPs were identified by analyzing 21 maize inbred lines (Hansey et al., 2012). In autotetraploid potato, over 60 000 high quality SNPs have been identified using a combination of Sanger sequencing and NGS data (Hamilton et al., 2011) with similar results in allopolyploid peanut (Khera et al., 2013). These and similar data sets have the potential to aid breeding and improvement in polyploid crops, even without a polyploid reference genome.

Sequencing needs to be combined with phenotypic analyses to tackle the challenges of understanding the past effects of strong directional and diversifying selection accompanying domestication and improvement and to harness this powerful technology for future crop improvement efforts. Following the use of genome-wide association studies (GWAS) to identify loci associated with human disease, such studies are now regularly used with plant populations to identify loci important in the context of agronomic improvement in breeding programs. Association studies use a set of genetically diverse crop lines and rely on inference of linkage disequilibrium between regions of diversity and loci responsible for traits of interest. For example, in maize, GWAS have revealed ~30 QTL associated with leaf morphology (Tian et al., 2011), while analysis of over 400 lines of rice have revealed a multitude of QTL covering a variety of important agronomic traits (Zhao et al., 2011). Similarly, in barley, GWAS analysis of over 500 cultivars identified 18 loci associated with 15 phenotypes (Cockram et al., 2010). Such studies are useful for identifying regions of importance in determining desirable phenotypes in crop species and will likely be increasingly important in world food security in the coming years. Because of the high frequency of neopolyploidy among crop species, few crops fulfill the requirements for effective use of GWAS and for a number of reasons (Harper et al., 2012). Perhaps the most obvious of these is the current absence of high-quality polyploid genome assemblies, as is the case for nearly all polyploid crops, including cotton, wheat, peanut, and sugarcane.

Recently, and remarkably, despite the lack of a genome sequence for allopolyploid *B. napus*, Harper et al. (2012) used associative transcriptomics to look for loci important during domestication and crop improvement. Using RNA-seq data, the authors simultaneously assessed variation in exonic sequences and investigated divergence in gene expression profiles. Using a previously published SNP linkage map (Bancroft et al., 2011), the authors reoriented segments of the progenitor genomes, creating pseudomolecules that more accurately represent the genome of the derived allopolyploid. The 81 analyzed lines of *B. napus* resolved into seven distinct crop types, and the authors identified two QTL deletions in the allopolyploid genome that contributed to the glucosinolate content of seeds (Harper et al., 2012).

Another approach, which has been reasonably successful in identifying regions that have been under selection during domestication, involves assessing genome-wide diversity for patterns consistent with recent selection, potentially highlighting genes that have played a key role during domestication (Olsen and Wendel, 2013). The action of selection will generally reduce genetic diversity around a locus under strong selection, as only the variation closely linked with the allele of interest will persist within the population. Thus, regions closely linked to an allele that has experienced recent positive selection will generally have reduced neutral variation compared with other regions of the genome. Such an analysis has a few limitations, however, including lack of sensitivity with regard to "soft-sweeps" that occur when selecting for a genetic variant that is already a component of the standing genetic variation. Despite these, and other limitations, this approach has identified a number of loci that appear to have been important in the domestication history of rice (He et al., 2011; Xu et al., 2012), maize (Chia et al., 2012; Jiao et al., 2012; van Heerwaarden et al., 2012) and soybean (Lam et al., 2010). This kind of information is important as it allows for more targeted and refined improvement designs in crop species; notably, there is potential for this type of analysis in polyploids, particularly when combined with a SNP linkage map, similarly to recent efforts in *Brassica napus* (Harper et al., 2012). A case in point is for allohexaploid bread wheat (Cavanagh et al., 2013). The NGS data from a diverse panel of wheat cultivars were generated in conjunction with a large, multiparental, advanced generation intercross. This allowed the positioning of over 7000 SNPs on a genetic map. Using the SNP map and analyzing distribution of variation at these SNPs allowed the identification of a number of loci that experienced a selective sweep in wheat, including pivotal genes in the flowering time network.

***Section conclusion*—**Neopolyploid plants present particular challenges for analyzing domestication history and crop improvement traits, due to the high genic and often repeat similarity between their constituent genomes. We anticipate that these methodological challenges will soon be overcome by advances in genome sequencing technologies (Faino and Thomma, 2014). In addition, other powerful approaches have emerged in the last few years that promise to improve our ability to connect genotype to phenotype, an essential prerequisite to targeted breeding efforts.

## CONCLUDING REMARKS

Many crop species are relatively recent allopolyploids, and thus an appreciation of the evolutionary consequences of (allo) polyploidy is central to our understanding of crop plant domestication, agricultural improvement, and the natural history of the flowering plants. Many insights into plant biology have been gleaned from crops, revealing a multitude of evolutionary processes that affect polyploid genomes, including rapid and substantial genome reorganization, fractionation, gene conversion, genome downsizing, transgressive gene expression alterations, and sub- and/or neofunctionalization of duplicate genes. Often these genomic changes are accompanied by heterosis, robustness, and the improvement of crop yield, phenomena thought to be important to the success of polyploids as crops. Advances in multiple "-omics" technologies and other analytical approaches promise to reveal in exquisite detail the connections between genotype and phenotype, thus facilitating our ability to manipulate the "systems biology" of polyploid plants toward desired objectives. We anticipate that these integrative approaches will facilitate both deep insight into the architecture of important traits and the feeding of a burgeoning human population.

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