

李响总计：120+5*0.6*0.6+40*0.6*0.6+120*0.6+

60*0.6*0.6*0.6*0.6=215.976*0.4=86.3904

1. 2025 年中国研究生“美丽中国”创新设计大赛——生物多样性保护与利用创新大赛，三等奖，（二类竞赛），1/4，
分值 120



2. 2025 年中国研究生“美丽中国”创新设计大赛——生物多样性保护与利用创新大赛，参与，（二类竞赛），3/3，
分值 $5 * 0.6 * 0.6 = 1.8$



3. 第九届青岛市大学生科技节——“潮引科技·智创未来”
大学生科普视频大赛，三等奖，（地厅级），3/3，分值 $40 * 0.6$
 $* 0.6 = 14.4$



4.Synthetic microbial community in pristine environment promotes the growth of the endangered plant *Lilium tsingtauense*. *Microbiome*, 2025.12, (Z-C) , 2/12 , 分值 $120 \times 0.6 = 72$

Synthetic microbial community in pristine environment promotes the growth of the endangered plant *Lilium tsingtauense*

Received: 06 Aug 2025

Accepted: 13 Oct 2025

Published online: 16 December 2025

Cite this article as: Liu, B., Li, X., Yang, J. et al. Synthetic microbial community in pristine environment promotes the growth of the endangered plant *Lilium tsingtauense*. *Microbiome* (2025). <https://doi.org/10.1186/s40168-025-02281-w>

Boda Liu, Xiang Li, Jinming Yang, Wanpei Lu, Guohao Tang, Yaru Shi, Jiaxing Li, Anning Ding, Hai Wang, Xuebin Song, Qingchao Liu & Xinqiang Jiang

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5. Multi-omics analysis identifies Rch-miR156 as a regulator of salt tolerance in heterografted Rosa plants. *Plant Stress*, 2025.09, (Z-D), 5/9, 分值 $60 \times 0.6 \times 0.6 \times 0.6 \times 0.6 = 7.776$



Multi-omics analysis identifies Rch-miR156 as a regulator of salt tolerance in heterografted *Rosa* plants

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ARTICLE INFO

Keywords:
Rosa chinensis
Grafting
Salt stress
Rch-miR156
RcNAC31

ABSTRACT

Rosa chinensis is commonly grafted onto salt-tolerant rootstocks to mitigate salinity stress, yet the molecular mechanisms underlying heterografting-induced adaptations in both the scion and rootstock remain unclear. Through systematic rootstock screening, we identified *R. multiflora* 'Inermis' as an optimal salt-tolerant rootstock for grafting purposes. Integrated analysis combining small RNA and transcriptome sequencing of heterografted plants after 24 days revealed 142 and 273 differentially expressed miRNAs (DEMs) in the scion (*R. chinensis*) and rootstock (*R. multiflora* 'Inermis'), respectively. Target prediction analyses indicated that these DEMs primarily modulate transcription factors (TFs) of the AUX/IAA, AP2/ERF, ARF, HD-ZIP, MYB, NAC, and bZIP families. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis demonstrated significant enrichment of DEM targets in histidine metabolism and lysine biosynthesis pathways, which are essential for osmotic adjustment and stress signaling. Notably, the Rch-miR156 isoform was markedly downregulated in heterografted scions, with RcNAC31 identified as its putative direct target TF. Functional validation demonstrated that Rch-miR156 overexpressing compromised salt tolerance in both *R. chinensis* and *R. multiflora* 'Inermis', as evidenced by increased reactive oxygen species (ROS) accumulation, elevated malondialdehyde (MDA) levels, and reduced chlorophyll content. Conversely, overexpression of RcNAC31 mitigated ROS accumulation, decreased MDA content, and consequently enhanced salt stress tolerance in *R. chinensis*. Collectively, these findings elucidate that heterografting in *Rosa* plants reshapes miRNA-mRNA regulatory networks and validates the Rch-miR156-RcNAC31 module for salt adaptation.

Introduction

Small RNAs (sRNAs) are non-coding RNAs typically 18 to 30 nucleotides (nt) in length, primarily categorized into short interfering RNAs (siRNAs) and microRNAs (miRNAs) (Carthew and Sontheimer, 2009). Among these, miRNAs represent a crucial class of sRNAs, functioning as key post-transcriptional regulators of plant genes (Rosatti et al., 2024). miRNAs play pivotal roles in diverse plant biological processes, including the regulation of plant growth and development, plant-microbe interactions, disease resistance, and the mitigation of abiotic stresses (Yang and Huang, 2014; Aslam et al., 2022; Masoomi et al., 2024). It has been established that miR156, miR159, miR160, miR164, miR166, miR167, miR168, miR169, and miR172 are

responsive to salt stress (Mallory and Vaucheret, 2006; Gao et al., 2022). For example, salt tolerance in transgenic *Arabidopsis thaliana* can be enhanced by overexpressing miR156 to regulate the miR156-SPL-DFR pathway (Cui et al., 2014). Conversely, cotton plants with silenced miR160b exhibit increased sensitivity to salt stress (Zhang et al., 2021).

Grafting is a pivotal horticultural technique involving the vascular reunion of a scion (bud or shoot) with a rootstock (a rooted plant), enabling their integration as a single physiological entity (Moore, 1982). This technique is extensively utilized to enhance crop tolerance to both abiotic (e.g., salinity, drought, chilling) and biotic stresses (e.g., soil-borne pathogens, pests) by leveraging rootstock-mediated adaptations (Zhang et al., 2021; Wang et al., 2025). In this symbiotic system,

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<https://doi.org/10.1016/j.plantstress.2025.101065>

Received 19 August 2025; Received in revised form 23 September 2025; Accepted 28 September 2025

Available online 29 September 2025

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