

Figure S1 Related to Figure 1. Biochemical Methods to Detect S-nitrosylation in *S. aureus* Lysates

(A) Experimental strategy to identify S-nitrosylated proteins following NO treatment of bacterial lysates by mercury resin-assisted capture of S-nitrosopeptides and mass spectrometry-based identification. NEM, N-ethylmaleimide.

(B) Biotin-switch assay of NO-treated bacterial lysates containing hemagglutinin-tagged AgrA with biotinylation of *S*-nitrosylated sulfhydryl groups and detection by immunoprecipitation-western blot. HA, hemagglutinin; IP, immunoprecipitation.

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S. aureus AgrA C. perfrigens VirR C. difficile CdtR/AgrA1 C. difficile AgrA2 L. monocytogenes AgrA E. faecalis DR75 1828 S. pyogenes FasA S. pneumoniae BlpR K. pneumoniae YehT E. coli YehT K. pneumoniae KPHS38090 E. coli YpdB	1 1 1 1 1 1 1 1 1 1 1 1 1 1		P 40 E 41 A 40 E 60 P 41 P 41 P 41 P 40 A 36 A 36 G 40 G 35
S. aureus AgrA C. perfrigens VirR C. difficile CdtR/AgrA1 C. difficile AgrA2 L. monocytogenes AgrA E. faecalis DR75 1828 S. pyogenes FasA S. pneumoniae BlpR K. pneumoniae YehT E. coli YehT K. pneumoniae KPHS38090 E. coli YpdB	41 42 41 61 42 42 42 41 37 37 37 41 36	C55 VL E GAK NMND - I G CY FLDIQL STDINGIKLGS EIRK HDPVGN I I FVT SHSEL DLLREY PENLDMLFLDIQM GELTGMETARKVRKYDDKVE I I FITALWDY LLLK ELTEKNK - VKIYFIVDAKYKISNELCDGLWIAQKIRESDYISPIIFLTNHIEM ELLNNYPKDLDILIMDIQM KTINGMDTARKIREFDHKLE I I FVT SFVEFI ELVSRMPTHQG-MGLYFLDIDLG QPDMNGFELAQEIRK FDPRGFIIFITTHAELS VLEFVKSQSRIIGLYFLDVDL QHEMSGLTLAAKIRDYDNLGK IVFVTTHGELS QLLAEVHEKGA - HQLFFLDIEIG EYTRCGLELAAAIRQKDPNAV IVFVTTHSEFI EAIGAVHKLRP - DVLFLDIQM PRISGLEMVG - MLDPEHRPY IVFLTAFDEY EGIGAVHKLRP - DVLFLDIQM PSLDGVLLAQNISQFAHKPFIVFITAWKEH	T 94 91 99 M 110 S 96 S 96 S 96 M 95 A 96 87 A 87 87 A 87 87 A 87
S. aureus AgrA C. perfrigens VirR C. difficile CdtR/AgrA1 C. difficile AgrA2 L. monocytogenes AgrA E. faecalis DR75 1828 S. pyogenes FasA S. pneumoniae BlpR K. pneumoniae YehT E. coli YehT K. pneumoniae KPHS38090 E. coli YpdB	95 92 100 111 97 97 96 88 88 88 93 88	C123 LTEVYKVAAMDFIFKD - DPAELRTRIIDCLETAHTRL QLLSKDNSVETIELKRGS (G - YEVRAFRYLIK PVKFKELQEQVTACVENILHKR YTYLT	- 149 - 137 S 153 - 156 K 150 - 149 - 148 H 142 H 142 D 150 D 144
S. aureus AgrA C. perfrigens VirR C. difficile CdtR/AgrA1 C. difficile AgrA2 L. monocytogenes AgrA E. faecalis DR75 1828 S. pyogenes FasA S. pneumoniae BlpR K. pneumoniae YehT E. coli YehT K. pneumoniae KPHS38090 E. coli YpdB	150 138 154 157 151 150 149 143 143 143 151	SVYVQY DDIMFFESSTKSHRLIAHLDNRQIEFYGNLKELSQLDDR - FFRCHNSFVVN /LKIRTEDILFLETF - ERKVIIHTNSQDYIVKMSMNKLEKELNNKGFFRCHTSYIVN LWKISFDEVIYFETSAIPHKIKLVTTSRIFEFYKSLRSLSDLDAC - FIRVHKSFVVN /DRIKIDSITYIETD - RPNILIYTHDDMYITKMSISKIEKILNEYGFFRCHNSYIVN IIHELLDDILFFETAPTIHKVILHGKNRQVEFYGKLKNIEKMLDES - FYRCHRSYIVN IRSVDMATIIFFESSSVSHKIVLHLENGEIEFYGSLKEIEEQSND - FYRCHKSYLINN QFQYPFKEVYYLETSPRAHRVILYTKTDRLEFTASLEEVFKQEPR - LLCHRSYLVN QFQYPFKEVYYLETSPRAHRVILYTKTDRLEFTASLEEVFKQEPR - LLCHRSYLVN RIVLLQMEDVAFVSSRMSGIYVTDREGKEGFTELTLRTLESRTP LLRCHRQYLVN RIYLLQMKDVAFVSSRMSGVYVTSHEGKEGFTELTLRTLESRTP LLRCHRQYLVN RIIVTSIHDIYYAEAHEKMTFVYTRR - ESFVMPMNITEFCSKLPPSHFFRCHRSFCVN	R 207 - 194 K 211 - 213 K 209 R 208 L 207 P 206 M 199 L 199 L 209 L 203
S. aureus AgrA C. perfrigens VirR C. difficile CdtR/AgrA1 C. difficile AgrA2 L. monocytogenes AgrA E. faecalis DR75 1828 S. pyogenes FasA S. pneumoniae BlpR K. pneumoniae YehT E. coli YehT K. pneumoniae KPHS38090 E. coli YpdB	208 195 212 214 209 208 207 200 200 200 210 204		

E. coli YpdB

Figure S2 Related to Figure 3. Amino Acid Sequence Alignment of AgrA with LytTR Transcription Regulators

Amino acid similarities and identities are shaded gray; stars show the position of cysteine residues also present in *S. aureus* AgrA; red stars indicate cysteines shown to mediate NO inhibition in this study.



Figure S3 Related to Figure 4. Nitric Oxide-Sensitivity of AgrA-Activitated Genes in

S. aureus with Constitutive Expression of AgrA from a Non-Native Promoter

RT-qPCR of AgrA-regulated genes after NO-treatment of *S. aureus* $\Delta agrA$ pagrA cultures expressing AgrA from the T5X non-native promoter (n=3). Data are represented as means with error bars showing standard deviation.

Student's t test, *p<0.05; ns, not significant.





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Figure S4 Related to Figure 5A. Body Surface Temperature of Mice Infected

with S. aureus

(A) Surface temperature of C57BL/6 (black circles, n=15) and congenic iNOS-/-

(red circles, n=15) mice at indicated time points post-infection with *S. aureus* Newman.

Individual values are plotted with horizontal lines showing medians of groups. X= mice euthanized due to a moribund state; Mann-Whitney U test, *p<0.05.

(B) Measurements of body surface temperature in surviving (top) and moribund (bottom) mice

(C57BL/6, black lines, n=15; iNOS^{-/-}, red lines, n=15) at indicated time points post-infection.

Dashed line at y=25°C marks one criterion used for euthanasia. Other euthanasia criteria included low mobility, labored breathing and a moribund state.





Against Bacterial Burden and Serum Cytokines

Relationship of mouse body surface temperature with log10 transformed bacterial burden (CFU/Lung) and cytokine serum levels (pg/mL) in C57BL/6 (black) and congenic iNOS knockout mice (red).

 R^2 indicates goodness of fit; **p*<0.05 indicates slope is different from zero, n=20.



Figure S6 Related to Figure 6. Deficiency in Host Nitrc Oxide Production Alters the Histopathological Pattern of Staphylococcal Pneumonia

(A) Representative H&E stains of lung sections at 20x magnification from C57BL/6 and iNOS knockout female mice infected with ~1 x 10^8 CFU at 4 h (top panels) and 8 h (bottom panels) post-infection.

(B) Representative H&E stains of lung sections at 20x magnification from C57BL/6 and iNOS knockout female mice infected with \sim 5 x 10⁷ CFU at 8 h post-infection.



Figure S7 Related to Figure 7. AgrA cysteine double mutant is partially resistant to Agr-inhibition by NO *in vitro* but not hypervirulent *in vivo*

(A) RT-qPCR of RNAIII in PAPA/NO-treated *S. aureus* Newman and *agrA* C55S C199S (double cysteine mutant) (n=3). Data are represented as means with error bars showing standard deviation. Student's t test, *p<0.05.

(B) Mouse percent mortality at indicated time points post-infection. C57BL/6 and congenic

iNOS^{-/-} mice were infected with either S. aureus Newman or agrA C55S C199S (~5 x 10⁷ CFU,

n > 12). Kaplan-Meier plot (left) and *p* values (right), **p*<0.05.

Mouse Group (n=mice per group)	Predominant Lesion Pattern	Mean Inflammatory Cell Accumulation (scale: 1-4)	Mean Bacterial Load (scale: 1-4)
4 h post-infection Inoculum: ~1 x 10 ⁸ CFU			
C57BL/6 Males (n=6)	Alveolar	1.2	2.2
C57BL/6 Females (n=5)	Alveolar	1.2	2.4
iNOS ^{-/-} Males (n=5)	Mixed	1	2
iNOS ^{-/-} Females (n=6)	Mixed	1.3	1.8
8 h post-infection Inoculum: ~1 x 10 ⁸ CFU			
C57BL/6 Males (n=7)	Focal Aggregation	3.9	3
C57BL/6 Females (n=8)	Focal Aggregation	2.4	2.5
iNOS ^{-/-} Males (n=6)	Alveolar	1.8	3.7
iNOS ^{-/-} Females (n=8)	Alveolar	2.1	2.5
8 h post-infection Inoculum: ~5 x 10 ⁷ CFU			
C57BL/6 Females (n=7)	Mixed	2.1	1.3
iNOS ^{-/-} Females (n=5)	Alveolar	1	1.8

Table S2 Related to Figure 7. Histology Scores for Lung Sections

Primer	Sequence 5'-3'	Reference
Cloning primers		
RU044	ATATGGTACCCTCGGATGAAGCTAAAGTAATAAG	This paper
RU045B	GACTTTATTATCTTATTACATACATTCACATCCTT	This paper
	A TGGCTAG	
RU048B	GGATGTGAATGTATGTAATAAGATAATAAAGTCA	This paper
	G TTAACGGC	
RU049	ATATGCGGCCGCCGTAAGCCCTCTGCTGATATG	This paper
RU044A	ATATGGTACCCTGCGCAAGTTCCGTCATGATTAT	This paper
	GTC	
RU049AA	ATATGCGGCCGCTCATTTATACGAAGGGAGCAG	This paper
	A TG	
pIMAY∆ <i>agrC</i>		
RU076	ATATGGTACCCGTATAATGACAGTGAGGAG	This paper
RU077	CACATCCTTATGGCTACATTTGAGTTAATACGAA	This paper
	TAAAAC	
RU078	CGTATTAACTCAAATGTAGCCATAAGGATGTGAA	This paper
	T GTATG	
RU079	ATATGCGGCCGCTCACCGATGCATAGCAGTG	This paper
pIMAYagrA-HA		
RU138	TTAAGCATAATCTGGAACATCATATGGATATATTT	This paper
	T TTTAACGTTTCTCACCGATGCATAGC	
RU139	TATCCATATGATGTTCCAGATTATGCTTAATAAGA	This paper
	T AATAAAGTCAGTTAACGGCG	
p <i>agrA</i>		
RU106	ATATGGTACCCATAAGGATGTGAATGTATG	This paper
RU107	ATATGGATCCAACAAGATTTACAATTGAATACGC	This paper
p <i>agrA-HA</i>		
RU116	AGCATAATCTGGAACATCATATGGATATATTTTT	This paper
	TAACGTTTCTCACCGATGCATAGCAGTGTTC	
Site-directed		
mutagenesis		
p <i>agrA</i> C6V		
RU094	GGATGTGAATGTATGAAAATTTTCATTGTCGAAG	This paper
	AC GATCCAAAACAAAGAGAAAACATG	
RU095	CATGTTTTCTCTTTGTTTTGGATCGTCTTCGACAA	This paper
	T GAAAATTTTCATACATTCACATCC	
p <i>agrA</i> C55S		
RU070	GCAAGCTAAAAATATGAATGACATAGGCTCTTAC	This paper
	TT TTTAGATATTCAACTTTC	
RU071	GCAAGCTAAAAATATGAATGACATAGGCTCTTAC	This paper
	TT TTTAGATATTCAACTTTC	
p <i>agrA</i> C123N		

Table S3 Related to STAR METHODS. Primers Used in This Paper

	-	
RU352	GCTGAATTAAGAACTCGAATTATAGACAATTTA GAAACTGCACATACACGCTTAC	This paper
RU353	GTAAGCGTGTATGTGCAGTTTCTAAATTGTCTAT	This paper
	AA TTCGAGTTCTTAATTCAGC	
p <i>agrA</i> C199S		
RU050	GAGTCAATTAGATGATCGTTTCTTTAGATCTCAT	This paper
	AA TAGCTTTGTCGTCAATCGC	
RU051	GCGATTGACGACAAAGCTATTATGAGATCTAAAG	This paper
	A AACGATCATCTAATTGACTC	
pIMAY <i>agrC</i>		
C915 C3715		
R0080	GTAACGTTTATTGTTATGAATAAATCCGCTGATG	This paper
DU004		T I :
R0081		i nis paper
		This paper
RU082		i nis paper
DI 1002		This paper
R0003		This paper
aPCR primers		
agrA F		This naner
agrA_I	GTCATTCATATTTTTAGCTTGCTC	This paper
agr/_r		This paper
agrB_R	GCACCATGTGCATGTCTTC	This paper
agriB_R	GAAGATACGTGGCAAACTGGTC	This paper
agriR_R		This paper
ChIP ₂ F	CAAATGCACTGTATAGCTGGC	This paper
ChIP, R	CAAAATAAGATTCACGGAGTAGG	This paper
amk F	AAGGTGCAAAGCAAGTTAGAA	Hirschhausen
9		et al., 2012
amk R	CTTTACGCGCTTCGTTAATAC	Hirschhausen
5 _		et al., 2012
gyrB F	TTATGGTGCTGGGCAAATACA	Goerke et al.,
		2000
gyrB_R	CACCATGTAAACCACCAGATA	Goerke et al.,
		2000
hmp_F	CGTTTAACGCCAAAAGTTAAATGG	Richardson et
		al., 2006
hmp_R	TGACTTTAGTGAATTTACACCAGG	Richardson et
		al., 2006
nrdG_F	CAGTGTTTATGTATCAGGATGTCC	Richardson et
		al., 2006
nrdG_R	GTTCGCCACCTAATAGACTTAGCC	Richardson et
		al., 2006
proC_F	GGCAGGTATTCCGATTGA	Theis et al.,

		2007
proC_R	CCAGTAACAGAGTGTCCAAC	Theis et al.,
		2007
psmα_F	CATCGCTGGCATCATTAAAG	This paper
psmα_R	5-ACCAGTGAATTTCTCAATTAATCC	This paper
psmβ_F	CGCAATTAAAGATACCGTAACTG	This paper
psmβ_R	CGATTGCTTCTGCTAGTCCAG	This paper
RNAIII_F	GAAGGAGTGATTTCAATGG	Goerke et al.,
		2000
RNAIII_R	TAAGAAAAATACATAGCACTGAG	Goerke et al.,
		2000
rpoD_F	AACTGAATCCAAGTGATCTTAGTG	Richardson et
		al., 2006
rpoD_R	TCATCACCTTGTTCAATACGTTTG	Richardson et
		al., 2006