Genomic Insights into the Evolution of the Nicotine Biosynthesis Pathway in Tobacco\textsuperscript{1}[CC-BY]

Masataka Kajikawa\textsuperscript{2,3}, Nicolas Sierro\textsuperscript{2}, Haruhiko Kawaguchi, Nicolas Bakaher, Nikolai V. Ivanov, Takashi Hashimoto, and Tsubasa Shoji*  
Graduate School of Biological Sciences, Nara Institute of Science and Technology, Ikoma, Nara 630-0101, Japan (M.K., H.K., T.H., T.S.); and Philip Morris International R&D, Philip Morris Products S.A., 2000 Neuchâtel, Switzerland (N.S., N.B., N.V.I.)  
ORCID IDs: 0000-0003-0361-2769 (M.K.); 0000-0003-2793-5896 (N.S.); 0000-0002-8398-5479 (T.H.); 0000-0002-6917-3773 (T.S.).

In tobacco (\textit{Nicotiana tabacum}), nicotine is the predominant alkaloid. It is produced in the roots and accumulated mainly in the leaves. Jasmonates play a central signaling role in damage-induced nicotine formation. The genome sequence of tobacco provides us an almost complete inventory of structural and regulatory genes involved in nicotine pathway. Phylogenetic and expression analyses revealed a series of structural genes of the nicotine pathway, forming a regulon, under the control of jasmonate-responsive ETHYLENE RESPONSE FACTOR (ERF) transcription factors. The duplication of NAD and polyamine metabolic pathways and the subsequent recruitment of duplicated primary metabolic genes into the nicotine biosynthesis regulon were suggested to be the drivers for pyridine and pyrrolidine ring formation steps early in the pathway. Transcriptional regulation by ERF and cooperatively acting MYC2 transcription factors are corroborated by the frequent occurrence of cognate cis-regulatory elements of the factors in the promoter regions of the downstream structural genes. The allotetraploid tobacco has homologous clusters of ERF genes on different chromosomes, which are possibly derived from two ancestral diploids and include either nicotine-controlling \textit{ERF189} or \textit{ERF199}. A large chromosomal deletion was found within one allele of the nicotine-controlling \textit{NICOTINE2} locus, which is part of one of the ERF gene clusters, and which has been used to breed tobacco cultivars with a low-nicotine content.

In plants, a large number of structurally diverse specialized metabolites are produced through long, multistep, and often branched pathways (Arimura and Maffei, 2017). The proper functioning of such pathways, allowing massive metabolic flows leading to complex products from simple precursors, largely relies on the concerted expression of a large set of metabolic and transport genes, or structural genes, in different developmental and environmental contexts. The transcription factors regulating these pathways play a critical role in such coordination, which often occurs at the transcription level. The regulatory transcription factors and downstream structural genes, which form regulatory networks of multiple genes, or regulons, have begun to be explored intensively through molecular and genomics studies (De Geyter et al., 2012; Patra et al., 2013).

\textit{Nicotiana tabacum}, hereafter called tobacco, is cultivated as an economically important crop around the globe (Davis and Nielsen, 1999). The main cultivated species, tobacco, is a natural allotetraploid possibly derived through the hybridization between two ancestral diploids that are closely related to current \textit{N. sylvestris} and \textit{N. tomentosiformis} (Murad et al., 2002; Sierro et al., 2013; Wang and Bennetzen, 2015). In tobacco, nicotine is an abundant predominant alkaloid produced in the roots and accumulating mainly in the leaves (Shoji and Hashimoto, 2011a; Dewey and Xie, 2013). As a defense toxin, nicotine production is drastically increased in response to damage caused by grazing herbivores (Baldwin, 1989), and jasmonates play a central signaling role in the damage-induced nicotine biosynthesis (Baldwin et al., 1994; Shoji et al., 2000, 2008). Nicotine has heterocyclic pyridine and pyrrolidine rings (Shoji and Hashimoto, 2011a; Dewey and Xie, 2013); the pyrrolidine ring is formed through consecutive reactions catalyzed by Orn decarboxylase (ODC; Imanishi et al., 1998; DeBoer et al., 2011a), putrescine N-methyltransferase (PMT; Hibi et al., 1994), and N-methylputrescine oxidase (MPO; Heim et al., 1996).
2007; Katoh et al., 2007), whereas enzymes involved in early steps of NAD synthesis, Asp oxidase (AO), quinolinate synthase (QS), and quinolinate phosphoribosyltransferase (QPT) are responsible for the formation of the pyridine ring (Sinclair et al., 2000; Katoh et al., 2006; Fig. 1). It has been proposed that PMT and MPO have evolved from spermidine synthase (SPDS) and diamine oxidase (DAO), two homologous enzymes with different catalytic activities, both of which accept putrescine as a substrate and thus are involved in polyamine metabolism (Hibi et al., 1994; Hashimoto et al., 1998; Junker et al., 2013; Naconsie et al., 2014). Two orphan oxidoreductases of different families, A622 (Hibi et al., 1994; DeBoer et al., 2009; Kajikawa et al., 2009) and berberine bridge enzyme-like (BBL) proteins (Kajikawa et al., 2011), are required for later steps including coupling of the two rings (Fig. 1), but the exact biochemical reactions catalyzed by these enzymes have yet to be determined. In tobacco roots, a pair of tonoplast-localized multidrug and toxic compound extrusion (MATE) family transporters, MATE1 and MATE2 (Shoji et al., 2009), mediate compound extrusion (MATE) family transporters, nicotine uptake permease 1 (NUP1), localized at plasma membranes (Hildreth et al., 2011; Kato et al., 2014). In addition to the transport function, NUP1 was proposed to be involved in the regulation of root growth and nicotine biosynthesis, and thus may have a regulatory role as well (Hildreth et al., 2011; Kato et al., 2015).

Nicotine contents in tobacco plants are genetically controlled by two distinct loci NICOTINE1 (NIC1) and NIC2, and their mutant alleles nic1 and nic2 have been used to breed a low-nicotine tobacco cultivars (Legg and Collins, 1971; Chaplin, 1975; Hibi et al., 1994). A small group of genes encoding closely related ETHYLENE RESPONSE FACTOR (ERF) transcription factors, which are in a clade within group IXa subfamily (Nakano et al., 2006), are clustered at NIC2 locus, and at least seven such genes (ERF17, ERF104ΔC, ERF115, ERF168, ERF179, ERF189, and ERF221), called NIC2-locus ERFs, were found to be deleted in the nic2 mutant (Shoji et al., 2010). In tobacco, all the NIC2-locus ERFs and their homologs are induced by jasmonates (Shoji et al., 2010), whereas salt stress induces the expression of most of the ERFs but not ERF189 and its closest homolog ERF199 (Shoji and Hashimoto, 2015). As master transcription factors regulating the pathway, jasmonate-inducible ERF189 and ERF199 directly up-regulate a nearly complete set of genes involved in nicotine biosynthesis and transport (all the genes mentioned above except NUP1) by recognizing GC-rich P box elements, which resemble, but differ from a typical GCC box, in the promoters of the downstream genes (Shoji and Hashimoto, 2011b, 2011c, 2012, 2013; Shoji et al., 2010, 2013). Interestingly, ORCA3 from Catharanthus roseus (van der Fits and Memelink, 2000) and JRE4/GAME9 from tomato (Solanum lycopersicum) and potato (Solanum tuberosum; Cárdenas et al., 2016; Thagun et al., 2016) are homologs of tobacco ERF189, and also regulate jasmonate-inducible defense metabolism, a part of indole alkaloid pathway and a nearly complete pathway for steroidal glycoalkaloid biosynthesis, respectively. Moreover, JRE4/GAME9 is in a cluster of related ERF genes in tomato and potato genomes, just like the NIC2-locus genes in tobacco (Cárdenas et al., 2016; Thagun et al., 2016). Through interaction with the nicotine-regulating ERF factors, a bHLH-family transcription factor MYC2, a key component in conserved jasmonate signaling (Goossens et al., 2016), positively regulates the nicotine pathway genes by directly binding to G box elements found in their promoters, as well as in way of the ERF genes (DeBoer et al., 2011b; Shoji and Hashimoto, 2011c; Zhang et al., 2012).

Genomics has greatly facilitated our understanding on specialized metabolism in plants. The genome sequence of tobacco (Sierro et al., 2014) allows us to characterize a whole range of features of the entire suite of genes involved in nicotine biosynthesis and related NAD and polyamine metabolism, such as fine molecular phylogenies, genomic arrangements, cis-element distributions in the promoters, and expression of individual genes. Here, we discuss the evolution of this specialized metabolic pathway specific to the Nicotiana lineage, with particular focus on gene regulatory aspects.

Figure 1. Pathways of nicotine, NAD, and polyamine metabolism in tobacco. Each defined enzymatic step is represented by an arrow and enzyme name, whereas undefined single or multiple step processes are represented by broken arrows. Boxes denote enzymes hypothesized to be involved predominantly in the nicotine biosynthesis pathway, whereas enzymes predominantly associated with related primary metabolopathic pathways are not framed. QS is underlined as it contributes to both nicotine and NAD pathways.
RESULTS

Genes in the Tobacco Genome Involved in Nicotine and Related Pathways

The genes encoding metabolic enzymes and transporters involved in nicotine and related primary metabolism (Fig. 1) were retrieved from tobacco genome sequence of TN90 cultivar (Sierro et al., 2014) using the BLAST functionality at the SOL Genomic Network (https://solgenomics.net/tools/blast/; Supplemental Table S1). To investigate the phylogenetic relationships, the tobacco enzymes, except A622 and BBL, were aligned with their homologs from N. sylvestris, N. tomentosiformis, tomato, pepper (Capsicum annuum), and Arabidopsis (Arabidopsis thaliana; Supplemental Fig. S1). In the phylogenetic trees, most proteins have two copies in tobacco, which group with their counterparts in ancestral diploids, forming a homologous group of orthologs. It is possible to divide the proteins in each tree into multiple such orthologous groups. According to the groupings and ancestral origins of their products, the tobacco genes were, to our knowledge, newly named in this study (Supplemental Table S1; Supplemental Fig. S1), if not identical to already named ones. For A622 (Kajikawa et al., 2009), MATE (Shoji et al., 2009), and NUP (Hildreth et al., 2011) genes, orthologous genes (greater than 98% identity at the nucleotide level) were found in the genome. ODC and PMT genes were given the names, due to no clear matching to the reported ones (Riechers and Timko, 1999; Xu et al., 2004), and so were BBLd2 and BBLe with their relations to other Nicotiana BBLs (Kajikawa et al., 2011; Supplemental Fig. S2).

Tobacco QPT1.2 and QPT2.2 of distinct groups, both from N. tomentosiformis, are ~75 kb apart on Super Scaffold (SS) 1382, suggesting a relatively recent duplication giving rise to these two genes (Shoji and Hashimoto, 2011b). A two-gene cluster of nonhomologous A622L and MATE2 was found on chromosome 12; these genes from N. tomentosiformis are ~128 kb away from each other on SS753. Other than those, no clustering was found at the SS level for the listed genes (Supplemental Table S1). Because of their uncertain placements in the genome, we could not confirm the genomic clustering of N. sylvestris-derived counterparts of the clustered genes.

Expression of Nicotine and Related Primary Metabolic Genes

Transcript levels were estimated by RNA-seq analysis, which yields expression levels in fragments per kilobase of exon per million mapped sequence reads (FPKM), for each gene assigned on the genome. Based on the FPKM values in various tobacco tissues, all of the metabolic and transport genes were clustered (Fig. 2A); QPT1.2 and QPT2.2 were excluded because of apparently duplicate mapping of the reads. There is a discrete cluster of 19 genes, including nearly all genes in the nicotine biosynthesis regulon (Fig. 2A). The genes in this cluster are expressed preferentially in the nicotine-producing roots. Such characteristic expression largely restricted to the roots is not evident for genes that are possibly involved in related primary pathway rather than the alkaloid production and form other clusters (Fig. 2A). Although included in the regulon, ODC2.1 and ODC2.2 with substantial expression also in stems and flowers, and BBLc and BBLd2 with very low FPKM values, are exceptional in this clustering.

To complement the RNA-seq results and further address the differential regulation, we examined the expression patterns with quantitative reverse transcription (qRT)-PCR of the metabolic genes involved in early parts of the pathways, which overlap or work in parallel with related primary pathways (Fig. 1). Primer pairs were designed to specifically amplify each gene or group of orthologs (Supplemental Table S2). Transcript levels in organs from tobacco plants, including roots of nic1nic2 mutant with a low-nicotine trait (Legg and Collins, 1971), and cultured BY-2 cells elicited with methyl jasmonate (MeJA), were measured and represented relative to those of a housekeeping gene EF1α (Fig. 2B). As reflected in hierarchal clustering, the expression patterns were again clearly distinguished into two major groups of genes, one possibly forming nicotine biosynthesis regulon and one presumably devoted to parallel primary pathways (Fig. 1). ODC1 clusters with the genes of the former group, but only at a low level of statistical significance, which is likely to be due to its very low expression levels. Thus ODC1 was assigned to the latter group. The genes of the former, including ODC2, PMT, MPO1, AO2, QS1, and QPT2, strongly or often nearly exclusively express in the roots of wild-type tobacco and their levels are decreased to 18% to 68% levels in nic1nic2 mutant roots, reflecting the regulation by NIC loci and therefore by NIC2-locus ERFs. The genes of this group are markedly up-regulated by MeJA in the cultured cells, leading to alkaloid induction, except for MPO1 as has been reported in Shoji and Hashimoto (2008). In contrast to the genes involved in nicotine formation, expression of ODC1, SPDS2, DA01, AO1, and QPT1 are not restricted to nicotine-producing tissues; they occur more ubiquitously, although their expression levels are generally lower (except SPDS2), which possibly reflects their contribution to primary pathways.

cis-Elements Predicted in Promoter Regions

The availability of genomic sequences prompted us to predict ERF189-binding P box and MYC2-binding G box elements in the promoter regions of the genes involved in nicotine and related pathways. We examined whether such elements were enriched in nicotine pathway genes. Using weighted matrices (Shoji and Hashimoto 2011b, 2011c) representing P and G boxes, we computationally searched for the binding elements
with cutoff scores of 5.0 for 10-mer P box and of 5.5 for 8-mer G box in 5'-flanking regions (−1,500 to −1 bp; counted from the first ATG). The scores of the predicted elements in each 100-bp bin along the entire promoter sequences are visualized in a heat map (Fig. 3A). For both elements in the primary metabolic genes, these average score for each bin are relatively low (upper block), whereas for the nicotine pathway genes there are a number of bins with high scores (lower two blocks). Bins scoring highly for both P and G boxes (squared with white lines in the right column) are present in 14 out of the 20 gene promoters of nicotine pathway, implying that these elements are crucial to the expression of these genes.

To retrieve the cis-elements shared among the coregulated genes in a nontargeted way, Multiple EM for Motif Elicitation (MEME) analysis (http://meme-suite.org; Bailey et al., 2006) was conducted using the 5'-flanking sequences (−1,500 to −1 bp) of 20 genes, included in the lower two blocks in Figure 3A, as queries. Highly scoring sequences related to P box (rank, 2; e-value, 9.5e-004; log likelihood ratio, 203) and those to G box (rank, 4; e-value, 2.9e+0.00; log likelihood ratio, 188) were found in all 20 and 19 promoters, respectively. Logo graphics (Crooks et al., 2004) representing conservation among the retrieved sequences are shown (Fig. 3B).

Regulation of BBL Gene Promoter in Tobacco

In concert with other genes involved in nicotine biosynthesis, BBL genes are strongly expressed in the roots and induced by jasmonates in tobacco (Kajikawa et al., 2011). To gain insight into the transcriptional regulation of BBL genes, promoter reporter analyses were performed for NsBBLa from N. sylvestris (Supplemental Fig. S2). Because the genomic sequence was not available when we began the experiment, the region from −1.126 to −1 bp (counted from the first ATG) of NsBBLa was obtained with TAIL-PCR; the sequence was later confirmed 99% identical to that in the genome database and 97% to that of BBLa gene in tobacco genome. Four P box (scores 5.8 to 6.9) and two G box (scores 9.1 and 5.5) elements were predicted within the promoter sequence. To generate transgenic plants and hairy roots, a GUS reporter gene driven by the promoter was introduced into tobacco via Agrobacterium tumefaciens-mediated transformation.

Expression patterns of the BBL promoter in transgenic seedlings and hairy roots were analyzed by visualizing GUS activities histochemically (Fig. 4). In transgenic seedlings at 2, 5, and 14 d after germination, GUS staining was visible in the roots, but not in any aerial tissues (Fig. 4, A–C). Strong staining was also observed in transgenic hairy roots (Fig. 4, D–F).
apical regions of the hairy roots, promoter activity was detected in differentiated cells as well as in actively dividing and elongating cells, but was absent in the root cap and in epidermal cells (Fig. 4, E and F). A cross section of the stained hairy roots in a differentiated zone was made to identify cell types associated with the activities; the promoter was expressed most strongly in the outmost cortex layer and moderately in the endodermis and parenchyma cells in the stele, but not in the epidermis (Fig. 4D). This expression pattern of the BBL promoter is quite similar to those reported for other nicotine pathway genes, such as PMT (Shoji et al., 2000), QPT2 (Shoji and Hashimoto, 2011a), A622 (Shoji et al., 2002), and MATE1 (Shoji et al., 2009).

To examine the jasmonate-mediated response of the BBL promoter, seven transgenic lines were treated with MeJA for 24 h, and the GUS activities in crude root extracts were measured fluorometrically. In five lines, significant increases of the activity (2.3 to 5.1 folds) relative to mock-treated controls were observed (Supplemental Fig. S3A). Indeed, GUS staining intensities were increased in transgenic hairy roots treated with MeJA, compared to the controls (Fig. 4E). To demonstrate the regulation of the BBL promoter by NIC loci, multiple lines of transgenic hairy roots with the promoter reporter were generated in wild-type and nic1 nic2 mutant genotypes. Higher GUS activities in the wild-type background were clearly observed in histochemical (Fig. 4F) and fluorometric (Supplemental Fig. S3B) assays.

Figure 3. ERF189-binding P box and MYC2-binding G box elements predicted in 5′-flanking regions from −1,500 to −1 (numbered from the first ATG) of metabolic and transport genes involved in nicotine and related primary metabolism. A, Heat map visualizing distributions of the elements predicted with Regulatory Sequence Analysis Tools (http://rsat.ulb.ac.be/rsat/); elements with scores greater than 5.5 for P box and 5.0 for G box were included. Colors reflect scores of the elements (or sums of those when multiples are predicted) in each bin. At borders between bins, elements were assigned into those proximal to the first ATG. Sums of scores for both boxes are in the right column (merge), where the bins including both P box and G box are squared with white lines. The values are averaged for a gene set in each block. Genomic sequence of a region from −1,500 to −1,200 is not available for MPO1.1 and BBLe.2. PMT3 and BBLe were excluded, because 5′-flanking sequences available were too short (<200 bp). B, Sequence logos representing conservations of sets of sequences related to P box (left) and G box (right) retrieved by MEME analysis from the promoter regions of the genes included in the lower two blocks of (A). NA, Not available.

Gene Clusters of NIC2-Locus ERFs and Their Homologs

Clustering of ERF genes at NIC2 locus was presumed in a previous study (Shoji et al., 2010). To understand the genomic organization of the NIC2-locus gene cluster and its possible counterpart from another ancestral diploid, NIC2-locus ERF genes and their homologs were retrieved from the tobacco genome sequence. Twenty-two ERF genes were retrieved in total, including four genes on unplaced SSs (Supplemental Table S3). Two clusters of multiple ERF genes of the relevant group are found in the genome: one 12-gene cluster (spanning ∼660 kb, flanked with genetic maker PT53353) from N. tomentosiformis on chromosome (chr.) 19 and one six-gene cluster (∼320 kb, ...
flanked with PT51405 and PT50089) from *N. sylvestris* on chr. 7 (Fig. 5; Bindler et al., 2011). A phylogenetic tree of the retrieved ERFs and their homologs can be found in Supplemental Figure S4. Although most ERFs retrieved are practically identical (≥98% at nucleotide level) to the queries, ERF91Ls, ERF17Ls, and JRE5Ls were, to our knowledge, newly defined according to their phylogenies (Supplemental Fig. S4), and the ERF91L genes differ by an N-terminal 64 amino acid extensions, but are nearly identical to ERF91 (not in the tree). Also, the ERF17L genes are not orthologous to ERF17 or JRE4 from tomato, the nearest neighbor in the tree. Some ERFs are truncated and do not include full-length DNA-binding domains, and therefore may be nonfunctional as transcription factors; these are denoted with ΔN or ΔC. As reflected in disproportional gene numbers between the clusters, only five out of ten functional NIC2-locus ERFs in the T-genome have clear counterparts in the S-genome; there are at least four pairs of such ERFs in the clusters (Fig. 5).

To delimit the genomic region deleted in *nic2* mutant, genomic PCR analysis (Supplemental Fig. S5) was performed with primers designed to detect the sequences at various positions around the NIC2-locus gene cluster (Supplemental Table S4). Genomic DNAs from various NIC genotypes in two cultivars, Burley 21 and NC95, were used for the analysis. Some of the amplified fragments were sequenced to confirm the specific amplifications (Supplemental Fig. S5), which are sometimes unsuccessful possibly due to highly repetitive nature of tobacco genome (Sierro et al., 2014). A large chromosomal region (~650 kb) including 10 out of 12 clustered ERF genes is missing in *nic2* genetic background, whereas the remaining two genes, ERF163 and ERF91L1, are retained in the genotype (Fig. 5; Supplemental Fig. S5), in agreement with the previous data (Shoji et al., 2010). ERF91L1 was considered an equivalent of former ERF91. These results were also in line with expression data in *nic2* mutant of the clustered ERFs and a gene that encodes COP9 signalosome subunit 7 and resides between ERF91L1 and the putative breakpoint of the deletion. Expression levels of the genes within the deleted region are very low, or below reliable detection limits, in *nic2* mutant (Supplemental Fig. S6). As expression levels of ERF168L1ΔC and ERF104ΔC are also below the detection limits (Supplemental Fig. S6), these genes on unplaced SS3881 were assumed to reside somewhere in the deleted part of the cluster.

Because genes were predicted with transcriptomics data, only a small fraction of the high-expressed ERF genes are found in this database (Supplemental Table S3), and can be assigned FPKM data; eight ERF genes were annotated, including only one orthologous pair of functional genes, ERF189 and ERF199. FPKM data indicate that ERF189 and ERF199 are expressed almost exclusively in the roots, whereas a similar root-specific expression (albeit at a lower level) was observed for ERF16 and nonfunctional ERFs, ERF17L3ΔC and ERF168L1ΔC (Fig. 5C). Expression of JRE5L2 and ERF91L1 is not restricted to the roots, but is also apparent in flowers and other tissues (Fig. 5C).

**Responses of ERF189 and Its Close Homologs to Jasmonates and Salt Stress**

The availability of the genome sequence allowed us to detect individual ERF genes with qRT-PCR by using...
We analyzed the responses to jasmonates and salt stress of ERF189 and ERF199, which were proposed to regulate the nicotine pathway (Shoji et al., 2010; Shoji and Hashimoto, 2015), and their close homologs, ERF16, ERF29, ERF115, and ERF221, which had been detected collectively in previous studies, in tobacco hairy roots; the cultured roots were treated with MeJA at 100 μM and NaCl at 300 mM. A pair of ERF189 and ERF199 are gradually induced by MeJA, whereas NaCl treatment has negative impact on their expression (Fig. 6), as reported previously (Shoji et al., 2010; Shoji and Hashimoto 2015). ERF16 is from N. sylvestris and has no obvious counterpart from N. tomentosiformis (Supplemental Fig. S4). ERF16 is induced by both MeJA and NaCl (Fig. 6) and has the highest expression levels among the examined genes (according to qRT-PCR data; Figs. 5C and 6); it boasts a 7-fold induction at 0.5 h by MeJA and 5-fold induction at 5 h by NaCl. The expression levels of ERF29, ERF115, and ERF221, which are highly similar to each other at the sequence level (Supplemental Fig. S4), have very low expression relative to ERF16, ERF189, and ERF199 (Fig. 6), and thus may be not annotated as genes in the database. MeJA treatment caused rapid (reaching maximums within 0.5 to 1.5 h) and substantial induction (15 to 33 times) of ERF29, ERF115, and ERF221, whereas their expression also rapidly rose and reached 59- to 226-fold levels after 5 h upon NaCl treatment (Fig. 6); such large fold changes may reflect their low basal expression.

**Genomic Deletions Found in the nic1nic2 Mutant of Burley 21 Cultivar**

To identify the genomic deletions in a nic1nic2 double mutant other than the ERF gene cluster (Fig. 5), genomic PCR analysis was carried out for the genes strongly down-regulated in the low-nicotine mutant (Supplemental Fig. S7); the genes highly ranked in a microarray-based screen (Shoji et al., 2010) along with ERF189 (rank, 8; signal ratio of nic1nic2 mutant to wild type, 0.025) were analyzed. We found that 13 genes have been deleted (rank, 1 to 38; ratio, 0.013 to 0.133), including presumed genes residing on the same SSs with the confirmed ones, on six SSs associated with at least four regions on three chromosomes in the nic1nic2 double mutant of cv Burley 21, or cv LA Burley 21 (Legg and Collins, 1971; Supplemental Table S5). The presumptive deletions encompass a relatively large chromosomal region, i.e. ~1,730 kb deletion at one end of chr. 17 (Supplemental Table S5). The deletions were found only in LA Burley 21 but not in other lines, such as the nic1 and nic2 single mutants of the same Burley 21 cultivar and the nic1nic2 double mutant of cv NC95 (Chaplin, 1975; Supplemental Fig. S7). As these are specific to a single line of LA Burley 21, the correlations of these deletions with NIC genotypes and thus nicotine biosynthesis are unlikely. The deletions found at two distinct positions on chr. 19 are far away and thus are apparently different from the deletion at NIC2 locus (Fig. 5A).
biological replicates. The levels are expressed relative to those of
Note that different vertical scales are adapted for
PCR in tobacco hairy roots treated with 100
stress in tobacco hairy roots. Transcript levels were analyzed with qRT-
NaCl (B) for 0, 0.5, 1.5, 5, or 24 h. The error bars indicateSDs over three
Figure 6. Response of ERF189 and related genes to jasmonate and salt
stresses in tobacco hairy roots. Transcript levels were analyzed with qRT-
c to the nicotine
formations branches of nicotine pathway are presumed
to have evolved from universal polyamine and NAD
pathways through gene duplication followed with
functionalization or neofunctionalization of the
duplicates (Fig. 1; Supplemental Fig. S1; Shoji and Hashimoto, 2011b;
Naconsie et al., 2014). The Orn-derived pyrrolidine ring
utilized as a common building block for formation of
tropane, nortropane, and nicotine alkaloids in a number
of species of Solanaceae and other families (Shoji and
Hashimoto, 2011a). The pyrrolidine formation branch,
composed with ODC, PMT, and MPO, may have arisen
before the diversification of the plants producing alkaloids containing the Orn-derived moiety. The
assumption is supported with the fact that tomato and
pepper have at least one gene of ODC2, PMT, and
MP01 (Supplemental Fig. S1; Stenzel et al., 2006).
Whereas ODC2, which acts in parallel with ODC1, has
retained its original catalytic activity, PMT and MPO1,
which have been derived from SPDS and DAO re-
respectively, have acquired novel catalytic activities through
refunctionalization (Juncker et al., 2013; Naconsie
et al., 2014), thus contributing to the innovation of the
pyrrolidine-forming extension (Fig. 1). In contrast to
the relatively ancient diversification of the pyrrolidine
branch from polyamine metabolism, establishment of
paralleled routes including AO, QS, and QPT for pyri-
dine formation (Fig. 1), which supply the ring to NAD
and nicotine production in tobacco, is presumed to
have occurred around the time of the diversification of the
Nicotiana lineage, given the specificity of AO2 and
QPT2 to the lineage (Supplemental Fig. S1; Shoji
and Hashimoto, 2011b; Ryan et al., 2012). This scenario

DISCUSSION

A Regulon for Nicotine Biosynthesis Pathway

Concerted and substantial expression of structural
genes involved in certain pathways is required for
massive metabolic flows allowing production and ac-
cumulation of specialized metabolites. Such coordi-
nation of multiple genes is often extended into preceding
primary pathways that supply precursors to down-
stream metabolism (van der Fits and Memelink,
2000; Cárdenas et al., 2016; Thagun et al., 2016; van
Moerkercke et al., 2015). In tobacco, a series of metabolic
and transport genes involved in a pathway leading to
nicotine from Orn and Asp express nearly exclusively in
the roots and jasmonate-elicited cultured cells (Fig. 2;
Shoji and Hashimoto, 2011a). Such coexpression of these
genes largely depends on pathway-controlling ERF
transcription factors (Shoji and Hashimoto, 2013). The
organization of these genes into such a regulon allows
the coordination of distinct portions of the pathway from
early ring formation steps to late steps, including ring
coupling and nicotine transport (Fig. 1).

Detailed phylogenies (Supplemental Fig. S1) and
expression profiling (Fig. 2) clearly distinguished the
genes involved in the regulon, as shown in Figure 1.
Genes involved in each step specific to the nicotine
pathway, such as PMT, MPO, A622, BBL, and MATE,
which generally belong to a single orthologous group
(Supplemental Figs. S1 and S2), are commonly regu-
lated as members of the regulon (Fig. 2). In contrast to
the nicotine-specific genes, ODC, AO, QS, and QPT
genes are involved in early steps that overlap with the
polyamine or NAD pathway (Fig. 1). To satisfy the
metabolic demands of different downstream pathways,
two types of genes (genes from two groups of ortho-
logs), are present for every overlapping step, except QS
(Fig. 1; Supplemental Fig. S1); ODC2, AO2, and QPT2
are involved in the nicotine biosynthesis regulon,
whereas ODC1, AO1, and QPT1 are not subjected to the
regulation by the ERFs and jasmonates and are possibly
devoted to the primary housekeeping pathways (Figs.
1 and 2). Of course, because such functional differenti-
ations among the genes were presumed from their bi-
ased, but not mutually exclusive, expression patterns,
transgenomic or mutational approaches may be required
to validate the contributions of each gene to specific
metabolic pathways. Although no differences other
than the transcriptional regulation between the gene
types have been suggested to date, slight differences in
the protein sequences (Supplemental Fig. S1) could give
rise to functional differentiations, thus allowing for
distinct metabolic roles (Schenck et al., 2015).

As reflected by the existence of two types of the genes
for the overlapping steps, pyridine and pyrrolidine
formation branches of nicotine pathway are presumed
to have evolved from universal polyamine and NAD
pathways through gene duplication followed with
functionalization or neofunctionalization of the
duplicates (Fig. 1; Shoji and Hashimoto, 2011b;
Naconsie et al., 2014). The Orn-derived pyrrolidine ring
is utilized as a common building block for formation of
tropane, nortropane, and nicotine alkaloids in a number
of species of Solanaceae and other families (Shoji and
Hashimoto, 2011a). The pyrrolidine formation branch,
composed with ODC, PMT, and MPO, may have arisen
before the diversification of the plants producing alkaloids containing the Orn-derived moiety. The
assumption is supported with the fact that tomato and
pepper have at least one gene of ODC2, PMT, and
MP01 (Supplemental Fig. S1; Stenzel et al., 2006).
Whereas ODC2, which acts in parallel with ODC1, has
retained its original catalytic activity, PMT and MPO1,
which have been derived from SPDS and DAO re-
respectively, have acquired novel catalytic activities through
neofunctionalization (Juncker et al., 2013; Naconsie
et al., 2014), thus contributing to the innovation of the
pyrrolidine-forming extension (Fig. 1). In contrast to
the relatively ancient diversification of the pyrrolidine
branch from polyamine metabolism, establishment of
paralleled routes including AO, QS, and QPT for pyri-
dine formation (Fig. 1), which supply the ring to NAD
and nicotine production in tobacco, is presumed to
have occurred around the time of the diversification of the
Nicotiana lineage, given the specificity of AO2 and
QPT2 to the lineage (Supplemental Fig. S1; Shoji
and Hashimoto, 2011b; Ryan et al., 2012). This scenario
is also in agreement with existence of a gene cluster of QPT1.1 and QPT2.1 in the tobacco genome (Supplemental Table S1) that may have arisen by a relatively recent gene duplication event. It remains to be addressed how and when the ERF factors, which play a central regulatory role in the nicotine biosynthesis regulon in present-day tobacco, have evolved to regulate distinct portions of the pathways that may have developed independently at different points in time.

Clusters of genes encoding nonhomologous proteins involved in specialized pathways has been widely recognized in plants (Nützmann and Osbourn, 2014), and alkaloid pathways follow suit (Winzer et al., 2012). In the tobacco genome, a cluster of A622L and MATE2 genes, which encode enzymes (DeBoer et al., 2009; Kajikawa et al., 2009) and transporters (Shoji et al., 2009), and which are both involved in late steps of the pathway, is situated on chromosome 12 (Supplemental Fig. S1). Localization of the cluster opens up the possibility of identifying genes for as yet undefined late steps based on their proximities to the cluster. Apart from this cluster, we could not find any clustering of the other nonhomologous genes; of course, before concluding, exact placements of unplaced SSs should be determined (Supplemental Fig. S1). The dispersion of these structural genes throughout the genome (Supplemental Table S1) implies that regulation of this functionality is dependent on promoter-binding transcription factors, rather than the chromatin-level regulation proposed for clustered genes (Wegel et al., 2009).

A number of P and G box elements, which are targeted by ERF189 and MYC2 transcription factors, respectively, were computationally predicted in the promoter regions of the genes (Fig. 3A). Occurrences of the predicted elements are more frequent among nicotine pathway genes regulated by those transcription factors, than they are among primary metabolic genes (Fig. 3A). This finding was complemented by the identification of P and G boxes as motifs conserved among the regulated promoters (Fig. 3B). These results support the notion that downstream structural genes have been recruited into the regulons under the control of the transcription factors through generating cognate cis-elements in their promoters (Shoji and Hashimoto, 2011b; Moghe and Last, 2015). Proximities of the two distinct boxes within the promoters (Fig. 3A; Shoji et al., 2010; Shoji and Hashimoto, 2011b, 2011c) imply the importance of such arrangements of functional cis-elements that possibly support cooperative action of the two transcription factors. As observed previously, both elements are likely to be present in similarly situated proximal promoter regions (Shoji et al., 2010; Shoji and Hashimoto, 2011b; Thagun et al., 2016); this is observed for genes such as PMT, QPT2, BBL, and MATE (Fig. 3A). However, this seems not always to be the case; the likely elements, though none of them have been validated experimentally, are also present in relatively distal promoter regions of some genes (Fig. 3A; Xu et al., 2004). It remains to be addressed whether such different placements of cis-elements in the promoters account for slight but significant differences in the expression patterns of the generally coregulated genes involved in the regulon, such as no elicitation of MPO1 in cultured cells and relatively relaxed suppression of ODC2 and MPO1 in nic1nic2 mutant (Fig. 3A; Shoji and Hashimoto, 2008).

Promoter of the BBLa gene follow the pattern of those of other genes involved in the regulon (Shoji et al., 2000, 2002, 2009; Shoji and Hashimoto 2011b) in terms of cell-type specificity (Fig. 4), response to jasmonates (Fig. 4E; Supplemental Fig. S3A), and suppression in the nic1nic2 mutant (Fig. 4F; Supplemental Fig. S3B). By recognizing resident P box elements, pathway-controlling ERF factors, with the help of MYC2, may mainly contribute to transcriptional regulation underlying such common characteristic expression. The functional importance of P and G box elements for regulation has been demonstrated by loss-of-function experiments with mutated promoters (Shoji et al., 2010; Shoji and Hashimoto, 2011b, 2011c). As yet, no gain-of-function analyses have been performed for these elements (Shoji et al., 2000; Xu and Timko, 2004). Compared to regulation by jasmonates and NIC genotypes, it has remained less clear how much the ERF factors contribute to the tissue-specific expression of the promoters. In tomato, expression of JRE4 is well correlated with those of downstream structural genes during developmental progressions (Cárdenas et al., 2016; Thagun et al., 2016). Root-specific expression of ERF189 and ERF199 indicated by RNA-seq (Fig. 5C) gives a first important cue to this issue. Cell-type specificity, in addition to root specificity, is considered characteristic to the regulon, as reflected by the epidermal expression of the NUP1 promoter contrasted with those of the ERF-regulated promoters (Kato et al., 2014).

Evolution of Clustered Transcription Factor Genes

The genetic locus NIC2 controlling nicotine content in tobacco (Legg and Collins, 1971; Hibi et al., 1994; Shoji et al., 2010) was finally elucidated; complete sequence of the tobacco genome (Siervo et al., 2014) allowed us to figure out the structure of ERF gene clusters at the NIC2 locus that originated from N. tomentosiformis and its counterpart from N. sylvestris (Fig. 5, A and B). A similar cluster of five ERF genes is present in the tomato genome (Cárdenas et al., 2016; Thagun et al., 2016). Whereas ERF and COP9 signalosome genes conserved between distantly related tomato and tobacco are similarly situated around the peripheral area of the clusters, central regions are occupied by ERF genes specific to each lineage, such as ERF189 and JRE4 (Fig. 5B; Supplemental Figs. S4 and S6). The structural arrangement of the clusters suggests more dynamic rearrangement of the divergent central area, which may favor formation of the ERFs devoted to lineage-specific alkaloid regulation. Tobacco has two sequences with similarities to JRE6 from tomato (not shown in
Supplemental Table S3 and Supplemental Fig. S4 because of incomplete reading frames). In tomato, apart from the ERF gene cluster on chr. 1, JRE6 is present as a singleton on chr. 5 (Thagun et al., 2016). The tobacco JRE6-like sequences may be situated somewhere around clusters, because they reside on unplaced SSs associated with same chromosomes. The possible association of the JRE6-like sequences with the clusters in tobacco implies the involvement of JRE6 orthologs in ancient clusters and consequent relocation of them to other chromosomes during formation of the tomato cluster.

There is considerable structural divergence even between the two clusters originating from distinct Nicotiana diploids in tobacco (Fig. 5), suggesting relatively frequent loss and gain of ERF genes and their replacements within the clusters even after diversification of the two ancestral diploids. Tandem repeats of homologous sequences may have contributed to highly frequent unequal crossing-over events leading to such chromosomal changes around the regions. A number of genes encoding truncated ERFs (Fig. 5; Supplemental Table S3) may be vestiges of recombination events that have occurred in the intragenic regions. Phylogenetic analysis revealed the existence of only a very few homeologous pairs of functional ERF genes in the tobacco genome as well as a considerable number of remaining unpaired or possibly nonfunctional genes (Supplemental Fig. S4). For these, the biological relevance is unclear, considering evolutionary proximity of N. tomentosiformis and N. sylvestris. Phylogenetic (Supplemental Fig. S4) and gene expression (Figs. 5C and 6) evidence point to the functional importance of a pair of ERF189 and ERF199, one of the three Nicotiana-specific pairs (Fig. 5B; Supplemental Fig. S4). These have been previously proposed to function as a regulator of the nicotine pathway (Shoji et al., 2010; Shoji and Hashimoto, 2015). A pair of genes, ERF221 and ERF29, which is the nearest functional pair to ERF189 and ERF199 in the phylogenetic tree (Supplemental Fig. S4), is expressed basally at low levels and is induced not only by MeJA but also by NaCl (Figs. 5C and 6). It is intriguing to uncover how only a certain ERF gene (or a certain pair of genes in tobacco case), among the many clustered genes, has become the predominant regulatory gene (Figs. 5C and 6; Thagun et al., 2016), and functionally important for a specialized pathway in each plant lineage.

Genomic Deletions in Low-Nicotine Mutants

Molecular basis of nlc2 mutation was described; the mutant allele has a large chromosomal deletion that encompasses ten ERF genes in the cluster at NIC2 locus on chr. 19, including ERF189 (Fig. 5B; Supplemental Fig. S5). Repetitive sequences present throughout the tobacco genome (Sierro et al., 2014) prevented further delimitation of the deleted region; regions of ~13 and 20 kb in size remain to be elucidated (Supplemental Fig. S5). Whole-genome or targeted resequencing and cytogenetic analyses may help to precisely determine breakpoints of the deletion and to detect possible structural changes at chromosomal level, respectively. Absence of a major deletion in the counterpart locus on chr. 7 has yet to be confirmed in nic1 genetic background (T. Shoji, unpublished data).

We found a number of genomic deletions other than that at NIC2 locus in the nic1nic2 mutant of Burley 21 cultivar, or cv LA Burley 21, on at least four positions on three chromosomes (Supplemental Table S5; Supplemental Fig. S7). A lot of genes, the expression of which is severely suppressed in the nic1nic2 mutant (signal ratio of nic1nic2 to wild type < 0.113; Shoji et al., 2010), are missing in the mutant (Supplemental Table S5; Supplemental Fig. S7). These deletions are specific to LA Burley 21 and not found in other varieties, and may not be associated with the NIC genotypes and thus with nicotine biosynthesis. Note that the nic1nic2 double mutant was not generated by crossing the corresponding single mutants, but rather derived from an original Cuban cigar cultivar as its genotype (Legg and Collins, 1971). The presence of multiple deletions specific to a certain line implies that the nature of the tobacco genome is highly prone to structural variations.

MATERIALS AND METHODS

Plant Growth and Treatment

Sterilized seeds of Nicotiana tabacum (tobacco), N. sylvestris, and N. tomentosiformis were germinated and grown to seedlings on half-strength Gamborg B5 medium solidified with 0.3% (w/v) gellan gum and supplemented with 2% (w/v) Suc. The wild-type, nic1, nic2, and nic1nic2 (registered as cv LA Burley 21) genotypes in the tobacco genome (Legg and Collins, 1971) were obtained from the USDA, the wild-type and nic1nic2 (registered as LAFCS35) genotypes in the NIC95 cultivar (Chaplin, 1975) from John Hamill (Deakin University), and N. tabacum cv Petit Havana line SR1, N. sylvestris, and N. tomentosiformis from Japan Tobacco. Two-week-old seedlings were transferred onto soil in pots and grown to maturity in the greenhouse. Tobacco BY-2 cells were cultured as described by Nagata et al. (1992). To induce nicotine biosynthesis genes, 4-d-old BY-2 cells were rinsed five times to remove auxin, transferred to auxin-free medium supplemented with MeJA at 100 μM, and cultured for 24 h.

RNA-Seq Analysis

Sequencing data for RNA from dry capsule (SRX495517, SRX495518, and SRX495519), senescent flower (SRX495530 and SRX495531), mature flower (SRX495520, SRX495521, and SRX495522), immature flower (SRX495602, SRX495603, and SRX495605), senescent leaf (SRX495532, SRX495534, and SRX495535), mature leaf (SRX495523, SRX495524, and SRX495525), young leaf (SRX495606, SRX495607, and SRX495608), stem (SRX495998, SRX495600, and SRX495601), and root (SRX495526, SRX495527, and SRX495529) of N. tabacum TN90 were obtained from BioProject PRJNA28029 (https://www.ncbi.nlm.nih.gov/bioproject/; Sierro et al., 2014).

Reads were mapped to the genome of N. tabacum TN90 (ftp://ftp.soltgenomics.net/genes/Nicotiana_tabacum/assembly/Ntab-TN90_AYMY-SS.fa.gz) using the software HISAT2 (v2.0.5; https://ccb.jhu.edu/software/hisat2/; Kim et al., 2015) and filtered using the software SAMtools (v1.3.1; http://samtools.sourceforge.net/; Li et al., 2009) to retain properly paired read pairs not annotated as "secondary," "QC failed," "duplicate," or "supplementary." For each N. tabacum TN90 gene model (ftp://ftp.soltgenomics.net/genes/Nicotiana_tabacum/annotation/Ntab-TN90_AYMY-SS_NGS_maseq.gff3), expression was calculated from the filtered mapped reads using the
software StringTie (v1.3.1c; https://ccb.jhu.edu/software/stringtie/; Pertea et al., 2016). Gene level expression values were obtained by summing the FPKM of the gene’s isoforms.

**qRT-PCR Analysis**

Total RNA was isolated from samples using RNeasy kit (Qiagen) and then converted to first-strand cDNA using ReverTra Ace qPCR RT Master Mix (Toyobo). The cDNA templates were amplified using a LightCycler 96 (Roche) with SYBR Premix Ex Taq (Takara) according to Shoji et al. (2010). The primer sequences are given in Supplemental Table S2. EFi-A was used as a reference gene. Each assay was repeated at least three times. Based on amplifications from equal molar quantities of cloned amplicons, amplifications from different primer pairs were normalized.

**Computational Analyses**

Full-length protein sequences were aligned with the software ClustalW (http://www.genome.jp/tools/clustalw/; Thompson et al., 1994), and using the alignments, phylogenetic trees were generated with the software MEGA6 (http://www.megasoftware.net/; Tamura et al., 2013) with the neighbor-joining algorithm.

The putative ERF189 and MYC2-binding elements in the 5′-flanking regions from −1,500 to −1 bp (numbered from the first ATG) of metabolic and transport genes (Supplemental Table S1) were searched and scored with Regulatory Sequence Analysis Tools (http://rsat.ulb.ac.be/rsat/; Turatsinze et al., 2008), using weight matrices for P box (Shoji and Hashimoto, 2011a) and G box (Shoji and Hashimoto, 2011b).

MEME analysis (v. 4. 11.2; http://meme-suite.org/; Bailey et al., 2006) was performed by selecting an option of zero or one occurrence per sequence and setting minimum width to 6 and maximum width to 15 and 12 when retrieving P box- and G box-related sequences, respectively.

**Plant Transformation**

The 5′-flanking region of NsBBLa was cloned from *N. sylvestris* genomic DNA by a TAIL-PCR method (Liu et al., 1995). A promoter region from −1,126 to −1 (numbered from the first ATG) of NsBBLa was placed upstream of a GUS coding sequence on pGBW3 using Gateway Technology (Thermo Fisher Scientific). To generate transgenic tobacco plants and hairy roots, leaf discs from *N. tabacum* cv NC95 of wild type and nic1nic2 mutant were infected with *Agrobacterium tumefaciens* strain EHA105 and *A. rhizogenes* strain ATCC15834 harboring the GUS reporter construct, respectively (Horsch et al., 1985). Wild-type tobacco hairy roots used in Figure 6 were induced in a similar fashion, but with *N. tabacum* cv Petit Havana line SR1 and the *A. rhizogenes* strain without the binary vector. The hairy root lines were subcultured every week in 125-mL glass flasks filled with 30 mL of liquid B5 medium supplemented with 2% (w/v) Suc with shaking at 100 rpm in the dark. MeJA and NaCl were directly added to 4-d-final concentrations of 100 μM and in-

**GUS Reporter Assays**

The GUS activity was detected histochemically and cross sections of the hairy roots were prepared as described by Shoji et al. (2000). Images of the stained tissues and sections were captured with a model no. SZX12 (Olympus) or a model no. Eclipse E-1000 (Nikon) microscope, both equipped with a model no. DP-70 digital camera (Olympus).

Frozen hairy roots were homogenized in 50 mM potassium P buffer (pH 7.0), 10 mM EDTA (pH 8.0), 0.1% (v/v) Triton X-100, and 0.1% (w/v) Sarcosyl. After centrifugation, the supernatants were desalted through NAP-5 columns (GE Healthcare) with P-buffered saline. Protein concentrations were determined with a Coomassie Protein Assay Reagent (Thermo Fisher Scientific). The protein solutions was supplemented with 4-methylumbelliferyl-P-D-glucuronide at 150 μmol and incubated at 37°C for the reactions. The amount of 4-methylumbelliflorone formed was measured by using a model no. F-4500 fluorescence spectrophotometer (Jitachi).

**Genomic PCR Analysis**

Genomic DNA was isolated using the CTAB method (Murray and Thompson, 1980) and used for PCR with Ex Taq DNA polymerase (Takara). The thermal program details for each primer pair are available upon request.

**Accession Numbers**

The promoter sequence of *NsBBLa* genes from *N. sylvestris* can be found in the GenBank/EMBL/DDBJ database under accession number LC201808.

**Supplemental Data**

The following supplemental materials are available.

**Supplemental Figure S1.** Phylogenetetic trees of enzyme proteins involved in nicotine and related primary metabolism.

**Supplemental Figure S2.** A phylogenetic tree of BBL proteins from tobacco and its ancestral *Nicotiana* diploids.

**Supplemental Figure S3.** GUS activities in tobacco hairy roots transformed with the reporter gene driven by NsBBLa promoter.

**Supplemental Figure S4.** A phylogenetic tree of NIC2-locus ERFs and related proteins.

**Supplemental Figure S5.** A chromosomal region deleted in nic2 mutant was delimited with genomic PCR analysis.

**Supplemental Figure S6.** Transcript levels of genes around NIC2 locus in the roots of wild-type and nic2 mutant tobacco were analyzed by qRT-PCR.

**Supplemental Figure S7.** Genes deleted in LA Burley 21 of nic1nic2 genotype were found by genomic PCR analysis.

**Supplemental Table S1.** Metabolic enzyme and transporter genes involved in nicotine and related metabolism in tobacco.

**Supplemental Table S2.** Primer sequences for qRT-PCR analysis.

**Supplemental Table S3.** NIC2-locus ERF genes and their homologs in tobacco.

**Supplemental Table S4.** Primer sequences for genomic PCR analysis to detect the chromosomal deletion around NIC2 locus in the mutants.

**Supplemental Table S5.** Gene found to be deleted in LA Burley 21.

**Supplemental Table S6.** Primer sequences for genomic PCR analysis to detect genes deleted in LA Burley 21.

**ACKNOWLEDGMENTS**

We thank Drs. Tsuyoshi Nakagawa (Shimane University) and John Hamill (Deakin University) for providing the pGBW3 vector and seeds of the NC95 cultivar, respectively. We are grateful to Drs. James Battey and David Page for critically reading and correcting the manuscript.

Received January 25, 2017; accepted April 13, 2017; published April 18, 2017.

**LITERATURE CITED**


Nicotine Biosynthesis Regulon in Tobacco
Zhang HB, Bokowiec MT, Rushton PJ, Han SC, Timko MP (2012) Tobacco transcription factors NtMYC2a and NtMYC2b form nuclear complexes with the NtJAZ1 repressor and regulate multiple jasmonate-inducible steps in nicotine biosynthesis. Mol Plant 5: 73–84