Subsystem: Ammonia Assimilation

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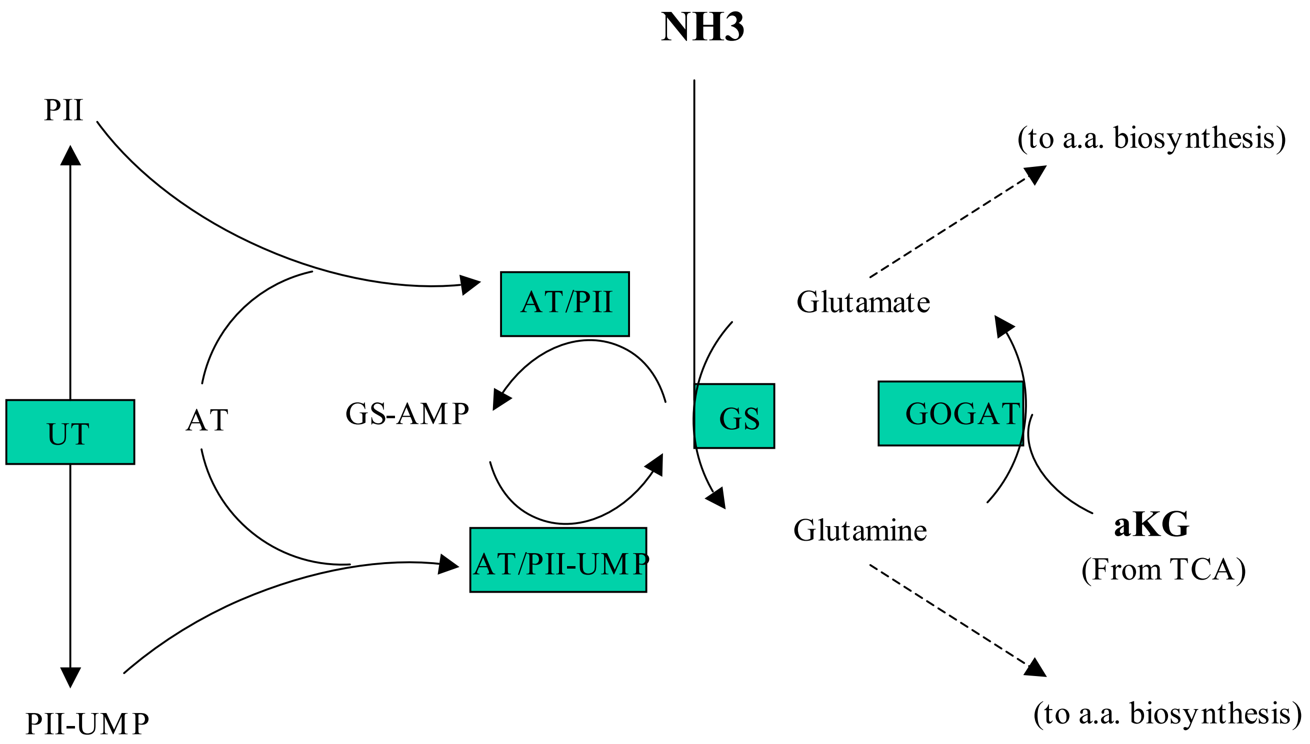
Introduction

Abbrev	Functional Role
GS1	Glutamine synthetase (EC 6.3.1.2)
AT	Glutamate-ammonia-ligase adenylyltransferase (EC 2.7.7.42)
PII	Nitrogen regulatory protein P-II
PIIK	Nitrogen regulatory protein P-II, glnK
UT	[Protein-PII] uridylyltransferase (EC 2.7.7.59)
GOGDP1	Glutamate synthase [NADPH] large chain (EC 1.4.1.13)
GOGDP2	Glutamate synthase [NADPH] small chain (EC 1.4.1.13)
GOGATF	Ferredoxin-dependent glutamate synthase (EC 1.4.7.1)
GOGD	Glutamate synthase [NADH] (EC 1.4.1.14)
NRI	Nitrogen regulation protein NR(I)
NRII	Nitrogen regulation protein NR(II) (EC 2.7.3.-)
NtcA	Global nitrogen regulatory protein, CRP family of transcriptional regulators
IF7	Glutamine synthetase inactivating factor IF7
IF17	Glutamine synthetase inactivating factor IF17

- ***Ammonia, nitrite and nitrate assimilation supply nitrogen for biosynthesis.***
- ***Ammonia assimilation can occur via glutamate dehydrogenase (GDH) or GS-GOGAT pathways. The latter is shown here. When both capabilities exist in an organism, GS-GOGAT route prevails in low ammonia conditions.***
- ***The subsystem is particularly interesting because of the regulatory aspects involved: post-translational modification of several enzymes and a signaling system.***
- ***The system holds little functional clustering compared to other subsystems. This and the difficulty of identifying signaling genes made this an interesting test case: Can a clear classification of the variations in the GS, GOGAT, and AT subsets be used to help identify or constrain the possible signaling and regulatory variations?***

Ammonia Assimilation: Subsystem diagram



- ***In some organisms, Glutamine synthetase is partly regulated by adenylylation. The effector, Adenylyltransferase is itself regulated by the regulatory protein, PII: binding PII vs. PII-UMP determines whether de-adenylylation or adenylylation occurs. Interconversion of PII and PII-UMP is accomplished by Uridylyltransferase, UT. This is the story in some bacteria (e.g. E. coli) but not all. In cyanobacteria the control is not by adenylylation but perhaps by phosphorylation of a related compound and/or the action of IF7 and IF17.***

Ammonia Assimilation Spreadsheet : Examples of variations

Organism	**GS1**	**AT**	**PII**	**PIIK**	**UT**	**GOGDP1**	**GOGDP2**	**GOGATF**	**GOGD**	**NRI**	**NRII**	**IF7**	**IF17**
Anabaena variabilis ATCC 29413			3138					4866				3127	
Synechococcus elongatus PCC 7942	1461							237				247	
Synechococcus sp. WH 8102	1068							2125					
Trichodesmium erythraeum IMS101	5780		4778					4553					
Crocosphaera watsonii WH 8501	3868		3936					4121					
Gloeobacter violaceus PCC 7421	1052		256, 689					1508					
Prochlorococcus marinus MED4	1377		709					659					
Prochlorococcus marinus str. MIT 9313	601		1475					1771					
Nostoc sp. PCC7120	2635		2626					4651				2636	
Synechocystis sp. PCC 6803	1933,476		1956			439	198	2982				571	415
Escherichia coli O157:H7 EDL933	4803	3936	3417		169	4094	4095			4801	4802		
Escherichia coli CFT073	4717	3715	3000	546	196	3882	3382, 3883			4715	4716		
Escherichia coli K12	3790	3001	2523	447	167	3155	3156			3788	3789		

Open problems, comments, conjectures

- ***Protein PII (glnB) has a variant (glnK). Clustal alignment yields a tree that can be painted with data from organisms discussed in (Arcondeguy, et al., 2001). The result (a calibrated tree) appears useful for making assignments in other organisms.***
- ***Ferredoxin-dependent, NADH-dependent, and NADPH-dependent GOGAT can be distinguished by length and functional clustering: the NADPH-dependent occurs as a pair while Fd-dependent appears singly and equal in size to the large subunit of the NADPH-dependent. NADH-dependent appears singly but equal in length to the sum of the two chains of NADPH-dependent.***
- ***The NADPH-dependent large and small subunits are functionally clustered to the NRI and NRII. Is this true in all cases when NRI and NRII are present or only in the organisms studied so far? Projection of this cluster across organisms reveals a number of possible incorrectly called genes.***
- ***Are the NADPH-dependent assignments in Synechocystis correct?***
- ***Why are so few IF7 and IF17 found in the cyanobacteria?***

References:

1. Merrick MJ, Edwards RA. Nitrogen Control in Bacteria. Microbiological Reviews **59**, 604-22 (1995)
2. Arcondeguy T, Jack R, Merrick M. PII Signal Transduction Proteins, Pivotal Players in Microbial Nitrogen Control. Microbiology and Molecular Biology Reviews **65,** 80-105 (2001)
3. Herroro A, Muro-Pastor AM, Flores E. Nitrogen Control in Cyanobacteria. J. of Bacteriaology. **183,** 411-25.
4. Rhodes D. http://www.hort.purdue.edu/rhodcv/hort640c/INDEX.HTM