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2 Fig. 1 Biological identification of strain RHTA01. (A. Colony morphology of strain RHTA01; B.

3 Microscopic morphology of strain RHTA01 (×40); C. Phylogenetic analysis based on the multiple

4 sequence alignment of 16S rRNA sequences; D. Phylogenetic analysis based on the multiple sequence

5 alignment of the SSU sequence; E. Phylogenetic analysis based on the multiple sequence alignment of the

6 LSU sequence; F. Phylogenetic analysis based on the multiple sequence alignment of the RPB2 sequence.

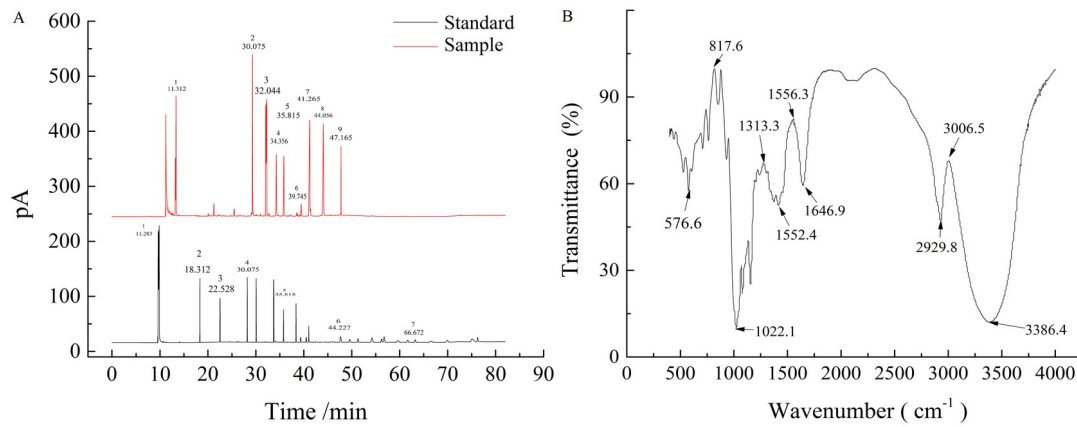7 The number of the sequence in NCBI are C1904170071/M1.Contig1: MT374076,

8 C1904170071/M3.Contig1: MT374081, C1904170071/M4.Contig1: MT377726 and the sequence number

11Fig. 2 Fatty acid analysis and functional group analysis of strain RHTA01. (A. Fatty acid analysis by gas

12chromatography. Red curve marked is the sample and black curve is the standard；B. Infrared spectrum of

13strain RHAT01 by FT-IR.)
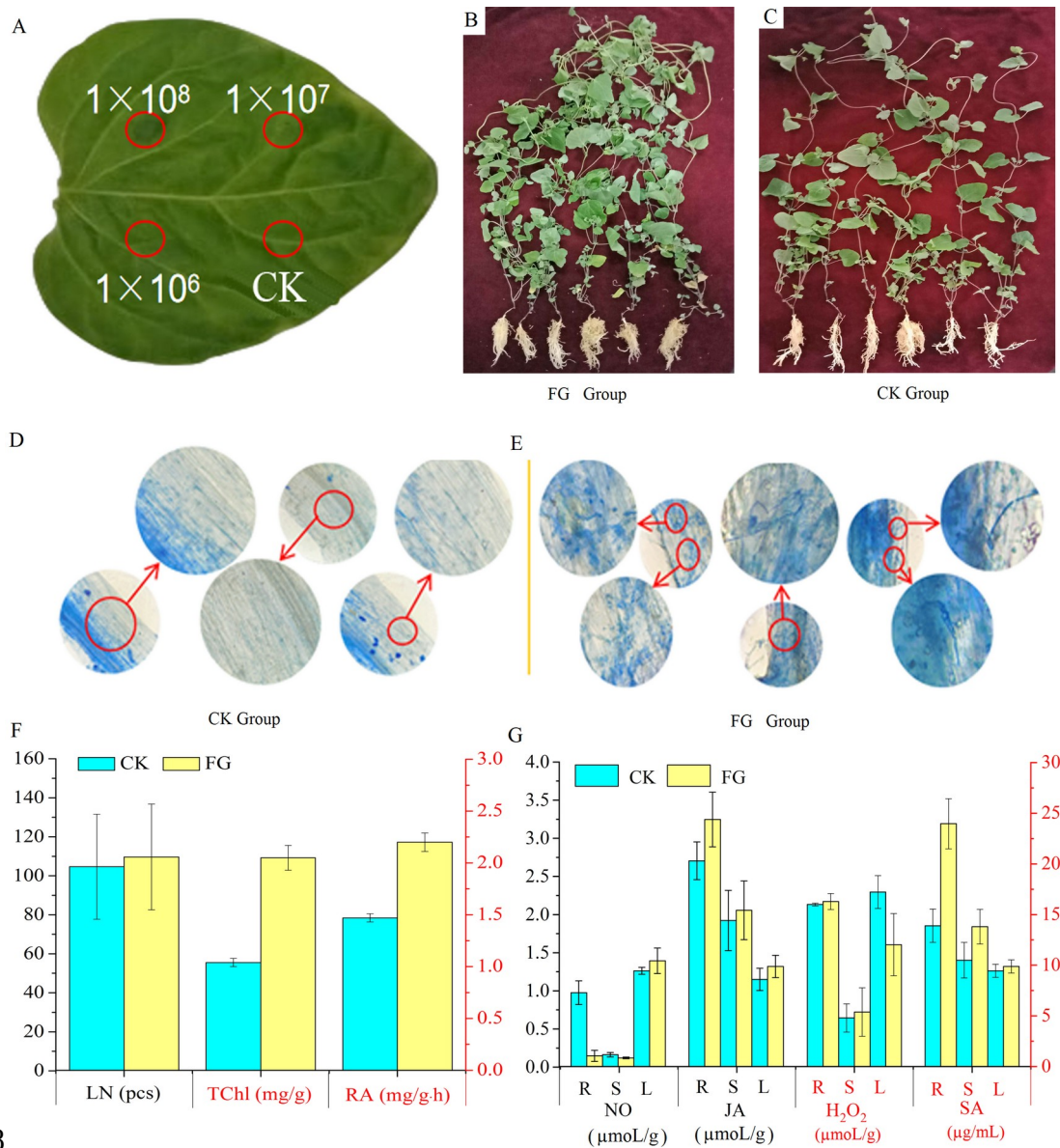
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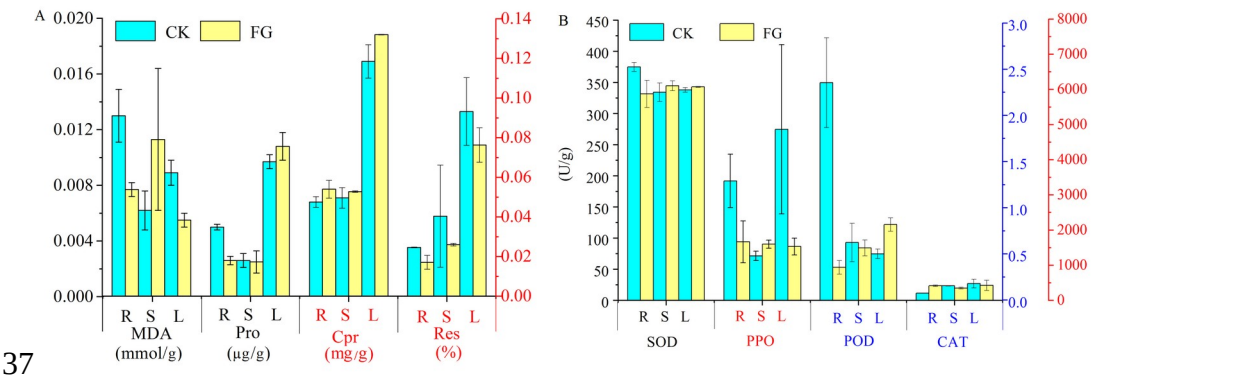17

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29Fig. 3 Effect of strain RHTA01 on the Growth of *C. pilosula*. A. Biological tests of strain RHTA01

30inoculated with *C. pilosula* leaves; B. The growth of *C. pilosula without the treatment by* strain RHTA01

31(CK, control group); C. The growth of *C. pilosula with the treatment by* strain RHTA01 (FG, treatment

32group); D. Colonization determination of strain RHTA01 in the roots of *C. pilosula*.without the treatment

33by strain RHTA01 (CK, control group); E. Colonization determination of strain RHTA01 in the roots of *C.*

34*pilosula* treated with strain RHTA01 (FG, treatment group); F. Chlorophyll content (Tchl), root activity

35(RA) and Leaf number (LN) of *C. pilosula* in the control group and treatment group; G. Signal molecular

36(SA, JA, H_2O_2 and NO) content of *C. pilosula* in the control group (CK) and FG treatment group (FG).

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38Fig. 4 The content of non-enzymatic ingredients (A) and various antioxidant enzymes activities (B) in

39different parts of *C. pilosula*. (A. The content of MDA, Pro, Cpr, Res in different parts of *C. pilosula* in

40the control group and the treatment group; B. The content of SOD, CAT, PPO, POD in different parts of *C.*

41*pilosula* in the control group and the treatment group.)

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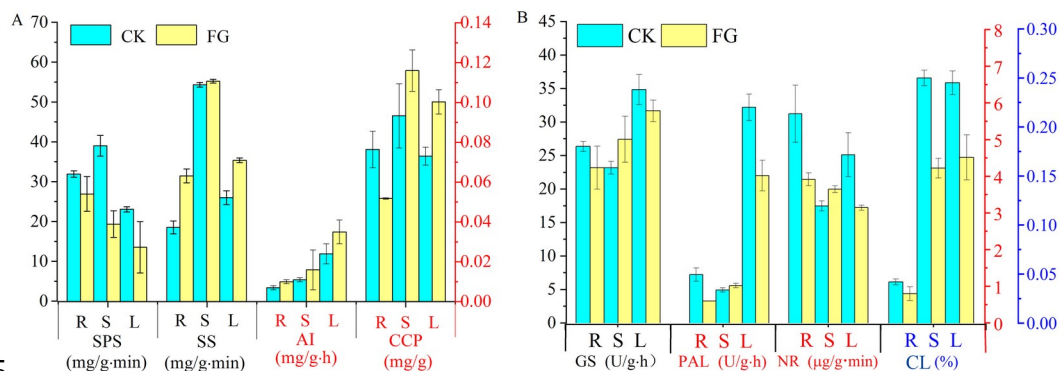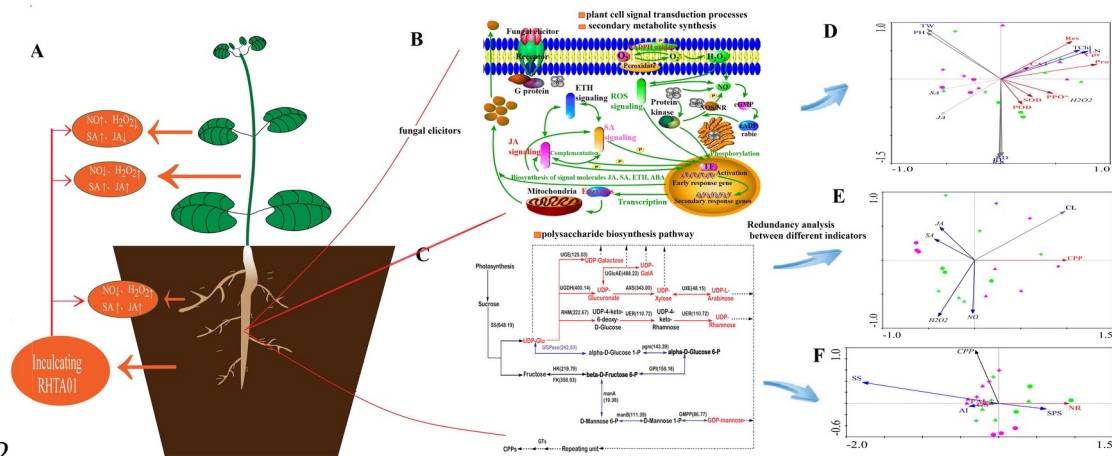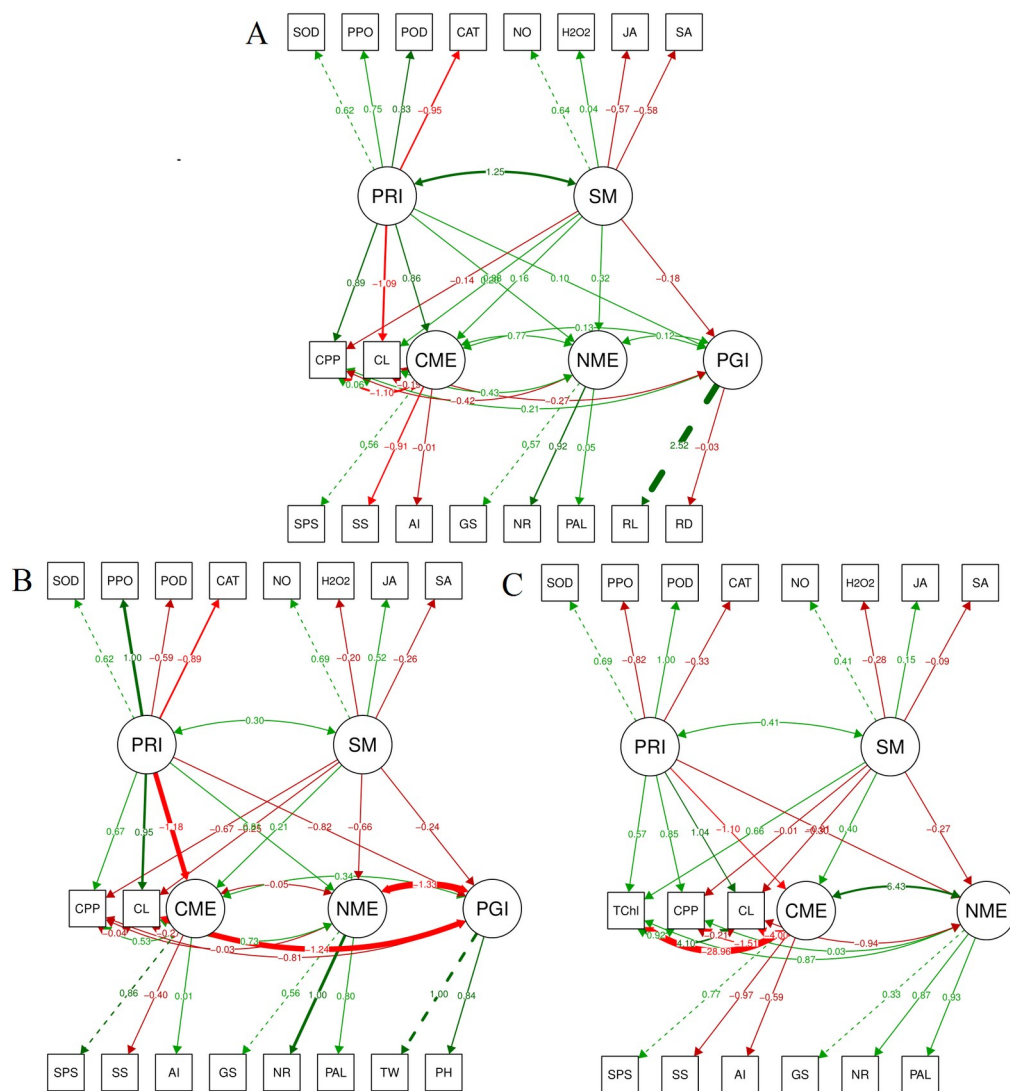52

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56 Fig. 5 The key enzymes involved in the synthesis of polysaccharide and Lobetyolin in different parts of *C.*

57 *pilosula* in the control group and the treatment group. (A. The key enzymes activity involved in

58 polysaccharide synthesis and content of polysaccharide (CCP) in different parts of *C. pilosula* in the

59 control group and the treatment group; B. The key enzymes activity involved in Lobetyolin synthesis and

60 content of Lobetyolin (CL) in different parts of *C. pilosula* in the control group and the treatment group.)

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73 Fig. 6 The correlation analysis among various biological indicators. (A. After inoculation the endophytic 74 *Trichoderma* strain RHTA01 in C. *pilosula*, the biological indicators of various parts of the host plant had 75 changed; B. After inoculated with the strain, regulated the expression of related genes, participated in plant 76 resistance and secondary metabolites accumulation; C. the biosynthesis pathway of C. *pilosula* 77 polysaccharide; D. RDA analysis showed the correlation among the contents of plant index (TChl and LN), 78 plant stress resistance index (MDA, Pro, Cpr, ReS, PPO, SOD, CAT, POD) and signaling molecules (NO, 79 H2O2, JA, SA); E. RDA analysis showed the correlation among the contents of signaling molecules (NO, 80 H2O2, JA, SA), polysaccharide synthesis (CPP) and Lobetyolin (CL); F. RDA analysis showed the 81 correlation among the contents of sucrose metabolism (sucrose phosphate synthase, SPS; sucrose synthase, 82 SS; soluble acid invertase, AI), compound synthesis (glutamine synthetase GS; phenylalanine ammonia 83 lyase ,PAL; nitrate reductase, NR) and polysaccharide synthesis (CPP).)

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85Fig. 7 Structural equation model (SEM) showed the causal relationships among Plant resistance index 86(PRI), Signal molecule (SM), Carbon metabolism enzyme (CME), Nitrogen metabolism enzyme (NME), 87Content of polysaccharide and Plant growth_index (PGI) from different parts of *C. pilosula*. (A. SEM was 88used for analysis the relationship of different indexs in the plant root; B. SEM was used for analysis the 89relationship of different indexs in the plant stem; C. SEM was used for analysis the relationship of different 90indexs in the plant leave.)