

## Interaction between nitric oxide and silicon on leghaemoglobin and S-nitrosothiol levels in soybean nodules

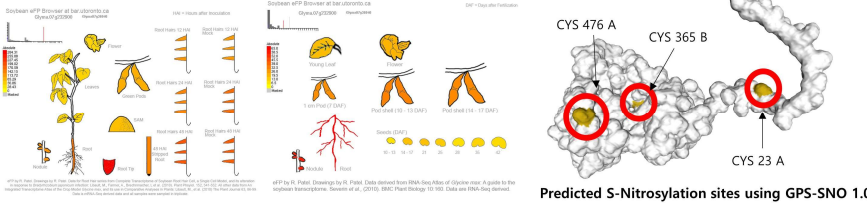
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**Table S1.** Primer lists used in the study.

Locus ID	Gene	Sequence
Glyma.19G170100	<i>Gmgsnor19g_F</i>	ATGGGAAGAGTCGGTTCTCG
	<i>Gmgsnor19g_R</i>	TTTCTCCAGAGGTGCCTTCG
Glyma09g37280	<i>GmNIP2-1_F</i>	ATCATCTTCCCCTGGCTCTCT
	<i>GmNIP2-1_R</i>	TAGCCCAGCAGAACCACTTC
GLYMA_11G121700	<i>GmLba_F</i>	AACATTCCCTCAATACAGCGTTGTG
	<i>GmLba_R</i>	CCCGTGAGCTTAGGATTAG
Glyma07g36040.1	<i>GmFLbR-1_F</i>	TGTGAAATCTCTGCCTGGGA
	<i>GmFLbR-1_R</i>	GCCCCATACTGAGCCCATT
Glyma17g04210.1	<i>GmFLbR-2_F</i>	GGGGATGGTGTGAAGCTAAC
	<i>GmFLbR-2_R</i>	GTCCAACCCAAGTTCGGCA
Glyma02g10170	<i>GmActin-F</i>	ACCCAGCAGCATGAAGATCA
	<i>GmActin-R</i>	CACATCTGCTGGAAGGTGCT

AT3G17240.1 (dihydrolipoamide dehydrogenase), Orthologs I (Glyma07g36040.1) ferric leghemoglobin reductase 1, FlbR-1

>Glyma07g36040.1 sequence type=CDS gene model=Glyma07g36040 sequence assembly version=Glyma 1.0 annotation version=1.1 JGI Gene Call confidence=high  
ATGGCGATGGCAAACTTGGCTCGACGGAAAGGTTACGCCGTCGTTTTGTCTGCGAGGTGCTGCGCTTTGTCTGACAAAGGTGGAGGGGTTCCGCTCCGGATCTGACGAAAAACGACGTCTGGTTCATCGGGCGG  
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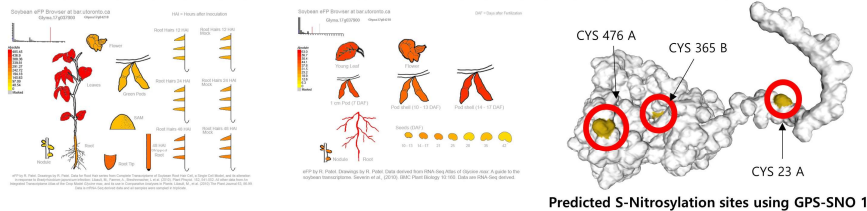
>Glyma07g36040.1 sequence type=predicted peptide gene model=Glyma07g36040 sequence assembly version=Glyma 1.0 annotation version=1.1 JGI Gene Call confidence=high  
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GKLVSPSEVSDTTEGGNTVVKGHIIATGSDVKSLPGITIDEKKVVSSTGALALTEIPKRLVIGAGYIGLEMSVWGLRGEITVVEFASEIVPTMDAIEVRKQFQRLSKQGMFKLTKVGVGDTSGDGKLTLEPAAGDQTLLEADV  
VLSAGRPTTAEGLDKIGVETDKIGIRLVNERFATNVSGVYAGDVIPIGPMPLAHKAEDGVACVEYIAGKGVGHVDYDKVPGVVYTMPEVASVGKTEQVKELGVYRKGFPFLANSRAKIDNAEGLVKILAETDKILGVHMAPNAGE  
LHEAAALQYDASSEDIARVCHAHPTMSEAVKEAMATYDKPIH\*

Threshold	Position	Peptide	Score	Cutoff	Cluster
High	365	AEEGDAVCVEYIAGK	2.565	2.443	Cluster B
Low	476	SEDIARVCHAHPTMS	1.224	0.797	Cluster A

Figure S1. Predicted S-Nitrosylation sites in the protein sequence of FlbR-1.

AT3G17240.1 (dihydrolipoamide dehydrogenase), Orthologs II (Glyma17g04210.1) ferric leghemoglobin reductase 2, FlbR-2

>Glyma17g04210.1 sequence type=CDS gene model=Glyma17g04210 sequence assembly version=Glyma 1.0 annotation version=1.1 JGI Gene Call confidence=high  
ATGGCGATGGCAAACTTGGCTCGACGGAAAGGTTACGCCGTCGTTTTGTCTGCGAGGTGCTGCGCTTTGTCTGACAAAGGTGGAGGGGATTCCGCTCCGGATCTGACGAAAAACGACGTCTGGTTCATCGGGCGG  
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GCTAATAGCAGAGCTAAGGCAATTGCAATGCTGAAGGACTGGTGAAGATATTGGCTGAAAGGAGACAGACAAGATATTGGGAGTGCACATTATGGCACCCCAATGAGGAGAGGCTTATTTCATGAAGCAGCAATAGCAGTAC  
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>Glyma17g04210.1 sequence type=predicted peptide gene model=Glyma17g04210 sequence assembly version=Glyma 1.0 annotation version=1.1 JGI Gene Call confidence=high  
MAMASLARRKGYAVVLSRRSFLTSWRGFASGSDENDVVVIGGGPGGYVAAKAAQLGLKTTIEKRGTLGGTCLNVGCPKALLHSHMYEAKHAFANHGKVFSSVEVDLPAMMAQDKAVSNLTKEGLFKKNKVN  
YVKGYSVSPSEVSDTTEGGNTVVKGHIIATGSDVKSLPGVITIDEKKVVSSTGALALTEIPKRLVIGAGYIGLEMSVWGLRGEITVVEFASEIVPTMDAIEVRKQFQRLSKQGLFKLTKVGVGDTSGDGKLTLEPAAG  
GQQTLEADVVLVSAGRPTTAEGLDKIGVETDKIGIRLVNERFATNVSGVYAGDVIPIGPMPLAHKAEDGVACVEYIAGKGVGHVDYDKVPGVVYTMPEVASVGKTEQVKELGVYRKGFPFLANSRAKIDNAEGLVKILA  
EKETDKILGVHMAPNAGELHEAAALQYDASSEDIARVCHAHPTMSEAVKEAMATYDKPIH\*

Threshold	Position	Peptide	Score	Cutoff	Cluster
High	365	AEEGDAVCVEYIAGK	2.565	2.443	Cluster B
Low	476	SEDIARVCHAHPTMS	1.224	0.797	Cluster A

Figure S2. Predicted S-Nitrosylation sites in the protein sequence of FlbR-2.

Glyma07g36040.1	MAMANLARRKGYAVVLSSRSSLC	LT	RWRGFASGSDENDVVVIGGGPGGYVAAIKAAQLGLKTT	63
Glyma17g04210.1	MAMASLARRKGYAVVLSSRSSF	CL	TSWRGFASGSDENDVVVIGGGPGGYVAAIKAAQLGLKTT	63
Glyma07g36040.1	CIEKRGTLGGTCLNVGCI	PSKALLHSSSHMYHEAKHAFANHG	VKFFSSVEVDLPAMMAQKDKAVS	126
Glyma17g04210.1	CIEKRGTLGGTCLNVGCI	PSKALLHSSSHMYHEAKHAFANHG	VKFFSSVEVDLPAMMAQKDKAVS	126
Glyma07g36040.1	NLTKGIEGLFKKKNKVNYVKGYGKL	VSPSEVSVD	TTGGNTVVKGKHI	189
Glyma17g04210.1	NLTKGIEGLFKKKNKVNYVKGYGKF	VSPSEVSVD	TTGGNTVVKGKHI	189
Glyma07g36040.1	DEKKVVSSTGALALTEIPKRL	IVIGAGYIGLEMGSVWGRLGSE	ITVVEFASEIVPTMDAEVRK	252
Glyma17g04210.1	DEKKVVSSTGALALTEIPKRL	LVIGAGYIGLEMGSVWGRLGTE	ITVVEFASEIVPTMDAEVRK	252
Glyma07g36040.1	QFQRSLEKQGMKFKLKT	KVVGVDTSGDGVKLTLEPAAGGDOTT	LEADVVLVSAGRTPFTAE	315
Glyma17g04210.1	QFQRSLEKQGLKFKLKT	KVVGVDTSGDGVKLTLEPAAGGDOTT	LEADVVLVSAGRTPFTAE	315
Glyma07g36040.1	LDKIGVETDKIGRI	LVNERFATNVSGVYAGDV	IPGPMLAHKAEEDGVACVEYIAGKVGHVDY	378
Glyma17g04210.1	LDKIGVETDKIGRI	LVNERFATNVSGVYAGDV	IPGPMLAHKAEEDGVACVEYIAGKVGHVDY	378
Glyma07g36040.1	DKVPGVVYTMPEVASVGKTEEQVKELGV	EYRVGKFPFLANSRAKAIDNAEGLVKILAEKETDK		441
Glyma17g04210.1	DKVPGVVYTMPEVASVGKTEEQVKELGV	EYRVGKFPFMAN	SRAKAIDNAEGLVKILAEKETDK	441
Glyma07g36040.1	ILGVHIMAPNAGELI	HEAAIALQYDASSEDI	ARVCHAHPTMSEAVKEAAMATYDKPIHI	501
Glyma17g04210.1	ILGVHIMAPNAGELI	HEAAIALQYDASSEDI	ARVCHAHPTMSEAVKEAAMATYDKPIHI	501

**Figure S3.** Peptide sequence alignment of two FLbR genes.