Supporting Information

Table S1. Primer sequences used for qRT-PCR analysis of gene transcript abundance.

Gene symbol	Annotation	Primer	Gene Sequence
Nitrogen metabolism			
gdh	NADH-glutamate dehydrogenase	gdh 414F	5´-CCTGACCAGCCTTCCTATGG -3´
		gdh 513R	5´-CATGAAGCTCTGGCAGAAACG-3´
gdhA	NADPH-glutamate dehydrogenase	gdhA 324F	5´-GGGCTTTGAGCAGATCTTCAA -3´
		gdhA 432R	5´-TTCTCTGTCGGACTTGCCCTTA -3´
glnA	Glutamine synthetase, type I	glnA 257F	5´-GCAGGGTGGTGAGGTTTTTC-3´
		glnA 356R	5´-CGCGCATATTCAACTGCATT-3´
glnN	Glutamine synthetase, type III	glnN 749F	5´-TGTGGAAGCTGGGCATCTATG-3´
		glnN 848R	5´-TCAGTGGCGATGTTGGTAGTG-3´
gltB	Glutamate synthase, large subunit	gltB 785F	5´-ATGTATCACGCACGCGAATG-3´
		gltB 884R	5´-TATACCAGCTGACGCAGGTCTTC-3´
gltD	Glutamate synthase, small subunit	gltD 757F	5´-GGCAACTCCGCTATGGATGT-3´
		gltD 856R	5´-CAGTGATGCTTGCGGCTATATG-3´
amtB	Ammonium transporter	amtB 732F	5´-CACCACCACCAACCTTTCG-3´
		amtB 831R	5´-TGCGTTGAGGGTCATGGAA-3´
glnK	Nitrogen regulatory protein P-II	glnK 136F	5´-TATCGCGGCGCTGTTATAGA-3´
		glnK 235R	5´-TTCTTGCGGTGTCGATGACA-3´
nifH	Nitrogenase reductase iron protein	nifH 418F	5´-GGCTATGCCGACAAGATATTCG-3´
		nifH 517R	5´-CGCGTCCCTTGAAATTATCC-3´
ureC	Urease, alpha subunit	ureC 870F	5´-GGCAGCGTTCCCGAATG-3´
		ureC 969R	5´-ATGACACACCATGAGCATATCCA-3´
Internal control genes (ICG)			
atpD	Beta subunit of membrane ATP synthase	atpD 776F	5´-TGGCGGAGTATTTCCGTGAT-3´
		atpD 875R	5´-AGCAGAGCCGAAACCTCAGA-3´
groEL	GroEL protein	groEL 794F	5´-AGGTCGGCTACGGCTTCAA-3´
		groEL 893R	5´-TTCTGGAGAGCGCTTCTTGTG-3´
infB	Initiation factor IF2	infB 1479F	5´-CGTTGCAGAGGGTGAAGCA-3´
		infB 1578R	5´-GTGACCGGGAGTGTCCAAGA-3´
rpoB	RNA polymerase beta-subunit	rpoB 1624F	5´-TTTGAAGTCCGCGATGTTCA-3´
		rpoB 1725R	5´-GAATGATGCCAGATAGGAGATCAGA-3´
murB	UDP-N-acetylenolpyruvoylglucosamine reductase	murB 389F	5´-CCTACGGCATACCCGGAAGT-3´
		murB 488R	5´-TCAACAGCTCTGCCCAGCTT-3´
pgi	Glucose-6-phosphate isomerase	pgi 580F	5´-TTCGTTGTGCCTGATGATGTC-3´
		pgi 679R	5´-GCATCAATGCGTCGATATCG-3´

Table S2. qRT-PCR analyses of ten different nitrogen metabolism genes in *R. albus* 8 grown on different nitrogen sources.

Nitrogen source and gene annotation	Gene	Locus Tag	Transcript abundance	
			Mid	Late
Ammonium sulfate				
NADH-glutamate dehydrogenase	*gdh*	CUS_6029	$58.61^{\#b}$	82.11^{*b}
NADPH-glutamate dehydrogenase	*gdhA*	CUS_5926	$0.05^{\#a}$	0.75^{*a}
Glutamine synthetase, typeI	*glnA*	CUS_5560	$10.57^{\#a}$	20.86^{*a}
Glutamine synthetase, typeIII	*glnN*	CUS_5996	$37.52^{\#a}$	$22.67^{\#a}$
Glutamate synthase, large subunit	*gltB*	CUS_7682	$0.06^{\#a}$	9.44^{*a}
Glutamate synthase, small subunit	*gltD*	CUS_7183	$53.46^{\#b}$	106.22^{*c}
Ammonium transporter	*amtB*	CUS_5997	$0.43^{\#a}$	35.81^{*a}
Nitrogen regulatory protein P-II	*glnK*	CUS_5997	$0.82^{\#a}$	136.17^{*a}
Urease, alpha subunit	*ureC*	CUS_4996	$0.22^{\#a}$	16.33^{*a}
Nitrogenase iron protein	*nifH*	CUS_5275	$59.32^{\#b}$	95.76^{*b}
Urea				
NADH-glutamate dehydrogenase	*gdh*	CUS_6029	$31.28^{\#a}$	$41.33^{\#a}$
NADPH-glutamate dehydrogenase	*gdhA*	CUS_5926	$18.91^{\#c}$	$47.99^{\#b}$
Glutamine synthetase, typeI	*glnA*	CUS_5560	$19.43^{\#b}$	39.35^{*a}
Glutamine synthetase, typeIII	*glnN*	CUS_5996	$38.73^{\#a}$	$26.36^{\#a}$
Glutamate synthase, large subunit	*gltB*	CUS_7682	$0.64^{\#b}$	11.51^{*a}
Glutamate synthase, small subunit	*gltD*	CUS_7183	$39.63^{\#b}$	59.36^{*b}
Ammonium transporter	*amtB*	CUS_5997	$4.69^{\#b}$	35.95^{*a}
Nitrogen regulatory protein P-II	*glnK*	CUS_5997	$11.96^{\#b}$	124.41^{*a}
Urease, alpha subunit	*ureC*	CUS_4996	$5.23^{\#b}$	34.59^{*b}
Nitrogenase iron protein	*nifH*	CUS_5275	$37.11^{\#b}$	90.28^{*b}
Peptides				
NADH-glutamate dehydrogenase	*gdh*	CUS_6029	$76.08^{\#b}$	$69.79^{\#b}$
NADPH-glutamate dehydrogenase	*gdhA*	CUS_5926	$1.21^{\#b}$	218.44^{*c}
Glutamine synthetase, typeI	*glnA*	CUS_5560	$57.23^{\#c}$	274.46^{*c}
Glutamine synthetase, typeIII	*glnN*	CUS_5996	$32.57^{\#a}$	111.41^{*b}
Glutamate synthase, large subunit	*gltB*	CUS_7682	$5.54^{\#c}$	412.94^{*b}
Glutamate synthase, small subunit	*gltD*	CUS_7183	21.10^{a}	19.58^{a}
Ammonium transporter	*amtB*	CUS_5997	$8.67^{\#c}$	354.43^{*b}
Nitrogen regulatory protein P-II	*glnK*	CUS_5997	$7.40^{\#b}$	202.98^{*b}
Urease, alpha subunit	*ureC*	CUS_4996	$7.93^{\#b}$	351.04^{*c}
Nitrogenase iron protein	*nifH*	CUS_5275	15.49^{a}	14.86^{a}

Symbols are used to represent statistical differences. When comparing nitrogen source or growth phase, absence of a symbol indicates no statistical difference. Otherwise, data is grouped: those that are not statistically different from one another have the same letter or character, while those that are statistically different have different letters or characters. ^{a}, ^{b}, and ^{c} denote significant ($P < 0.05$) differences between nitrogen sources, while $^{\#}$, *, and $^{\$}$ denote significant ($P < 0.05$) effects by different growth phase.

Table S3. Effect of ammonia and urea on enzyme activities in *R. albus* 8 in early log phase growth.

Nitrogen source	Log phase	GDH		GS		GOGAT		Urease
		nmol/min/mg		U/min/mg	nmolPi/min/mg	nmol/min/mg		U/min/mg
		NADPH	NADH	γ-transferase	Biosynthetic	NADPH	NADH	
Ammonia	Early	5.3$^{\#a}$	95.4$^{\#a}$	2.2$^{\#c}$	2699.9$^{\#c}$	0.1	< 0	11.4$^{\#a}$
Urea	Early	6.8$^{\#a}$	90.0$^{\#a}$	0.4$^{\#b}$	2378.9$^{\#b}$	< 0	< 0	39.7$^{\#b}$
SE		3.7	18.0	0.1	94.0	0.1	0.1	3.0

Symbols are used to represent statistical differences. When comparing nitrogen source or growth phase, absence of a symbol indicates no statistical difference. Otherwise, data is grouped: those that are not statistically different from one another have the same letter or character, while those that are statistically different have different letters or characters. ^{a}, ^{b}, and ^{c} denote significant ($P < 0.05$) differences between nitrogen sources, while $^{\#}$, *, and $^{\$}$ denote significant ($P < 0.05$) effects by different growth phase.

Table S4. qRT-PCR analyses of ten different nitrogen metabolism genes in *R. albus* 8 grown on ammonia and urea in early log phase growth.

Nitrogen source and gene annotation	Gene	Locus Tag	Transcript abundance
			Early
Ammonium sulfate			
NADH-glutamate dehydrogenase	*gdh*	CUS_6029	$48.01^{\#a}$
NADPH-glutamate dehydrogenase	*gdhA*	CUS_5926	$0.04^{\#a}$
Glutamine synthetase, typeI	*glnA*	CUS_5560	$10.97^{\#a}$
Glutamine synthetase, typeIII	*glnN*	CUS_5996	$27.58^{\#a}$
Glutamate synthase, large subunit	*gltB*	CUS_7682	$0.07^{\#a}$
Glutamate synthase, small subunit	*gltD*	CUS_7183	$35.42^{\#a}$
Ammonium transporter	*amtB*	CUS_5997	$0.15^{\#a}$
Nitrogen regulatory protein P-II	*glnK*	CUS_5997	$0.30^{\#a}$
Urease, alpha subunit	*ureC*	CUS_4996	$0.17^{\#a}$
Nitrogenase iron protein	*nifH*	CUS_5275	$29.93^{\#a}$
Urea			
NADH-glutamate dehydrogenase	*gdh*	CUS_6029	$32.59^{\#a}$
NADPH-glutamate dehydrogenase	*gdhA*	CUS_5926	$27.51^{\#c}$
Glutamine synthetase, typeI	*glnA*	CUS_5560	$14.35^{\#a}$
Glutamine synthetase, typeIII	*glnN*	CUS_5996	$36.47^{\#a}$
Glutamate synthase, large subunit	*gltB*	CUS_7682	$0.54^{\#b}$
Glutamate synthase, small subunit	*gltD*	CUS_7183	$35.33^{\#a}$
Ammonium transporter	*amtB*	CUS_5997	$3.23^{\#b}$
Nitrogen regulatory protein P-II	*glnK*	CUS_5997	$6.46^{\#b}$
Urease, alpha subunit	*ureC*	CUS_4996	$3.24^{\#a}$
Nitrogenase iron protein	*nifH*	CUS_5275	$27.80^{\#a}$

Symbols are used to represent statistical differences. When comparing nitrogen source or growth phase, absence of a symbol indicates no statistical difference. Otherwise, data is grouped: those that are not statistically different from one another have the same letter or character, while those that are statistically different have different letters or characters. ^{a}, ^{b}, and ^{c} denote significant ($P < 0.05$) differences between nitrogen sources, while $^{\#}$, *, and $^{\$}$ denote significant ($P < 0.05$) effects by different growth phase.