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SHORT COMMUNICATION

Major latex-like proteins identified from *Cucurbita pepo* control primary root elongation

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Abstract
Major latex-like proteins (MLPs) play a crucial role in the accumulation of hydrophobic organic pollutants in the Cucurbitaceae family. MLPs bind to hydrophobic organic pollutants in roots, and their complexes are secreted into xylem vessels. Consequently, hydrophobic organic pollutants are transported to the aerial parts. MLP-PG1 and MLP-GR3 serve as transporting factors for hydrophobic organic pollutants in zucchini (*Cucurbita pepo*) and are highly expressed in the roots. However, the biological functions of these MLPs in the roots remain elusive. In the current study, we show that MLP-PG1 and MLP-GR3 control primary root elongation. We found that both MLP-PG1 and MLP-GR3 bound to indole-3-acetic acid (IAA) in vitro. Primary root elongation was suppressed in the transgenic tobacco plants overexpressing *MLP-PG1* and *MLP-GR3*, while it was promoted in one of the *Arabidopsis thaliana mlp* mutants. Furthermore, these MLPs did not influence the endogenous IAA content. These results suggest that MLPs control primary root elongation by inactivating IAA in the roots.

Keywords Auxin · Molecular interaction · Root growth · Zucchini

Introduction

Major latex-like proteins (MLPs) were first identified in the latex of opium poppy (*Papaver somniferum*) in 1985 (Nessler et al. 1985) and, to date, have been identified in both monocots and dicots (Fujita and Inui 2021). MLPs belong to the birch pollen allergen Bet v 1 family, which consists of pathogenesis-related class 10 proteins, cytokinin-specific binding proteins (Pasternak et al. 2006), abscisic acid receptor PYLs (Miyazono et al. 2009), and plant allergens (Geroldinger-Simic et al. 2011).

A significant feature of MLPs is their internal hydrophobic cavity, which enables them to exhibit a broad spectrum binding affinity for hydrophobic compounds (Choi et al. 2015; Goto et al. 2019; Inui et al. 2013; Lytle et al. 2009). Another feature of MLPs is their ability to respond to abiotic and biotic stress. *Cis*-acting regulatory elements in the promoter regions of *MLP* genes contain plant hormone- and pathogen-responsive elements, and the expression of *MLP* genes is regulated by abiotic and biotic stresses (Chen and Dai 2010; Fujita et al. 2022). *MLP43,* identified from *Arabidopsis thaliana,* is suppressed by abscisic acid (ABA), functions as a positive regulator of the ABA signaling pathway, and confers drought tolerance (Wang et al. 2016). MLPs interact with ethylene-responsive factors, thereby increasing their binding affinity to the promoter regions of *pathogenesis-related protein* (*PR*) genes, leading to the induction of *PR* genes (Yang et al. 2015). Previous studies have shown that MLPs confer resistance against bacteria (Gai et al. 2018), fungi (Yang et al. 2015), and viruses (Song et al. 2020).

MLP-PG1 and MLP-GR3 have been identified in zucchini (*Cucurbita pepo*) as transport factors for hydrophobic organic pollutants (Inui et al. 2013). These MLPs bind to hydrophobic organic pollutants in the roots, forming MLP-hydrophobic organic pollutant complexes which are secreted into the xylem vessels and, finally, transported to the aerial parts (Goto et al. 2019; Inui et al. 2013; Iwabuchi

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et al. 2020). Consequently, crop contamination occurs in the Cucurbitaceae family. *MLP-PG1* and *MLP-GR3* are highly expressed in the roots of *C. pepo* (Fujita et al. 2022; Goto et al. 2019); however, the biological functions underlying this high expression in the roots remain elusive. In the present study, we demonstrate the involvement of MLP-PG1 and MLP-GR3 in root development. First, the binding affinity of MLPs toward indole-3-acetic acid (IAA), a natural auxin, was examined. We evaluated the primary root elongation in the transgenic tobacco plants overexpressing *MLP* genes and *A. thaliana mlp* mutants to understand the role of MLPs in root development. Our study showed that MLPs control primary root elongation by interacting with auxins.

Materials & methods

Plant materials and growing conditions

Sterile seeds of transgenic tobacco plants overexpressing *MLP-PG1* and *MLP-GR3* and *A. thaliana mlp* mutants were sown on Murashige and Skoog (MS) medium and cultivated at 24 °C for 8 days and 22 °C for 2 weeks, respectively, under a 16/8 h light/dark cycle. The transgenic tobacco seedlings were transferred to MS medium containing 0, 0.1, 1.0, and 10 µM 1-naphthylacetic acid (1-NAA), and the *A. thaliana* seedlings were transferred to MS medium. The synthetic auxin 1-NAA is used as an alternative to IAA because IAA is sensitive to light. The plates with seedlings were positioned at an angle of nearly 90° for 13 (tobacco) and 7 (*A. thaliana*) days, and the primary root length was measured.

Production of transgenic tobacco plants and selection of *A. thaliana* mutants

Transgenic tobacco plants overexpressing *MLP-PG1* and *MLP-GR3* from *C. pepo* were generated as previously described (Stoykova and Inui 2021).

A. thaliana mutants were purchased from TAIR (https://www.arabidopsis.org). Genomic DNA was extracted from the leaves of 3-week-old plants using ISOPLANT (Wako Pure Chemical Industries, Ltd., Osaka, Japan), and PCR was conducted under the following conditions: 5 min at 94 °C; 25 cycles of 30 s at 94 °C, 30 s at 58 °C, 30 s at 72 °C; 7 min at 72 °C using primers listed in Supplementary Table 1. The *tubulin* gene was also amplified under the same conditions. The amplified fragments were electrophoresed on a 0.8% agarose gel and detected using ethidium bromide.

Expression analysis of each *MLP* gene was conducted using total RNAs extracted from the roots of the mutants grown for 3 weeks using TRIzol RNA Isolation Reagent (Thermo Fisher Scientific Inc., Waltham, MA, USA). Following cDNA synthesis using a ReveTra Ace qPCR Mix (Toyobo Co., Ltd., Osaka, Japan), RT-PCR was performed using Quick Taq HS DyeMix (Toyobo Co., Ltd.) under the following conditions: 5 min at 95 °C; 35 cycles of 30 s at 94 °C, 30 s at 58 °C; 30 s at 72 °C; and 7 min at 72 °C using primers listed in Supplementary Table 1. The *tubulin* gene was amplified as an internal standard under the same conditions. The amplified fragments were detected on a 2% agarose gel. Quantitative RT-PCR was performed by Light Cycler 480 II (Roche Applied Science, Indianapolis, IN, USA) under the following conditions: 1 min at 95 °C; 40 cycles of 15 s at 95 °C, 30 s at 60 °C; 5 s at 95 °C; and 1 min at 65 °C using primers listed in Supplementary Table 1. The *tubulin* gene was amplified as an internal standard under the same conditions. Relative expression levels were calculated using the ΔΔCT method, and the specific amplification of the *MLP* genes was checked by generating melting curves.

Purification of recombinant MLPs

Recombinant MLPs were purified from *Escherichia coli* as described in our previous report (Inui et al. 2013). Briefly, *E. coli* expressing *MLP-PG1* and *MLP-GR3* fused with His-tags at the C-terminus were sonicated and then centrifuged at 4 °C for 15 min at 26,700 × *g*. The supernatant was incubated with TALON® metal affinity resin (Takara Bio Inc., Shiga, Japan), and the mixture was washed with 50 mM sodium phosphate buffer (pH 7.0) and loaded to the column. Imidazole (150 mM) dissolved in 50 mM sodium phosphate buffer (pH 7.0) was added to the column. The elution was centrifugated at 4 °C for 30 min at 26,700 × *g*, and the supernatant was collected and stored at 4 °C until use.

Binding assay with MLPs to IAA

The binding ability of MLPs to IAA was examined in accordance with our previous report (Fujita et al. 2020). Briefly, 200 µL of 60 mM IAA dissolved in dimethylformamide was reacted with 1 mg of NH_2 magnetic beads (Tamagawa Seiki, Co., Ltd, Nagano, Japan) according to the manufacturer's instruction. The binding buffer (50 mM potassium phosphate buffer [pH 5.6], 100 mM KCl, 1 mM dithiothreitol, 0.2 mM phenylmethylsulfonyl fluoride) was added to IAA-immobilized NH_2 magnetic beads, and the beads were washed thrice. 200 µL of recombinant MLP-PG1 (832.42 µg/mL) and MLP-GR3 (900.886 µg/mL) were added to IAA-immobilized NH_2 magnetic beads and thoroughly dispersed. After rotation at 4 °C for 4 h at 25 rpm, the beads were washed eight times with the binding buffer. The supernatant from the eighth wash was used as the wash fraction. 35 µL of the binding buffer and 7 µL of the Sample Buffer Solution with Reducing Reagent for SDS-PAGE (Nacalai Tesque, Inc., Kyoto, Japan) were added to the washed beads. After boiling at 98 °C for 5 min, the

supernatant was subjected to SDS-PAGE on a 15% acrylamide gel, and the gel was then stained using a Silver Staining kit (Wako Pure Chemical Industries).

Quantification of IAA content

IAA was extracted and quantified as previously described (Matsuo et al. 2020). Transgenic tobacco plants were cultivated in the soil at 24 °C under a 16/8 h light/dark cycle for 13 weeks. Soil particles were removed with water, and the cleaned roots were frozen in liquid nitrogen. IAA was extracted from 200 mg of roots into 5 mL of 80% methanol containing 1% acetic acid, followed by the addition of [$^{13}C_6$] IAA (Cambridge Isotope Laboratories, Inc., Tewksbury, MA, USA) as an internal standard. After centrifugation, IAA was extracted at 4 °C overnight and re-extracted using the same extraction solution. The extract was purified by solid-phase extraction, dissolved in water/methanol/acetic acid (80:19.95:0.05, v/v/v), and analyzed using high-performance liquid chromatography coupled with tandem quadrupole mass spectrometry (HPLC/MS/MS; Prominence20A Series HPLC [Shimadzu Corporation, Kyoto, Japan] equipped with a 3200 QTrap LC/MS/MS System [AB Sciex LLC, Framingham, MA, USA]).

Construction of a phylogenetic tree

The amino acid sequences of the MLPs from *C. pepo* and *A. thaliana* were obtained from the UniProt database (https://www.uniprot.org/; Table S2). A phylogenetic tree was constructed using ClustalW (Larkin et al. 2007).

Statistical analysis

Dunnett's multiple comparison test was used to determine significant differences among plant lines using RStudio software version 2023.12.1 + 402 (http://www.rstudio.com) SimComp package.

Results & discussion

MLP-PG1 and MLP-GR3 bind to IAA

Since MLP homologs contain an internal cavity (Fujita and Inui 2021), it is conceivable that plant hormones act as ligands for MLP homologs (Pasternak et al. 2006; Ruszkowski et al. 2014). We investigated the ability of MLP-PG1 and MLP-GR3 to bind IAA, a natural auxin compound. After incubating the recombinant MLP-PG1 and MLP-GR3 with beads immobilized with IAA, we detected a distinct band at approximately 17 kDa, which corresponded to the molecular weight of the MLPs (Fig. 1). In contrast, the band intensity of MLPs incubated with the beads without IAA immobilization was remarkably reduced. No visible bands were observed in the wash fraction (Figure 1). These results clearly showed that MLP-PG1 and MLP-GR3 specifically bind to IAA in vitro. Our previous chemical screening showed that MLP-PG1 and MLP-GR3 bind to a compound with an indole ring-like structure (Fujita et al. 2020). The Kiwi allergen Act d 11 shows a high binding score for compounds with indole-like structures in silico (Chruszcz et al. 2013). Thus, the binding of MLP-PG1 and MLP-GR3 to IAA was reasonable.

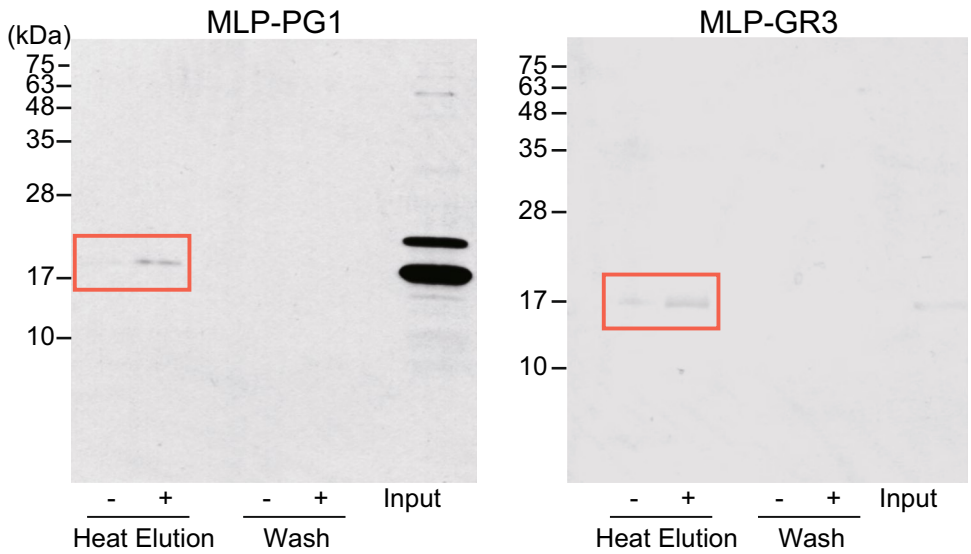
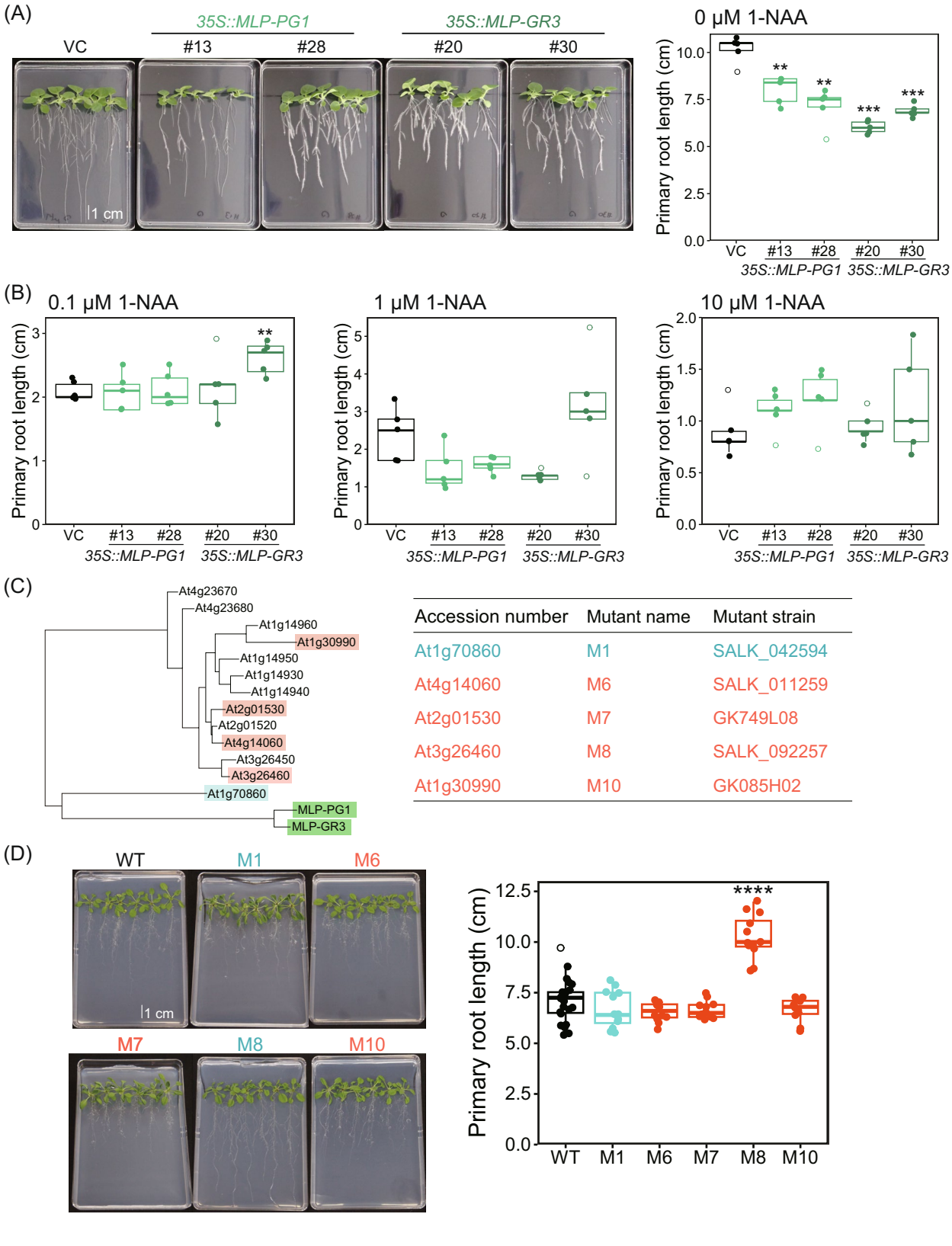


Fig. 1 Major latex-like proteins (MLPs) from *Cucurbita pepo* bind to indole-3-acetic acid (IAA). The binding affinity of MLP-PG1 and MLP-GR3 to IAA. –, incubation with magnetic beads; +, incubation with magnetic beads immobilized with IAA



Accession number	Mutant name	Mutant strain
At1g70860	M1	SALK_042594
At4g14060	M6	SALK_011259
At2g01530	M7	GK749L08
At3g26460	M8	SALK_092257
At1g30990	M10	GK085H02

◂**Fig. 2** Major latex-like proteins (MLPs) from *Cucurbita pepo* suppress the primary root elongation. **A** Primary root length of transgenic tobacco plants overexpressing *MLP-PG1* or *MLP-GR3* gene cultivated in 1-NAA free medium. Asterisks indicate significant differences compared to the primary root length of transgenic tobacco plants expressing *empty vector* (VC) (**, $p < 0.01$; ***, $p < 0.001$). **B** Primary root length of transgenic tobacco plants overexpressing *MLP-PG1* or *MLP-GR3* gene cultivated in 1-NAA medium. **C** Phylogenetic tree of MLPs from *Arabidopsis thaliana* and *C. pepo*. **D** Primary root length of *A. thaliana mlp* mutants. Asterisks indicate significant differences compared to the primary root length of wild-type (WT) plants (****, $p < 0.0001$)

MLP-PG1 and MLP-GR3 suppress primary root elongation

Next, we examined the biological functions of MLP-PG1 and MLP-GR3 in root development. The transgenic tobacco plants overexpressing *MLP-PG1* and *MLP-GR3* were cultivated vertically in MS medium. The primary root lengths of transgenic tobacco plants overexpressing *MLP-PG1* (lines #13 and #28) and *MLP-GR3* (lines #20 and #30) were significantly shorter than those of transgenic tobacco plants expressing *empty vector* as a control (Fig. 2A). IAA is light-sensitive; therefore, 1-NAA was added to the MS medium at concentrations of 0, 0.1, 1, and 10 µM (Uchida et al. 2018). However, the negative effects of MLP-PG1 and MLP-GR3 on primary root elongation were negligible (Fig. 2B).

The transformation of the Cucurbitaceae family remains challenging, and it is difficult to construct knockdown or knockout mutants of *C. pepo*. We examined the effects of *A. thaliana MLP* genes on primary root elongation. We selected *At1g70860,* which is closely related to *MLP-PG1* and *MLP-GR3* (Fig. 2C), and *At4g14060*, *At2g01530*, *At3g26460*, and *At1g30990*, which are highly expressed in the roots of *A. thaliana* seedlings (Supplementary Fig. 2). We purchased *A. thaliana mlp* T-DNA insertion mutant lines (SALK_042594, SALK_011259, GK749L08, SALK_092257, and GK085H02) and evaluated the expression levels of *MLP* genes (Supplementary Figure 1). Primary root elongation was evaluated as described above (Fig. 2D). Four *mlp* mutants (M1 [*at1g70860*], M6 [*at4g14060*], M7 [*at2g01530*], and M10 [*at1g30990*]) showed equivalent primary root elongation with wild-type plants (Fig. 2D); however, primary root elongation was significantly promoted in M8 (*at3g26460*). Considering that the overexpression of *MLP-PG1* and *MLP-GR3* suppressed primary root elongation in the transgenic tobacco plants (Fig. 2A), MLPs may have a negative impact on primary root elongation and control root development. *MLP329* identified from *A. thaliana* promotes seed dormancy and is highly expressed in the roots (Chong et al. 2022); however, *mlp329* mutants and transgenic *A. thaliana* plants overexpressing *MLP329* exhibited an equivalent primary root length with that of wild-type plants. *At4g14060*, *At2g01530*, and *At1g30990* were highly expressed in the roots (Supplementary Figure 2), whereas the *A. thaliana mlp* mutants (M1, M6, and M7) did not show significant primary root elongation (Fig. 2D). These results suggest that not all the *MLP* genes highly expressed in the roots suppress primary root elongation. Several *MLP* genes confer resistance against fungi that infect the roots of cotton (*Gossypium hirsutum*) (Yang et al. 2015). In contrast, our previous study showed that MLP-PG1 confers resistance against *Botrytis cinerea* (Fujita et al. 2022). MLP-PG1 may have dual functions in the roots: resistance against fungi and suppression of primary root elongation. Additionally, *MLP* genes are induced by infection of arbuscular mycorrhiza (Pawlowski et al. 2003). Therefore, *MLP* genes that are highly expressed in roots play a role in the stress response, root endosymbiosis, and root development.

These results led us to hypothesize that MLP-PG1 and MLP-GR3 decrease the endogenous IAA content in the roots. Several MLP homologs function as enzymes in the biosynthesis of secondary metabolites. PR-10s in *P. somniferum* catalyze the codeine and morphine biosynthesis pathways (Dastmalchi et al. 2019). MLPL shows cyclase activity and is involved in the biosynthesis of *cis-trans*-nepetalactol, an intermediate product of the catmint *cis-trans*-nepetalactone (Lichman et al. 2020; Lozada et al. 2022). To assess whether MLP-PG1 and MLP-GR3 decrease the endogenous IAA content in the roots, we quantified the endogenous IAA content in the roots of transgenic tobacco plants. The endogenous IAA content did not significantly decrease in the roots of transgenic tobacco plants overexpressing *MLP-PG1* or *MLP-GR3* (Fig. 3). Our previous report shows that overexpression of *MLP-PG1* in *Nicotiana tabacum* dramatically induces the auxin-signaling related genes encoding auxin-binding proteins (Fujita et al. 2022). Several *A. thaliana MLP* genes in the root apex are induced by gravitational stimuli (Kimbrough et al. 2004). Auxins play a central role in gravitropism (Blancaflor and Masson 2003), suggesting that MLPs are also involved in gravitropism. Overall, these results indicate that MLPs deactivate IAA in the roots and control primary root elongation, thereby regulating the auxin signaling pathway. MLPs have been identified as a transporter of hydrophobic compounds from roots to aboveground parts of the Cucurbitaceae family (Inui et al. 2013). One of the physiological functions of MLPs is the responses and controls toward abiotic and biotic stresses (Fujita and Inui 2021). Root elongation controls by MLPs revealed in this study may play a role in defense responses to environmental stresses.

Conclusion

In the present study, we investigated the biological functions of *MLP-PG1* and *MLP-GR3* in the roots of *C. pepo*, which are highly expressed in the roots. Our results show

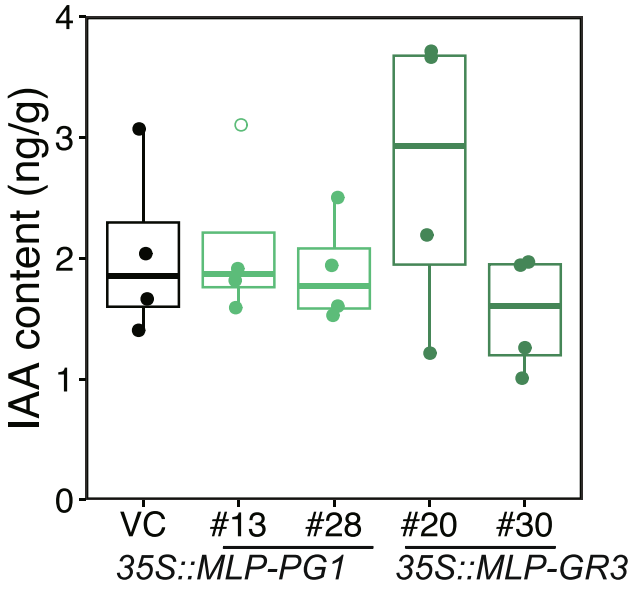


Fig. 3 Endogenous indole-3-acetic acid (IAA) content in the roots of transgenic tobacco plants overexpressing *major latex-like proteins* (*MLP*) gene

the profound effects of MLP-PG1 and MLP-GR3 on primary root elongation. Based on the reverse genetics results, MLP-PG1 and MLP-GR3 suppressed primary root elongation. Considering that MLPs bound to IAA without influencing the endogenous IAA content, we hypothesized that MLPs deactivated IAA in the roots to control primary root elongation. However, the molecular mechanisms underlying the regulation of primary root elongation by MLP-PG1 and MLP-GR3 remain elusive. The involvement of MLP-PG1 and MLP-GR3 in the auxin signaling pathway requires further investigation. Besides, the influence of MLPs toward auxin distribution should be assessed, thereby inhibiting primary root elongation.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s10725-025-01292-9.

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Author contribution KF and HI: designed the research; KF, JG, EI, MC, NC, MY, CS, and HI: performed the experiments; HI: provided the materials; and KF and HI: analyzed the data and wrote the manuscript, which was revised and approved by all the authors.

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Data availability The datasets generated and analyzed in the current study are available from the corresponding author upon reasonable request.

Declarations

Competing interests The authors have no conflicts of interest to declare that are relevant to the contents of this article.

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References

Blancaflor EB, Masson PH (2003) Plant gravitropism. unraveling the ups and downs of a complex process. Plant Physiol 133:1677–1690. https://doi.org/10.1104/pp.103.032169

Chen JY, Dai XF (2010) Cloning and characterization of the *Gossypium hirsutum* major latex protein gene and functional analysis in *Arabidopsis thaliana*. Planta 231:861–873. https://doi.org/10.1007/s00425-009-1092-2

Choi SH, Hong MK, Kim HJ et al (2015) Structure of ginseng major latex-like protein 151 and its proposed lysophosphatidic acid-binding mechanism. Acta Crystallogr Sect D Biol Crystallogr 71:1039–1050. https://doi.org/10.1107/S139900471500259X

Chong SN, Ravindran P, Kumar PP (2022) Regulation of primary seed dormancy by MAJOR LATEX PROTEIN-LIKE PROTEIN329 in Arabidopsis is dependent on DNA-BINDING ONE ZINC FINGER6. J Exp Bot 73:6838–6852. https://doi.org/10.1093/jxb/erac337

Chruszcz M, Ciardiello MA, Osinski T et al (2013) Structural and bioinformatic analysis of the kiwifruit allergen Act d 11, a member of the family of ripening-related proteins. Mol Immunol 56:794–803. https://doi.org/10.1016/j.molimm.2013.07.004

Dastmalchi M, Chen X, Hagel JM et al (2019) Neopinone isomerase is involved in codeine and morphine biosynthesis in opium poppy. Nat Chem Biol 15:384–390. https://doi.org/10.1038/s41589-019-0247-0

Fujita K, Inui H (2021) Review: biological functions of major latex-like proteins in plants. Plant Sci 306:110856. https://doi.org/10.1016/j.plantsci.2021.110856

Fujita K, Kondoh Y, Honda K et al (2020) Pesticide treatment reduces hydrophobic pollutant contamination in *Cucurbita pepo* through competitive binding to major latex-like proteins. Environ Pollut 266:115179. https://doi.org/10.1016/j.envpol.2020.115179

Fujita K, Asuke S, Isono E et al (2022) MLP-PG1, a major latex-like protein identified in *Cucurbita pepo*, confers resistance through the induction of pathogenesis-related genes. Planta 255:10. https://doi.org/10.1007/s00425-021-03795-x

Gai YP, Yuan SS, Liu ZY et al (2018) Integrated phloem sap mRNA and protein expression analysis reveals phytoplasma-infection responses in mulberry. Mol Cell Proteomics 17:1702–1719. https://doi.org/10.1074/mcp.RA118.000670

Geroldinger-Simic M, Zelniker T, Aberer W et al (2011) Birch pollen-related food allergy: clinical aspects and the role of allergen-specific IgE and IgG4 antibodies. J Allergy Clin Immunol 127:616–622. https://doi.org/10.1016/j.jaci.2010.10.027

Goto J, Iwabuchi A, Yoshihara R et al (2019) Uptake mechanisms of polychlorinated biphenyls in *Cucurbita pepo* via xylem sap containing major latex-like proteins. Environ Exp Bot 162:399–405. https://doi.org/10.1016/j.envexpbot.2019.03.019

Inui H, Sawada M, Goto J et al (2013) A major latex-like protein is a key factor in crop contamination by persistent organic pollutants. Plant Physiol 161:2128–2135. https://doi.org/10.1104/pp.112.213645

Iwabuchi A, Katte N, Suwa M et al (2020) Factors regulating the differential uptake of persistent organic pollutants in cucurbits and non-cucurbits. J Plant Physiol 245:153094. https://doi.org/10.1016/j.jplph.2019.153094

Kimbrough JM, Salinas-mondragon R, Boss WF, Brown CS (2004) The fast and transient transcriptional network of gravity and mechanical stimulation in the Arabidopsis root apex. Plant Physiol 136:2790–2805. https://doi.org/10.1104/pp.104.044594

Larkin MA, Blackshields G, Brown NP et al (2007) Clustal W and Clustal X version 2.0. Bioinformatics 23:2947–2948. https://doi.org/10.1093/bioinformatics/btm404

Lichman BR, Godden GT, Hamilton JP et al (2020) The evolutionary origins of the cat attractant nepetalactone in catnip. Sci Adv 6:20. https://doi.org/10.1126/sciadv.aba0721

Lozada NJH, Hong B, Wood JC et al (2022) Biocatalytic routes to stereo-divergent iridoids. Nat Commun 13:4718. https://doi.org/10.1038/s41467-022-32414-w

Lytle BL, Song J, de la Cruz NB et al (2009) Structures of two *Arabidopsis thaliana* major latex proteins represent novel helix-grip folds. Proteins Struct Funct Bioinforma 76:237–243. https://doi.org/10.1002/prot.22396

Matsuo S, Miyatake K, Endo M et al (2020) Loss of function of the *Pad-1* aminotransferase gene, which is involved in auxin homeostasis, induces parthenocarpy in Solanaceae plants. Proc Natl Acad Sci USA 117:12784–12790. https://doi.org/10.1073/pnas.2001211117

Miyazono KI, Miyakawa T, Sawano Y et al (2009) Structural basis of abscisic acid signalling. Nature 462:609–614. https://doi.org/10.1038/nature08583

Nessler CL, Allen RD, Galewsky S (1985) Identification and characterization of latex-specific proteins in opium poppy. Plant Physiol 79:499–504. https://doi.org/10.1104/pp.79.2.499

Pasternak O, Bujacz GD, Fujimoto Y et al (2006) Crystal structure of *Vigna radiata* cytokinin-specific binding protein in complex with zeatin. Plant Cell 18:2622–2634. https://doi.org/10.1105/tpc.105.037119

Pawlowski K, Swensen S, Guan C et al (2003) Distinct patterns of symbiosis-related gene expression in actinorhizal nodules from different plant families. Mol Plant-Microbe Interact 16:796–807. https://doi.org/10.1094/MPMI.2003.16.9.796

Ruszkowski M, Sliwiak J, Ciesielska A et al (2014) Specific binding of gibberellic acid by cytokinin-specific binding proteins: a new aspect of plant hormone-binding proteins with the PR-10 fold. Acta Crystallogr Sect D Biol Crystallogr 70:2032–2041. https://doi.org/10.1107/S1399004714010578

Song L, Wang J, Jia H et al (2020) Identification and functional characterization of NbMLP28, a novel MLP-like protein 28 enhancing *Potato virus Y* resistance in *Nicotiana benthamiana*. BMC Microbiol 20:55. https://doi.org/10.1186/s12866-020-01725-7

Stoykova P, Inui H (2021) Transport enhancement of hydrophobic pollutants by the expression of zucchini major latex-like protein genes in tobacco plants. J Plant Physiol 263:153464. https://doi.org/10.1016/j.jplph.2021.153464

Uchida N, Takahashi K, Iwasaki R et al (2018) Chemical hijacking of auxin signaling with an engineered auxin-TIR1 pair. Nat Chem Biol 14:299–305. https://doi.org/10.1038/nchembio.2555

Wang Y, Yang L, Chen X et al (2016) Major latex protein-like protein 43 (MLP43) functions as a positive regulator during abscisic acid responses and confers drought tolerance in *Arabidopsis thaliana*. J Exp Bot 67:421–434. https://doi.org/10.1093/jxb/erv477

Yang CL, Liang S, Wang HY et al (2015) Cotton major latex protein 28 functions as a positive regulator of the ethylene responsive factor 6 in defense against *Verticillium dahliae*. Mol Plant 8:399–411. https://doi.org/10.1016/j.molp.2014.11.023

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