Impacts of Whole-Genome Triplication on MIRNA Evolution in Brassica rapa

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Abstract

MicroRNAs (miRNAs) are a class of short non-coding, endogenous RNAs that play essential roles in eukaryotes. Although the influence of whole-genome triplication (WGT) on protein-coding genes has been well documented in Brassica rapa, little is known about its impacts on MIRNA. In this study, through generating a comprehensive annotation of 680 MIRNA for B. rapa, we analyzed the evolutionary characteristics of these MIRNA from different aspects in B. rapa. First, while MIRNA and genes show similar patterns of biased distribution among subgenomes of B. rapa, we found that MIRNA are much more overretained than genes following fractionation after WGT. Second, multiple-copy MIRNA show significant sequence conservation than that of single-copy MIRNA, which is opposite to that of genes. This indicates that increased purifying selection is acting upon these highly retained multiple-copy MIRNA and their functional importance over singleton MIRNA. Furthermore, we found the extensive divergence between pairs of miRNAs and their target genes following the WGT in B. rapa. In summary, our study provides a valuable resource for exploring MIRNA in B. rapa and highlights the impacts of WGT on the evolution of MIRNA.

Key words: MIRNA, whole-genome triplication, retention, coevolution, Brassica rapa.

Introduction

MicroRNAs (miRNAs) are a class of endogenous small RNA sequences, mainly 20–22 nt in length, and regulate gene expression at the transcriptional or posttranscriptional level, by cleaving the transcripts of target genes or inhibiting their translation (Chen 2009; Voinnet 2009; Vazquez et al. 2010; Axtell 2013). MiRNAs are derived from single-stranded RNA precursors which are transcribed by RNA polymerase II, and further processed by the DICER-like complex to generate self-complementary fold-back structures (stem-loop, hairpin or pri-miRNAs) (Ghildiyal and Zamore 2009; Czech and Hannon 2011; Ameres and Zamore 2013). Mature miRNAs are incorporated into RNA-induced silencing complexes, which targets miRNAs and other larger RNAs based on sequence complementarity (Vazquez et al. 2010; Cuperus et al. 2011). Plant miRNAs play crucial regulatory roles in diverse biological processes related to plant development (Mallory and Vaucheret 2006) such as: seed germination (Liu et al. 2007), organ formation (Moxon et al. 2008), developmental timing and patterning (Wu et al. 2013), phase transition (Aukerman and Sakai 2003), and biotic/abiotic stress resistance (Ruiu-Ferrer and Voinnet 2009; Jeong et al. 2011), etc. In many cases, MIRNA (precursor genes of mature miRNAs) can be grouped into families of different loci that encode similar or identical mature miRNAs (Meyers et al. 2008). Previous research reported that only a small part of annotated MIRNA families are well conserved in multiple species, whereas the majority are lineage or species-specific (Axtell 2008; Cuperus et al. 2011; Jones-Rhoades 2012). Some plant MIRNA families are conserved for hundreds of millions of years in multiple lineages, they have higher expression than less conserved or species-specific miRNAs, possess more paralogous loci, and have a higher diversity of target genes. Unlike highly conserved MIRNA, young MIRNA families are often weakly expressed, processed imprecisely, they lack targets, and display patterns of neutral variation. Based on these
features, previous reports suggest that these young miRNAs are rapidly changing and evolutionarily transient (Fahlgren et al. 2010; Ma et al. 2010), with only a subset of them stabilizing by integrating into regulatory networks (Fahlgren et al. 2007).

Whole-genome duplication (WGD) is widespread in plant genomes and may result in extensive genetic redundancy (Wang, Wang, et al. 2012). At least five ancient WGD events characterize the evolutionary history of the model plant, Arabidopsis thaliana (A. thaliana) (Cheng, van den Bergh, et al. 2013). Being from the Brassicaceae, the Brassica genus experienced the same events, with additional and relatively recent whole-genome triplication (WGT, hexaploidy) event (Br-α) (Wang et al. 2011). Since this triplication, both the number and expression of genes differentiated among the three subgenomes. The subgenomes that had fewer genes (more highly fractionated) are enriched for genes that were expressed at relatively lower mRNA levels compared with the paralogs (Cheng, Wu, Fang, Sun, et al. 2012). Such phenomenon was defined as "subgenome dominance," which was also observed in maize (Schnable et al. 2011).

Brassica rapa is a widely cultivated and economically important vegetable and oil crop around the world. The functional analysis of miRNAs in B. rapa has been the focus of several recent studies, which is potentially important for the genetic improvement of B. rapa crops (Yu et al. 2012). A less conserved miRNA, bra-miR1885, can regulate specific TIR-NBS-LRR transcripts in response to pathogen stress, particularly to turnip mosaic virus (TuMV) infection (He et al. 2008). Bra-miR398a and bra-miR398b are conserved miRNAs involved in heat response (Yu et al. 2012). Bra-miR156 affects BraSPL9-2, which controls the heading time in Chinese cabbage (Wang et al. 2014), whereas bra-miR319a targets TCP genes to modulate head shape in Chinese cabbage (Mao et al. 2014). Considering the important role of miRNAs in the regulation of development of B. rapa, several miRNAs and their putative target genes have been identified in B. rapa, but an analysis of the evolutionary relationship between miRNAs and their target genes is still lacking. At the time of this study, 157 mature miRNA sequences (127 unique sequences), representing 96 (Yu et al. 2012; Jiang et al. 2014) miRNAs have been released in the latest version of miRBase (version 21, June 2014; http://www.mirbase.org/, last accessed November 04, 2015) (Griffiths-Jones et al. 2008; Kozomara and Griffiths-Jones 2010). Apart from the miRNAs recorded in miRBase, two studies (Kim et al. 2012; Wang, Li, et al. 2012) annotated of 587 nonredundant miRNAs in B. rapa by small RNA sequencing and analyzing relative sequencing reads. However, only a limited number of studies have inferred that many miRNAs vary in paralogous gene copy number (deletion of one or more redundant paralogs) in B. rapa (Kim et al. 2012; Yu et al. 2012). The additional WGT experienced by B. rapa may have important consequences for the evolution of miRNAs, and thus a systematic and comprehensive study is needed to elucidate the subsequent changes.

In this study, we annotated B. rapa miRNAs globally by analyzing small RNA sequencing data, comparing the data with previous studies, and performed microsynteny predictions to the well annotated miRNAs in Arabidopsis. We then investigated the patterns of preservation/conservation of miRNAs from different subgenomes of the palehexaploid genome of B. rapa. Our results provide a valuable resource to explore the function of miRNAs and highlight the evolutionary consequences of miRNAs following WGT.

Materials and Methods
Small RNA Sequencing and Annotation
Small RNA sequencing data (Woodhouse et al. 2014) was generated from three tissues (root, stem, and leaf) in B. rapa cultivar Chiifu-401/42 and used to annotate miRNAs. We used “cutadapt” to trim both 5′- and 3′-adaptors from sequencing data (Martin 2011) as described (Woodhouse et al. 2014). Clean reads were aligned to the B. rapa genome (V1.5; http://brassicadb.org, last accessed November 04, 2015) (Cheng et al. 2011) using Bowtie (Langmead et al. 2009). Only reads that matched perfectly to less than 30 genomic regions in the B. rapa genome were used for miRNA annotation. The mapped regions were subjected to secondary hairpin structure prediction using “Mireap” (http://sourceforge.net/projects/mireap/, last accessed November 04, 2015). The predicted structures with less than −18 kcal mol⁻¹ free energy, less than 300 nt spaces between the miRNA and its complementary sequence, greater than 16 matched nucleotides, and less than 4 nt bulge of miRNA or its complementary sequence were subjected to further analysis. Only the secondary hairpin structures without any overlap of the annotated coding region and RNAs (tRNA, rRNA, snRNA, and snoRNA) were considered reliable miRNAs.

Integration of MiRNA Annotation Data Sets
The mature and precursor miRNA sequences of B. rapa from four previous studies (Kim et al. 2012; Wang, Li, et al. 2012; Yu et al. 2012; Jiang et al. 2014) were aligned to the B. rapa genome using BLASTN with e-value of 0.001. BLASTN hits with less than 80% coverage of the precursor were removed. If the precursors could be mapped to multiple positions in the genome, the best hit of the precursor was considered as the candidate locus of the miRNA. The position of mature miRNAs was then determined by the position of their precursors. Altogether, we combined four data sets (Kim et al. 2012; Wang, Li, et al. 2012; Yu et al. 2012; Jiang et al. 2014) and these annotation results with our aforementioned data set into a comprehensive miRNA atlas of B. rapa.
Microsynteny Comparisons among Species to Identify B. rapa MIRNAS

For the microsynteny-based identification of B. rapa MIRNAS, the mature miRNA sequences of A. thaliana, Arabidopsis lyrata were downloaded from the latest version (21.0, June 2014) of miRBase (Griffiths-Jones et al. 2008). These sequences were mapped to the B. rapa genome by “PatMan” (Prüfer et al. 2008) with a maximum of two mismatches allowed. The syntenic genes between B. rapa and each outgroup, A. thaliana and A. lyrata, were predicted by SynOrths (Cheng, Wu, Fang, Wang, et al. 2012). Twenty protein-coding genes in the respective upstream and downstream regions of the miRNA queries and mapped miRNA loci were extracted and compared. The syntenic miRNA pairs, defined with at least four syntenic gene pairs among the 40 flanking gene windows, were analyzed further. Then, we extended the flanking genomic sequences (300 nt) around each mapped locus in B. rapa genome and submitted them to MiRcheck to determine secondary hairpin structures (Jones-Rhoades and Bartel 2004). The mapped loci which passed the criterion of MiRcheck were considered accurate. The method was also used to determine orthologous MIRNAS of annotated B. rapa MIRNAS in A. thaliana, A. lyrata, and Schrenkiella parvula, respectively. In this analysis, the A. thaliana genome was downloaded from The Arabidopsis Information Resource (TAIR10; http://www.Arabidopsis.org/index.jsp, last accessed November 04, 2015) (Arabidopsis Genome Initiative 2000). The genomic data set for A. lyrata was obtained from the Joint Genome Initiative database (http://genome.jgi-psf.org/Araly1/Araly1.home.html, last accessed November 04, 2015; Hu et al. 2011) and S. parvula data set was retrieved from Dassanayake et al. (2011).

MIRNA Nucleotide Divergence Analysis

Syntenic pairs of MIRNA precursors between A. thaliana and B. rapa were divided into five regions: 5’-region, miRNA-5p, region between miRNA-5p and miRNA-3p, miRNA-3p, and 3’-region. The 5’-region was defined as 60 nt upstream of miRNA-5p, whereas the 3’-region was defined as 60 nt downstream of miRNA-3p. Using the A. thaliana MIRNAS as reference, we used the strategy reported by Ma et al. (2010) to analyze the nucleotide divergence of single-copy MIRNAS, multiple-copy MIRNAS, and MIRNAS among subgenomes. We divided each of the five regions into seven equal-length bins and calculated the average variation ratio by counting mismatches in the bins between pairwise MIRNAS based on MUSCLE alignments (Edgar 2004).

The Prediction of miRNA Targets Genes

MiRNAs bind to target genes with perfect or near-perfect complementarity, this nature motivates the prediction of potential targets through computational approaches. We utilized multiple methods to reduce false positive predictions of target genes (Dai et al. 2011; Wang and Adams 2015). Three tools for plant-specific miRNA target prediction, TargetFinder (Fahlgren et al. 2007, 2010), psRNAtarget (Dai and Zhao 2011), and psRobot (Wu et al. 2012) were used to identify the target genes of miRNAs in A. thaliana and B. rapa under default parameters. The final miRNA target genes were predicted by at least two of the three tools. Specifically, the predicted target genes of miRNAs from MiR5658, MiR5021, and MiR414 were discarded because of the massively amplified trinucleotide repeats in the mature sequences (UGA, GAA, and UCA, respectively).

Results

A Comprehensive Annotation of MIRNAS Genes in the B. rapa Genome

To obtain a complete data set of B. rapa MIRNAS, we utilized a comprehensive approach to annotate MIRNAS, including an analysis of small RNA sequencing reads, integrating the previous MIRNAS data sets of B. rapa, and a microsynteny relationship to well-annotated MIRNAS in Arabidopsis.

Previous sRNA-seq data (Woodhouse et al. 2014) from three tissues (root, stem, and leaf) of the reference genome B. rapa Chiifu was used to annotate B. rapa MIRNAS. After adaptor trimming, the numbers of unique and total reads were calculated and mapped to the B. rapa genome (supplementary table S1, Supplementary Material online). In summary, the MIRNAS size distributions share similar patterns between unique reads (supplementary fig. S1A, Supplementary Material online) and total reads (supplementary fig. S1B, Supplementary Material online), with 24 nt small RNAs being the most abundant, followed by 23 and 21 nt small RNAs, consistent with observations in Brassica napus (Huang et al. 2013). Approximately 3–4.6 million reads from each tissue were mapped perfectly to the B. rapa genome and were used for further analysis. After performing secondary structure predictions with the help of Mireap, we filtered the secondary hairpin structures of coding region and RNAs (rRNA, tRNA, snRNA, and snoRNA) in B. rapa (Materials and Methods). Finally, a total of 326 MIRNAS in the B. rapa genome were found with perfect hairpin structures, as expected by miRNA. Among these MIRNAS, 161 (49.4%), 50 (15.3%), and 115 (35.2%) are expressed as mature miRNAs in all three tissues, two tissues and only one tissue, respectively. The percentage of expressed tissue-specific MIRNAS in three tissues is 9.2–13.8%, with the leaf tissue expressing the most miRNAs.

We merged our annotated MIRNAS with previously reported data sets to include miRNAs that are expressed in other tissues or in different conditions. We compared our results with four previously reported MIRNA data sets in B. rapa (Kim et al. 2012; Wang, Li, et al. 2012; Yu et al. 2012; Jiang et al. 2014) and integrated them with our data set into a comprehensive MIRNAS annotation (Materials and
In total, 670 MIRNAs were combined into the MIRNA annotation (fig. 1). While almost one-third of the MIRNAs, 202 out of 670, were present in at least two data sets, only 20 (2.99%) were in all five data sets, indicative of spatial-, time-, or condition-specific expression.

As a complement to de novo MIRNA annotation based on sequence, interspecific microsynteny comparisons of MIRNA loci have also been widely used in MIRNA analysis (Maher et al. 2006; Fahlgren et al. 2010; Ma et al. 2010; Shen et al. 2014). The numerous studies of MIRNA in A. thaliana and A. lyrata provide abundant information to annotate B. rapa MIRNAs orthologues. Candidate MIRNA loci in B. rapa were found using the microsynteny relationships of B. rapa, A. thaliana, and A. lyrata. The candidates MIRNAs were then submitted to MiRcheck to identify the secondary structures (Jones-Rhoades and Bartel 2004). The MIRNAs that remained after MiRcheck were considered as reliable. A total of 181 orthologous syntenic MIRNAs between B. rapa and Arabidopsis were detected (supplementary fig. S2, Supplementary Material online).

Intriguingly, only ten MIRNAs were not present in the integrated annotation, but raise the total number of annotated MIRNAs in B. rapa to 680. Among these ten MIRNAs, mature miRNAs of three (MIR4245a, MIR840a, and MIR848a) were expressed under a specific condition or treatment in Arabidopsis (Rajagopalan et al. 2006; Fahlgren et al. 2007; Moldovan et al. 2010; Zhang et al. 2012; Vidal et al. 2013).

Altogether, we curated a comprehensive annotation of 680 MIRNAs (supplementary table S2, Supplementary Material online) in B. rapa, with precise and accurate genome locations that, to our knowledge, constitutes the most extensive effort to characterize the complete B. rapa MIRNA genes to date.

Retention Bias of B. rapa MIRNAs Following WGT

The complete MIRNA annotation was subjected to an interspecific microsynteny comparison with three diploid species A. lyrata, A. thaliana, and S. parvula. These three species were selected as outgroups due to their prominence in the evolutionary history of Brassicaceae, as A. lyrata and S. parvula were reported to represent the ancestral karyotypes of Brassicaceae family (Lysak et al. 2006; Schranz et al. 2006; Mandáková and Lysak 2008) and Brassica tribe (Cheng, Mandáková, et al. 2013). Arabidopsis thaliana is also part of the Brassicaceae and a model dicot system with thorough MIRNA studies. All of the aforementioned annotated B. rapa MIRNAs were used for microsynteny comparisons among these four species. From these 680 MIRNAs, we found that 204 retained a syntenic relationship to 97 nonredundant MIRNA loci from the three diploid species. The 204 MIRNAs belong to 178 B. rapa MIRNA loci, with 42 MIRNAs compressed into 16 MIRNA tandem arrays (Maher et al. 2006) (supplementary table S3, Supplementary Material online). Among the 97 nonredundant MIRNA loci in the diploid species, 40 had one, 33 had two, and 24 had three syntenic orthologs (1*40+2*33+3*24=178 orthologs) from the three subgenomes of B. rapa.

The ratio of single-copy to multiple-copy (duplicated/tripled) MIRNA (0.70; 40/57) was significantly lower (P value = 0.002, χ² test) than that of genes in the whole genome (1.34, 9,175/6,836. Wang et al. 2011; Li et al. 2014), indicating that MIRNAs were more highly retained following the fractionation subsequent to WGT. We then compared the retention of MIRNA to their neighbor gene loci (tandem genes were considered as a locus). As shown in figure 2, it is clear that MIRNAs have a higher ratio of retention than that of their neighbor gene loci. We also found that the MIRNAs’ retention was associated with the retention of local genomic fragments. Taking the first gene adjacent to an individual MIRNA as an example, of the 114 genes flanking the 57 aforementioned multiple copy MIRNAs, 47 (41.2%) retained multiple copies and 67 (58.8%) had only one copy. For the 80 genes flanking the 40 single-copy MIRNAs, 26 (32.5%) were multiple-copy and 54 (67.5%) were single-copy. The retention ratio of genes flanking the multiple-copy MIRNAs was higher than that of genes flanking the single-copy MIRNAs.

MIRNAs showed a biased distribution in the three subgenomes of B. rapa. Among the 178 syntenic MIRNA loci in B. rapa, 75 MIRNA loci were located in subgenome LF (the least fractionated subgenome), 54 at MF1 (the more fractionated subgenome one), and 49 at MF2 (the more fractionated

FIG. 1.—Distribution of integrated B. rapa MIRNAs among five data sets. Distribution of B. rapa MIRNAs in the five data sets I, our data set; II, data set from Jiang et al. (2014); III, data set from Wang, Li, et al. (2012); IV, data set from Yu et al. (2012); V, data set from Kim et al. (2012). The numbers of MIRNAs present in each data set are given in the individual sections.
strained than single-copy MIRNA that multiple-copy constraint following WGT. In conclusion, our results reveal a significant difference in sequence variability was found for observation (De Smet et al. 2013). In another analyses, no MIRNA (fig. 4), indicating that these parts were under fewer evolutionary constraints than that of miRNA-5p/miRNA-3p (fig. 4B).

Although the patterns of divergence in the regions of single-copy and multiple-copy MIRNAS were qualitatively similar, there was clearly more divergence in the single-copy MIRNAS, especially in sequences of mature miRNA-5p (fig. 4B). This observation indicates that the single-copy MIRNAS may have less constraint to keep the function of mature miRNA sequences, which is in contrast to the genic observation (De Smet et al. 2013). In another analyses, no significant difference in sequence variability was found for MIRNAS located in different subgenomes (fig. 4C), indicating constraint following WGT. In conclusion, our results reveal that multiple-copy MIRNAS are evolutionarily more constrained than single-copy MIRNAS.

Functional Divergence of miRNA Target Genes

MiRNAs have been found to target the genes of transcription factors (Willmann and Poethig 2007; Chen 2009; Voinnet 2009; Zhang et al. 2009; Li et al. 2010; Luo et al. 2013), and thus can have a broad influence on the biological functions in B. rapa. Therefore, it is important to identify the miRNA target genes to characterize function. Plant miRNAs have perfect or near-perfect complementary sequences to their target genes (Mallory and Vauchet 2006; Axtell 2013) which allow many computational approaches to predict target genes. The combination of different computational tools to predict miRNA targets is beneficial in that false results are minimized (Dai et al. 2011; Wang and Adams 2015). Here, we generated reliable pairs of miRNAs and target genes with replicated reports from at least two plant-specific target prediction tools. Based on this criterion, a total of 2,559 pairs of miRNA family target genes were identified and submitted to further analysis, including 2,396 unique putative genes targeted by 689 miRNAs that belong to 255 miRNA families. Among the 2,396 predicted target genes, 1,995 (83.3%) have functional InterPro annotations (Zdobnov and Apweiler 2001). We found that 72 miRNA families corresponded to 227 miRNAs targeted to 277 transcription factors genes (supplementary table S4, Supplementary Material online).

To gain a better understanding of the functional roles of the predicted miRNA target genes in B. rapa, we annotated miRNAs with Gene Ontology (GO) categories for the current B. rapa genome version (1.5). Of the predicted targets, 1,431 (59.7%) had GO assignments. We found that miRNA families preferentially target genes involved in a wide spectrum of regulatory functions and biological processes, including gene expression/transcription, metabolism, transport, signal transduction, and translation, etc (supplementary table S5, Supplementary Material online).

Coevolution of MIRNAS and Target Genes

The MIRNAS and their target genes are fractionated in B. rapa after the WGT event. The gain and loss of parwise relationships between miRNAs and target genes are two important processes in the coevolution of miRNAs and their targets (Guo et al. 2008; Wang and Adams 2015). The systematic annotation of MIRNAS and the determination of their target genes in B. rapa provide an opportunity to study the gain/loss dynamics of their parwise relationships following a WGT event. The 1,236 pairs of miRNA family targets in A. thaliana were used as a reference to assess their conservation in B. rapa. Orthologs of A. thaliana miRNAs and their target genes were determined in B. rapa with SynOrths (Cheng, Wu, Fang, Wang, et al. 2012). In total, out of the 1,236 A. thaliana miRNA-target pairs, only 111 (~10%) were retained in B. rapa, with 71 pairs whose target genes have paralogs and 40 with single-copy target genes (fig. 5). These results show the fast evolution and fractionation of this interactive relationship between miRNAs and target genes in B. rapa. As mentioned above, among the 71 multiple-copy target genes, 41 pairs keep miRNA binding sites on all retained paralogs, suggesting that these genes most developed their miRNA binding sites.
prior to WGT and maintained them subsequently. For the remaining 30 multiple-copy genes, only one or two (not all) paralog(s) were targeted by miRNAs, indicative of the gain or loss of miRNA target sites after WGT. These observations reveal the coevolutionary relationship between miRNAs and their target genes following WGT in *B. rapa*, and the rapid divergence of miRNA binding sites during this process.

**Fig. 2.**—Retention rates of miRNAs and their neighboring gene loci (20 flanking genes on either side of the miRNAs) in *B. rapa*. Retention of orthologs among the miRNAs (position 0) and their immediate neighbors in the three subgenomes of *B. rapa* using miRNAs of *A. lyrata* (*A*), *A. thaliana* (*B*), and *S. parvula* (*C*) as reference. Blue line indicates subgenome LF, red line indicates subgenome MF1, and green line indicates subgenome MF2.
Discussion

In this study, we carried out a comprehensive annotation of B. rapa MIRNAs through high-throughput small RNA sequencing, integrating previously reported B. rapa MIRNAs, and interspecies microsynteny comparisons to well-annotated MIRNAs in Arabidopsis. A complete data set of B. rapa MIRNAs was generated, which serves as a valuable resource to promote the studies of MIRNAs in B. rapa. Based on this, we further performed a systematic analysis of MIRNA evolution in the mesohexaploidized genome of B. rapa.

MIRNAs are essential regulators of gene expression in both plants and animals (Axtell et al. 2011). According to the latest miRBase database (Release 21), 325 and 205 MIRNAs were annotated in genomes of A. thaliana and A. lyrata, respectively. Brassica rapa is a paleohexaploid with a much larger and more complex genome than that of Arabidopsis. In this study, we annotated 969 miRNAs (765 unique sequences) from 680 MIRNA genes in B. rapa, which were about twice the number in A. thaliana. This result is consistent with the nature of the larger polyploid genome of B. rapa. Among the 680 MIRNAs,
FIG. 4.—Nucleotide divergence within fold-backs of MIRNAs in B. rapa. (A) MIRNA fold-backs were divided into five regions, and miRNA can be miRNA-5p or miRNA-3p. (B) Average sequence divergence between single-copy and multiple-copy MIRNA fold-backs. Single-copy MIRNA fold-backs are more diverged than that of multiple-copy MIRNA in both miRNA-5p region and region between miRNA-5p and miRNA-3p. (C) Average sequence divergence among MIRNA fold-backs located at different subgenomes of B. rapa. Similar variation patterns of MIRNA fold-backs were found across all the five regions. The fold-backs of orthologous MIRNAs in A. thaliana were used as references.
only 204 (~30%) MIRNA*s had orthologous MIRNA*s in A. thaliana, A. lyrata, or S. parvula. The large number of B. rapa-specific MIRNA*s may indicate the expansion of recently evolved MIRNA*s that undergoing frequent births and deaths (Fahlgren et al. 2007, 2010; Ma et al. 2010) after the Arabidopsis–Brassica divergence and Schrenkiella–Brassica divergence.

As a frequently used complement to small RNA sequencing annotation, microsynteny-based methods have been widely used in the identification of plant MIRNA*s (Maher et al. 2006; Ma et al. 2010; Shen et al. 2014). It detected MIRNA*s with low expression or condition-specific expression in specific pathways. In our study, three MIRNA*s (bra-MIR4245a, bra-MIR840a, and bra-MIR848a) that were not detected by the small RNA sequencing were found using microsynteny comparisons. In Arabidopsis, miR4245 plays a role in the regulation of the jasmonate pathway by targeting AT1G57620, AT5G11020 (emp24/gp25L/p24 family protein, kinase), and AT5G46470 (disease resistance protein, TIR-NBS-LRR class) (Zhang et al. 2012). MiR840 targets the WHIRLY transcription factor AT2G02740 (Rajagopalan et al. 2006; Fahlgren et al. 2007) and may take part in the process of nitrate regulation, coordination of carbon, and nitrogen metabolism (Vidal et al. 2013). MiR848 plays a role in gene regulation and developmental responses to hypoxia, which is likely to be dependent on mitochondrial function (Moldovan et al. 2010). Based on the syntenic relationships between B. rapa and Arabidopsis, complete or similar functions can be inferred for MIRNA*s in B. rapa. With the development of sequencing technology, more and more plant genomes will be sequenced, and the abundant information of annotated MIRNA*s in model species can be applied to predict MIRNA*s of newly sequenced species using interspecies microsynteny comparisons.

Following WGT, the deletion of one or more MIRNA* para-logs among subgenomes resulted in differential conservation MIRNA* copies (Kim et al. 2012). Our observation of biased fractionation in MIRNA*s among the three subgenomes in B. rapa genome provided further evidence for the subgenome dominance phenomenon in polyploids (Schnable et al. 2011; Wang et al. 2011; Cheng, Wu, Fang, Sun, et al. 2012). This findings is consistent with previous studies of grass MIRNA*s (Abrouk et al. 2012) and recent studies on duplicated gene retention (some miRNA targets) following whole-genome duplications in many plant genomes (Thomas et al. 2006; Freeling 2009; Throude et al. 2009; Schnable et al. 2011, 2012; Cheng, Wu, Fang, Sun, et al. 2012). Compared with total genes in the whole genome or flanking genes of MIRNA*s, the MIRNA*s were highly retained after WGT, suggestive of the higher conservation and important regulatory functions of MIRNA*s. In B. rapa, genes in the least fractionated subgenome (LF) were dominantly expressed over the genes in more fractionated subgenomes (MFs: MF1 and MF2) (Cheng, Wu, Fang, Sun, et al. 2012). However, the expression among MIRNA* paralogs in three subgenomes could not be distinguished due to their identical or highly similar mature sequences. Besides, the nucleotide variation of paralogous MIRNA*s was not significantly different among three subgenomes, although it was different from genes (Cheng, Wu, Fang, Sun, et al. 2012). One possible explanation is that the MIRNA*s are more sensitive to mutations than genes.
and need higher conservation to maintain their regulatory roles.

Because multiple-copy miRNAs could produce identical miRNAs to regulate the same target gene, whereas a single-copy miRNA could regulate expression of multiple target genes, it is complex to study the coevolution of miRNAs and their target genes, especially in polyploid genomes. To simplify the analysis of this coevolutionary relationship between miRNAs and their target genes in B. rapa, we only extracted genes regulated by miRNAs from a single miRNA locus in the 97 nonredundant loci. We found that target genes of miRNA multiples tend to be retained as multiples rather than singletons, whereas target genes of miRNA singletons tend to be retained as singletons. Such a tendency was coincident with previous research in soybean (Zhao et al. 2015), which suggested coevolution between miRNAs and their target genes. Additionally, the massive gain and/or loss of miRNA binding sites among paralogs demonstrated the divergence of the miRNA-target genes in B. rapa, which may be an important factor that affects gene divergence following WGT (Guo et al. 2008; Wang and Adams 2015). These analyses highlight the role of miRNA regulation in the evolutionary fate of duplicated genes following WGT.

Conclusion

Our work provides a valuable resource for B. rapa miRNAs and systematic information of miRNA evolution following WGT in B. rapa. The combined miRNA annotation led to the development of a comprehensive data set of 969 miRNAs from 680 miRNAs in B. rapa. Furthermore, miRNAs are more likely to be retained than genes following WGT, while biased distributions of miRNAs among subgenomes is similar to that of genes. Interestingly, compared with singleton miRNAs, the multiple-copy miRNAs are under strong purifying selection during evolution, indicating their functional importance to be highly retained and more conserved than the singleton miRNAs. Together, our comprehensive annotation and evolutionary analysis of miRNAs in B. rapa contributes a clear picture of species-specific miRNA evolution and a greater understanding of the impact that whole-genome duplication has on miRNA evolution.

Supplementary Material

Supplementary figures S1 and S2 and tables S1−S5 are available at Genome Biology and Evolution online (http://www.gbe.oxfordjournals.org).

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Impacts of WGT on miRNA Evolution in *B. rapa*


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