Plant Physiology Preview. Published on January 5, 2017, as DOI:10.1104/pp.16.01923

Validating Genome-Wide Association candidates through quantitative variation in nodulation

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One Sentence Summary:

GWAS combined with multiple mutagenesis technologies, including CRISPR/Cas9, were used to functionally validate novel candidate genes contributing to phenotypic variation in symbiosis between legume plants and rhizobial bacteria.

Author contributions:
S.J.C., P.T., N.D.Y., and R.M.S. designed research;
S.J.C., P.T., J.G., R.D., P.A., N.J.B., J.M., A.D.F., and D.F.V. performed research;
S.J.C, P.T., and N.D.Y. analyzed data;
S.J.C, P.T., and N.D.Y wrote the paper.

The authors declare no conflict of interest.

This work was supported by NSF award IOS-1237993.

Abstract

Genome wide association (GWA) studies offer the opportunity to identify genes that contribute to naturally occurring variation in quantitative traits. However, GWA relies exclusively on statistical association, so functional validation is necessary to make strong claims about gene function. We used a combination of gene-disruption platforms (Tnt1 retro-transposons, hairpin RNA-interference constructs, and CRISPR/Cas9 nucleases) together with randomized, well-replicated experiments to evaluate the function of genes that an earlier GWAS in *Medicago truncatula* had identified as candidates contributing to variation in the symbiosis between legumes and rhizobia. We evaluated ten candidate genes found in six clusters of strongly associated SNPs, selected on the basis of their strength of statistical association, proximity to annotated gene models, and root or nodule expression. We found statistically significant effects on nodule production for three candidate genes, each validated in two independent mutants. Annotated functions of these three genes suggest their contributions to quantitative variation in nodule production occur through processes not previously connected to nodulation, including phosphorous supply and salicylic acid-related defense response. These results demonstrate the utility of GWA combined with reverse mutagenesis technologies to discover and validate genes contributing to naturally occurring variation in quantitative traits. The results highlight the potential for GWA to complement forward genetics in identifying the genetic basis of ecologically and economically important traits.

Genome wide association (GWA) studies offer the promise of identifying genes responsible for quantitative trait variation in plants and animals (Mackay et al., 2009). Relative to forward genetic screens, GWA has the potential to identify genes of much smaller phenotypic effect. Moreover, the genes identified through GWA are expected to contribute to naturally occurring phenotypic variation. By contrast, forward genetic screens identify genes that are functionally necessary but may or may not contribute to natural variation. An important limitation of GWA analyses, however, is that the statistical approach used to identify candidate genes is also expected to identify many false positives. Therefore, functional validation of GWA candidates is essential for confirming the biological importance of the identified genes (Ioannidis et al., 2009).

The symbiosis between legume plants and rhizobial bacteria is responsible for large inputs of nitrogen into both natural and agricultural systems through symbiotic nitrogen fixation (Vance, 2001). The ecological and economic importance of this symbiosis has made identifying its genetic basis an important goal for plant biologists (Oldroyd et al., 2011). More than 30 plant genes that play central roles in the formation and growth of plant nodules, the site of rhizobial symbiosis, and nitrogen fixation have been identified (Popp and Ott, 2011; Pislariu et al., 2012). These genes were identified primarily through forward genetic screens. In standard forward genetic screens, a mutant phenotype is identified based on the effects seen within individual organisms, something that will bias these screens towards detecting genes of large effect. Forward genetic screens are likely to miss genes of small phenotypic effects, such as those that contribute to naturally occurring quantitative variation in nodulation (Stanton-Geddes et al., 2013; Friesen et al., 2014). Identification of these genes of subtle effect will provide a fuller understanding of the symbiosis between legumes and rhizobia, and may provide targets for selection in important agronomic legumes.

Here we report on the application of three reverse genetics mutagenesis tools: *M. truncatula* Tnt1 retrotransposon mutant collection (Tadege et al., 2008; Pislariu et al., 2012), hairpin RNA-interference knock-down constructs (Wesley et al., 2001), and CRISPR/Cas9 site-specific nuclease (SSN) (Baltes et al., 2014) to empirically evaluate the functional importance of ten genes that a previous sequence-based GWA study identified as candidates for naturally occurring phenotypic variation in the legume-rhizobia symbiosis (Stanton-Geddes et al., 2013). We used 17 whole-plant, stable mutants (six Tnt1, three hairpin, and eight CRIPSR mutants) in well replicated phenotypic assays to evaluate the function of each of the ten GWA candidates. The functional importance of three (*PHO2-like, PNO1- like and PEN3- like*) was validated by two independent mutations, confirming the importance of genes found in three of the six clusters investigated. These results not only identify genes not previously identified as being involved in

86 legume-rhizobia symbiosis, they also illustrate the power of combining GWA with newly-developed
87 gene-disruption technologies to identify genes that contribute to naturally occurring variation in
88 quantitative traits.
89
90
91

RESULTS

Association mapping SNF-associate candidate genes in *Medicago*

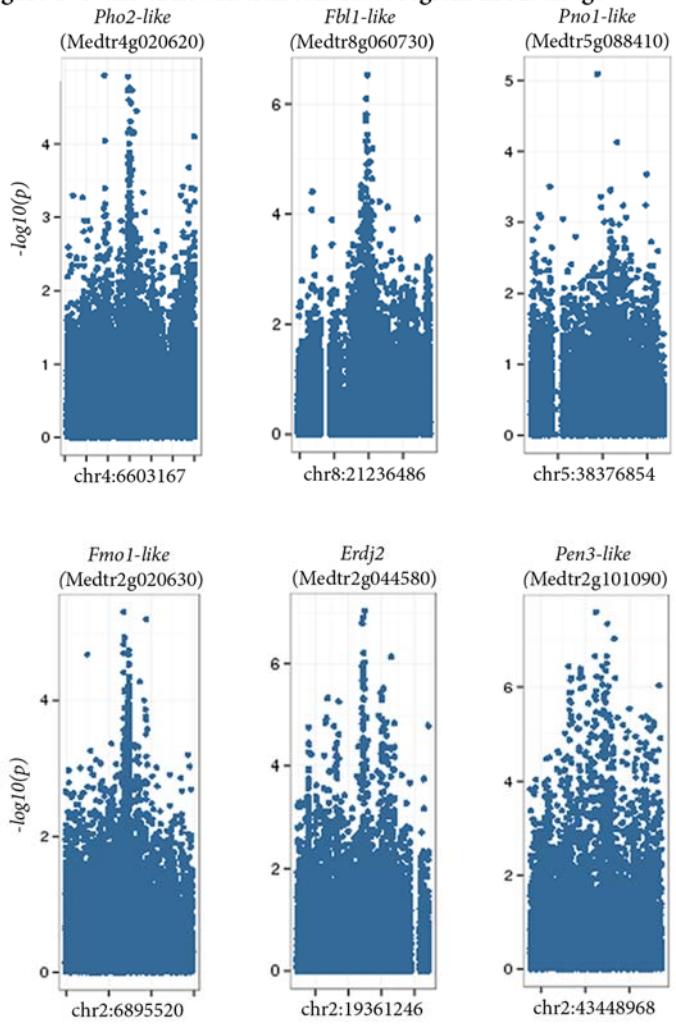
To generate a list of candidates underlying variation in nodulation, we previously carried out GWA analysis involving over 6 million SNPs on a panel of 226 *M. truncatula* accessions (Stanton-Geddes et al., 2013). In brief, nodulation data were collected on eight replicates of each accession and GWA was conducted using the GLMM implemented in TASSEL (Bradbury et al., 2007). From this GWA we selected the 100 SNPs with the strongest association to variation in the number of nodules per plants, producing an initial list of nodulation candidates. This list then was filtered based on several criteria: 1) Statistical support and ranking for an association from the GWA, 2) Candidate being in linkage-disequilibrium (LD) with other SNPs with strong statistical support (*i.e.*, located in a peak), 3) Location within or proximate to annotated coding regions, and 4) Expression in root and or nodule tissue. GWA was performed twice over the course of the research as a new assembly of the *M. truncatula* genome (Mt4.0) was released mid-experiment (Tang et al., 2014), replacing the earlier assembly (Mt3.5) (Young et al., 2011) used in the original analysis.

Based on these criteria, we selected ten candidates (noting that we did not require all candidates to meet all of the filtering criteria) to target for mutagenesis and phenotypic validation (Table 1). Six of the candidates were physically proximate to other candidates (two within 15 kb of each other and four within 80 kb of one another). These candidates were chosen to evaluate the potential to identify the causative gene when clusters of statistically associated SNPs identified by GWA spanned multiple genes (Fig. 1).

Generation of whole plant mutants

To empirically evaluate the functional importance of GWA-identified candidate genes underlying naturally occurring variation in nodulation, we generated a suite of whole-plant mutants using three mutagenesis platforms: Tnt1 retrotransposons, RNA hairpin knockdown, and CRISPR/Cas9 (SSNs) (Fig. 2a-c). We identified Tnt1 insertions in seven candidates by either querying the Noble Foundation Tnt1 database (Tadege et al., 2008) or through PCR screening of pools of Tnt1 mutant lines (Table S1). For each of the seven putative Tnt1 mutants, we used a PCR assay with gene and insertion-specific primers to identify lines that were either homozygous for the Tnt1 insertion or wild-type at the respective candidate locus; hereafter referred to as *pho2-like*$_{Tnt}$, *fbl1-like*$_{Tnt}$, *pno1-like*$_{Tnt}$, *fmo1-like*$_{Tnt}$, *rfp1-like*$_{Tnt}$, *hlz1-like*$_{Tnt}$ and *pen3-like*$_{Tnt}$ (Fig. 3a-c, Fig. S1, Fig. S9). We then used homozygous insertion and WT lines

Figure 1 GWAS of nodulation candidate regions in Medicago

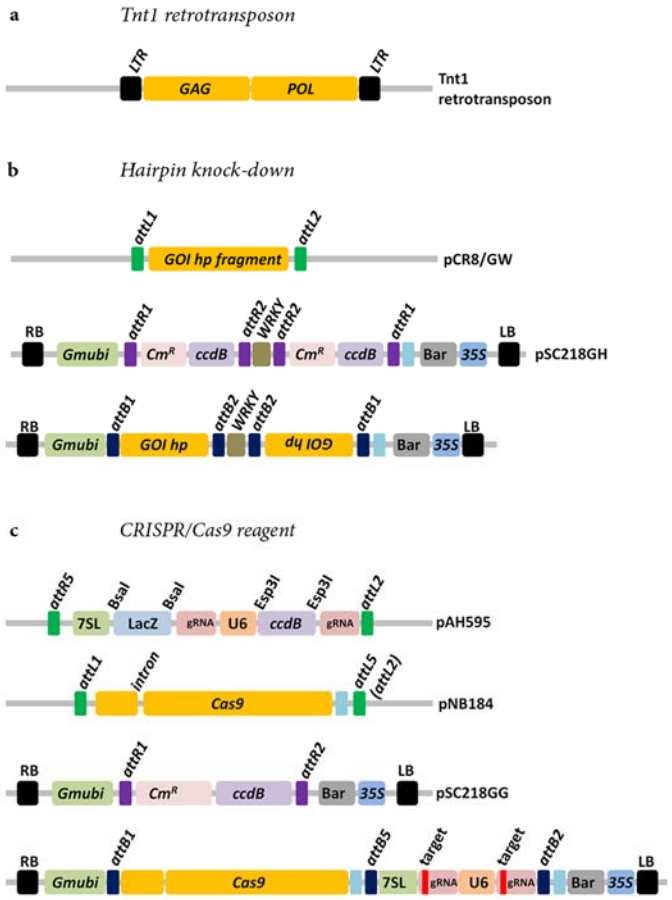


identified in this screen as parent plants to generate self-pollinated seeds for use in phenotype assays described below. Preliminary analyses revealed that the *fbl1*$_{Tnt}$ line as well as the WT line derived from the same grandparent plant were also segregating for a super-nodulating phenotype (> 100 nodules on root systems < 5 cm long), and therefore these were excluded from further analyses.

We also attempted to generate hairpin knock-downs for all ten candidates and successfully recovered multiple independently transformed whole plant mutant lines for four: *PHO2-like*, *FBL-like*, *PNO1-like*, and *ERDJ2*. Using TAIL-PCR we were able to determine the genomic location of hairpin transgene and identify homozygous hairpin lines for three of these genes, hereafter referred to as *fbl-like*$_{HP}$, *pno1-like*$_{HP}$, and *erdj2*$_{HP}$ (Fig. 3b and Fig. S2a-c). These lines were grown to produce self-pollinated seed that was used for phenotype assays.

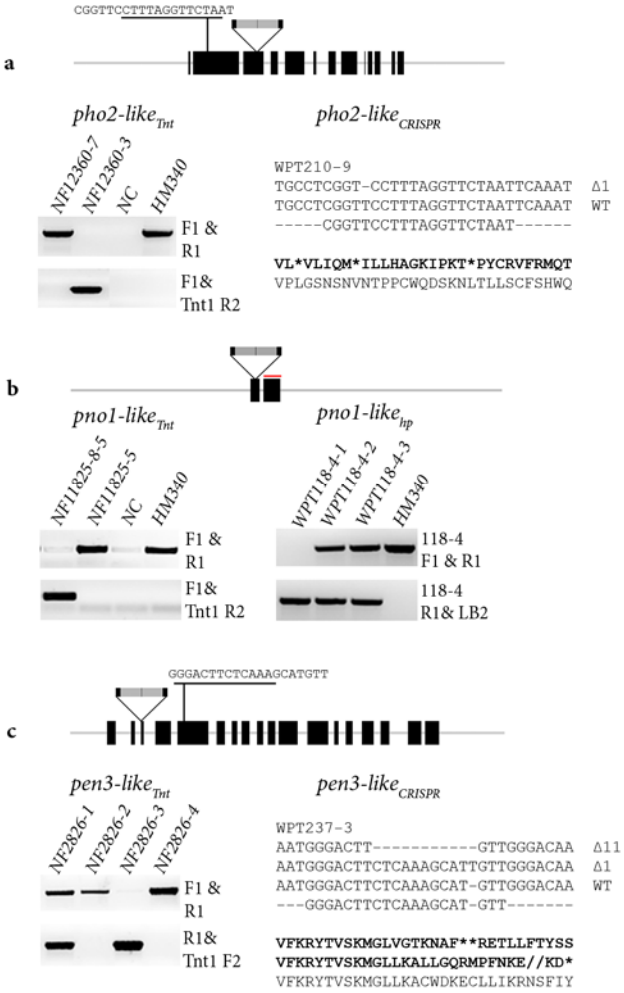
Because hairpin technologies are expected to reduce but not eliminate expression of target genes, we also targeted all ten candidates for whole-plant knock-outs using CRISPR/Cas9 and successfully generated whole-plant knock-out lines for seven candidate genes: *PHO2-like*, *FMO1-like*, *ERDJ2*, *ACRE1*,

Figure 2 Mutagenesis platforms



HLZ1-like, *MEL1* and *PEN3-like* (Fig. 3a-c and Fig. S3-S7). We recovered multiple T_0 homozygous mutant plants with mutation efficiencies ranging from 50-70% for many candidates genes including *PHO2-like,* *FMO1-like* , *ERDJ2*, and *PEN3-like* candidates, whereas germ-line mutations in *ACRE1*, *HLZ1-like*, *MEL1* mutant plants had to be confirmed in later generations (Fig. S3-S7). The CRISPR/Cas9 reagent was useful for mutating smaller sized genes (<500 bp) such as *Acre1* since the mutagenesis of these genes are typically more challenging using random mutagenesis strategies. Indeed, we could not identify a Tnt1 insertion in this gene by querying the Noble database and were also unsuccessful using the Tnt1 PCR-reverse-screen (Fig. S7a). By contrast, using the CRISPR system, we generated several *Acre1* candidate mutants and could generate mutations at the *ACRE2* paralog located 16-kbp upstream of *ACRE1* (Fig. S7b-c). For the *ERDJ2* candidate we recovered two T_0 homozygous mutant plants, one with a bi-allelic 3-bp and 85-bp frame-shift deletion and a second plant with two 6-bp mutant alleles (Fig. S4) and tested both mutants since we suspected the plant might be homozygous lethal. We hereafter referred to the

Figure 3 Screening of candidate mutant lines.



CRISPR mutant lines as *pho2-like*$_{\text{CRISPR}}$, *fmo1-like*$_{\text{CRISPR}}$, *erdj2*$_{\text{CRISPR-3/85}}$, *erdj2*$_{\text{CRISPR-6}}$, *acre1-like*$_{\text{CRISPR}}$, *hlz1-like*$_{\text{CRISPR}}$, *mel1*$_{\text{CRISPR}}$ and *pen3-like*$_{\text{CRISPR}}$. We were unable to confirm homozygous mutant plants for the remaining three candidates (*FBL1-like*, *PNO1-like* and *RFP1-like*). The apparent poor mutation rate of these three targets might be due to errors in the sequence used to construct the CRISPR reagent. However, we grew all of the stable transformants to produce self-pollinated seeds that were then used for phenotype assays.

Mutation and knockdown of gene candidates affect nodulation

We assayed nodule production in 17 mutant and paired control lines in a series of randomized and well-replicated phenotype experiments. The assays were performed with an average of 22 mutant and 22 WT plants including six candidates tested with two independent mutation events to evaluate whether results were robust to the specific mutation and genomic background.

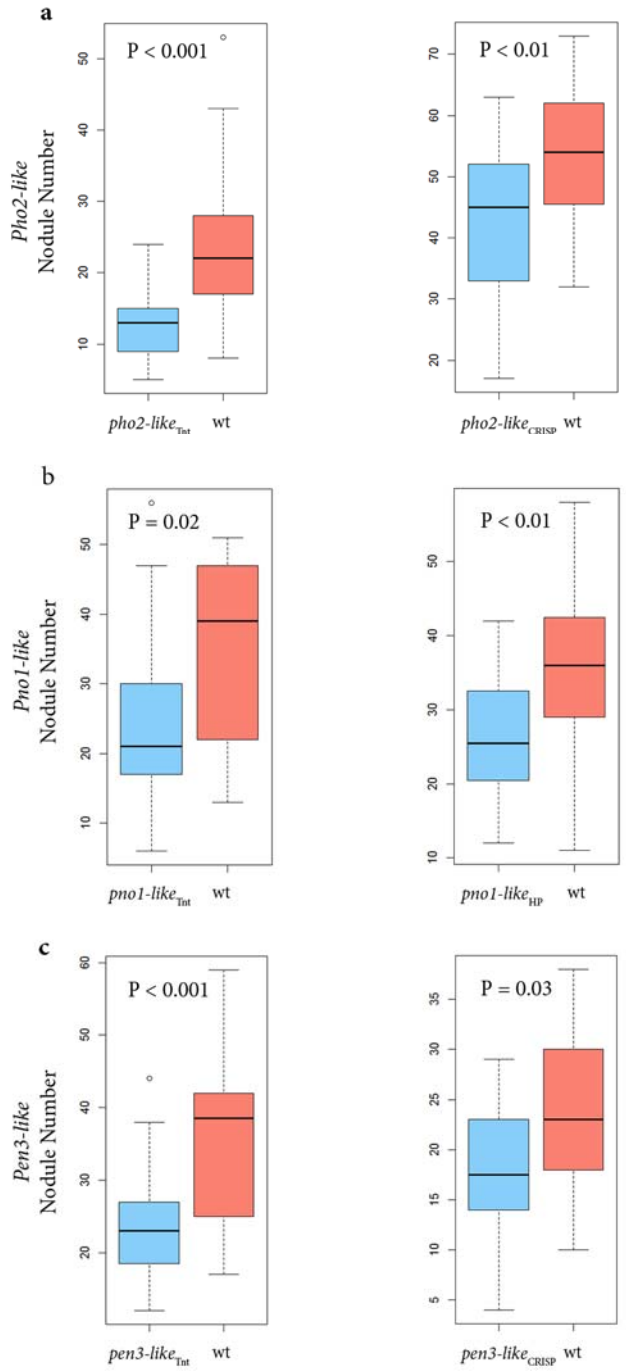
Phenotype assays revealed that lines carrying mutations in three of the candidates, *PHO2-like* (4g020620), *PNO1-like* (5g088410), and *PEN3-like* (2g101090), produced significantly fewer nodules than control plants ($P < 0.03$ for each mutant by wild-type line comparison; Fig. 4a-c and Table S2). In each of these cases, the phenotypic effects were validated by two independent mutations (Fig. 3). The *PHO2-like* mutants were generated by the insertion of a Tnt1 element (*pho2-like*$_{Tnt}$) in one plant and a CRISPR/Cas9 generated mutant harboring a homozygous 1-bp frame-shift mutation (*pho2-like*$_{\text{CRISPR}}$) in the other. *PNO1-like* mutant plants were generated by insertion of a Tnt1 element (*pno1-like*$_{Tnt}$) and a plant homozygous for a hairpin transgene targeting the *PNO1-like* transcript (*pno1-like*$_{HP}$). Similarly, two *PEN3-like* mutants were identified by Tnt1 insertion (*pen3-like*$_{Tnt}$) and a CRISPR/Cas9 induced 11-bp and 1-bp bi-allelic frame-shift mutation in each allele (*pen3-like*$_{\text{CRISPR}}$) (Fig. 3a-c).

Surprisingly, two Tnt1 insertion lines (*fmo1-like*$_{Tnt}$ and *hlz1-like*$_{Tnt}$) produced significantly more nodules than control lines (Table S2). However, second mutations in these candidates, both generated using CRISPR/Cas9, exhibited results inconsistent with the Tnt1 mutants ($P_{\text{mut\_wt x assay}} < 0.05$). Indeed, the number of nodules formed by lines carrying CRISPR mutations in these genes did not differ from controls. Potentially, the greater nodule number in the Tnt1 lines may have been due to Tnt1 insertions in non-target genes (two of the control Tnt1 plants when assaying the *hlz1-like*$_{Tnt}$ had no nodules and five others had ≤ 10 nodules – many fewer than expected). Consequently, we decided to focus on the three candidates with mutants showing reproducibly reduced nodule numbers compared than controls (*PHO2-like*, *PNO1-like*, and *PEN3-like*) for further analysis.

Nitrogen content and nodule morphology of validated candidate lines

Although plants with mutations in the three validated candidate genes (*PHO2-like*, *PNO1-like*, *PEN3-like*) produced significantly fewer nodules, N concentration and nodule morphology were not affected. Foliar nitrogen concentrations did not differ significantly between any of the mutants and their control (t-tests, all $p_{df=4} > 0.1$, Supplemental Table S2). Moreover, longitudinal sections of nodules from all validated mutant lines indicated they were structurally sound, with distinct meristematic, infection, and pink nitrogen fixation zones (Supplemental Figs. S10, S11). Both *pho2-like*$_{tnt1}$ mutants and their corresponding WT controls had lighter pink nodules overall, however *pho2-like*$_{CRISPR}$ nodules exhibited similar color intensity compared with the HM340 control (Fig. S11). This suggests that differences in the pink color of *Pho2-like*$_{tnt1}$ is probably due to the Tnt1 background rather than disruption of the *PHO2-like* gene itself.

Figure 4 Distribution of nodule number produced by mutant and wild



193 **Effects of forward genetic mutants**

194 To better understand the quantitative nature of nodulation mutants, we compared effects of the
195 validated GWA mutants to nodulation mutants in genes originally discovered through forward genetics.
196 Considering only "confirmed" candidates from our GWA study (*PHO2-like*, *PNO1-like*, *PEN3-like*), GWA
197 mutants produced ~ 60% of the number of nodules on wild-type plants. These results were then

compared to phenotype assays on two well-known and previously characterized nodulation mutant lines: the calcium and calmodulin-dependent kinase *dmi3* (Catoira et al., 2000) and *ipd3-2*, which encodes for a protein that interacts with DMI3 (Messinese et al., 2007). Under exactly the same experimental conditions used to test the GWA mutant lines, these forward genetics mutants exhibited drastic reductions in nodule number – an average of just 0.5 nodules on *dmi3* lines and 1.5 nodules on *ipd3* lines compared with 39 on WT plants ($P < 0.0005$, Fig. S8).

DISCUSSION

Genome wide association analyses provide an opportunity for identifying functionally important genes that contribute to naturally occurring variation in quantitative traits, genes that are unlikely to be detected by forward genetic screens. However, the approach is challenged by several statistical issues including an expected high number of statistical false positives due to the large number of statistical tests and the difficulty of fully eliminating confounding effects of relatedness among assayed individuals. This means that GWA is best viewed as a statistical approach for identifying genomic regions that are likely to contribute to variation. Moving beyond such a candidate status requires empirical validation of gene function (Ioannidis et al., 2009). In this work, we applied a suite of mutagenesis platforms, retrotransposon insertions, hairpin knock-down RNAi constructs, and CRISPR/Cas9, to disrupt the function of ten genes that GWA had identified as candidates in contributing to variation in the legume-rhizobia symbiosis through nodulation (Stanton-Geddes et al., 2013). Our evaluation experiments revealed that mutations in three of the ten candidate lines produced significantly fewer nodules than wild-type plants, thereby identifying new genes contributing to quantitative variation in nodule production.

Three out of ten candidate genes were empirically validated in this study. However, there was more than one candidate gene for some genomic intervals. Therefore, the validation rate is better represented as three validated genes among the six intervals evaluated. These findings demonstrate that GWA coupled with well-replicated validation experiments is an effective means to identify genes contributing to quantitative variation. The high rate of success in validating the functional importance of GWA candidates is likely due to at least two reasons. First, in creating an initial list of candidates for functional evaluation, we did not limit our efforts to only those variants with the strongest statistical support from the GWA. Rather, we considered the 100 SNPs with the strongest statistical associations with phenotypic variation as potential candidates and then applied genetically informed criteria for identifying which candidates to pursue for validation. These criteria included SNPs in or near annotated genes, genes expressed in roots or nodules, and SNPs that formed clusters of statistical associations, (peaks in the Manhattan plots) (Fig. 1).

Despite the criterion that chosen SNPs either were in or near a coding region, only four of the GWA variants that we pursued were actually in annotated coding regions, with the remainder anywhere from 168 to 5819 bp from annotated CDS. Our data do not allow us to determine whether the SNPs near, but not in, coding regions cause functionally important variation in gene expression as opposed to linkage-disequilibrium (LD) with un-assayed SNPs in coding regions. Nevertheless, non-coding SNPs are often

associated with phenotypic variation (Hindorff et al., 2009) through effects on gene expression (Cookson et al., 2009; Cubillos et al., 2012). We also prioritized candidates that showed expression in root or nodule tissue, although such a criterion might have biased against lowly expressed genes (like many transcription factors) or gene products expressed elsewhere in the plant affecting nodulation (Krusell et al., 2002). The third criterion we applied, that candidates be physically proximate to other SNPs showing strong associations, is likely to favor alleles that are maintained in contemporary populations through balancing selection where the optimal trait value varies among populations or that have recently increased in frequency (Barton and Turelli, 1989; Yeaman and Whitlock, 2011).

Also central to our evaluation experiments was the use of well-replicated experiments when evaluating phenotypic effects. Each of the phenotypic assays we conducted involved an average of 22 mutant and 22 WT (minimum of 7 mutant and 6 wild-type) individuals. This was important because the distributions of mutant and WT phenotypes often showed considerable overlap (Fig. 4a-c). The importance of replication also helps to explain why the genes we identified had not been detected in earlier forward-genetic screens conducted on nodulation in *M. truncatula* (Catoira et al., 2000; Oldroyd and Long, 2003; Schnabel et al., 2005; Pislariu et al., 2012; Domonkos et al., 2013). If the mutations we evaluated had been tested in only a single individual, the mutant phenotype would likely have fallen into the range of phenotypes exhibited by WT plants generally and thus would not have been picked up in a standard genetic screen. The phenotypic effects of genes identified through forward genetic screens relative to those we validated here is highlighted by the comparison of *dmi3* and *ipd3* to the three GWA-selected candidates: *dmi3* and *ipd3* plants produced an average of approximately 2% of the number of nodules produced on WT plants whereas the validated genes first identified as candidates through GWA produced roughly 60% of the number of nodules compared with WT plants.

Genetics of nodulation

Although we identified candidates without prior knowledge of their function, the molecular functions of homologs for the validated candidates are known and all are interesting in the context of nodulation. One of the validated candidates, *PHO-like* (Medtr4g020620), suggests a potentially important role for phosphorous in quantitative variation in nodulation. *PHO2-like* is annotated as encoding an E2 ubiquitin conjugating enzyme and its *Arabidopsis thaliana* ortholog (35% AA identity, E value = 4e-104) is involved in phosphorous accumulation (Park et al., 2014). Not only can phosphorous availability affect nodulation and N_2 fixation (Graham and Rosas, 1979; Jakobsen, 1985; Graham, 1992, Sulleman 2013) but in *A. thaliana*, *AtPHO2* ortholog interacts directly with the E3 product of Nitrogen

Limitation Adaption (*Nla*), which mediates plant responses to N limitation (Park et al., 2014). Moreover, E2 ubiquitin conjugate enzymes are presumed to interact with multiple E3 partners that could lead to the proteolytic degradation of a larger range of uncharacterized substrates (Smalle and Vierstra, 2004). *Medicago PHO2-like* is expressed at modest levels throughout nodule development (and also in uninoculated roots), but reaches a distinct peak in expression at 20 dpi (Fig. S12). This is a timepoint when nodules are fully differentiated, actively fixing nitrogen, and still prior to the initiation of senescence.

A second interesting validated gene is the annotated ABC transporter (*PEN3-like*) (Medtr2g101090). ABC transporters are involved in a wide range of plant activities, including pathogen metabolite detoxification, non-host pathogen resistance, stomatal function, and Ca^{2+} sensing associated plant immunity (Rea, 2007; Campe et al., 2016). The *A. thaliana* gene with greatest similarity to Medtr2g101090 is *PEN3* (66% identical AA sequence across 97% of the gene length. E-value = 0), which has been shown to be an essential component of salicylic acid-related defense against biotrophic fungi (Stein et al., 2006; Johansson et al., 2014). The formation of nodules requires direct interaction with bacteria and there is growing evidence that defense responses can negatively affect nodule formation (Ramu et al., 2002; Lopez-Gomez et al., 2012; Larrainzar et al., 2015). Interestingly, ABC transporters have been shown to be significantly and highly up-regulated in several nodulation mutants relative to wild-type controls (Lang and Long, 2015). *PEN3-like* is strongly expressed in *Medicago* nodules throughout development, though even more highly expressed in roots, with a slight peak in nodule expression at 14 dpi (Fig. S12).

The final validated candidate is annotated as encoding an RNA-binding *PNO1-like* protein (Medtr5g088410). How this protein might affect nodulation is not clear, although recent work has identified roles for members of this gene family in the regulation of miRNAs (Karlsson et al., 2015), suggesting that Medtr5g088410 could affect the expression of genes involved in nodulation. It is expressed at a comparatively low level in both nodules and roots with no distinct peak in time of expression (Fig. S12).

Mutation platforms for GWA validation

Efficient means to validate the functional importance of GWA candidate genes are necessary for GWAS to be effective in discovering genes of subtle effects, fulfilling the promise of linking molecular genetics with quantitative trait variation. Here we applied multiple genomic technologies

(retrotransposon mutagenesis, hairpins, and CRISPR/Cas9) to make this link. Each of these technologies has advantages and disadvantages when being applied as a reverse genetics tool. The *M. truncatula* Tnt1 collection has the advantage of ease: the Noble Foundation in Ardmore, OK has over 21,000 mutant lines that have largely saturated the genome with random Tnt1 insertion events and the collection is easily searchable online. Although easy to use for validation experiments, there is the problem of background mutations (*e.g.,* Fig. S9). On average, there are 25 insertions in each Tnt1 lines and as many as 97 independent Tnt1 loci have been reported (Veerappan et al., 2016). These background mutations can make phenotyping data potentially unreliable, complicating their use as the sole validation tool in reverse genetics phenotyping experiments. In our experiments, one Tnt1 line expressed an (unexpected) super-nodulation phenotype, while two Tnt1 lines produced more nodules than control plants, though neither of these phenotypes could be validated with a second (non-Tnt1) mutation.

Both hairpin and CRISPR require more effort to create, involving construction of vectors, infecting plants with *Agrobacterium*, and regeneration of whole plants from callus. Despite these challenges, we had a high rate of success in creating stable whole-plant transformants using both hairpin and CRISPR/Cas9 at high efficiency and frequency. For example, CRISPR/Cas9 targeting the *PHO2-like* and *PEN3-like* genes induced homozygous mutations in multiple independent T_0 plants (Fig S3- S7).

Hairpin technologies seem promising in two situations: when genes of interest are members of multi-gene families where gene redundancy might mask phenotype effects and for genes that are gametophytic or homozygous lethal. This is illustrated by the *ERDJ2* candidate in our mutant screening. We identified a CRISPR/Cas9 *ERDJ2* mutant with an in-frame 3-bp and a frame-shift 85-bp mutant alleles and confirmed that the gene is homozygous lethal by segregation analysis. PCR analysis of approximately 30 $erdj2_{CRISPR\_3/85}$ mutants failed to identify plants with both frame-shift 85-bp mutant alleles, suggesting that the combination of frame shift mutations results in a homozygous lethal phenotype (Fig. S4). Nevertheless, we successfully created a hairpin mutant that decreased transcript expression without the lethality of a knock-out to use in candidate validation. For some genes, however, "knocking down" rather than "knocking out" expression could also limit the phenotypic effects of the mutations.

CRIPSR technologies have advanced rapidly in recent years and hold promise for altering gene sequence and expression in many systems including plants (Baltes and Voytas, 2015; Luo et al., 2016). Although producing stable germ-line whole-plant mutants has proven challenging in some species, including *A. thaliana* (Fauser et al., 2014; Feng et al., 2014), we were able to produce stable mutant lines

with high efficiency. The mechanism behind this success rate is not clear, although we suspect that the transformation method might be a factor. *Medicago* transformation generates callus tissue that undergoes strong herbicide selection in contrast to floral dip transformation that requires infection of individual embryos. Moreover, we were often able to remove the CRISPR transgene from the mutant lines by genetic segregation to obtain non-transgenic mutant plants that can be used for future complementation studies. Given the rapid development of CRISPR multi-plex platforms, it should soon be feasible to mutate and test large numbers of GWA identified candidates. Doing so would allow researchers to move beyond validating small numbers of candidates and allow robust empirical evaluation of the genes that control variation underlying complex quantitative traits.

MATERIALS AND METHODS

Insertional mutant screening and genotyping

To identify mutants in the 10 candidates selected for validation, we first searched for Tnt1 insertional mutants using the Noble Foundation's *M. truncatula* Mutant Database (http://medicago-mutant.noble.org/mutant/blast/blast.php) (Tadege et al., 2008; Pislariu et al., 2012). Searches of this database, which is comprised of more than 21,000 mutants, identified insertions in five of seven candidates with the remaining two candidates identified by a PCR reverse-screen performed at the Noble Foundation (Table S1). Seeds for Tnt1 mutant lines were obtained from the *M. truncatula* Tnt1 collection, planted, and genotyped for homozygous and wild-type (null) insertion alleles at the locus of interest. Mutant plants for *Erdj2*, *Acre1* and *Mel1* candidates could not be identified either from the Tnt1 database or from the PCR-reverse screen and we therefore relied upon the CRISPR/Cas9 platform to generate these mutants.

Hairpin and CRISPR/Cas9 transgenes and whole plant transformation

We attempted to create hairpin constructs to reduce gene expression in all 10 candidates and successfully identified homozygous hairpin transgenic plant lines for three: *FBL1-like*, *PNO1-like*, and *ERDJ2*. To create hairpins, targeted coding sequences were amplified by PCR using primer sequences (Table S3) from cDNA derived from *M. truncatula* accession R108. These amplicons were cloned into the pCR8/GW/TOPO entry vector (Life Technologies, CA) and incorporated into the hairpin destination vectors pSC218GH (see below) by a Gateway™ LR clonase reaction.

Finally, we generated CRISPR/Cas9 SSN to introduce frame-shift mutations in all 10 candidates and recovered homozygous mutants for seven. Target sequences were identified by BLAST searches of the *Medicago* R108 (HM340) genome assembly (www.medicagohapmap.org/downloads/r108) using the Mt 4.0 reference sequence as a query. Resulting sequences were then used to query the sgRNA designer v.1 for selection of target guide RNAs (www.broadinstitute.org/rnai/public/analysis-tools/sgrna-design-v1) (Doench et al., 2014). The targets were created by a primer annealing assay and cloned into the *Esp3*I and *Bsa*I sites of the U6/At7SL guide RNA entry vector (pAH595) (Table S3). The completed guide RNA entry vector sequence was confirmed and combined with a second entry vector that harbored the *Arabidopsis* optimized Cas9 cassette (pNJB184) by a multi-site Gateway LR clonase reaction into the pSC218GG destination vector (see below) for *Agrobacterium* transformation (Li et al., 2013; Baltes et al., 2014). A detailed protocol can be found in the Supplemental Methods.

Whole plant transformation of R108 plants, the same genetic background used in the *M. truncatula* Tnt1 collection, with hpRNA and CRISPR/Cas9 constructs was carried out using a slightly modified version of an established protocol (Cosson et al., 2006). In brief, transformation was carried out by inoculating leaf tissue explants with *A. tumefaciens* strain EAH105 transformed with either a hairpin or CRISPR SSN. The transformations were conducted using a modified version of the binary vector backbone pNB96 (pSC218) (Curtin et al., 2011) with an introduced inverted-repeat cassette to facilitate cloning of hairpin RNA fragments (pSC218GH) and a reading-frame cassette to incorporate both the Cas9 and target guide RNA entry vectors (pSC218GG). The inverted-repeat and reading-frame cassettes were derived from previously reported pTDT-DC-RNAi and pTDTO vectors (Valdes-Lopez et al., 2008) and were driven by the constitutively expressed *Glycine max* Ubiquitin promoter (Hernandez-Garcia et al., 2010).

After co-cultivating the leaf tissue with *Agrobacterium* for three days, explants were washed in an antibiotic liquid media and transferred to a media for callus induction with bi-weekly transfers. After approximately six weeks, callus tissue was transferred to a shoot induction media and incubated in 16:8 light:dark hour photoperiod. Developing shoots were transferred to a rooting media to encourage root development before planting to soil. Both binary vectors pSC218GH and pSC218GG contain the 35S::BAR cassette for phosphinothricin herbicide selection of transgenic plants. T_0 plants were rapidly screened using a previously reported DNA extraction method and PCR-CAPS assay to identify target mutations (Curtin et al., 2011).

Nodulation assays

To evaluate the effects of candidate gene mutations on nodulation we grew mutant and wild-type plants in well-replicated (an average of 22 mutant and 22 wild type plants per assay, see Table S2 for details) in completely-randomized experiments. Prior to planting, seeds were treated in concentrated sulfuric acid for 5 min, washed with sterile dH_2O, and then kept in the dark on wet filter paper at 4°C for 7–10 days before planting into 650 ml conetainers with 4:1 parts autoclaved sand:perlite mixture. Five days after planting, seedlings were inoculation with a 30mL suspension (OD600 ~0.015) of *S. meliloti* strain Sm2011 carrying the *hemA*::LacZ reporter (Ardourel et al., 1994). Plants were grown at 22-25°C, 75 % humidity and 200-350 $\mu molm^{-2}s^{-1}$ 16h-8 h photoperiod, fertilized 15 and 21 days post inoculation with Fähreus nutrient solution, and otherwise watered as needed. Thirty-five to 41 days after inoculation, plants were harvested and nodule number was determined. Each mutant was compared against a separate set of WT control plants. To reduce the effects of background insertions, controls for the Tnt1 mutants were grown from seeds from a full-sib of the mutant plants. R108 seeds were used for the control treatment for hairpin and CRISPR lines. For each assay experiment, we tested for statistically significant differences between the phenotype of the mutant line and the phenotype of the wild-type control line using a t-test using R (R Development Core Team, 2013). For the six candidates (*PHO2-like*, *PNO1-like*, *FMO1-like*, *ERDJ2*, *HLZ1-like* and *PEN3-like*) where we evaluated two independent mutation lines, we also used ANOVA to test for between-line differences in nodulation. Similarly, for the two mutant lines ($pho2_{CRIPSR}$, $mel1_{CRISPR}$) for which the phenotypic assays were repeated, we used ANOVA to test for differences between mutant and wild-type lines between assays. All data are available at datadryad.org (dx.doi.org xxxxxxxx).

Nodule morphology and nitrogen content

To complement phenotypic data collected during initial validation experiments, we also grew the three mutants exhibiting validated nodulation phenotypes (*PHO2-like*, *PNO1-like*, and *PEN3-like*) to test for differences in foliar N concentration and to examine nodule morphology. These plants were grown under the same conditions as those for initial phenotype assays. At 14 dpi, three plants per treatment were harvested in order to make visual observations of nodules. Plants were washed to remove surrounding substrate and 10 cm of roots with nodules were isolated to obtain close up pictures of nodules (Figure S10). One nodule (second or third from the top) was then harvested from each plant, sliced in half longitudinally by hand, and then observed under a stereo microscope (Figure S11). At 28 dpi, four plants grown in parallel were harvested for N concentration assays, which were conducted by the University of Minnesota Research Analytical Lab using the Dumais method (Matejovic, 1995).

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434 **Table 1.** Genome Location, GWAS statistics, and Expression of Candidate Genes

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Mt4.0 Designation	Candidate Gene	Rank	P-value	GWAS	Expression	Confirmed
Medtr2g020630	Flavin-containing Monooxygenase-like (FMO1-LIKE)	41	8.14E-06	Mt3.5	Root & nodule specific	
Medtr2g044570	Ring finger protein1-like (RFP1-like)	8	1.62E-07	Mt3.5	All tissues	
Medtr2g044580	Endoplasmic reticulum DNAJ protein (ERDJ2)	5	1.30E-07	Mt3.5	Nodule upregulated	
Medtr2g101040	Malic enzyme-like1 (MEL1)	15	2.22E-07	Mt4.0	All tissues	
Medtr2g101090	Penetration3-like (PEN3-like)	1	2.56E-08	Mt4.0	Root & nodule upregulated	YES
Medtr2g101120	AVR9/CF-9 rapidly elicited protein 1 (ACRE1)	23	3.55E-07	Mt4.0	All tissues	
Medtr2g101190	Homeodomain leucine zipper1-like (HLZ1-like)	72	9.65E-07	Mt4.0	All tissues	
Medtr4g020620	Ubiquitin conjugate24 like (PHO2-like)	12	5.58E-06	Mt3.5	Nodule upregulated	YES
Medtr5g088410	Partner of NOB1-like (PNO1-like)	36	7.08E-06	Mt3.5	Root & nodule specific	YES
Medtr8g060730	F-box like 1 (FBL1-like)	2	4.26E-08	Mt3.5	Below detection limit	

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439 **FIGURE LEGENDS**

440 **Figure 1. GWAS of nodulation candidate regions in *Medicago***. From left to right, Manhattan
441 plots extending 300,000 bp either side of the candidate SNP for each of the six candidate gene
442 regions.

443 **Figure 2. Mutagenesis platforms. a.** Tnt1 retrotransposon insertional mutagenesis in *Medicago*
444 was developed in the R108 (HM340) accession. The original transformant harbored five Tnt1
445 copies. The Tnt1 element can transpose by a copy and paste mechanism during callus
446 regeneration leading to progeny lines with random stable insertions. **b.** Schematic
447 representations of the hairpin entry and destination vectors. Typically, a 300-500 bp amplicon
448 from the candidate gene of interest is amplified from *Medicago* whole-plant cDNA template
449 and cloned into the pCR8/GW entry vector. The entry vector is then used to clone the hairpin
450 fragment into the pSC218GH binary vector, followed by *Agrobacterium* transformation. **c.** The
451 construction of the CRISPR/Cas9 reagent requires a multi-site Gateway cloning reaction utilizing
452 two entry vectors and a destination binary vector. The CRIPSR targets are cloned into pAH595,
453 and along with the Cas9 entry vector (pNB184) are cloned into pSC218GG vector, followed by
454 *Agrobacterium* transformation. A detail protocol of the CRISPR/Cas9 assembly is provided in the
455 Supplemental Methods.
456

457 **Figure 3. Screening and identification of candidate mutant alleles. a**. Two independent *PHO2-*
458 *like* mutant alleles, *pho2-like*$_{Tnt}$ and *pho2-like*$_{CRISPR}$. Seeds from the Tnt1 line NF12360 were
459 screened by PCR assay to determine homozygous and null insertions at the *PHO2-like* locus,
460 identifying null insertion NF12360-8 plant and homozygous mutant NF12360-7 (Supplemental
461 Figure S9). A second mutant allele for *PHO2-like* was identified using plants transfromed with a
462 CRISPR/Cas9 reagent that targeted the open-reading frame of *PHO2-like*. Several homozygous
463 T_0 mutant plants were identified and the WPT210-9 plant was selected for downstream
464 phenotype analyses. WPT210-9 had a 1-bp deletion in the coding region of both alleles,
465 effectively disrupting the reading frame as indicated by the three stop codons depicted in the
466 amino acid sequence. Heritable transmission of the 1-bp mutation was confirmed by screening
467 T1 plants by a PCR-digestion assay and sequencing. **b**. Two independent *PNO1-like* mutant
468 alleles, *pno1-like*$_{Tnt}$ and *pno1-like*$_{HP}$.Tnt1 mutant alleles were identified for *PNO1-like* by
469 screening seed from the NF11825 line. *Pno1-like* mutant and null insertion lines were identified,
470 NF11825-8 and NF11825-5 respectively. Since an insufficent number of seed was recovered
471 from the NF11825-8 plant for phenotype analysis, seed from the next generation (NF11825-8-5)
472 was used as wild-type plant. For the second mutant allele, a hairpin line was identified. TAIL

PCR was used to identify the genomic location of the transgene and a PCR assay using both the genome location and transgene specific primers were used to identify a plant homozygous for the hairpin transgene (WPT118-4-1). **c,** Two independent *PEN3-like* mutant alleles, *pen3-like*$_{Tnt}$ and *pen3-like*$_{CRISPR}$. Seed from the NF2826 Tnt1 line were used to identify homozygous (NF2826-4) and null (NF2826-2) insertion mutant plants using both *PEN3-like* and Tnt1 specific primers. For the second mutant allele, we identified several CRISPR/Cas9 homozygous T_0 mutant plants such as WPT237-3 which had a segreagting a bi-allelic mutation consisting of a 11bp deletion and a 1bp insertion. Screening of WPT237-3 T1 mutant plants confirmed heritable transmission of both mutations.

Figure 4. Nodule number produced by mutant and wild type plants. Nodules were counted 32-42 days post inoculation. Data are shown for two independent mutants for each of three candidate genes. a, *PHO2-like*, b, *PNO1-like*, and c, *PEN3-like*. For each figure, the horizontal black bar represents the median value, the box the middle quartiles, and the whiskers the range of data, except for outliers shown as a single data point.

Supplemental Data

The following supplemental materials are available.

Supplemental Figure S1. The characterization of three Tnt1 mutant lines
Supplemental Figure S2. The characterization of two whole-plant hairpin lines
Supplemental Figure S3. The characterization of the Pho2-like CRISPR/Cas9 mutants
Supplemental Figure S4. The characterization of the Erdj2 CRISPR/Cas9 mutants
Supplemental Figure S5. The characterization of the Acre-1 CRISPR/Cas9 mutants
Supplemental Figure S6. The characterization of the Pen3-like CRISPR/Cas9 mutants
Supplemental Figure S7. The characterization of the Fmo1-like, Hlz-1 and Mel1-like CRISPR/Cas9 mutants
Supplemental Figure S8. Nodulation phenotype of dmi3 and ipd3-2
Supplemental Figure S9. The Tnt1 insertion background of the NF12360 Tnt1 mutant line
Supplemental Figure S10. WT and Pho2-like, Pen3-like, and Pno1-like mutant nodules at 14 dpi
Supplemental Figure S11. WT and Pho2-like, Pen3-like, and Pno1-like mutant dissected nodules at 14 dpi
Supplemental Figure S12. The expression analysis of validated genes, derived from the Medicago truncatula Gene Expression Atlas ((http://mtgea.noble.org/v3/index.php)

Supplemental Table S1. List of Tnt1 mutant lines obtained from Noble Foundation Tnt1 mutant database
Supplemental Table S2. Statistical tests comparing phenotype between mutant and wild-type control plants
Supplemental Table S3. Primer sequences for PCR assays and vector construction (SEPARATE EXCEL FILE)

Supplemental Methods 1. CRISPR reagent design and construction

ACKNOWLEDGMENTS

We thank Catalina Pislariu, Jianqi Wen, Sarah Hoerth for assistance with mutant characterization, Nathan Henning for plant care assistance, Aaron Hummel for the pAH595 vector, Ryan Morrow for technical assistance with plant transformation and media preparation and Jean-Michel Ané for *dmi3* and *ipd3* mutant seeds.

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