An HD-Zip IV transcription factor protein NbGL3 regulates glandular trichome initiation in tobacco

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Abstract

Glandular trichomes, a specialized multicellular structure, are considered as biofactories due to their capability to synthesize and secrete a large amount of secondary metabolites. Tobacco leaves have a high density of glandular trichomes that produce huge amounts of secondary metabolites, which can be used as important industrial raw materials. However, molecular mechanisms controlling glandular trichome development in tobacco still remain largely unknown. In the present study, we found that \( NbGL3 \), an HD-Zip IV family gene from \textit{Nicotiana benthamiana}, was highly expressed in mature leaves, and ethylene or auxin application could increase the expression of \( NbGL3 \). Virus induced gene silencing \( NbGL3 \) resulted in a decreased glandular trichome density on leaves. Putative downstream genes, such as \textit{micro trichome}, \textit{cyclin B2}, and \textit{wax inducer 1 like} were down regulated in \( NbGL3 \) silenced plants. Our results demonstrate that \( NbGL3 \) could positively regulate initiation of glandular trichomes in tobacco.


Introduction

Plant trichomes, the epidermal outgrowths covering most aerial plant tissue surfaces, are found in a very large number of plant species. According to their morphology, trichomes could be classified into glandular or non-glandular, unicellular or multicellular, branched or non-branched (Werker 2000, Pattanaik et al. 2014). Trichomes play various roles in plant growth and development, including protection of plant from UV radiation, arthropod herbivores, and pathogens (Kang et al. 2016), and from excess transpiration (Kang et al. 2014). Glandular trichomes are characterized by the ability of head cells to secrete or store large quantities of secondary metabolites (Huchelmann et al. 2017).

Tobacco shoots are covered with a high density of glandular trichomes. Tobacco glandular trichome cells secret and store huge amounts of terpenes, alkanes, acyl sugars, nicotine, fatty acid derivatives, and flavonoids (Rodà et al. 2003), together representing up to 16 % of the dry mass of the leaf (George 1991, Wagner et al. 2004). These exudates are important for aromas, flavours, and pharmaceuticals (Schilmiller et al. 2010, Huchelmann et al. 2017). Molecular mechanisms controlling trichome development in model plant \textit{Arabidopsis} have been extensively studied and reviewed (Serna and Cathie 2006, Pesch and Hülskamp 2009, Pattanaik et al. 2014, Yan et al. 2014). However, previous study indicated that transcription networks controlling trichome development are different between tobacco and \textit{Arabidopsis}. Overexpression of \textit{myeloblastosis related transcription factor} (MIXTA) from \textit{Antirrhinum majus} and \textit{Wo1} gene from tomato could promote glandular trichome initiation in tobacco (Payne et al. 1999, Yang et al. 2015). Most recent reports demonstrated that C2H2 type zinc finger \textit{NbGIS}, \textit{AIGIS} from \textit{Arabidopsis}, and \textit{JcZFP8} from \textit{Jatropha curcas} can also promote glandular trichome development in tobacco through gibberellic acid (GA) signaling (Liu et al. 2017, 2018, Shi et al. 2018). However, the molecular mechanism of glandular trichomes initiation and development in tobacco still remains largely unknown.

The homeodomain-leucine zipper (HD-Zip) transcription factor family is unique to the plant kingdom, and characterized by two indispensable conserved domains: the
homeodomain (HD) and the leucine zipper (Zip) domain (Schena and Davis 1992, Ariel et al. 2007). Based on the distinctive features of DNA-binding specificities, gene structures, additional common motifs, and physiological functions, the members of HD-Zip family can be divided into four groups, HD-Zip I to IV (Henriksson et al. 2005, Ariel et al. 2007). HD-Zip proteins play a wide variety of roles during plant growth and development, including lateral organ initiation (Otsuga et al. 2010), leaf cell expansion and endoreduplication (Hur et al. 2015), floral meristem regulation (Williams et al. 2005), and responses to biotic or abiotic stresses (Ariel et al. 2007, Brandt et al. 2014). The HD-Zip IV proteins have been demonstrated to play a pivotal role in trichome initiation in numerous plants. Glandular trichomes are terminally differentiated and organized structures that are specialized for chemical defense. GLABROS 2 (Gb2) is a member of the Arabidopsis GLABROS family, which is responsible for the development of glandular trichomes. The identification of Gb2 and its role in trichome development highlight the importance of this family in plant biology. GLABROS 2 is expressed in specific regions of the plant, including the petiole, petal, sepal, and fruit. The expression of Gb2 is regulated by plant hormones and environmental factors, which demonstrate the complexity of trichome development. The wild type tobacco plants about two months after transplantation which had entered flowering stage were used to collect samples (root, stem, mature leaf, young leaf, petiole, petal, sepal, fruit) for NbGL3 expression pattern analysis. Systemic leaves 20 days after infiltration (DAI) were used for RNA extraction and VIGS gene verification. The leaves one week after infiltration were collected for RNA extraction and downstream gene expressions.

**Materials and methods**

**Plants and growth conditions:** Tobacco (Nicotiana benthamiana Domin) seedlings were cultured in a greenhouse under a 16-h photoperiod, an irradiance of 100 µmol m⁻² s⁻¹, day/night temperatures of 23/19 °C, and a relative humidity of 80 %. The seeds were germinated, the seedlings were grown until the second leaf could be observed, and then transplanted into the small basins. Then the seedlings with 4 - 5 true leaves (about 20 d after transplantation) were used for Agrobacterium infiltration.

**Vector construction:** For VIGS vector construction, a 660 bp fragment from the NbGL3 coding sequence was amplified with specific primers: 5’ - AAGGTTACCGAATTCTCTATAGCTTGTTAATTCAGGCTCGC - 3’ and 5’ - TGCTTCGGAATGCCCGGGTCTGAACCATTCTGG TAGTATC-3’. Linearized pTRV2 vector was generated using the XbaI and Scal restriction enzymes. The PCR product was ligated with linearized pTRV2 vector using the ClonExpress II one step cloning kit (Vazyme, Nanjing, China). The reconstructed vector was transformed into competent Escherichia coli cells and verified by sequencing. The verified pTRV2:NbGL3, empty pTRV2, and pTRV1 vectors were introduced into Agrobacterium tumefaciens strain GV3101 by heat shock method.

**Agrobacterium infiltration:** A. tumefaciens strains carrying TRV-mediated vectors were cultured overnight at 28 °C in the appropriate antibiotic selection medium. Then the cultures were spun down and resuspended in infiltration medium (10 mM MES, 10 mM MgCl₂, 200 mM acetosyringone) to an absorbance of 1 at 600 nm. The resuspended cells were incubated at room temperature for 3 h. Before infiltration, A. tumefaciens strains harboring pTRV1 vector were mixed with that harboring pTRV2:NbGL3 or pTRV2 empty vector at a volume ratio of 1:1. The strain harboring pTRV2:NbPDS was used as a positive control to assess the efficiency of VIGS system. N. benthamiana infiltration was performed as previously reported (Senthilkumar et al. 2014).

**Plant hormone treatment:** To examine the effect of plant hormones on NbGL3 expression, the tobacco plants (20 DAI) were sprayed with GA (100 µM), 6-benzylaminopurine (6-BA; 50 µM), methyl jasmonate (MeJA; 100 µM), naphthaleneacetic acid (NAA; 100 µM), methyl jasmonate (MeJA; 100 µM), or 1-amino-1-cyclopropanecarboxylic acid (ACC; 1 µM), respectively. The control plants were sprayed with their corresponding mock solutions. The fourth leaf from the top at least from three plants at 3 and 6 h after treatment were harvested for RNA extraction.

**Real-time quantitative PCR (qPCR) analysis:** Total RNA was extracted using the plant total RNA isolation kit (Foregene, Chengdu, China). The cDNA was synthesized using PrimeScript™ RT reagent kit (TaKaRa, Dalian, China) according to the manufacturer's instructions. The qPCR was performed on a CFX96™ real-time PCR system using SYBR Green Master Mix (Vazyme). The housekeeping gene GAPDH was used as an internal reference. The primers used are listed in Table 1Suppl.
**Scanning electron microscopy:** Systemic leaves, stems, and sepals from the plants 20 DAI with pTRV2:NbGL3 or pTRV2 empty vector were used for SEM analysis. Samples treatment and SEM images were conducted as previously described (Chen et al. 2014).

### Results

To determine the **NbGL3** function in glandular trichome development, we first investigated the expressions of **NbGL3** in different organs and developmental stages. Our results showed that **NbGL3** was expressed in all organs, and the highest expression occurred in mature leaves. Sepals and petals also possessed relatively high transcript abundance, while transcript abundance in root was quite low (Fig. 1A). The expression pattern of **NbGL3** was relatively consistent with the distribution of glandular trichomes, which indicated that **NbGL3** probably participated in glandular trichome development in tobacco.

Plant hormone plays an important role in trichome development. In order to study whether **NbGL3** controls the trichome initiation through hormone signaling, we first examined whether the expression of **NbGL3** in mature leaves could be induced by the application of plant hormones. Tobacco plants were sprayed with 100 μM GA, 50 μM 6-BA, 100 μM MeJA, 100 μM NAA, or 1 μM ACC and the leaves were harvested at 3 and 6 h after hormone application. The real-time qPCR analysis was performed to examine the **NbGL3** transcript abundance. The expression of **NbGL3** was significantly higher in NAA and ACC treated plants than in their negative controls. However, GA, 6-BA, and MeJA treatment plants had no effect on **NbGL3** expression. These results suggest that **NbGL3** expression could be induced by auxin and ethylene.

In order to explore the role of **NbGL3** in tobacco, we employed VIGS system to silence its expression. The *Nicotiana benthamiana* phytoene desaturase gene was used as a positive control to assess the efficiency of VIGS system. At 20 DAI, tobacco plants showed systematical bleaching phenotype, which indicated successful silencing *Nicotiana benthamiana* phytoene desaturase (Fig. 1 Suppl.). Real-time qPCR analysis performed on leaves, stems, and sepals collected from the infiltrated plants at 20 DAI further confirmed silencing *Nicotiana benthamiana* phytoene desaturase (Fig. 1 Suppl.). The transcription of **NbGL3** gene was significantly decreased in the pTRV2: **NbGL3** infiltrated plants comparing with that infiltrated with the pTRV2 empty vector (Fig. 1C). These results suggested that **NbGL3** gene was successfully silenced.

The expression of **NbGL3** was significantly reduced in pTRV2: **NbGL3** infiltrated plant (Fig. 1C). To assess the effect of **NbGL3** on glandular trichome development, we checked the glandular trichome density on leaves, stems, and flower sepals from pTRV2: **NbGL3** and pTRV2 empty vector infiltrated plants. Compared to empty vector control plants, a decrease in glandular trichome density was observed in **NbGL3** silenced plants (Figs 2A and 3A). In order to determine whether **NbGL3** regulates glandular trichome initiation in tobacco, we counted the number of glandular trichomes in pTRV2: **GL3** and pTRV2 empty vector infiltrated plants. The results showed that trichome number per area was significantly decreased on **GbGL3** gene silenced leaves, stems, and sepals comparing with the negative control plants (Figs 2B and 3B).

There are two kinds of glandular trichomes on *N. benthamiana*: short glandular trichomes (SGTs) and the tall glandular trichomes (TGTs) (Fig. 2 Suppl.). The SGTs...
have a short unicellular stalk, on the top of which sits a head containing several nonchlorophyllous cells. The TGTs have a multicellular stalk and a head with a single or several chlorophyllous cells (Nielsen et al. 1991). 

Silencing NbGL3 in tobacco resulted in inhibition of long glandular trichome initiation; this result indicated that NbGL3 might function in a similar way as its homologous genes in cucumber and tomato (Yang et al. 2011, Cui et al. 2016). In order to further confirm the function of NbGL3 in tobacco, real-time qPCR analysis was conducted to examine the transcripts abundance of the genes whose homologs were differentially expressed in tril and csgl3 mutant plant. As shown in Fig. 4, expression of all downstream genes were decreased in NbGL3 silenced plants, and our results were consistent with previous reports (Yang et al. 2011, Cui et al. 2016).

Discussion

A key and unique feature of glandular trichomes is their ability to synthesize and secrete large amounts of specialized metabolites (Huchelmann et al. 2017). As such, they can be considered as “chemical factories”, making them interesting targets for metabolic engineering (Schilmiller et al. 2010, Huchelmann et al. 2017). Elucidating the transcription network regulating glandular trichome development will provide great foundation for metabolic engineering targeting to the chemicals produced by glandular trichomes. Genes controlling trichome development have been extensively studied in Arabidopsis. However, according to the present knowledge, mechanisms controlling the multicellular glandular trichome development in tomato and tobacco is partially different from that of unicellular trichomes in Arabidopsis and cotton (Serna and Cathie 2006). GLABROUS1 (GL1) is a myeloblastosis gene required for trichome development in Arabidopsis (Marks and Feldmann 1989). However, overexpression of GL1 in tobacco could not induced trichome formation (Payne et al. 1999). Overexpression
Fig. 3. Glandular trichomes analyzed by scanning electron microscopy. A - Glandular trichomes on different organs from NbGL3 silenced and control (pTRV2) plants. Scale bars: 1.00 mm (left and middle) and 500 μm (right). B - Glandular trichome density on different organs from NbGL3 silenced and control (pTRV2) plants. TGT - tall glandular trichome, SGT - short glandular trichome. Means ± SEs, n = 3, * - P < 0.05, ** - P < 0.01 (the Student’s t-test).

Fig. 4. Real-time quantitative PCR analysis of seven putative downstream genes of NbGL3. Leaves from NbGL3 silenced and control (pTRV2) plants were used for analysis. GL2-like - glabrous 2 like, CycB2 - cyclin B2, HD-8 - homeodomain 8, MIXTA - myeloblastosis related transcription factor, WIN1-like - wax inducer 1 like, MYB76-like - myeloblasosis 76-like, Mict - micro trichome. Means ± SEs, n = 3, * - P < 0.05 (the Student’s t-test).
of MIXTA, a myeloblastosis related transcription factor controlling conical cell formation in snapdragon, could boost trichome initiation in tobacco (Payne et al. 1999) and A. majus (Glover et al. 1998). Whereas ectopic expression of MIXTA in Arabidopsis gl1 mutant plants failed to rescue the glabrous phenotype (Payne et al. 1999). As described above, HD-Zip IV proteins seem to play an important role in trichome development. In this study, we investigated the role of NbGL3, a HD-Zip IV protein, in N. benthamiana. The expression pattern of NbGL3 showed that NbGL3 has a relatively higher transcription in leaves and sepals (Fig. 1A), this expression pattern was consistent with the TGTs distribution. In Arabidopsis, glabrous 2 promotes trichome initiation in shoots, but acts as a repressor in root hair development (Qing and Aoyama 2012). The low expression of NbGL3 in root indicated that NbGL3 may not play an important role in root hair development in tobacco.

Plant hormones play an important role in trichome development in most plant. However, hormone regulation pathways are not conserved among different plants. In addition, different hormones may regulate trichome development through different transcription networks in the same species (Pattanaik et al. 2014). Previous reports showed that AtGIS and NbGIS regulated glandular trichomes in tobacco through GA signaling pathway. In our study, expression of NbGL3 only showed response to ethylene and auxin, and external gibberellin, cytokinin, and jasmonic acid methyl ester had no effect on NbGL3 expression (Fig. 1B). These results indicated that NbGL3 might regulate glandular trichome development in tobacco through ethylene and auxin signaling.

In tobacco plant, tall and short glandular trichome types have been identified (Nielsen et al. 1991). While the former have been extensively studied and match the classic picture of trichome function, the short trichomes have remained less characterized (Sallets et al. 2014). TGTs were completely disappeared on NbGL3 silenced plant surfaces (Fig. 3A,B). However, the changes of SGTs densities were more complex, with an increase on leaves and a decrease on sepals and stems (Fig. 3B). These results indicated that development of TGTs and SGTs might be controlled by different mechanisms and NbGL3 mainly functioned in TGTs initiation. Wo is a HD-Zip IV protein and regulates glandular trichomes development in tomato. Wo could induce the expression of a cell cycle protein coding gene, cyclin B2, and further physically interacted with cyclin B2 protein to regulate glandular trichome development (Yang et al. 2011, 2015). Transcriptomic analysis in cucumber csgl3 and tril mutant (Zhao et al. 2015, Cui et al. 2016, Wang et al. 2016), tomato wolly plant (Yang et al. 2011), and tobacco plant transformed with Wo from tomato (Yang et al. 2015) identified a number of putative downstream genes. Several putative downstream genes were analyzed by real-time qPCR in the present study and our results were consistent with previous reports (Fig. 4). However, further studies have to be conducted to confirm if the NbGL3 protein could directly bind to the promoter region of the downstream genes to regulate their expression.

References

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