A novel stress response mechanism, triggered by indole, involved in quorum quenching enzyme MomL and iron-sulfur cluster in *Muricauda olearia* Th120

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Running title: Study of a novel stress response mechanism

Figure S1. The OD_{600} value comparison between with (black) or without indole (transparent) conditions. Error bars represent the standard deviations of three replicates. For statistical analysis, ***/ ** /* means $P<0.001$, $P<0.01$, and $P<0.05$, respectively.

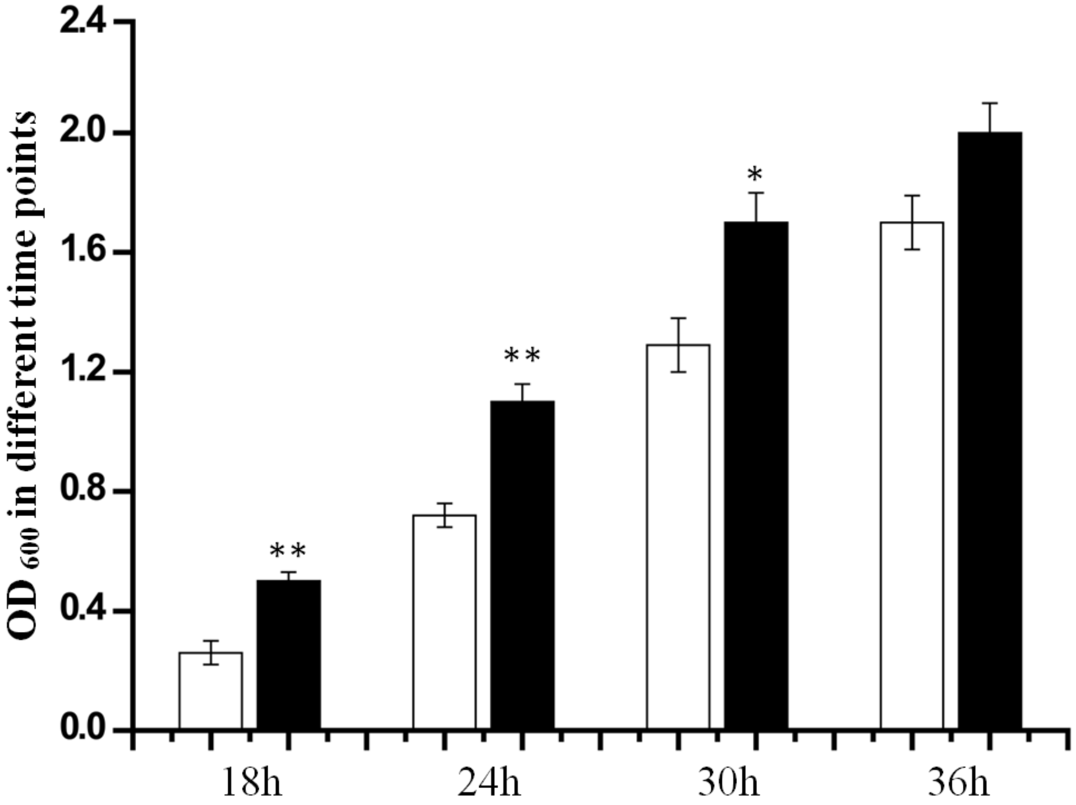
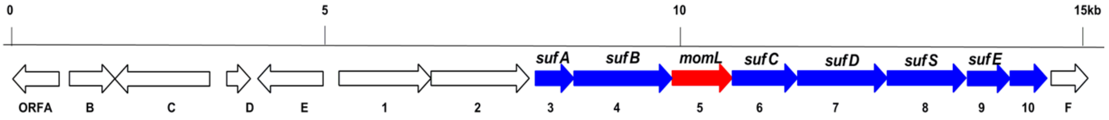
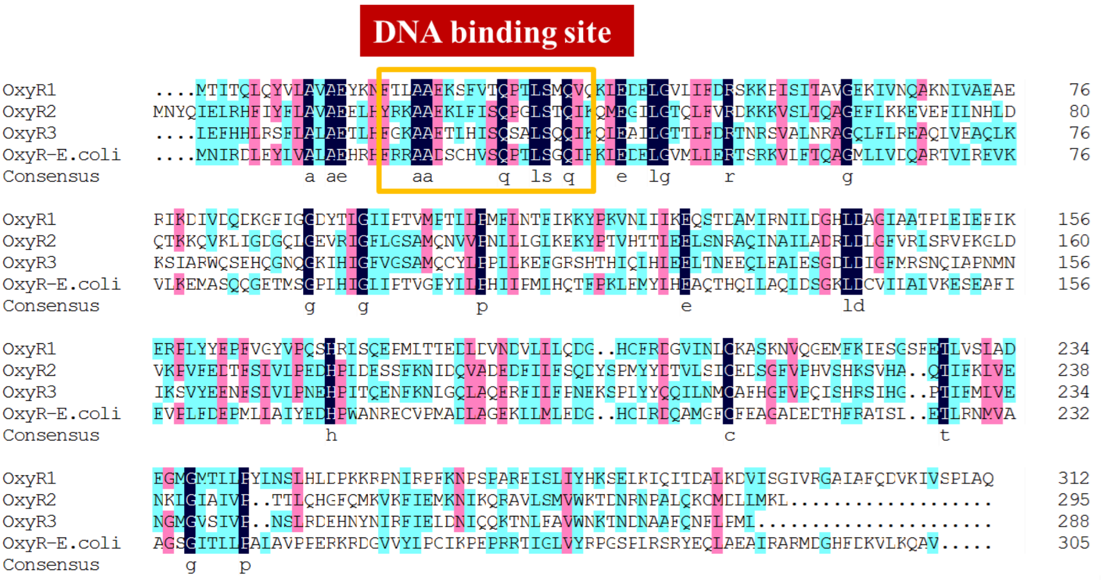


Figure S2. The gene cluster of *suf-momL* of *Muricauda olearia* Th120.



ORF	Blast homolog	#aa
ORFA	member protein	229
ORFB	membrane-associated phospholipid phosphatase	230
ORFC	branched-chain amino acid transport system carrier protein	429
ORFD	hypothetical protein	84
ORFE	thiamine-monophosphate kinase	347
ORF1	regulator/secreted protein	414
ORF2	hypothetical protein	445
ORF3	Fe-S binding protein SufA	109
ORF4	Fe-S metabolism associated SufB	481
ORF5	AHL-lactonase MomL	294
ORF6	ABC transporter ATP-binding protein SufC	249
ORF7	FeS assembly protein SufD	439
ORF8	cysteine desulfurase SufS	408
ORF9	Fe-S metabolism associated SufE	140
ORF10	Fe-S assembly suf system protein	106
ORFF	hypothetical protein	108

Figure S3. Sequence alignment of *oxyR* genes.



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OxyR1           ....MTITQLQYVLAVAEYKNFTLAAEKSFVTQPTLSMQVQKIEDELGVLIFDRSKKPISITAVGEKIVNQAKNIVAEAE    76
OxyR2           MNYQIELRHFIYFLAVAEELHYRKAAEKLFISQPGLSTQIKQMEGILGTQLFVRDKKKVSLTQAGEFIKKEVEFIINHLD    80
OxyR3           ....IEFHHLRSFLALAETLHFGKAAETIHISQSALSQQIKQIEAILGTTLFDRTNRSVALNRAGQLFLREAQIVEAQLK    76
OxyR-E.coli     ....MNIRDLEYLVALAEHRHFRRAADSCHVSQPTLSGQIRKLEDELGVMLLERTSRKVLFTQAGMLLVDQARTVLREVK    76
Consensus                     a ae      aa      q  ls q    e  lg     r          g

OxyR1           RIKDIVDQDKGFIGGDYTIGIIPTVMPTILPMPLNTFIKKYPKVNLIIKEQSTDAMIRNILDGHLDAGIAATPLEIEFIK   156
OxyR2           QTKKQVKLIGDGQLGEVRIGFLGSAMQNVVPNILLGIKEKYPTVHTTIEELSNRAQINAILADRLDLGFVRISRVPKGLD   160
OxyR3           KSIARWQSEHQGNQGKIHIGFVGSAMQCYLPPILKEFGRSHTHIQIHIEELTNEEQLEAIESGDLDIGFMRSNQIAPNMN   156
OxyR-E.coli     VLKEMASQQGETMSGPLHIGLIPTVGPYLLPHILPMLHQTFPKLEMYLHEAQTHQLLAQLDSGKLDCVILALVKESEAFI   156
Consensus                     g    g          p                  e              ld

OxyR1           ERPLYYEPFVGYVPQSHRISQEPMITTEDLDVNDVLILQDG..HCFRDGVINLCKASKNVQGEMFKIESGSFETLVSLAD   234
OxyR2           VKPVFEDTFSIVIPEDHPIDESSFKNIDQVADEDFIIFSQDYSPMYYDTVLSICEDSGFVPHVSHKSVHA..QTIFKIVE   238
OxyR3           IKSVYEENFSIVIPNEHPITQENFKNIGQLAQERFIIFPNEKSPLYYQQILNMCAFHGFVPQISHRSIHG..PTIFMIVE   234
OxyR-E.coli     EVPLFDEPMLLAIYEDHPWANRECVPMADLAGEKLLMLEDG..HCLRDQAMGFCFEAGADEDTHFRATSL..ETLRNMVA   232
Consensus                        h                                    c                   t

OxyR1           EGMGMTILPYINSLHLDPKKRPNIRPFKNPSPAREISLIYHKSELKIQITDALKDVISGIVRGAIAFQDVKIVSPLAQ     312
OxyR2           NKLGIAIVP..TTLQHGFQMKVKFIEMKNIKQRAVLSMVWKTDNRNPALQKCMDLIMKL...................     295
OxyR3           NGMGVSIVP..NSLRDEHNYNIRFIELDNIQQKTNLFAVWNKTNDNAAFQNFLPMI......................     288
OxyR-E.coli     AGSGITLLPALAVPPERKRDGVVYLPCIKPEPRRTIGLVYRPGSPLRSRYEQLAEAIRARMDGHFDKVLKQAV.....     305
Consensus          g    p
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Figure S4. the R^2value (Pearson correlation coefficient) of the transcriptome assay and real-time PCR.

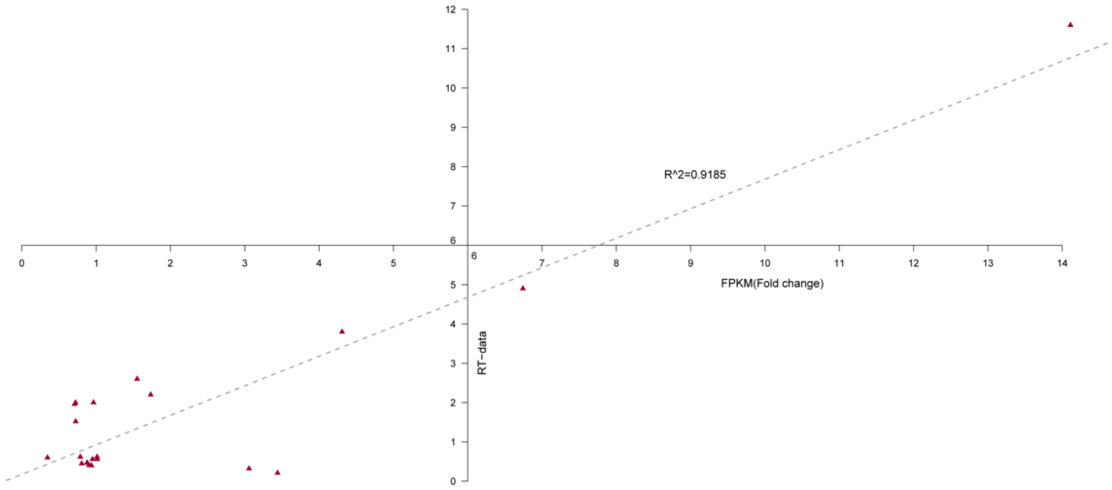

Table S1. Primer information for transcriptional analysis of target genes.

16S-forward	TACGGGAAGAAACCACC
16S-reverse	GCCAGTATCAAAGGCAAT
orfE-forward	GCCTTGCTTCCCTTTC
orfE-reverse	CCACCCAAGTCACTGTTTC
orf1-forward	TGCCTTGGTGGGTCTG
orf1-reverse	TGCCGTGATTACTTGCTT
sufA-forward	TCGGAAACAGCCAAGC
sufA-reverse	CACGGCATTATCCTCAAA
sufB-forward	TGCCGTGGATATTGTCA
sufB-reverse	CCCTTTCGGAATGTAGC
momL-forward	TCTTCCAGAGCCCTTTAC
momL-reverse	GGTTGTCCTCGCTTGTC
sufC-forward	GTCCAGAAAGGCAAGGG
sufC-reverse	CAGAATCGGTCTCATCCA
sufE-forward	TGTCAGAGTAAGGTTTGGGTA
sufE-reverse	AGTTGCTTTACCATACTCACC
orf10-forward	GAAGAAACCACCATAGATACAC
orf10-reverse	GGCAAACTTTCCGCTAC
orfF-forward	CTTGGAAACTGCGCTCTA
orfF-reverse	GATTGGCACCGAGGAA
oxyR1-forward	TGCTACTACAGGACGGACAT
oxyR1-reverse	TTGAGGGCATCGGTTAT
oxyR2-forward	TATCCTACCGTGCATACC
oxyR2-reverse	AAATCTTCATCGGCTACT
oxyR3-forward	TTGGCAATCCGAACACC
oxyR3-reverse	GGTTGGACCGCATAAAA
fur-forward	CGTGTTCACTGCCTTCC
fur-reverse	GCTTGCGTACCAGTTTG
himA-forward	ATCTTTCTTGGGAAATGTAG
himA-reverse	TCAATTCTGCTCCTGCT
himD-forward	CTTGGAGAATGGAGACA
himD-reverse	TTACGCCTTCTACAAAA

Table S2. Survival rate of *Pcc* under Km condition.

Condition	Survival rate of *Pcc*
LB+20 µg/mL Km	0
LB+25 µg/mL Km	0
LB+50 µg/mL Km	0

Table S3. The affect of boiled inactived MomL towards survival rate of *M. olearia* Th120 and *Pcc*.

Condition	Survival rate of *M. olearia* Th120	Survival rate of *Pcc*
Strains Co-culture	41%	39%
Strains Co-culture with 0.1U/ml inactived MomL	40%	40%
Strains Co-culture with 1U/ml inactived MomL	43%	42%

Table S4. List of *suf* related genes regulated by indole in the transcriptome assay.

Gene description	Fold change
sufA-sufE	5.1-8.7
momL	6.3
oxyR1	4.1

Table S5. Significantly enriched pathways and mapped genes regulated by indole based on KEGG pathway analysis.

gene categories	***p* value**	**enrich DEGs**	**NR function**	**KEGG function**	**KEGG detailed function**
Lysine biosynthesis (ko00300)	0.0184	*gene301*	diaminopimelate epimerase	K01778|*dapF*	K01778(diaminopimelate epimerase)
		gene1097	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase	K01929|*murF*	K01929(UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase)
		gene2657	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase	K01928|*murE*	K01928(UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase)
		gene3005	aspartate kinase	K00928|*lysC*	K00928(aspartate kinase)
Vancomycin resistance (ko01502)	0.0247	*gene882*	D-alanyl-D-alanine dipeptidase	K08641|*vanX*	K08641(D-alanyl-D-alanine dipeptidase)
		gene1097	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanyl ligase	K01929|*murF*	K01929(UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase)
		gene2656	phospho-N-acetylmuramoyl-pentapeptide-transferase	K01000|*mraY*	K01000(phospho-N-acetylmuramoyl-pentapeptide-transferase)
C5-Branched dibasic acid metabolism (ko00660)	0.0323	*gene160*	3-isopropylmalate dehydrogenase	K00052|*leuB*	K00052(3-isopropylmalate dehydrogenase)
		gene676	succinyl-CoA synthetase subunit beta	K01903|*sucC*	K01903(succinyl-CoA synthetase beta subunit)
		gene170	acetolactate synthase large subunit	K01652|E2.2.1.6L, *ilvB*, *ilvG*, *ilvI*	K01652(acetolactate synthase I/II/III large subunit)
Two-component system (ko02020)	0.0577	*gene1134*	LuxR family transcriptional regulator	K11618|*liaR*	K11618(two-component system, NarL family, response regulator LiaR)
		gene1255	acriflavin resistance protein	K07787|*cusA*, *silA*	K07787(Cu(I)/Ag(I) efflux system membrane protein CusA/SilA)
		gene2036	copper/silver resistance-related transport membrane protein	K07787|*cusA*, *silA*	K07787(Cu(I)/Ag(I) efflux system membrane protein CusA/SilA)
		gene882	D-alanyl-D-alanine dipeptidase	K08641|*vanX*	K08641(D-alanyl-D-alanine dipeptidase)

Table S6. List of TonB transfer system genes regulated by indole.

Gene description	Fold change
TonB-dependent receptor-1	2.3
TonB-dependent receptor-2	3.4
TonB-1	6.5
TonB-2	7.8
TonB-3	7.2