Evolutionary Variation in MADS Box Dimerization Affects Floral Development and Protein Abundance in Maize

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INTRODUCTION

Floral organ morphology is diverse, but the master regulators controlling floral organ development are conserved. Many of the master regulators controlling floral organ development are transcription factors encoded by the ABC(DE) genes. The ABC(DE) model proposes how these transcription factors act together to regulate the development of floral organs. All but one of the original ABC(DE) genes encode MADS box transcription factors (reviewed in Krizek and Fletcher, 2005). Although derived from analyses of genetic mutants in the eudiots Antirrhinum majus and Arabidopsis (Arabidopsis thaliana), some aspects of the ABC(DE) model can explain the genetics of floral development in distantly related angiosperms. For example, B-class gene function is deeply conserved. B-class genes regulate stamen and petal development in many angiosperms, even when petal and stamen homologs are highly modified (reviewed in Litt and Kramer, 2010). How, then, can floral organs vary so extensively in form and function when they are specified by orthologous genes?

The combinatorial assembly of MADS box protein complexes provides a framework to answer this question, in the floral quartet model (Theissen and Saedler, 2001; Theissen et al., 2016). MADS box proteins may function as tetramers or “floral quartets,” with tetramer composition determining DNA binding and downstream gene regulation. For example, tetramers of B-, C-, and E-class proteins (BCE complexes) likely specify Arabidopsis stamen identity, and tetramers of C- and E-class proteins likely specify carpel identity (Honma and Goto, 2001; Theissen and Saedler, 2001; Theissen et al., 2016). Evidence for the floral quartet model includes genetic data, in vitro characterization of protein-protein interactions, and in planta evidence for MADS box complex formation and DNA binding, particularly in Arabidopsis (reviewed in Theissen et al., 2016). Beyond Arabidopsis, the paralogs available to form MADS box complexes differ between lineages, but general classes of interactions are conserved. For example, B-class genes have complex histories of lineage-specific duplications, but most B-class paralogs participate in BCE complexes in vitro (Veron et al., 2007; Zhang et al., 2018). This conservation of protein-protein interactions, coupled to the functional conservation of many MADS box genes, suggests that complexes of homologous MADS box proteins specify homologous floral organs in different lineages. Mixing and matching of MADS box paralogs in these
complexes may generate floral diversity by regulating different suites of downstream genes, thus contributing to evolutionary variation in organ shape and form (Mondragón-Palomino and Theissen, 2008; Theissen et al., 2016). For example, complexes of B- and E-class proteins may specify petal development in orchids (Orchidaceae species). However, the precise mix of B- and E-class proteins in these complexes likely differs between unelaborated petals and the highly elaborated petals that characterize orchid flowers (Hsu et al., 2015). Evolutionary changes to MADS box complexes, specifically to BCE MADS box complexes, may also have been important in the evolution of the flower itself (Wang et al., 2010; Theissen et al., 2016; Ruelens et al., 2017). Thus, combinatorial assembly of MADS box complexes may have been important in floral evolution and diversification.

Although differential MADS box complex assembly presents an appealing model for explaining floral diversification (Theissen and Saedler, 2001; Mondragón-Palomino and Theissen, 2009, 2011; Theissen et al., 2016; Bartlett, 2017), the consequences of changing MADS box protein-protein interactions have not been extensively tested in planta. If combinatorial MADS box complex assembly contributes to floral diversification, then we can predict (1) deep conservation of MADS box complexes like the BCE complex and (2) that evolutionary changes to floral MADS box protein-protein interactions should result in changes to gene regulation and, in turn, to floral development. Here, we test these predictions using the maize (Zea mays) B-class MADS box protein STERILE TASSEL SILKY EAR1 (STS1; a homolog of PISTILLATA in Arabidopsis; Goto and Meyerowitz, 1994; Bartlett et al., 2015). STS1 forms obligate heterodimers with SILKY1 (SI1; a homolog of APETALA3 in Arabidopsis; Jack et al., 1992; Ambrose et al., 2000; Whipple et al., 2004). We engineered an ancestral variant of STS1 that forms both homodimers and heterodimers with SI1 (Bartlett et al., 2016). We show that this facultative STS1 homodimerization has subtle, quantitative effects on stamen development but large effects on downstream gene expression. We also show that BCE complexes do form in maize. Lastly, we found that B-class dimerization affected MADS box complex composition and abundance. Our results show how coding change in a pleiotropic master regulator could have quantitative effects on MADS box complex composition and abundance and, in turn, contribute to quantitative variation in floral form.

RESULTS

STS1-HET and STS1-HOM Show Subtle Differences in Localization and Function

To explore the effects of B-class heterodimerization versus homodimerization, we developed transgenic maize plants that express a version of STS1 that can bind DNA as homodimers. We found that changing the Gly (G) residue at position 81 to Asp (D) reverts STS1 to its most likely ancestral dimerization state: able to form both homodimers and heterodimers (Bartlett et al., 2016). Additional amino acid residues differ between STS1 and its most likely ancestor. However, we chose to introduce a single change (G81D) to explicitly test the effects of heterodimerization versus homodimerization, to the exclusion of other differences between the extant and ancestral proteins. We introduced the critical G81D change into an STS1-yellow fluorescent protein (YFP) fusion construct that rescues sts1 (Bartlett et al., 2016). Additional amino acid residues differ between STS1 and its most likely ancestor. However, we chose to introduce a single change (G81D) to explicitly test the effects of heterodimerization versus homodimerization, to the exclusion of other differences between the extant and ancestral proteins. We introduced the critical G81D change into an STS1-yellow fluorescent protein (YFP) fusion construct that rescues sts1 (Bartlett et al., 2015) and used it to transform maize. We will refer to the obligate heterodimer construct (pSTS1:STS1-YFP) as STS1-HET and to the STS1 homodimer construct [pSTS1:STS1(G81D)-YFP] as STS1-HOM.

To understand how variable B-class dimerization affects floral development, we used identical crossing schemes to generate
lines carrying either STS1-HET or STS1-HOM in backgrounds that were segregating either si1 or sts1. In both si1 and sts1, stamen and lodicule (petal homolog) organ identity is lost (Ambrose et al., 2000; Bartlett et al., 2015). We found that both transgenes complemented sts1; neither organ identity nor organ number varied between STS1-HET and STS1-HOM (Figures 1D and 1E; Supplemental Table 1). In contrast, adult flowers in si1 mutants carrying STS1-HOM were indistinguishable from nontransgenic si1 mutants (Figures 1C and 1F). This indicates that STS1-HOM can rescue sts1 mutants and is functional, but it cannot compensate for the loss of SI1 function.

To explore differences between STS1-HET and STS1-HOM in more detail, we analyzed the development of complemented sts1 mutants. We examined protein localization of both STS1-HET and STS1-HOM over the course of development using confocal microscopy. We found that STS1-HET was restricted to lodicule and stamen primordia, as expected (Figures 1G and 1H; Bartlett et al., 2015). In contrast, protein localization was relaxed in STS1-HOM lines, appearing in gynoecia in addition to lodicule and stamen primordia (Figure 1J). However, this gynoecial localization was not evident in our immunolocalizations using an anti-STS1 antibody (Supplemental Figure 1). In contrast to the proteins, STS1-HET and STS1-HOM RNAs showed similar localization patterns (Supplemental Figure 1). This suggests that the subtle localization differences we detected were regulated at the protein level.

In addition to protein localization differences, morphology differed quantitatively between STS1-HOM and STS1-HET flowers. This included differences in anther aspect ratio, such that anthers of STS1-HOM flowers were wider and shorter than those of STS1-HET flowers while they were still developing (Student’s t test, \( P = 6.8 \times 10^{-10} \); Figures 1K and 1L; Supplemental Data Set 1). We assayed anther shape at anthesis using eFourier analysis, as implemented in the R package MOMOCS (Bonhomme et al., 2014). This analysis identified a small but significant difference in shape between anthers from si1 mutants complemented with either STS1-HET or STS1-HOM (MANOVA, \( P = 0.006 \)). Anthers from STS1-HET flowers occupied a larger morphospace and tended to be wider than STS1-HOM anthers (Supplemental Figure 2). Indeed,

Figure 1. B-Class Dimerization Has Subtle Effects on Floral Development in Maize.

(A) to (E) Stamen identity ([A]: marked with asterisks) is lost in both sts1 (B) and si1 (C) mutant flowers. At anthesis, sts1 mutant flowers complemented with either the STS1-HET (D) or STS1-HOM (E) transgene resemble wild-type flowers and each other.

(F) The STS1-HOM transgene did not complement the si1 mutant phenotype.

(G) to (J) Confocal microscopy showing localization of STS1-HET ([G] and [H]) and STS1-HOM ([I] and [J]) localization in developing flowers. Dotted lines in (H) and (J) indicate developing gynoecia, and numbers in top right corners indicate frequencies at which we observed the shown localization patterns.

(K) to (N) Anther shape metrics during development ([K] and [L]) and at anthesis ([M] and [N]).

(K) During development, anther aspect ratio (AR; anther width/length) was higher in STS1-HOM anthers than in STS1-HET anthers (\( P = 6.8 \times 10^{-10} \); left), while anther area (anther width \times anther length) was not significantly different (\( P = 0.2592 \); right). We measured 39 (STS1-HET) or 28 (STS1-HOM) anthers total from three individuals of each genotype. **Highly Significant (\( P < 0.01 \)); NS, not significant.

(L) Confocal images of developing anthers measured in (K).

(M) At anthesis, anther aspect ratio is lower in STS1-HOM anthers than in STS1-HET anthers (\( P = 0.003 \); left), while anther area is not significantly different (\( P = 0.367 \); right). Values were calculated using Student’s t test. *Significant (\( P < 0.01 \)); NS, not significant.

(N) Twenty-five randomly selected anthers from the first (bottom) and fourth (top) quartiles of anthers measured in (M), colored according to STS1 transgene genotype. We measured 10 anthers from 18 individuals of each genotype (180 anthers per genotype).
aspect ratio measurements of mature anthers showed that anthers from STS1-HOM flowers were narrower than those from STS1-HET flowers (Student’s t test, P = 0.003; Figures 1M and 1N; Supplemental Data Set 2). Differences in anther aspect ratio, both during development and at anthesis, were despite similarities in anther surface area, which we used as a proxy for size (developing anthers: Student’s t test, P = 0.259 [Figure 1K]; anthesis: Student’s t test, P = 0.367 [Figure 1M]). Taken together, our results suggest that B-class dimerization may affect anther shape, potentially by affecting anther growth dynamics over the course of development.

Differential Dimerization of Maize B-Class Proteins Affects Downstream Gene Regulation

The morphological differences between STS1-HET and STS1-HOM flowers were subtle, indicating small phenotypic consequences of differential B-class dimerization. We were curious if downstream transcription was similarly conserved between STS1-HET and STS1-HOM. To understand the effect of STS1 dimerization on gene expression, we performed RNA sequencing (RNA-seq) in sts1 or si1 mutants complemented with either STS1-HET or STS1-HOM. We harvested inflorescence tissue shortly after stamen primordium emergence to capture gene expression just after the initiation of STS1 expression (Bartlett et al., 2015). Because of the high genetic diversity in maize, we compared expression profiles within genetic backgrounds to control for potential differences due to incomplete introgression of the STS1 transgenes (Buckler et al., 2006). To this end, we measured differential expression by comparing expression in each line (STS1-HOM or STS1-HET) against expression in their mutant siblings.

These analyses revealed more differentially expressed genes in STS1-HOM than in STS1-HET, as compared with mutant siblings. At a 5% false discovery rate (FDR), there were 501 differentially expressed genes in inflorescences expressing STS1-HET, as compared with sts1 mutant siblings (Figure 2A; Supplemental Data Set 3). In inflorescences expressing STS1-HOM, we found 1257 differentially expressed genes, as compared with sts1 mutant siblings (Figure 2B; Supplemental Data Set 4). There were 109 genes differentially regulated by both STS1-HOM and STS1-HET. STS1-HOM can both homodimerize and heterodimerize with SI1 (Bartlett et al., 2016). To see how gene expression was affected specifically by STS1-HOM without the presence of SI1, we compared gene expression between inflorescences expressing either STS1-HET or STS1-HOM in a si1 mutant background. We found that only 5 genes were differentially expressed in STS1-HET inflorescences, as compared with si1 mutant siblings (Figure 2C; Supplemental Data Set 5). In contrast, in inflorescences expressing STS1-HOM, 91 genes were differentially expressed, as compared with si1 mutant siblings (Figure 2D; Supplemental Data Set 6). These contrasts indicate that B-class dimerization affects patterns of gene expression in developing inflorescences, either directly or indirectly. Therefore, evolutionary change in B-class dimerization can impact downstream gene expression.

To determine whether the general functions of genes regulated by STS1-HET and STS1-HOM were qualitatively similar, we performed Gene Ontology (GO) enrichment analyses with our differentially expressed gene sets in an sts1 mutant background (Supplemental Data Sets 7 and 8). To compare these lists of enriched GO terms, we used GO correlation plots (Figure 2E; Bergey et al., 2018). Since the STS1-HET and STS1-HOM constructs were so similar, and since our morphological data suggested subtle functional differences between STS1-HET and STS1-HOM (Figure 1), we reasoned that STS1-HET and STS1-HOM were regulating similar processes. Therefore, we made the threshold for calling a GO term unique to either data set very stringent; only GO terms with an enrichment P < 0.01 in one data set and an enrichment P > 0.25 in the other data set were called unique (Figure 2E, sectors i and v). Using these comparisons, we found many GO terms related to development shared between STS1-HET and STS1-HOM (Figure 2E). Indeed, 29 of the 65 enriched GO terms shared between STS1-HET and STS1-HOM were related to development (P < 0.01 in both data sets; Figure 1E). GO terms related to signaling and metabolism were also enriched in both data sets, although the majority of these terms were not significantly enriched in STS1-HOM. However, the most highly enriched GO terms in STS1-HOM were not significantly enriched in STS1-HET (P > 0.25). These GO terms, specific to STS1-HOM, were almost all related to chromatin assembly and protein modification (Figure 2E, sector ii). Thus, core floral developmental programs were activated in inflorescences expressing STS1-HOM, but B-class dimerization also affected the expression of unique sets of genes, particularly genes involved in chromatin assembly and remodeling.

A Complex of B-, C-, and E-Class Proteins Is Conserved in Maize

Differential dimerization may affect the composition of protein complexes, which is crucial for MADS box function (Theissen and Saedler, 2001; Theissen et al., 2016). To determine how differential B-class dimerization might impact the composition of MADS box complexes, we performed immunoprecipitations (IPs) of STS1-HET and STS1-HOM in an sts1 mutant background using a specific antibody against GFP (ChromoTek). We analyzed precipitated complexes using quantitative mass spectrometry (MS). After confirming the presence of STS1 in the IP complex through immunoblotting, we performed trypsin digestion and liquid chromatography-MS/MS followed by label-free protein quantification (Sinitcyn et al., 2018). We used protein from sts1 mutant siblings as a negative control to detect nonspecific proteins. We compared abundances of identified proteins using the intensity-based absolute quantification (IBAQ) method (Krey et al., 2014; He et al., 2019). Protein identification was based on at least five exclusive peptides, and two replicates were performed for each sample; protein abundances were similar between replicates (Supplemental Data Sets 9 and 10). We found 1278 total proteins in complex with STS1-HET; 453 of these were either specific to STS1-HET or were at least twofold higher than in mutant siblings (Supplemental Data Set 9). In contrast, we found 1597 proteins in complex with STS1-HOM; 486 of these proteins were either specific to STS1-HOM or were at least twofold higher than in mutant siblings (Supplemental Data Set 10). We found 125 proteins in common to both the STS1-HET and STS1-HOM IPs (either absent in sts1 siblings or twofold or greater change). This result indicates that, while many proteins are common to STS1-HET and STS1-HOM complexes, each STS1 variant is associated with a distinct set of proteins.
The first set of proteins in our IPs that we explored further were the MADS box proteins. Ancestral protein resurrection and in vitro surveys of protein-protein interactions predict that complexes of B-, C-, and E-class MADS box proteins are conserved across flowering plants (Veron et al., 2007; Theissen et al., 2016; Zhang et al., 2018). However, this prediction remains largely untested in planta, particularly in monocots. Therefore, we specifically searched for other MADS box proteins in our IP-MS data. In the STS1-HET IP-MS results, we found both STS1 and SI1 peptides as well as peptides for three E-class MADS box proteins (ZMM27, ZMM7, and ZMM6) and two C-class proteins (AGAMOUS co-orthologs ZAG1 and ZMM23; Supplemental Table 2; Münster et al., 2002; Zahn et al., 2005). ZMM6, ZMM7, and ZMM27 are all in a single clade of E-class proteins, co-orthologous to the Arabidopsis protein SEPALLATA3 (Zahn et al., 2005). In STS1-HOM, we found the same three E-class proteins and one C-class protein, ZAG1, but did not find ZMM23. ZMM23 was identified as one of the most enriched proteins in the STS1-HET IP and was the only MADS box protein specific to STS1-HET. This variability in complex abundance between STS1-HET and STS1-HOM indicates that differential dimerization affects the mix of precisely which BCE complexes are present during floral development. Our results also indicate broad conservation of B-, C-, and E-class protein complexes between maize and Arabidopsis, confirming predictions from in vitro assays (Veron et al., 2007; Ruelens et al., 2017).

B-Class Dimerization Affects Transcription Factor Complex Abundance

The MADS box proteins we identified in both IP data sets were at much higher levels in STS1-HOM than in STS1-HET (SI1 was the only exception). STS1-HOM was far more abundant than STS1-HET: IBAQ values for STS1-HOM were 4.0 times higher than for STS1-HET, 3.58 times higher normalized to SI1 (Figure 3). The higher abundance of STS1-HOM in our IPs could have been due to complex stoichiometry, where STS1-HOM homodimerization caused double the number of STS1-HOM proteins in MADS box complexes. Alternatively, STS1-HOM protein levels could also have been generally higher in developing flowers. We suspected that STS1-HOM levels were generally higher; our immunolocalizations suggested a higher abundance of STS1-HOM versus STS1-HET, despite the same experimental conditions (Supplemental Figure 1). However, these immunolocalizations were not quantitative. To directly measure protein levels, we performed immunoblotting using a polyclonal antibody against STS1. The same amount of protein for each sample was loaded. After immunoblotting (described in Methods), we performed densitometry analysis using ImageJ (1.4 NIH software; Schneider et al., 2012). Relative abundance was calculated by dividing the densitometry value of STS1 protein with the respective loading control (α-Tubulin). In these blots, STS1-HOM was seven times more abundant than STS1-HET (Figure 3C; Supplemental Table 3). Together with our IP-MS results, these data indicate that STS1-HOM accumulated to a higher abundance than STS1-HET in inflorescence tissue.

STS1-HOM protein could have been more abundant than STS1-HET protein because the STS1-HOM transgene was transcribed to higher levels than the STS1-HET transgene. To test for this, we performed RT-qPCR using specific primers for STS1 and SI1 in sts1 mutants complemented with either STS1-HET or STS1-HOM. We found that SI1 was expressed to the same level in both lines; however, the expression of STS1 in STS1-HET was 3.7-fold higher than in STS1-HOM (relative to Actin; Figure 3D). Similarly, in our RNA-seq results, normalized STS1-HET expression was consistently double normalized STS1-HOM expression: ~15,000 counts versus 8600 counts, respectively. Thus, despite relatively low STS1-HOM expression, STS1-HOM protein accumulated to higher levels than STS1-HET in floral tissue. This indicates that STS1 homodimerization led to increased protein accumulation independent of RNA levels. Therefore, the higher abundance of STS1-HOM is likely regulated posttranscriptionally.

The other MADS box proteins we detected in our IPs were also more abundant in STS1-HOM than in STS1-HET. ZAG1, ZMM6, and ZMM7 increased in abundance twofold to ninefold in STS1-HOM as compared with STS1-HET (Figure 3B; Supplemental Table 2). This higher abundance of ZAG1, ZMM6, ZMM7, and ZMM27 could also have been because of differences in transcription or differences posttranscriptionally. To distinguish between these possibilities, we looked for these genes in our RNA-seq data and determined that they were not differentially expressed between STS1-HOM and their sts1 mutant siblings (Supplemental Data Set 4). Therefore, the higher abundance of these C- and E-class MADS box proteins was likely not because of higher transcription. Of all the MADS box proteins we identified in our IPs, SI1 was the only one found at similar levels in both STS1-HET and STS1-HOM. This suggests that SI1 is able to compete with STS1-HOM to form heterodimers and that SI1 may be a limiting factor in MADS box protein complex assembly. Taken together, our results show that STS1 homodimerization affected the abundance of other MADS box proteins in transcription factor complexes, likely posttranscriptionally.

STS1-HET and STS1-HOM Form Complexes With Chromatin Remodelers, Kinases, and the Ubiquitination Machinery

To explore our IP-MS data sets further, we performed GO enrichment analyses with identified proteins in the STS1-HET versus STS1-HOM IPs. In these analyses, we only included proteins with at least a twofold change as compared with sts1 siblings. When we compared the resulting lists of enriched GO terms, our results were similar to the RNA-seq comparisons: development, signaling, and metabolism-related GO terms were enriched in both data sets. However, chromatin-related GO terms were no longer exclusively enriched in the STS1-HOM data set (Figures 2E and 3A; Supplemental Data Sets 11 and 12).

We found GO categories related to chromatin modification enriched in both the STS1-HOM and STS1-HET IP-MS results (Figure 3A). Many of the proteins that were in these enriched GO categories are homologs of Arabidopsis chromatin remodelers that act to relieve the chromatin-mediated repression of transcription (Wu et al., 2012; Hu et al., 2014; Li et al., 2015). This includes an ISWI chromatin-remodeling complex ATPase, CHR126b, a homolog of the Arabidopsis protein CHR11 (Smaczniak et al., 2012). CHR126b was enriched in both the STS1-HET and STS1-HOM IP-MS data.
Figure 2. B-Class Dimerization Remodels Transcription in Developing Tassel Flowers.

(A) to (D) Significantly more genes are differentially expressed in STS1-HOM versus STS1-HET inflorescences, as compared with mutant siblings. (A) and (B) Differential gene expression in sts1 mutants complemented with either the STS1-HET (A) or STS1-HOM (B) transgene, as compared with sts1 mutant siblings. (C) and (D) Differential gene expression in si1 mutants complemented with either the STS1-HET (C) or STS1-HOM (D) transgene, as compared with si1 mutant siblings. (E) GO term correlation plots comparing probabilities of GO term enrichments in STS1-HET versus STS1-HOM. GO categories related to chromatin assembly and remodeling are significantly enriched in the STS1-HOM DE gene set. The left panel shows all GO terms, and the right panel excludes highly enriched GO terms in STS1-HOM. Dot sizes are proportional to the number of genes in each enriched GO term category and colored according to which larger category they are associated with. P value cutoffs for sectors are as follows: (i) $P \text{ value } x > 0.25$ and $P \text{ value } y < 0.01$; (ii) $0.01 < P \text{ value } x < 0.25$ and $P \text{ value } y < 0.01$; (iii) $P \text{ value } x < 0.01$ and $P \text{ value } y < 0.01$; (iv) $P \text{ value } x < 0.01$ and $0.01 < P \text{ value } y < 0.25$; (v) $P \text{ value } x < 0.01$ and $P \text{ value } x > 0.25$. 
sets (Supplemental Table 2). We found three additional chromatin remodeling and scaffolding factors in complex only with STS1-HOM: BRAHMA1, CHR12, and FRIGIDA-LIKE PROTEIN4a (Supplemental Table 2). In Arabidopsis, BRAHMA, CHR12, and FRIGIDA modify specific chromatin states to regulate the transition to floral meristem identity, floral organ development, and meristem determinacy (Bezhani et al., 2007; Liu et al., 2009; Sang et al., 2012; Wu et al., 2012; Hu et al., 2014; Thouly et al., 2020). In complex with STS1-HOM, these proteins might be acting to open up chromatin surrounding MADS box binding sites, resulting in higher or more prolonged expression of MADS box targets in STS1-HOM plants (Figure 4).

We also found a class of proteins related to signaling in our IP data sets, specifically kinases. Ten kinases were immunoprecipitated with STS1-HET and 11 with STS1-HOM; only two of these were in both samples (Supplemental Data Sets 9 and 10; Supplemental

**Figure 3.** B-Class Dimerization Affects Protein Abundance and Protein Complex Assembly in Developing Tassels.

(A) GO term correlation plot comparing probabilities of GO term enrichments in the STS1-HET versus STS1-HOM IP-MS data sets. GO categories related to protein modification and chromatin remodeling are enriched in both data sets. Dot sizes are proportional to the number of genes in each enriched GO term category and colored according to which larger category they are associated with. P value cutoffs for sectors are as follows: (i) P value x > 0.25 and P value y < 0.01; (ii) 0.01 < P value x < 0.25 and P value y < 0.01; (iii) P value x < 0.01 and P value y < 0.01; (iv) P value x < 0.01 and 0.01 < P value y < 0.25; (v) P value x < 0.01 and P value x > 0.25.

(B) Relative abundances of MADS box proteins in the IP-MS data sets. STS1, as well as C- and E-class proteins, are higher in STS1-HOM than in STS1-HET IPs.

(C) Immunoblots with anti-STS1 (top) and anti-Tubulin (bottom) also show that STS1-HET is less abundant than STS1-HOM.

(D) RT-qPCR shows that STS1-HET RNA is more abundant than STS1-HOM RNA, relative to Actin. SI1 RNA occurs at similar levels, relative to Actin, in both STS1-HET and STS1-HOM.

(E) Immunoblots with anti-pSer and anti-ubiquitin show that STS1-HET and STS1-HOM are phosphorylated and likely in complex with ubiquitinated proteins. The same amount of immunoprecipitated STS1-HET and STS1-HOM protein was loaded for this experiment.
One new set of GO terms that emerged in our analysis was related to protein modification and ubiquitination. These GO terms were more enriched in STS1-HOM but were still present in STS1-HET (Figure 3A). When we explored which proteins might be associated with these enriched GO terms (Supplemental Table 5), we found that STS1-HOM was more abundant than STS1-HET in the upregulation of target genes. This transcription is likely halted by the proteasome-mediated degradation of MADS box complexes.

**STS1-HET and STS1-HOM Are Posttranslationally Modified**

STSI-HOM was more abundant than STSI-HET, and both proteins were in complex with ubiquitination machinery and kinases in our IP-MS results (Figure 3). Ubiquitination and (often) phosphorylation precede protein degradation in the proteasome (Schrader et al., 2009). Therefore, our IP-MS data suggested that STS1 degradation was regulated by posttranslational modification. To explore the posttranslational modification of STS1, we first predicted phosphorylation sites in STSI-HET and STSI-HOM using Usite (Gao et al., 2010; Yao et al., 2012). The results for STSI-HET and STSI-HOM were identical and revealed a high likelihood for STSI phosphorylation, mostly in Ser residues in the I and K domains, which mediate protein-protein interactions (Masiero et al., 2002; Yang et al., 2003; Bartlett et al., 2015). Similarly, in silico analyses using UbPred revealed low-confidence ubiquitination sites in both STSI-HET and STSI-HOM (Radivojac et al., 2010). These analyses led us to explore the phosphorylation and ubiquitination of STS1-HET versus STS1-HOM in vitro. To do this, after IP of STS1-containing complexes using an anti-GFP antibody (Roche), we performed immunoblotting using commercial anti-pSer or anti-ubiquitin monoclonal antibodies (Santa Cruz Biotechnology). We found that both STS1-HET and STS1-HOM proteins were phosphorylated. When we analyzed IP complexes with an anti-ubiquitin antibody, we identified potentially ubiquitinated proteins in both the STS1-HET and STS1-HOM complexes. We detected no obvious differences in phosphorylation or ubiquitination between STS1-HET and STS1-HOM (Figure 3E). However, these blots were not quantitative and would not have revealed subtle differences between STS1-HET and STS1-HOM posttranslational modifications. Our results do indicate that STS1-HET and STS1-HOM are potentially in complex with ubiquitinated proteins and are both phosphorylated.

**DISCUSSION**

We found that differential B-class dimerization did not result in qualitatively different organ identities in maize. Instead, the impacts of differential B-class dimerization on maize floral development were subtle and quantitative: anthers from STSI-HOM flowers were narrower than those from STSI-HET flowers at anthesis (Figure 1). At a molecular level, we found STS1 in complex with C- and E-class proteins, chromatin remodelers, and chromatin scaffolding proteins in Arabidopsis, MADS box proteins also associate with chromatin remodelers and scaffolding proteins (Smaczniak et al., 2012; Vachon et al., 2018). Thus, both BCE MADS box complexes and MADS box interaction with chromatin proteins are conserved between maize and Arabidopsis. We found that STSI-HOM was more abundant than STSI-HET and that the two STS1 variants were in complex with different mixes of ubiquitin ligase complex or the APC/C have been reported as interacting with MADS box proteins, the E3 ubiquitin ligase proteins we found in our IPs are in the same complexes in other species, giving us additional confidence in our results (Feng et al., 2004; Wertz et al., 2004; Adhvaryu et al., 2015; Chang et al., 2015). Thus, our IP-MS results indicate that MADS box complexes in maize interact with the ubiquitination machinery.
MADS box proteins and chromatin remodelers. In Arabidopsis, the differential abundance and composition of transcription factor complexes, as well as the differential recruitment of chromatin remodeling factors, can all impact the dynamics of transcription (Li et al., 2015; Hugouvieux et al., 2018; Clark et al., 2020). Indeed, we found that B-class dimerization had profound effects on gene expression (Figure 2). Importantly, while the DNA binding profiles of STS1-HET and STS1-HOM dimers may differ, this difference is not essential for altered transcriptional dynamics. Differential MADS box complex abundance and differential recruitment of chromatin-modifying machinery, mediated by protein-protein interactions, may result in quantitative tuning of transcription (Figure 4).

We found that STS1-HOM protein was more abundant than STS1-HET, despite lower levels of RNA (Figure 3). This means that STS1-HOM abundance was likely regulated posttranscriptionally, leaving either (1) impaired degradation of the STS1-HOM protein or (2) increased translational efficiency of the STS1-HOM transcript as explanations for higher STS1-HOM abundance (Schrader et al., 2009; Gingold and Pilpel, 2011). We favor impaired degradation of STS1-HOM for three reasons. First, the STS1-HET and STS1-HOM transcripts differ by a single nucleotide in the 81st codon (Bartlett et al., 2016). Although this single-nucleotide polymorphism could affect RNA secondary structure and translation efficiency, it is well downstream of the start codon, where RNA secondary structure is more likely to affect translational efficiency (Kudla et al., 2009; Tzeng et al., 2009; Tuller et al., 2010; Ding et al., 2014; Verma et al., 2019). Second, both STS1 variants coprecipitated with proteins related to ubiquitination. Third, STS1 includes a KEN box sequence, unaffected by the G81D change that differentiates STS1-HET from STS1-HOM. KEN boxes are short linear motifs (degrons) recognized by the APC/C, an E3 ubiquitin ligase (Davey and Morgan, 2016). This indicates that STS1 may be recruiting the APC/C. Indeed, we found three APC/C subunits in complex with STS1-HOM. The higher abundance of STS1-HOM may have allowed us to detect these transient interactions. Beyond our own data, many Arabidopsis MADS box proteins are ubiquitinated (Manzano et al., 2008), and some MADS box complexes are sent to the proteasome for degradation under phytoplasma infection (MacLean et al., 2014). Taken together, these data lead us to favor differential protein degradation as an explanation for higher STS1-HOM abundance.

It seems likely that STS1-HOM was more abundant than STS1-HET because of differential degradation. However, we are left wondering what mechanism may underlie this difference. Both differential dimerization and DNA binding ability can affect protein degradation in the proteasome (Johnson et al., 1998; Coppotelli et al., 2011; Kiparaki et al., 2015; Hickey et al., 2018); either may be responsible for differential degradation of STS1-HET versus STS1-HOM. For example, the yeast (Saccharomyces cerevisiae) homeodomain transcription factor MATα2 both homodimerizes and forms heterodimers with a paralog, MATα1. While the MATα2 homodimers are ubiquitinated and rapidly degraded, a degron in MATα2 is masked by heterodimerization with MATα1 (Johnson et al., 1998). In the case of STS1, the KEN box degron, or an as-yet unidentified degron (Moss et al., 2015; Geffen et al., 2016; Ella et al., 2019), may be masked or altered in STS1 homodimers but not in STS1/SI1 heterodimers, allowing for more rapid degradation of STS1/SI1 heterodimers. The strength of DNA binding by a protein can also affect degradation dynamics (Coppotelli et al., 2011; Hickey et al., 2018). In yeast, MATα2 mutant proteins that differ in their DNA binding profiles are far more stable than wild-type proteins, despite intact degron sequences (Hickey et al., 2018). Similarly, strong DNA binding of an Epstein-Barr virus protein inhibits its degradation in the proteasome (Coppotelli et al., 2011). STS1 homodimers and STS1/SI1 heterodimers may differ in their DNA binding profiles or affinity, which could, in turn, affect protein degradation dynamics.

We discovered that STS1 likely interacts with kinases and is phosphorylated (Figure 3). Phosphorylation is an important posttranslational modification that impacts protein function by controlling subcellular localization, DNA binding, and protein-protein interactions (Wang et al., 2018; Xu et al., 2018; Millar et al., 2019). A potential Ser/Thr phosphorylation site within the MADS box domain is deeply conserved in plants, suggesting the importance of phosphorylation for MADS box protein function (Angle at and Immink, 2009; Patharkar and Walker, 2016). Indeed, several MADS box proteins are phosphorylated. For example, phosphorylation of the mouse MADS box protein MEF2C enhances its DNA binding activity (Molkentin et al., 1996). In Arabidopsis, AGL24 is bound and phosphorylated by a meristic-omatic receptor-like kinase ( Fujita et al., 2003). AGL15 is bound and phosphorylated by MPK3/6, allowing for the expression of HAESA, a Leu-rich repeat receptor-like kinase gene that regulates floral organ abscission (Patharkar and Walker, 2016). Although phosphorylation of ribosomes impacts the translational efficiency of B-class mRNAs (Tzeng et al., 2009), we could find no reports of B-class protein phosphorylation. Our demonstration of in planta phosphorylation of STS1 could contribute to understanding of the regulation of B-class MADS box proteins.

We found that variation in B-class MADS box dimerization affected one aspect of anther shape in maize: anthers from STS1-HOM flowers were narrower than those from STS1-HET flowers. This could be because of altered transcription of genes regulating cell division or expansion in STS1-HET versus STS1-HOM (Figure 4). Indeed, GO categories specifically enriched in the STS1-HOM DE gene set include “regulation of cell size,” “cell proliferation,” and “response to gibberellin” (Supplemental Data Set 8). Upregulated genes in these GO categories encode putative cell cycle regulators and markers of proliferating cells, including proliferating cell nuclear antigens and histones (Citterio et al., 1992; Fobert et al., 1994). Importantly, many of these genes are also in the chromatin categories that were highly enriched in the STS1-HOM DE gene set (Figure 2). We think that this enrichment indicates both altered regulation of cell division and altered chromatin remodeling caused by the higher abundance of STS1-HOM. Three SHORT INTERNODE/STYLISH (SHI/STY) transcription factor genes are specifically upregulated in STS1-HOM. SHI/STY transcription factors regulate organ morphogenesis and plant architecture in many taxa, including in the grasses barley (Hordeum vulgare) and rice (Oryza sativa); Kuusk et al., 2006; Yuo et al., 2012; Landberg et al., 2013; Gomariz-Fernández et al., 2017; Youssef et al., 2017; Duan et al., 2019; Min et al., 2019). In barley and Arabidopsis, SHI/STY genes have specific roles in positive regulation of cell proliferation (Kuusk et al., 2006; Yuo et al., 2012).
The upregulated SHI/STY genes may similarly be regulating cell proliferation in STS1-HOM anthers. Thus, differential B-class dimerization might impact the regulation of cell division in developing anthers, resulting in quantitative differences in anther shape.

Small changes to floral organ development, regulated by MADS box genes, are significant in the evolution of floral diversity. Within families and genera, large-scale changes to floral Bauplan are rare. Instead, changes to organ shape, size, color, and micromorphology are more common (Endress, 1992; Rudal and Bateman, 2004; Bartlett and Specht, 2010; Cui et al., 2010). These small differences in organ form can have important consequences for floral function. For example, in Plantago and Thalictrum, stamen dimensions and material properties are important for efficient pollen release from anthers (Timerman et al., 2014; Timerman and Aquilegia (Sharma and Kramer, 2017), and petal fusion in and stamen size in Arabidopsis (Wuest et al., 2012), petaloidy in

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cases, in the pTF101 vector backbone, were transformed into

the maize (Zea mays) Hi-II genetic background at the Iowa State University

transformants were crossed to

STS1-HET versus STS1-HOM in

maize. Thus, evolutionary variation in a pleiotropic master regu

like STS1 could impact transcriptional dynamics and have small, quantitative effects on floral development and the evolution of floral diversity.

METHODS

Transgenic Lines and Plant Growth

STS1 transgenes, in the pTF101 vector backbone, were transformed into the maize (Zea mays) Hi-II genetic background at the Iowa State University plant transformation facility (annotated vector maps are included in the data repository). STS1-HET and STS1-HOM transformants were crossed to either sts1 or a1 mutants in the A619 genetic background. Resulting progeny carrying a transgene were identified by their ability to resist herbicide application and crossed again to sts1 or a1 mutants in the A619 genetic background. Once generated, plants for all molecular analyses were grown in the University of Massachusetts College of Natural Science greenhouse using a 50:50 soil mix of LC1 (SunGro Horticulture) and Turface (Turface). Field-grown plants were grown at the University of Massachusetts Crop and Animal Research and Education Farm in South Deerfield, Massachusetts.
RNA-Seq Tissue Collection and Sequencing

Plants were grown in the greenhouse as described above. Shortly after stamen primordium emergence (4 to 5 weeks after planting), plants were harvested and inflorescence meristems were flash frozen in liquid nitrogen. Samples were harvested at the same time of day, beginning at 3 PM. Three plants per genotype were pooled to generate one biological replicate, with three biological replicates per genotype (genotyping primers are listed in Supplemental Table 6). RNA was extracted from each pooled biological replicate using a combination of Trizol (Invitrogen) and Qiagen Plant RNAeasy columns including Qiagen on-column DNase digestion. One microgram of RNA from each biological replicate was used for RNA library preparation with the NEBNext Ultra library kit per the manufacturer’s instructions (three libraries per genotype). Samples were barcoded using NEBNext Set 1 Multiplex Oligos for Illumina to generate libraries for single-end 150-bp sequencing. DNA sequencing was performed at the Genomics Resource Laboratory, University of Massachusetts at Amherst, using an Illumina NextSeq500.

Differential Expression Analysis

Quality and adapter filtering were performed as part of the Illumina pipeline. Reads were mapped to the version 4 maize genome assembly Zm-B73-REFERENCE-GRAMENE-4.0 using STAR v2.5.3a (Dobin et al., 2013; Jiao et al., 2017). Mapping using STAR included default parameters for alignment and seeding, quality filtering, trimming, and removal of alignments with noncanonical splice junctions to obtain counts per gene (Dobin et al., 2013). Differential expression analysis was performed using the R package RUVseq for normalization followed by differential expression analysis with edgeR (Robinson et al., 2010; McCarthy et al., 2012; Risso et al., 2014). The RUVseq pipeline included upper quartile normalization using 7000 empirically determined control genes. These empirical control genes are the 7000 least differentially expressed genes in the data set as determined by the empirical variables (e.g., genetic background), those samples were not included in the downstream differential expression analysis, resulting in the exclusion of one STS1-HET and one STS1-HOM library.

GO Analysis

GO analysis was completed using the R package GOseq (Young et al., 2010), utilizing the maize-PANZER GO annotations from maize-QAER (Wimalanathan et al., 2018), using the default parameters. The RNA analysis included all genes from the STS1-HET and STS1-HOM RNA-seq analysis with FDR < 0.05, and the proteomics analysis included the 100 genes with the highest fold change from the STS1-HET and STS1-HOM data sets. Genes without a GO annotation were excluded during the analysis.

Confocal Microscopy

Plants were grown in the greenhouse as described above. Shortly after stamen primordium emergence (4 to 5 weeks after planting), plants were harvested and meristems were stained with 5 μM SynaptoRed membrane dye (VWR 80510-682) in DMSO. The confocal image data were gathered using an A1R: Nikon A1 Resonant Scanning Confocal Microscope.

Anther Shape Measurement and Analysis

For measuring anthers and counting floral organs, we grew plants in the greenhouse (young anthers) or field (anthers at anthesis) as described above. To measure anthers in young flowers, plants were harvested at the inflorescence meristem stage after glume development (5 to 6 weeks after planting). Developing flowers were imaged using Leica CTR5500 fluoroscence and Zeiss 710 confocal microscopes. Anthers were measured in three individuals per genotype, more than six anthers per individual. To measure anthers at anthesis, dehisced anthers were harvested from the central spike on the day that flowers first opened. Anthers with filaments attached were harvested from central spikes and scanned within 1 h after dehiscing. Individual anthers were placed on a slide (flat side down) and scanned using an Epson V700 scanner. Scanned images were separated into individual files, and images were made binary using ImageJ (Schneider et al., 2012). For the anther aspect ratio, individual anther image files were read into R, and anther length and width were measured using the R package MOMOCs (Bonhomme et al., 2014). Anther aspect ratio was calculated by dividing anther width by anther length (18 individuals per genotype, 10 anthers per individual). These aspect ratio values were log-transformed (log base 10) for normality (Shapiro-Wilk normality test, P = 0.66). Means of log-transformed aspect ratio values were compared using Student’s t test (Supplemental Table 7). For the eFourier analysis, individual anther image files were read into R, and analysis was completed using the R package MOMOCs (Bonhomme et al., 2014). The eFourier transformation was done using 12 harmonics and normalization of coefficients. Statistical analysis was completed using MANOVA.

For the organ counts, mature anthers were harvested from the central spike prior to dehiscence, and we counted lodicules and stamens in five spikelets from five individuals (50 florets total). All anther measurements are given in Supplemental Data Sets 1 and 2, and anther images are included in the data repository.

IP

For each genotype (STS1-HET, STS1-HOM, and matched sta1 mutant siblings), 5 g (40 plants) of pooled maize tassels (0.5 to 1.0 cm in length) was ground in liquid nitrogen using mortar and pestle. The resulting powder was mixed with 10 mL of an extraction buffer for proteins dynamically transported between nucleus and cytosol, in native conditions (50 mM Tris-HCl, pH7.5, 150 mM NaCl, 1% [w/v] IGEPAL-CA-630, and 1% protease inhibitor mix). Then, extract was filtered through four layers of Miracloth and centrifuged twice at 15,000g for 10 min at 4°C. Protein extract was incubated with 40 μL of GFP-trap MA bead slurry (ChromoTek), shaking for 2 h at 4°C. Beads with the bound target protein were magnetically separated and washed four times with 200 μL of ice-cold wash buffer containing 50 mM Tris, pH7.5, 150 mM NaCl, 0.1% [w/v] IGEPAL-CA-630, and 1% protease inhibitor mix. Bound proteins were eluted with 40 μL of elution buffer (0.05% [w/v] bromophenol blue, 0.1 M DTT, 10% glycerol [w/v], 2% SDS [w/v], and 0.05 M Tris-HCl, pH 6.8). Five microliters was used for immunoblotting to confirm the presence of the bait protein (STS1-YFP) by standard SDS-PAGE and detection by chemiluminescence with a monoclonal anti-GFP antibody (Mouse IgG1K, clones 7.1 and 13.1; Roche catalog no. 11814460001) at 1:1000 dilution and anti-mouse HRP-conjugated secondary antibody (Amersham ECL GE catalog no. 45,001,275) at 1:3000 dilution. Then, 35 μL was used to run a short SDS-PAGE gel, stained with GelCode Blue Safe protein stain (Thermo Fisher Scientific). Gel slices were sent for MS analysis to the University of Massachusetts Medical School MS facility. Two replicates were performed for each genotype.

Liquid Chromatography-MS/MS and Label-Free Protein Quantification

In-gel trypsin digestion was analyzed in a quadrupole-Orbitrap hybrid mass spectrometer (Thermo Sci Q-Exactive with Waters NanoAcquity UPLC). Forty individuals of each genotype (sts1 and sta1 mutants complemented with STS1-HET or STS1-HOM) were used for each IP experiment. When a high number of individuals is used, a lower number of technical replicates
in the mass spectrometer is needed to get robust results (Jorrín-Novó et al., 2015). In this experiment, the reproducibility can be observed in the high number of proteins identified in both replicates for each sample as well as in the similar abundance of each one (Supplemental Data Sets 9 and 10). For protein identification, Mascot in Proteome Discoverer 2.1.1.21 with the Uniprot Maize database was used. For label-free quantitation, Scaffold version 4.8.4 was used, with 90% minimum peptide threshold, three peptides minimum, and a peptide FDR of 0.05.

Antibody Production and Immunolocalization

Anti-STS1 antibody was developed from the full-length coding sequence of STS1 cloned into pDEST17 at the Bartlett lab, using the protocol described by Chuck et al. (2014) with some modifications. 6HIS-STS1 was expressed and purified from *Escherichia coli* Rosetta strain, using denaturing conditions. A total of 200 μg of purified protein was sent to Co-calcio Biologicals, where two guinea pig immunizations were performed. Serum was used for antibody affinity purification to the STS1 recombinant protein using magnetic beads from Invitrogen (Chuck et al., 2014). Validation of antibody was performed by immunoblotting with total protein extract from *sts1* complemented lines and *sts1* mutants as a negative control. Primary antibody was used at 1:2000 dilution and secondary anti-guinea pig HRP-coupled antibody (Thermo Fisher Scientific catalog no. A18769) at 1:3000 dilution. STS1 immunolocalizations were performed as previously described by Chuck et al. (2010) and Tsuda and Chuck (2019). Primary antibody was used at 1:200 dilution and secondary anti-guinea pig alkaline phosphatase-coupled antibody (Thermo Fisher Scientific catalog no. A18772) at 1:300 dilution.

Anti-STS1, Anti-Ubiquitin, and pSer Immunoblots

SDS-PAGE with 12% (w/v) acrylamide gel was performed with 30 μg of protein extract from *sts1* and STS1-HET and STS1-HOM complemented mutants. Then, semidy transfer, blocking, and incubation with 1:2000 affinity-purified anti-STS1 guinea pig polyclonal antibody were performed. Protein was detected using chemiluminescence with 1:3000 anti-guinea pig secondary HRP-coupled antibody (Thermo Fisher Scientific catalog no. A18769). Membrane was stripped and tubulin was detected as a loading control by incubation with 1:25,000 mouse monoclonal anti-TUB DM1A (Abcam catalog no. ab7291). Detection was done using 1:10,000 anti-mouse secondary HRP-conjugated antibody (Amerham ECL GE catalog no. 45,001,275).

For measurement of STS1 protein level, after immunoblot images were captured by scanning of x-ray films, densitometry analysis was performed using ImageJ (1.4 NIH software; Schneider et al., 2012). The detailed protocol is described by Abraham-Juárez (2019). The relative abundance of STS1 in each sample was calculated by dividing the densitometry value of STS1 protein with the respective loading control (α-Tubulin). Then, samples were normalized to STS1-HET to establish the fold change between them. Data are shown in Supplemental Table 5. Three replicates were done with similar results.

For the phosphorylation and ubiquitination assays, STS1-YFP HET and HOM IPs were performed with anti-GFP antibody as described for IP above; PhosSTOP (Roche) was added to the protein extraction buffer for the phosphorylation assay. Based on previous densitometry experiments we performed to estimate the amount of protein in the two samples, 3 μL of the STS1-HOM and 9 μL of the STS1-HET IP elutions were loaded on two different gels (one for anti-pSer and one for anti-ubiquitin blot). Blocking was performed with 2% (w/v) BSA. For the phosphorylation assay, primary anti-pSer 16B4 mouse monoclonal antibody (Santa Cruz Biotechnology catalog no. sc-8017) was used at 1:1000 dilution and the same secondary anti-mouse antibody as used before at 1:3000. For development, Clarity ECL reagents (Bio-Rad) and the Azure c-300 Chemiluminescent Immunoblot Imaging System (Azure Biosystems) were used. After development, anti-pSer and anti-ubiquitin blots were stripped, blocked, and incubated with anti-GFP antibody (Mouse IgG1K, clones 7.1 and 13.1; Roche catalog no. 11814460001) at 1:1000 dilution and the same secondary anti-mouse antibody as used before at 1:3000. All immunoblots were repeated three times.

In Situ Hybridization

*sts1* and *sts1* complemented in florescences were fixed overnight at 4°C in 4% (w/v) paraformaldehyde in 1× PBS. Fixed samples were dehydrated in an ethanol series and transferred into Histoclear, then embedded in Paraplast, sectioned, and hybridized according to Bartlett et al. (2015).

RT-qPCR

Total RNA was isolated from 1.8-cm tassels using Trizol reagent according to the manufacturer’s instructions. cDNA was synthesized using 1 μg of RNA, Oligo dt(20), and SSIII RT Reverse Transcriptase (Invitrogen) according to the manufacturer’s instructions, for three independent biological replicates. qPCR was performed for each cDNA replicate and samples were run in duplicate, using the SYBR Green PCR master mix (Thermo Fisher Scientific). Cycling was done with the following conditions: 95°C for 10 min, 40 cycles of 95°C for 15 s and 60°C for 1 min, and a final melt curve stage from 60 to 95°C, in a StepOne system (Applied Biosystems). Data were normalized using Actin as the reference gene. To get fold change values, the 2-ΔΔCT method was used.

Accession Numbers

Raw sequencing data are available at the National Center for Biotechnology Information Sequence Read Archive (Bioproject PRJNA625570). Supplemental data sets and anther images are available at dryad (https://datadryad.org/stash/dataset/doi:10.5061/dryad.4xgxd2573). Code for analyses and figure generation is available on GitHub (https://github.com/BartlettLab/B-class).

Supplemental Data

- **Supplemental Figure 1.** STS1 immunolocalizations and *in situ* hybridizations.
- **Supplemental Table 1.** Floral organ counts.
- **Supplemental Table 2.** MADS-box proteins and chromatin remodelers identified in IP-MS experiments.
- **Supplemental Table 3.** Kinases identified in IP-MS experiments.
- **Supplemental Table 4.** Kinases identified in IP-MS experiments.
- **Supplemental Table 5.** Ubiquitination machinery identified in IP-MS experiments.
- **Supplemental Table 6.** Primers for genotyping assays and RT-qPCR.
- **Supplemental Table 7.** Results of statistical tests.
- **Supplemental Data Set 1.** Anther dimensions early in floral development.
- **Supplemental Data Set 2.** Anther dimensions at anthesis.
**SUPPLEMENTAL DATA**

**Data Set 3.** Genes differentially expressed in STS1-HET vs st51 mutant siblings.

**Data Set 4.** Genes differentially expressed in STS1-HOM vs st51 mutant siblings.

**Data Set 5.** Genes differentially expressed in STS1-HET vs si1 mutant siblings.

**Data Set 6.** Genes differentially expressed in STS1-HOM vs si1 mutant siblings.

**Data Set 7.** Enriched GO-terms differentially expressed in STS1-HET vs st51 mutant siblings.

**Data Set 8.** Enriched GO-terms differentially expressed in STS1-HOM vs st51 mutant siblings.

**Data Set 9.** STS1-HET IP-MS two replicates IBAQ.

**Data Set 10.** STS1-HOM IP-MS two replicates IBAQ.

**Data Set 11.** Enriched GO-terms in proteins immuno-precipitated with STS1-HET.

**Data Set 12.** Enriched GO-terms in proteins immuno-precipitated with STS1-HOM.

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**AUTHOR CONTRIBUTIONS**

M.B., A.S.-L., M.J.A.-J., and C.W. designed the research; A.S.-L., M.J.A.-J., M.B., C.B., P.H., and J.M. conducted research and analyzed results; M.B., A.S.-L., M.J.A.-J., and C.W. designed the research; A.S.-L., M.J.A.-J., and C.W. provided helpful comments on the article. We also thank Craig Albertson, Peter Chien, Lilian Fritz-Laylin, Joshua Gendron, David Jackson, Zachary Lippman, Michelle Facette, Eric Strieuter, Beth Thompson, and three anonymous reviewers for helpful discussion and comments. This work was supported by the National Science Foundation (grants IOS-1652380 and IOS-1546837 to M.B.), the USDA National Institute of Food and Agriculture (grant NIFA-2018-67012-27998 to A.S.-L.), and the University of Massachusetts.

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