Transcriptional control of floral anthocyanin pigmentation in monkeyflowers (Mimulus)

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Summary

- A molecular description of the control of floral pigmentation in a multi-species group displaying various flower color patterns is of great interest for understanding the molecular bases of phenotypic diversification and pollinator-mediated speciation.
- Through transcriptome profiling, mutant analyses and transgenic experiments, we aim to establish a ‘baseline’ floral anthocyanin regulation model in Mimulus lewisii and to examine the different ways of tinkering with this model in generating the diversity of floral anthocyanin patterns in other Mimulus species.
- We find one WD40 and one bHLH gene controlling anthocyanin pigmentation in the entire corolla of M. lewisii and two R2R3-MYB genes, PELAN and NEGAN, controlling anthocyanin production in the petal lobe and nectar guide, respectively. The autoregulation of NEGAN might be a critical property to generate anthocyanin spots. Independent losses of PELAN expression (via different mechanisms) explain two natural yellow-flowered populations of M. cardinalis (typically red-flowered). The NEGAN ortholog is the only anthocyanin-activating MYB expressed in the M. guttatus flowers.
- The mutant lines and transgenic tools available for M. lewisii will enable gene-by-gene replacement experiments to dissect the genetic and developmental bases of more complex floral color patterns, and to test hypotheses on phenotypic evolution in general.

Introduction

Flower color produces some of the most beautiful displays in nature, and serves an important function in the ecology and evolution of plants by attracting animal pollinators (Glover, 2007; Davies et al., 2012). Many closely related plant species display dramatically different floral color patterns, and in some cases the flower color or pattern change may have produced a pollinator shift that leads to reproductive isolation and speciation (Bradshaw & Schemske, 2003; Hoballah et al., 2007; Streisfeld et al., 2013). A molecular description of the control of floral pigmentation in a multi-species group displaying various flower colors and patterns would, therefore, be of great interest for understanding the molecular bases underlying phenotypic diversification, plant–pollinator interactions and pollinator-mediated speciation. The monkeyflower genus, Mimulus, provides an excellent study system for such an endeavor.

The genus Mimulus contains 160–200 species that exhibit astonishing flower color variation (Fig. 1) and has been the subject of intensive ecological and evolutionary studies for over 60 yr (Hiesey et al., 1971; Beardsley et al., 2004; Wu et al., 2008). In the past decade a wealth of genomic and genetic resources as well as functional tools have been developed for multiple species in the genus (Wu et al., 2008; Cooley et al., 2011; Hellsten et al., 2013; Streisfeld et al., 2013; Yuan et al., 2013a,b), enabling in-depth genetic and developmental analyses of this traditionally ecological and evolutionary model system.

Two major pigment types determine flower color in Mimulus: anthocyanins are responsible for the pink/purple color and carotenoids for the yellow (Vickery & Olson, 1956; Hiesey et al., 1971; Streisfeld & Kohn, 2005; Cooley & Willis, 2009; Yuan et al., 2013b). A combination of the two pigment types often result in red color, as in the petal lobes of M. cardinalis and the spots on the corolla throat of M. guttatus (Fig. 1).

The core enzymes involved in both anthocyanin and carotenoid biosyntheses have been well characterized (reviewed in Grotewold, 2006; Glover, 2007; Ruiz-Sola & Rodriguez-Concepcion, 2012). The diversity of flower color in nature is largely determined by when and where these enzymes are expressed (i.e. transcriptional regulation of these enzymes) (Schwinn et al., 2006; Glover, 2007; Shang et al., 2011; Martins et al., 2013). While the transcriptional control of anthocyanin biosynthetic enzymes has been elucidated in multiple plant species (Paz-Ares et al., 1987; Ludwig et al., 1989; Goodrich et al., 1992; Quattrocchio et al., 1998; Walker et al., 1999; Borevitz et al., 2000; Spelt et al., 2000; Schwinn et al., 2006; Albert et al., 2011, 2014; reviewed in Koes et al., 2005; Hichri et al., 2011; Davies et al., 2012), the regulation of carotenoid biosynthetic pathway in flowers is little known (Grotewold, 2006; Glover, 2007; Ruiz-Sola & Rodriguez-Concepcion, 2012). As such, anthocyanin pigmentation provides...
a more suitable platform at the moment to understand the genetic and developmental bases of natural variation between different species (Sobel & Streisfeld, 2013).

The anthocyanin biosynthetic pathway (ABP) contains at least six essential structural genes encoding core enzymes: Chalcone synthase (CHS), Chalcone isomerase (CHI), Flavonoid 3-hydroxylase (F3H), Dihydroflavonol 4-reductase (DFR), Anthocyanidin synthase (ANS) and UDP-3-O-glucosyltransferases (UF3GT). In maize (Zea mays), Petunia and Arabidopsis, a highly conserved MYB-bHLH-WD40 (MBW) protein complex
has been shown to coordinately activate all or some of the ABP structural genes (Paz-Ares et al., 1987; Ludwig et al., 1989; de Vetten et al., 1997; Quattrocchio et al., 1999; Walker et al., 1999; Borevitz et al., 2000; Spelt et al., 2000; Zhang et al., 2003; Carey et al., 2004). In Antirrhinum majus flowers, three closely related R2R3-MYBs (Rosea1, Rosea2 and Venosa) and a bHLH (Della) protein coordinately activate at least four ABP genes (F3H, DFR, ANS and UFGT) (Martin et al., 1991; Goodrich et al., 1992; Schinn et al., 2006), but the WD40 component has yet to be identified. The MYB and bHLH proteins represent the two largest transcription factor families in flowering plants (Feller et al., 2011). The anthocyanin-activating MYBs and bHLHs belong to subgroup 6 of the R2R3-MYB family and subgroup IIIf of the bHLH family, respectively (Stracke et al., 2001; Heim et al., 2003; Feller et al., 2011). More recently, a group of single-repeat R3-MYBs has been shown to negatively regulate ABP gene expression by competing with the R2R3-MYB activators for the limited supply of bHLH proteins (Zhu et al., 2009; Nakatsuka et al., 2013; Yuan et al., 2013a; Albert et al., 2014).

The conserved nature of the ABP enzymes and their MBW regulators across flowering plants has enabled a number of investigations on the genetic control of floral anthocyanin pigmentation in nonmodel organisms, including Phalaenopsis orchids (Ma et al., 2009), Asiatic hybrid lilies (Lilium spp.) (Yamagishi et al., 2010, 2014), morning glories (Ipomoea spp.) (Des Marais & Rausher, 2010), Isocoma spp. (Smith & Rausher, 2011), Phlox drummondii (Hopkins & Rausher, 2011) and Clarkia gracilis (Martins et al., 2013). These studies provide valuable information on the potential players involved in flower color diversification in a wide range of angiosperm lineages. However, due to the lack of genetic resources or/and functional tools, reaching a deeper understanding of the precise molecular bases and developmental mechanisms that generate floral anthocyanin patterns (e.g. spots, stripes) or cause flower color variation between species, remains a formidable task in most of these systems.

Here we describe the major transcriptional regulators of ABP genes in the pink flowered Mimulus lewisi (Fig. 1), an emerging model system particularly suitable for studying the developmental genetics of ecologically important floral traits (Yuan et al., 2013a,b). Through transcriptome profiling, mutant analyses and transgenic experiments, we find one WD40 (MIWD40a) and one bHLH (MIANbHLH1) gene controlling anthocyanin biosynthesis in the entire corolla of M. lewisi; one R2R3-MYB, named Petal Lobe Anthocyanin (PELAN), controlling anthocyanin biosynthesis in the petal lobe, and another R2R3-MYB, named Nectar Guide Anthocyanin (NEGAN), controlling anthocyanin spot formation in the nectar guide. NEGAN, but not PELAN, is involved in an autoregulatory feedback loop, which might be a critical property required for the ‘spot’ pattern formation. Furthermore, using the M. lewisi model we demonstrate that two independent losses of PELAN expression (via different mechanisms) explain the yellow flower color of two natural populations of M. cardinalis (usually red-flowered), which is the sister species of M. lewisi. Our M. lewisi model also explains the M. guttatus anthocyanin pattern by successfully predicting the NEGAN ortholog as the only anthocyanin-activating MYB expressed in the predominantly yellow M. guttatus flowers.

Materials and Methods

Plant materials and growth conditions

The Mimulus lewisi inbred line LF10 and M. cardinalis inbred line CE10 were described in Yuan et al. (2013a). The M. lewisi boo mutants were generated by ethyl methanesulfonate (EMS) mutagenesis in the LF10 background (Owen & Bradshaw, 2011). Seeds of two natural yellow-flowered M. cardinalis strains, SM and CI, collected from the Siskiyou Mountains of Oregon (US) and Cedros Island (Baja California, Mexico), respectively, were provided by Bob Vickery (University of Utah). Seeds of M. guttatus inbred line IM767 were provided by John Willis (Duke University). Plants were grown in the University of Washington and University of Connecticut glasshouses under similar conditions as described in Yuan et al. (2013a).

Transcriptome sequencing and analyses

In order to obtain a comprehensive view of the expression profile of the ABP genes and their putative transcriptional regulators in the M. lewisi LF10 flowers, we isolated total RNA from the corolla of 15-mm flower buds (3 d before opening) for transcriptome sequencing. The 15-mm corolla stage is the intermediate stage between when anthocyanins first become visible (10-mm, 6 d before opening) and flower opening (Yuan et al., 2013a) – not too early to capture ABP gene expression and not too late to capture the expression of their transcriptional regulators.

The RNA-Seq library was prepared at the University of North Carolina High-Throughput Sequencing Facility (UNC-HTSF) using the Illumina (San Diego, CA, USA) TruSeq RNA Sample Preparation Kit v2. Briefly, mRNA was first purified from 2 μg of total RNA using oligo-dT attached magnetic beads, and then cleaved into 200-bp pieces under elevated temperature. The resulting RNA fragments were primed with random hexamers and were reverse transcribed into first strand cDNA, followed by second strand cDNA synthesis. The double strand cDNA was end repaired and A-tailed, and then ligated to adapters for PCR enrichment to generate the final cDNA library for Illumina sequencing at the UNC-HTSF.

The resulting c. 85 million 100-bp paired-end RNA-Seq reads (NCBI Sequence Read Archive PRJNA232780: SRX403785) were assembled into 80 602 contigs (N50 = 1.4 kb; average length = 834 bp) using CLC Genomics Workbench (Qiagen, Venlo, Netherlands) with default de novo assembly parameters. We then mapped the RNA-Seq reads to the de novo transcriptome assembly (available from http://www.eeb.ucconn.edu/people/yuan/resources) to determine the RPKM expression value (Mortazavi et al., 2008) of each transcript using the CLC Genomics Workbench ‘RNA-Seq Analysis’ tool, with the minimum read length fraction set to 0.9 and minimum similarity set to 0.97.

Previously characterized ABP genes and their MBW regulators from Arabidopsis were used as queries (Table 1) to retrieve the
Conjugating Enzyme (UBC) was used as a reference gene as tentative RT-PCR was performed using iQ SYBR Green Supermix before PCR. The thesis System for RT-PCR (Invitrogen), then diluted 40-fold DNase-treated RNA using the SuperScript III First-Strand Synthesis System and the SuperScript III First-Strand Synthesis System for RT-PCR (Invitrogen). cDNA was synthesized from 1 Kit (Sigma-Aldrich) and then treated with amplification grade Total RNA was isolated using the Spectrum Plant Total RNA Expression analyses by RT-PCR support was estimated by 200 bootstrap replicates. Maximum likelihood (ML) analyses were conducted using RAxML & Castresana, 2007) for subsequent phylogenetic analyses. Maxi-regions of the alignments were selected using Gblocks (Talavera & Castresana, 2007) for subsequent phylogenetic analyses. Transgenic experiments RNAi plasmids were constructed with a 133–350-bp fragment amplified from the coding regions of MIWD40a, MIANbHLHI, PELAN and NEGAN (Table S3), essentially following the protocol described in Yuan et al. (2013a). To ensure target specificity, the fragment included in each RNAi plasmid was BLASTed against the LF10 genome assembly with an E-value cutoff of 0.1 so that no other genomic regions perfectly match this fragment for a contiguous block longer than 16 bp. For PELAN, it was not possible to find a contiguous region longer than 100 bp in the coding region fulfilling this criterion. Therefore, we connected two shorter fragments (75 and 68 bp) with the required specificity by bridge PCR (Table S3).

In order to test whether NEGAN is self-activated, we generated an over-expression plasmid by cloning the 804-bp full-length NEGAN CDS (without the stop codon; Table S3) into the pEarleyGate 103 vector (Earley et al., 2006; Arabidopsis Biological Resource Center, CD3-685), following Earley et al. (2006). This vector drives the expression of the transgene by the CaMV 35S promoter.

The final plasmid constructs were verified by sequencing and then transformed into Agrobacterium tumefaciens strain GV3101 for subsequent plant transformation, as described in Yuan et al. (2013a).

Results

Identification of the putative ABP structural genes and MBW regulatory genes by BLAST searches

BLAST searches against the LF10 15-mm corolla transcriptome identified one copy of each of the six ABP structural genes (MICHSa, MICHI, MIF3Ha, MIDFR, MIANS and MIUF3GT) (Bio-Rad) in a CFX96 Touch Real-Time PCR Detection System (Bio-Rad). Samples were amplified for 40 cycles of 95°C for 15 s and 60°C for 30 s. Reactions were run with three biological replicates and two technical replicates. Amplification efficiencies for each primer pair were determined using critical threshold values obtained from a dilution series (1 : 4, 1 : 20, 1 : 100, 1 : 500).

Candidate gene sequencing of the boo mutants

The transcriptome analyses revealed one WD40, one bHLH and one R2R3-MYB as potential candidate genes encoding the major transcriptional regulators. To examine whether these genes harbor mutations in the four boo mutant lines that were identified as potential loss-of-function mutants of the MBW complex (see the Results section), full-length coding DNA sequences (CDS) of these candidate genes were amplified from the boo cDNAs. PCR products were treated with ExoSAP-IT (USB/Affymetrix, Santa Clara, CA, USA) and sequenced using the BigDye Terminator v3.1 system (Applied Biosystems, Foster City, CA, USA) following the manufacturers’ protocols. Primers used for amplification and sequencing are listed in Table S2.

Phylogenetic analyses

Multiple sequence alignments of R2R3-MYB and bHLH proteins were performed using MUSCLE (Edgar, 2004). Conserved regions of the alignments were selected using Gblocks (Talavera & Castresana, 2007) for subsequent phylogenetic analyses. Maximum likelihood (ML) analyses were conducted using RAxML 7.0.4 (Stamatakis, 2006), with the JTT amino acid substitution matrix and the GAMMA model of rate heterogeneity. Clade support was estimated by 200 bootstrap replicates.

Expression analyses by RT-PCR

Total RNA was isolated using the Spectrum Plant Total RNA Kit (Sigma-Aldrich) and then treated with amplification grade DNaseI (Invitrogen). cDNA was synthesized from 1 μg of the DNase-treated RNA using the SuperScript III First-Strand Synthesis System for RT-PCR (Invitrogen), then diluted 40-fold before PCR. The Mimulus ortholog of At5g25760 Ubiquitin-Conjugating Enzyme (UBC) was used as a reference gene as described in Yuan et al. (2013a). Gene-specific primers used for RT-PCR are listed in Supporting Information Table S1. Quantitative RT-PCR was performed using iQ SYBR Green Supermix (Bio-Rad) in a CFX96 Touch Real-Time PCR Detection System (Bio-Rad). Samples were amplified for 40 cycles of 95°C for 15 s and 60°C for 30 s. Reactions were run with three biological replicates and two technical replicates. Amplification efficiencies for each primer pair were determined using critical threshold values obtained from a dilution series (1 : 4, 1 : 20, 1 : 100, 1 : 500).

Table 1 Gene expression profile from the Mimulus lewissii LF10 15-mm corolla transcriptome

<table>
<thead>
<tr>
<th>Query</th>
<th>Gene</th>
<th>GenBank acc. no.</th>
<th>Expression value (RPKM)</th>
</tr>
</thead>
<tbody>
<tr>
<td>TT4(1)</td>
<td>MICHSa</td>
<td>KJ011133</td>
<td>2696.65</td>
</tr>
<tr>
<td></td>
<td>MICHsb</td>
<td>KJ099581</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>MICHsc</td>
<td>KJ099582</td>
<td>0</td>
</tr>
<tr>
<td>TT5(2)</td>
<td>MICHb</td>
<td>KJ011134</td>
<td>465.19</td>
</tr>
<tr>
<td>TT6(3)</td>
<td>MIF3Ha</td>
<td>KJ011135</td>
<td>368.86</td>
</tr>
<tr>
<td></td>
<td>MIF3Hb</td>
<td>KJ099583</td>
<td>49.33</td>
</tr>
<tr>
<td>TT3(4)</td>
<td>MIDFr</td>
<td>KJ011136</td>
<td>188.31</td>
</tr>
<tr>
<td>TT18(5)</td>
<td>MIANS</td>
<td>KJ011137</td>
<td>305.36</td>
</tr>
<tr>
<td>UF3GT(6)</td>
<td>MIUF3GT</td>
<td>KJ011138</td>
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</tr>
<tr>
<td>TTG1(7)</td>
<td>MIWD40a</td>
<td>KJ009140</td>
<td>30.34</td>
</tr>
<tr>
<td></td>
<td>MIWD40b</td>
<td>KJ009140</td>
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<tr>
<td></td>
<td>MIWD40c</td>
<td>KJ009141</td>
<td>5.78</td>
</tr>
<tr>
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<td>KJ011142</td>
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<tr>
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<td>KJ011144</td>
<td>124.83</td>
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<tr>
<td>PAP2(12)</td>
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<tr>
<td></td>
<td>NEGAN-L2</td>
<td>KJ099585</td>
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<tr>
<td></td>
<td>NEGAN-L3</td>
<td>KJ099586</td>
<td>0</td>
</tr>
</tbody>
</table>

The genes with ‘0’ RPKM values are found in the genome assembly, but not in the transcriptome.

corresponding transcripts from the LF10 de novo transcriptome assembly by TBLASTN searches (Altschul et al., 1997). To complement the transcriptome data, we also used the same query sequences to search against the genome assembly generated in a previous study (Yuan et al., 2013a). The genomic copies of these genes were annotated and the sequences were deposited in GenBank (accession numbers are listed in Table 1).
with high RPKM expression values, and an additional copy of the F3H gene (MIF3Hb) with relatively low RPKM value (Table 1). Searches against the LF10 genome assembly confirmed the single copy of CHI, DFR, ANS and UF3GT, and the two paralogs of F3H, but revealed two additional paralogs of CHS (MICHSb and MICHSc). RT-PCR across four corolla developmental stages (5-, 10-, 15- and 20-mm) suggests that MICHSb and MICHSc are not expressed in the corolla (Supporting Information Fig. S1a), explaining the absence of these two copies in the transcriptome. Furthermore, the RT-PCR experiments showed that MIF3Ha has much higher expression levels than MIF3Hb in the 10- and 15-mm stages. MIF3Hb expression was not detectable until later stages (15- and 20-mm) (Fig. S1b). Because anthocyanin pigments already become visible in the 10-mm corolla (Yuan et al., 2013a), we reasoned that MIF3Ha, not MIF3Hb, plays a primary role in anthocyanin biosynthesis in the corolla. Taking these results together, we concluded that MICHSa, MICHI, MIF3Ha, MIDFR, MIANS and MIUF3GT are the six key ABP structural genes responsible for LF10 corolla anthocyanin pigmentation.

Similarly, a combination of transcriptome and genome BLAST searches retrieved five paralogs of subgroup 6 R2R3-MYBs, three subgroup IIIf bHLHs paralogs and three WD40 paralogs. Although flowering plant genomes typically harbor hundreds of R2R3-MYB and bHLH genes (Stracke et al., 2001; Heim et al., 2003; Pires & Dolan, 2010; Feller et al., 2011), identification of the anthocyanin-activating subgroup 6 R2R3-MYBs and subgroup IIIf bHLHs are facilitated by the ‘signature’ amino acid sequence motif, ‘[R/K][P/R/Q][R/P][F/L]’ (Stracke et al., 2001; Fig. S2) and ‘NGxKTRKxxQxxExxx[D/E]xxxLxRSxQLREL YESLxxxE’ (Pires & Dolan, 2010; Fig. S3), that clearly distinguishes these two subgroups, respectively. Phylogenetic analyses including the M. lewisii sequences and previously characterized R2R3-MYB and bHLH sequences corroborated our identification based on the signature motifs (Fig. 2). The WD40 protein sequences are extremely different from other WD-repeat proteins.

![Fig. 2 Maximum likelihood (ML) phylogenies of R2R3-MYB (subgroup 6 and related subgroups) proteins (a) and bHLH (subgroup IIIf and related subgroups) proteins (b). Subgroup classifications followed Stracke et al. (2001) and Heim et al. (2003). Trees are rooted by midpoint rooting. Bootstrap support values > 50% are indicated along the branches. Mimulus lewisii sequences characterized in this study are highlighted in bold and have been deposited in GenBank (accession numbers see Table 1). All M. guttatus sequences were retrieved from Phytozone (http://www.phytozone.net), including MgMYB1-5 (MgMYB1: mgv1a023671m; MgMYB2: mgv1a024703m; MgMYB3: mgv1a024996m; MgMYB4: mgv1a025765m; MgMYB5: mgv1a019326m) and the three bHLHs (mgv1a00290, mgv1a00684, mgv1a00268). All Arabidopsis sequences were retrieved from the TAIR site (http://www.arabidopsis.org/). Other sequences were retrieved from GenBank as follows: Antirrhinum majus ROSEA1 (DQ275529); ROSEA2 (DQ275530); Venosa (DQ275531); AmMIXTA (X79108); AmDelia (AA382663); Lilium hybrid LhMYB6 (AB534587); LhMYB12 (AB534586); Lotus japonicus TT2a (BAG12893); Malus × domestica MdMYB10a (DQ267897); M. lewisii GUIDELESS (KC139356); Petunia × hybrida PhAN2 (AF146702); PhAN4 (HQ428105); PhDPL (HQ116169); PhPHZ (HQ116170); PhAN1 (AAG25928); PhJAF13 (AAC93455); Vitis vinifera VvMYBA1 (BAD18977); VvMYB3 (BAD18978); VvMYBPA2 (ACK56131); VvMYC1 (EU447172); VvMYCA1 (EF193002); Zea mays ZmP (P27898); ZmB (CA40544); ZmLc (AA33504).]
containing proteins, but highly conserved among WD40 members (Fig. S4). As such, the identification of WD40 sequences is straightforward. The transcriptome profiling suggests that only two of the five R2R3-MYB paralogs are expressed in the LF10 corolla; one has much higher expression value than the other. Likewise, only one bHLH paralog and one WD40 paralog are predominantly expressed in the corolla (Table 1). RT-PCR across different corolla developmental stages confirmed the transcriptome results (Fig. S1c–e).

**boo1, boo3, boo5 and boo14 are putative loss-of-function mutants of the MBW regulatory complex**

In order to determine whether these putative MBW genes retrieved from BLAST searches are actual transcriptional regulators of anthocyanin pigmentation in the *M. lewisii* flower, we set out to identify loss-of-function mutants of the MBW regulatory complex. We screened 12 recessive *boo* mutants with white flowers for coordinated downregulation of ABP structural genes. The rationale is that loss-of-function of one structural gene in the pathway should not affect the expression of other ABP genes, whereas loss-of-function of the MBW regulatory complex will lead to downregulation of multiple ABP genes simultaneously. Subsequent RT-PCR of the six key structural genes showed dramatic downregulation of *MIF3Ha, MIDFR* and *MIANS* in four of the 12 *boo* mutants (Fig. 3). Pair-wise complementation crosses suggest that these four mutant lines belong to three complementation groups: *boo3, boo1/boo5* and *boo14*.

Among the three complementation groups, *boo3* has the most specific phenotypic effect (i.e. least pleiotropy), only lacking the anthocyanin pigments on the petal lobe. The anthocyanin spots in the nectar guide and the purple color of the stem base remain unaffected. The seed coat color of *boo3* is also indistinguishable from the wild-type LF10 (Fig. 4), being deep brown, presumably due to proanthocyanidin accumulation (Lepiniec et al., 2006). The *boo1/boo5* lines show the most pleiotropy: petal lobes are white, anthocyanin spots in the nectar guide are completely absent, the stem base has no purple color and seed coat is pale yellow (Fig. 4). *boo14* shows intermediate phenotypes, with no anthocyanins in the petal lobes or stem base, weak anthocyanin spots towards the base of the nectar guide, but having a seed coat color indistinguishable from the wild-type (Fig. 4).

*boo3, boo1/boo5 and boo14 correspond to the R2R3-MYB, WD40 and bHLH genes, respectively*

The different degree of pleiotropy displayed by the *boo3, boo1/boo5* and *boo14* mutants suggest that they may correspond to the three different classes of transcriptional regulators: WD40 mutations are usually the most pleiotropic and R2R3-MYB mutations are the least pleiotropic (Zhang et al., 2003; Koes et al., 2005). The R2R3-MYB, bHLH and WD40 genes with the highest expression level in the corolla were considered as the most promising candidate gene underlying *boo3, boo14* and *boo1/boo5*, and were named *Petal Lobe Anthocyanin (PELAN), MIAnbHLH1* and *MIWD40a*, respectively (Table 1). To test this idea, we sequenced the full-length CDS of the three candidate genes for all four *boo* mutants. In each *boo* mutant line only one of the three candidate genes harbored a mutation. The *boo3* mutant has a premature stop codon at the end of the first exon of *PELAN* (Figs 5a, S2); *boo1* and *boo5* have an amino acid replacement in a highly conserved site and a premature stop codon, respectively, in *MIWD40a* (Figs 5b, S4), consistent with the complementation test indicating that they are allelic; *boo14* has a mutation in an intron/exon junction leading to nonsplicing of the last intron of *MIAnbHLH1* (Figs 5c, S3). These results support our hypothesis that *boo3, boo1/boo5* and *boo14* correspond to the R2R3-MYB gene *PELAN*, the WD40 gene *MIWD40a* and the bHLH gene *MIAnbHLH1*, respectively.

A second R2R3-MYB controls anthocyanin spot formation in the nectar guide

The fact that both *MIWD40a* and *MIAnbHLH1* mutations affect the anthocyanin spots in the nectar guide, whereas the *PELAN* mutation does not, suggests that there must be another R2R3-MYB responsible for anthocyanin spot formation in the nectar guide. The transcriptome and RT-PCR experiments did show one other R2R3-MYB paralog expressed in the corolla, although the RPKM expression value of this gene is much lower than *PELAN* (8.56 vs 124.83; Table 1). However, if this gene is only expressed in the nectar guide, the relatively low expression value estimated from the entire corolla can be explained by the fact that the nectar guide accounts for only a small proportion (c. 10%) of the corolla tissue. To test this hypothesis, we dissected the 15-mm corolla into petal lobes and nectar guide and isolated RNA from each tissue type. RT-PCR showed that *PELAN* is predominantly expressed in the petal lobe (Fig. 5d), whereas the other R2R3-MYB paralog is expressed exclusively in the nectar guide. These results strongly suggest that this second R2R3-MYB, designated as *Nectar Guide Anthocyanin (NEGAN)*, controls the anthocyanin spot formation in the nectar guide.

![Fig. 3](https://example.com/fig3.png) **Fig. 3** Semi-quantitative RT-PCR of the structural anthocyanin biosynthetic genes in the *Mimulus lewisii* *boo* mutants. *MIF3Ha, MIDFR* and *MIANS* are dramatically downregulated in these mutants; *MIUF3GT* is also downregulated, but to a lesser extent; *MICHa* and *MICHi* are not affected. *MIUBC* is shown as a reference gene. PCR cycle numbers are shown after the gene names. WT, wild-type.
RNAi transgenic lines accurately reproduce boo phenotypes

In order to further verify the function of these MBW regulators, we built gene-specific RNAi constructs to knock down the expression of each of the four players identified above, in the wild-type LF10 background. We generated 4, 92, 12 and 14 independent RNAi transgenic lines for PELAN, NEGAN, MlANbHLH1 and MlWD40a, respectively. For all genes but MlANbHLH1, more than half of the transgenic lines display a strong phenotype indistinguishable from the corresponding boo mutants; the remaining lines usually show an intermediate phenotype (Fig. 6). Even for MlANbHLH1, five of 12 independent lines have strong phenotypes indistinguishable from boo14.

The strong PELAN RNAi lines have white petal lobes, but have normal nectar guide anthocyanin spots (Fig. 6a), purple stem base and deep brown seed coat color, accurately phenocopying boo3. The strong NEGAN RNAi lines have no anthocyanin spots in the nectar guide, but are indistinguishable from LF10 in all other traits, including petal lobe color (Fig. 6b). The strong MlANbHLH1 lines have white petal lobes, weak anthocyanin spots towards the base of the nectar guide (Fig. 6c), a green stem base, but normal seed coat color, just like the boo14 mutant. The fact that both boo14 and the MlANbHLH1 RNAi lines have weak anthocyanin spots in the bottom part of the nectar guide suggests that there probably exists another functionally redundant bHLH paralog (e.g. MlANbHLH2, Table 1) with low expression level in the nectar guide. MlWD40a knock-down affects all of the aforementioned traits, as in boo5. Together with the mutant analyses, these transgenic results support the model that MlANbHLH1 and MlWD40a regulate anthocyanin biosynthesis in the entire corolla, while PELAN and NEGAN act more specifically in different parts of the corolla (Fig. 7).
NEGAN, but not PELAN, is involved in a self-activation loop

In order to verify that the target regulatory genes have been specifically knocked down in the RNAi lines, we selected three strong lines of each gene for molecular characterization. We first verified transgene presence in these RNAi lines by PCR using transgene specific primers (Fig. S5), then performed semi-quantitative RT-PCR (Fig. S5) and qRT-PCR (Fig. 6e) at the 15-mm corolla stage to examine gene expression. These two sets of experiments consistently showed that in the PELAN RNAi lines, the
expression level of PELAN is substantially lower than the wild-type control, and the expression levels of NEGAN, MlANbHLH1 and MlWD40a are not affected (Figs 6e, S5). Similarly, in the MlANbHLH1 RNAi lines, MlANbHLH1 shows clear downregulation but the other genes are not affected (except NEGAN, see the next paragraph).

Interestingly, in the NEGAN RNAi lines, while the other genes remain unaffected as expected, the NEGAN gene itself showed 100% knock-down (no NEGAN transcripts were detected after 40 cycles of PCR; Fig. 6e). This is somewhat surprising because based on our experience with several transcription factor genes characterized in the LF10 background (Yuan et al., 2013a; b; this study), RNAi usually results in 70–90% knock-down in strong transgenic lines, not a complete knock-down. Even more intriguingly, in the MlWD40a RNAi lines, not only was MlWD40a clearly knocked down, but expression of NEGAN also becomes undetectable, although the expression of PELAN is not affected (Fig. 6e). This suggests that MlWD40a is required for NEGAN, but not PELAN, expression. Assuming that MlWD40a functions as part of the MBW complex activating NEGAN expression, we could infer that NEGAN is involved in an autoregulatory feedback loop, which explains its 100% knock-down in the NEGAN RNAi lines. If NEGAN is indeed activated by the ‘NEGAN-MlANbHLH1-MlWD40a’ complex itself, one would predict that MlANbHLH1 RNAi should also result in substantial down-regulation of NEGAN. However, our qPCR experiment showed only c. 50% NEGAN knock-down (Fig. 6e). This is probably due to a redundant bHLH factor (e.g. MlANbHLH2) expressed in the nectar guide, consistent with the ‘weak anthocyanin spot’ phenotype of boo14 and the MlANbHLH1 RNAi lines.

In order to further test the NEGAN self-activation model, we generated 35S:NEGAN over-expression lines using the full-length NEGAN CDS without 5' or 3' UTR sequences. We focused our analysis on the leaf tissue, which expresses MlANbHLH1 and MlWD40a at comparable levels to flowers, but expresses no subgroup 6 R2R3-MYBs (unpublished leaf transcriptome data). The latter feature is important because that means any detectable endogenous NEGAN transcript, which can be distinguished from the transgene transcript by the presence of UTRs, must be activated by the transgene. We obtained 50 independent 35S:NEGAN lines. A representative whole plant phenotype is shown in Fig. 8(a). We selected three 35S:NEGAN lines with strong leaf phenotypes (an example shown in Fig. 8b), and performed RT-PCR using primers that can amplify part of the 3' UTR of NEGAN. Our results clearly showed that the endogenous NEGAN gene can be activated by the NEGAN transgene in the over-expression lines, and no NEGAN expression was detectable in the wild-type controls (Fig. 8c).

Independent losses of PELAN expression (via different mechanisms) explain natural yellow-flowered M. cardinalis populations

With a basic model of floral anthocyanin regulation established in M. lewisii (Fig. 7), next we explore the possibility of using this model to explain some simple cases of flower color variation in other Mimulus species. The first case involves two natural M. cardialis populations with yellow flowers.

M. cardinalis is the sister species of M. lewisii (Beardsley et al., 2003) and is typically red-flowered (Fig. 9a) due to the combination of high concentrations of both anthocyanins and carotenoids. The two yellow populations are found in the
northern (Siskiyou Mountains, Oregon) and southern (Cedros Island, Baja California) margins of the *M. cardinalis* geographic range (Vickery, 1995; Paul et al., 2011), and hereafter will be referred to as *M. cardinalis* SM and *M. cardinalis* CI, respectively. Both *M. cardinalis* SM and CI lack anthocyanins in the petal lobe, but have strong anthocyanin pigmentation in the nectar guide (Fig. 9b,c). Genetic crosses with *M. cardinalis* CE10 (Fig. 9a) show that yellow is recessive to red. The similarity of floral anthocyanin pigmentation pattern between *M. cardinalis* SM, CI and the *M. lewisii* boo3 mutant suggests that the phenotype of all three is likely to be caused by the loss of function of the same gene, *PELAN*. Indeed, complementation crosses between the three suggest that they are all allelic (Fig. S6).

Next we ask: What is the molecular nature of the loss-of-function *peIan* allele of *M. cardinalis* SM and CI? These two populations are geographically isolated from each other and display slightly different phenotypes (Fig. 9b,c), which suggests that they have evolved independently from the typical red-flowered phenotype. To address this question, we first attempted to amplify and sequence the full-length CDS of *PELAN* from *M. cardinalis* SM and CI corolla cDNA at the stage corresponding to the 15-mm corolla stage of *M. lewisii* LF10, to examine potential coding DNA mutations. However, although the *PELAN* CDS could be readily amplified from both *M. lewisii* LF10 and the red-flowered *M. cardinalis* CE10 corolla cDNA, it could not be amplified from either *M. cardinalis* SM or CI. This suggests that *PELAN* may not be expressed in the yellow *M. cardinalis*. Further RT-PCR experiments corroborate this inference (Fig. 9e). To rule out the possibility that this failure of detecting *PELAN* expression by RT-PCR is due to primer mismatch in SM and CI, we performed PCR on the genomic DNA as a control. The RT-PCR primers produced a band of the expected size with the CI genomic template, but, surprisingly, still failed to amplify any products in SM (Fig. 9f). These results indicate an intriguing possibility that the *PELAN* gene has been deleted from the SM genome. To test this idea, we designed multiple pairs of primers, from both exonic and intronic regions...
and with sequences conserved between LF10, CE10 and CI (Figs 9d,S7) – all of these primer pairs produced a clean band of expected size in CE10 and CI, but no bands in SM (Fig. 9f).

Taken together, these results suggest that the losses of petal lobe anthocyanins in *M. cardinalis* SM and CI are caused by independent molecular lesions in the *PELAN MYB* gene. The loss of *PELAN* expression in SM is linked with the probable deletion of the entire gene in the SM genome, whereas the loss of *PELAN* expression in CI is most likely to be caused by cis-regulatory changes because the complementation crosses have ruled out trans-acting factors as a potential cause.

The *NEGAN* ortholog is the only anthocyanin-activating MYB expressed in the *M. guttatus* corolla

The second case of using the *M. lewisii* model to explain floral anthocyanin pigmentation patterns in other *Mimulus* involves *M. guttatus*, for which many genomic resources are available (Wu et al., 2008; Hellsten et al., 2013). *M. guttatus* belongs to the ‘yellow flower’ clade (the top clade in Fig. 1), where most species do not have petal lobe anthocyanins but do have anthocyanin spots in the corolla throat (Fig. 10a), presumably serving as a nectar guide for pollinators.

The *M. guttatus* genome has five *R2R3-MYB* genes (*MgMYB1-5*) that are classified in the anthocyanin-activating group (Cooley et al., 2011; Fig. 2a). Phylogenetic analysis suggests that *MgMYB1-3* groups together with *PELAN* and *MgMYB5* groups with *NEGAN*. *MgMYB4* represents a more divergent lineage (Fig. 2a). Considering that *NEGAN* is the MYB that controls anthocyanin spot formation in the *M. lewisii* nectar guide, we predicted that the *NEGAN* ortholog, *MgMYB5*, is the only anthocyanin-activating *MYB* gene expressed in the *M. guttatus* corolla, to explain the fact that anthocyanins are restricted to the nectar guide spots in the *M. guttatus* flower. RT-PCR experiments clearly show that this is the case (Fig. 10b). These results suggest that the function of *NEGAN* – making anthocyanin spots in the nectar guide – is conserved between these two major clades of *Mimulus* (Fig. 1), and our *M. lewisii* model can be used to explain anthocyanin pigmentation patterns even in distantly related species.

**Discussion**

In this study we have identified four major transcriptional regulators of anthocyanin pigmentation in *M. lewisii* flowers, including the *MIWD40a* and *MIANbHLH1* genes that control anthocyanin pigmentation in the entire corolla, the *PELAN R2R3-MYB* that controls the petal lobe color, and the *NEGAN R2R3-MYB* that regulates the anthocyanin spot formation in the nectar guide. Furthermore, through two case studies in *M. cardinalis* and *M. guttatus*, we have demonstrated that the establishment of a baseline floral anthocyanin regulation model in *M. lewisii* is of great value towards understanding the molecular bases underlying the astonishing diversity of floral anthocyanin pigmentation patterns in other *Mimulus* species.

The identities and functions of all four regulatory genes are supported by multiple lines of evidence. Overall the different degrees of pleiotropy of these genes are consistent with the MBW regulatory network model characterized in other plant species (Zhang et al., 2003; Koes et al., 2005; Hichri et al., 2011) – *WD40* is the most pleiotropic, while the *R2R3-MYB* is the least pleiotropic and tends to act in a tissue-specific fashion. The identity and function of *PELAN* are supported by multiple alleles from both EMS-induced (box5) and natural mutants (*M. cardinalis* SM and CI), and by gene-specific RNAi knock-down experiments. The identity and function of *NEGAN* are supported by the tissue-specific expression pattern (only in the nectar guide) and the distinct RNAi transgenic phenotype, with only the anthocyanin spots in the nectar guide being affected. Similarly, a combination of EMS-induced loss-of-function alleles and RNAi phenocopies confirm the identity and function of *MIANbHLH1* and *MIWD40a*.

The autoregulation of *NEGAN* is noteworthy. Although the regulatory role of the MBW complex in ABP structural gene expression is highly conserved across all flowering plants characterized to date (Koes et al., 2005; Glover, 2007; Hichri et al., 2011; Davies et al., 2012), the transcriptional regulation of the MBW regulatory genes themselves is less understood. In *Petunia*, *Arabidopsis* and grapevine (*Vitis vinifera*), some anthocyanin-activating *bHLH* genes can be activated by the MBW complex itself (Spelt et al., 2000; Baudry et al., 2006; Hichri et al., 2011).

![Fig. 10 Anthocyanin pigmentation in *Mimulus guttatus* inbred line IM767. (a) Flower images showing the anthocyanin spots in the nectar guide. (b) The *NEGAN* ortholog is the only anthocyanin-activating MYB expressed in the corolla of IM767, indicated by the red arrow. Genomic DNA was used as control to test primer quality. The *M. guttatus UBC* ortholog (*MgUBC*) was used as a reference gene. The larger size of the *MgUBC* genomic amplicon is due to the presence of an intron in the amplified fragment. Primer sequences are listed in Table S1.](www.newphytologist.com)
2010). However, in maize, the three components of the MBW complex seem to be independently regulated (Carey et al., 2004). The bHLH in *M. lewisii* (MlANbHLH1) does not seem to be regulated by the MBW complex, either, as neither MIWD40a nor PELAN/NEGAN knock-down affects MlANbHLH1 expression. Little is known about the transcriptional control of the R2R3-MYBs, which usually show more tissue-specific expression patterns (e.g. PELAN and NEGAN). One interesting exception is the apple MYB10 that activates anthocyanin biosynthesis in the red-fleshed apple varieties. The rearrangement of the MYB10 upstream regulatory region in some apple varieties results in a tandem repeat of a 23-bp sequence that serves as binding site for the MYB10 protein itself, leading to the autoregulation of MYB10 (Espley et al., 2009). Our RNAi and over-expression experiments strongly suggest that NEGAN, but not PELAN, is activated by the MBW complex itself (Figs 6c, 8). The fact that the MBW complex regulates NEGAN but not PELAN suggests that these two R2R3-MYB genes have evolved distinct cis-elements that respond to different transcriptional regulators.

It is also interesting to note the link between the self-activation of NEGAN and the formation of anthocyanin spots rather than a solid pattern in the nectar guide. Formation of spotty patterns in biological objects is often explained by the reaction-diffusion model (Turing, 1952) or various modified versions of this model (Meinhardt, 1982; Meinhardt & Gierer, 2000; Kondo & Miura, 2010). The essence of these reaction-diffusion based models is an interacting network that contains a local autocatalytic feedback loop and a long-range inhibitory feedback loop (Meinhardt & Gierer, 2000). The activation of NEGAN by the NEGAN-MlANbHLH1-WD40a complex itself forms such an autocatalytic feedback, although what may constitute the long-range inhibitory feedback is not yet clear. Notably, the reaction-diffusion model has previously been proposed as a potential mechanism generating multicellular pigmented petal spots by Davies et al. (2012). In fact, the transcriptional network regulating anthocyanin pigmentation in *Petunia hybrida* contains both an autocatalytic activator and a potential long-range repressor – the bHLH gene AN1 is activated by the MBW complex itself, which also activates an R3-MYB repressor, MYBx; MYBx inhibits the activity of AN1 and is capable of intercellular movement (Albert et al., 2014). However, the flowers of *Petunia hybrida* do not usually display anthocyanin spots. This suggests that the existence of such feedback loops may be required, but may not necessarily be sufficient for spot formation. The specific properties of each component (e.g. the relative diffusion rate of the long-range inhibitor to the short-range activators) could be critical to form different patterns (Kondo & Miura, 2010). It will be interesting to determine whether one can ‘engineer’ anthocyanin spots in *Petunia* petals by fine-tuning the properties of these activators and repressors through transgenic manipulations.

In addition to the four major transcriptional activators, a single-repeat R3-MYB gene, ROI1, similar to the *Petunia* MYBs, has been previously identified as a negative regulator of anthocyanin biosynthesis in *M. lewisii* petal lobes (Yuan et al., 2013a). Yeast-two-hybrid experiments suggest that PELAN, NEGAN and ROI1 can all interact with MlANbHLH1 in yeast (Y-W. Yuan & H.D. Bradshaw, unpublished data), supporting the hypothesis that ROI1 negatively regulates anthocyanin biosynthesis by competing with the R2R3-MYB activators for the limited supply of bHLH proteins. At first glance ROI1 may appear as a good candidate fulfilling the ‘inhibitory feedback’ requirement as a competitor of NEGAN, to explain the spotty anthocyanin pattern in the nectar guide. However, this is unlikely to be the case because ROI1 has very low expression level in the nectar guide compared to petal lobes. Consistent with this, knocking down ROI1 in *M. lewisii* does not seem to have any effects on the nectar guide anthocyanin spots (Yuan et al., 2013a). There probably exists another yet-to-be-identified repressor specifically expressed in the nectar guide, forming inhibitory interactions with NEGAN.

The successful prediction of the molecular bases underlying the natural yellow *M. cardinalis* populations and the *M. guttatus* floral anthocyanin patterns using our *M. lewisii* model is particularly satisfying. The two yellow *M. cardinalis* populations are found in the northern (Siskiyou Mountains of Oregon) and southern limit (Cedros Island, Baja California) of the species range (Vickery, 1995; Paul et al., 2011), respectively, and thus represent a classical example of new forms evolving from isolated populations on the periphery of a species range (Mayr, 1976). Pollination observations in a common garden environment using the typical red flowers and the mutant yellow forms suggested that the color change from red to yellow in *M. cardinalis* is probably sufficient to ‘initiate partial, incipient reproductive isolation’ (Vickery, 1995). As such, by revealing the loss of PELAN expression as the cause for this color change, we might have recovered the molecular bases of two parallel incipient speciation events.

The *M. cardinalis* results also provide further evidence supporting the notion that phenotypic variation within and between species often involve the same ‘hotspot’ genes (Stern, 2011; Streisfeld & Rausher, 2011). The petal lobe-specific R2R3-MYB, PELAN, is such a hotspot gene occupying ‘a privileged position’ (Stern, 2011) in a genetic network that can ‘maximize the phenotypic output’ by causing the downregulation of multiple anthocyanin biosynthetic genes, but meanwhile can ‘minimize pleiotropy’ by changing only the petal lobe color without affecting any other traits. However, there could be many different ways leading to loss-of-function of the same hotspot gene. In the two isolated *M. cardinalis* populations, loss of PELAN expression has evolved independently by two completely different mechanisms: one is probably caused by cis-regulatory changes and the other likely involves the deletion of the entire gene.

The *M. guttatus* case study demonstrates that our *M. lewisii* floral anthocyanin regulation model is applicable not only to closely related species, but also to relatively distantly related species (for phylogenetic relationships see Fig. 1). None of the R2R3-MYBs in the *PELAN* clade (Fig. 2a) is expressed in *M. guttatus* corolla (Fig. 10b), explaining the lack of anthocyanins in petal lobes. The NEGAN orthog, MgMYB5, appears to be responsible for the formation of nectar guide anthocyanin spots in *M. guttatus.*

Ultimately, we would like to extend the two simple case studies presented here and use the *M. lewisii* model to examine the molecular tinkering underlying the evolution of more complex
floral anthocyanin patterns, such as the different anthocyanin shades in the petal lobes of *M. pulchellus* or the novel ‘spider-web’ pattern in *M. pictus* (Fig. 1). With the necessary mutant lines and the powerful transgenic tools available in *M. lewisii*, we can introduce genomic copies (including upstream regulatory regions) of each major anthocyanin regulator from other species, on a gene-by-gene basis, into the corresponding *M. lewisii* mutant background. In doing so, we will be able to address the question of how many gene replacements are required to change one complex pigmentation pattern into another. More importantly, given the gradient of phylogenetic distances between the various species and *M. lewisii*, the gene-by-gene replacement strategy will allow us to test whether phenotypic evolution at deeper phylogenetic levels (between distantly related species) involves different kinds of mechanisms, genes or mutations to those involved with phenotypic evolution within species or between closely related species (Stern & Orgogozo, 2009).

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**References**


**Supporting Information**

Additional supporting information may be found in the online version of this article.

**Fig. S1** RT-PCR of different paralogs of *CHS, F3H*, and the MBW regulatory genes.

**Fig. S2** Alignment of subgroup 6 R2R3-MYBs.
Fig. S3 Alignment of subgroup IIIf bHLHs.
Fig. S4 Alignment of WD40 proteins.
Fig. S5 Molecular characterization of the RNAi transgenic lines.
Fig. S6 Complementation test between *Mimulus lewisii* boo3, *M. cardinalis* SM and *M. cardinalis* CI.
Fig. S7 Alignment of PELAN sequences from *Mimulus lewisii* LF10, *M. cardinalis* CE10 and *M. cardinalis* CI.

Table S1 Primers used in RT-PCR experiments
Table S2 Primers used for candidate gene sequencing of the *boo* mutants
Table S3 Primers used for constructing RNAi and over-expression plasmids
Table S4 Primers used for PELAN amplification in *Mimulus cardinalis* strains

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