

# Engineering Plant C<sub>1</sub> Metabolism

- **Personnel** - 5 PIs & labs, funding
- **Background** - overview of plant C<sub>1</sub> metabolism
- **Objectives** - review of project aims
- **Progress** - methylene-THF reductase
  - genomics/pathway disc./compartmentation
  - development of transgenics/mutants
  - ME of glycine betaine (GB) synthesis in tobacco; labeling, metabolic modeling
  - comparison of wildtype & GB-deficient maize; labeling, C<sub>1</sub> DNA microarrays
- **Project outputs** - publications, workshops, websites

# Plant C<sub>1</sub> Metabolism Group

PI	(Univ)	Expertise	GAs/PDFs
Hanson	(UF)	Biochem/Mol Biol	1.5
Bohnert	(UA)	Mol Biol	1
Rhodes	(Purdue)	Modeling/Biochem	1
Gage	(MSU)	An Biochem/MS	1
Shachar-Hill	(NMSU)	NMR/P-Biochem	1

# Funding Agencies

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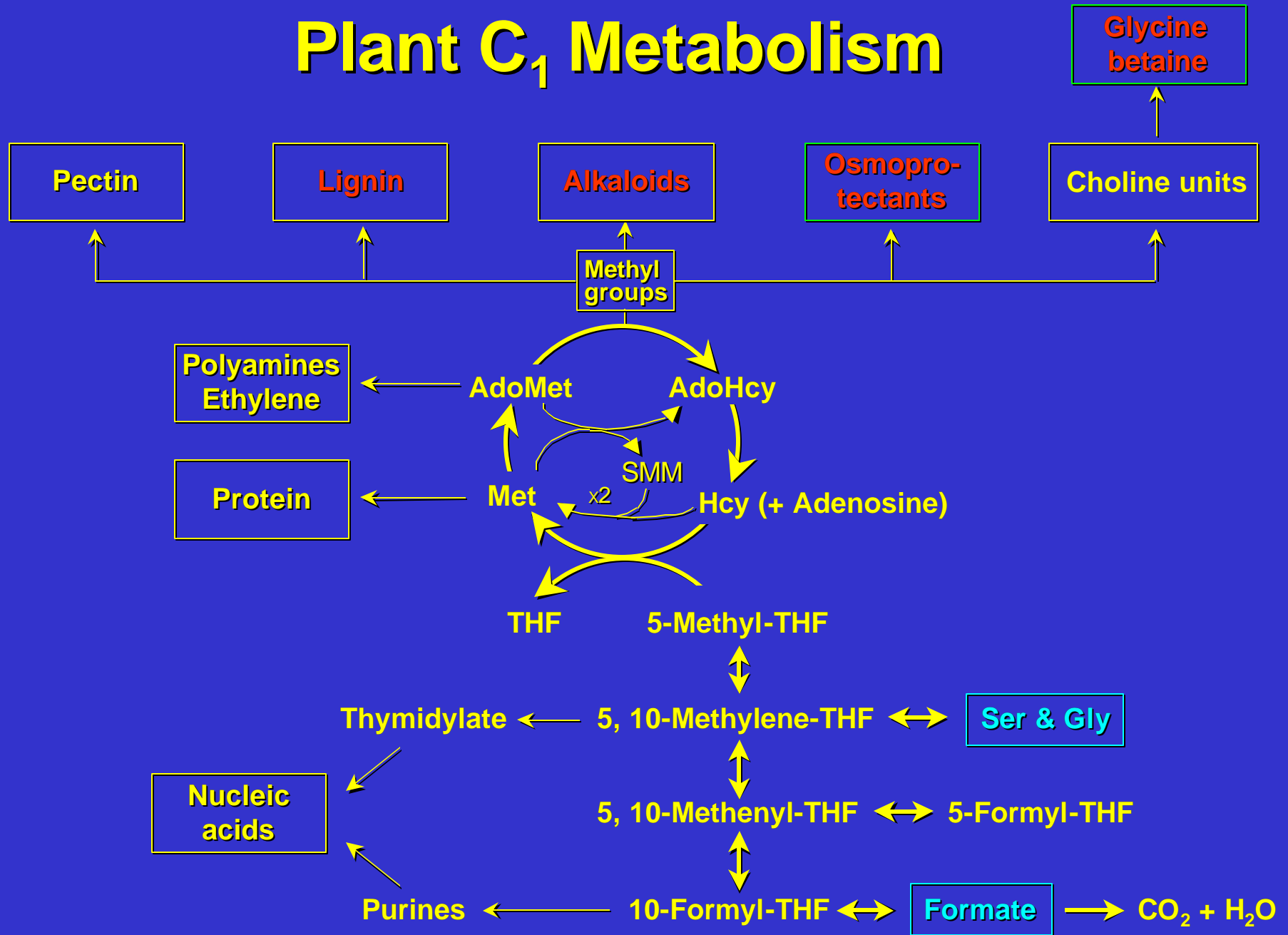
<b>PI</b>	<b>Agency</b>	<b>Award dates</b>
<b>Hanson</b>	<b>NSF-IBN</b>	<b>Feb 99 - Jan 02</b>
<b>Bohnert</b>	<b>NSF-IBN</b>	<b>Feb 99 - Jan 02</b>
<b>Gage</b>	<b>NSF-BES</b>	<b>Feb 99 - Jan 02</b>
<b>Rhodes</b>	<b>DOE-BES</b>	<b>Sep 99 - Aug 02</b>
<b>Shachar-Hill</b>	<b>NIST</b>	<b>May 00 - Apr 01</b>

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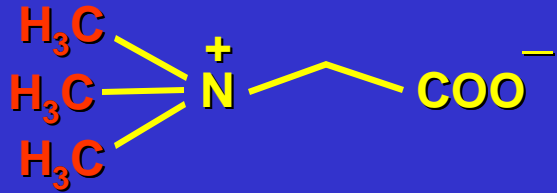
# Background on Plant C<sub>1</sub> Metabolism

- Provides C<sub>1</sub> units (methyl, methylene, formyl) for biosyntheses - all are essential
- Engineering high-methyl products (e.g. lignin, alkaloids, osmoprotectants) competes with other metabolism for C<sub>1</sub> units

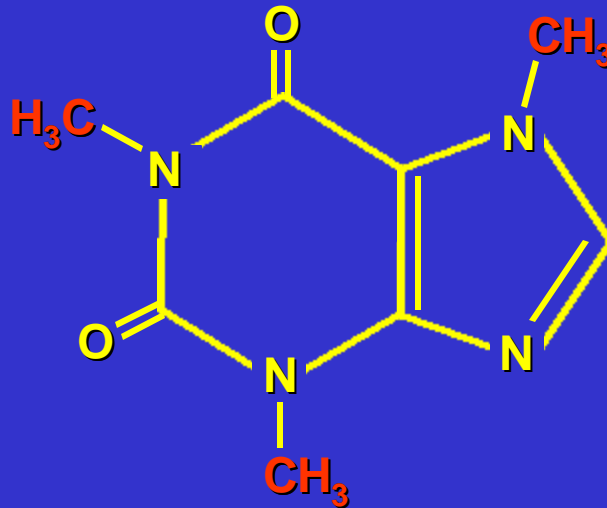
# Plant C<sub>1</sub> Metabolism



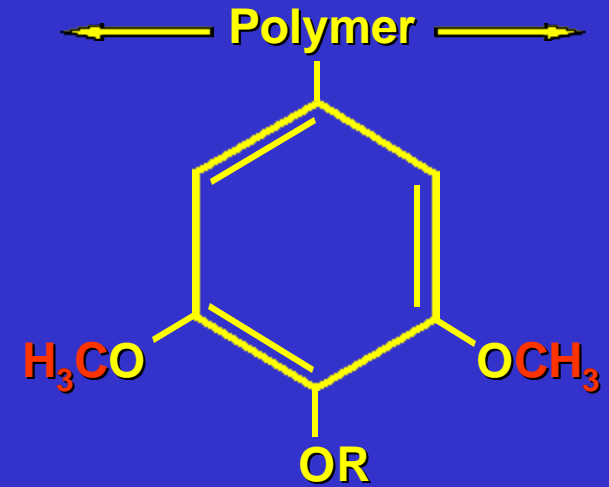
# High-Methyl Engineered Products



**Glycine betaine**  
(osmoprotectant)

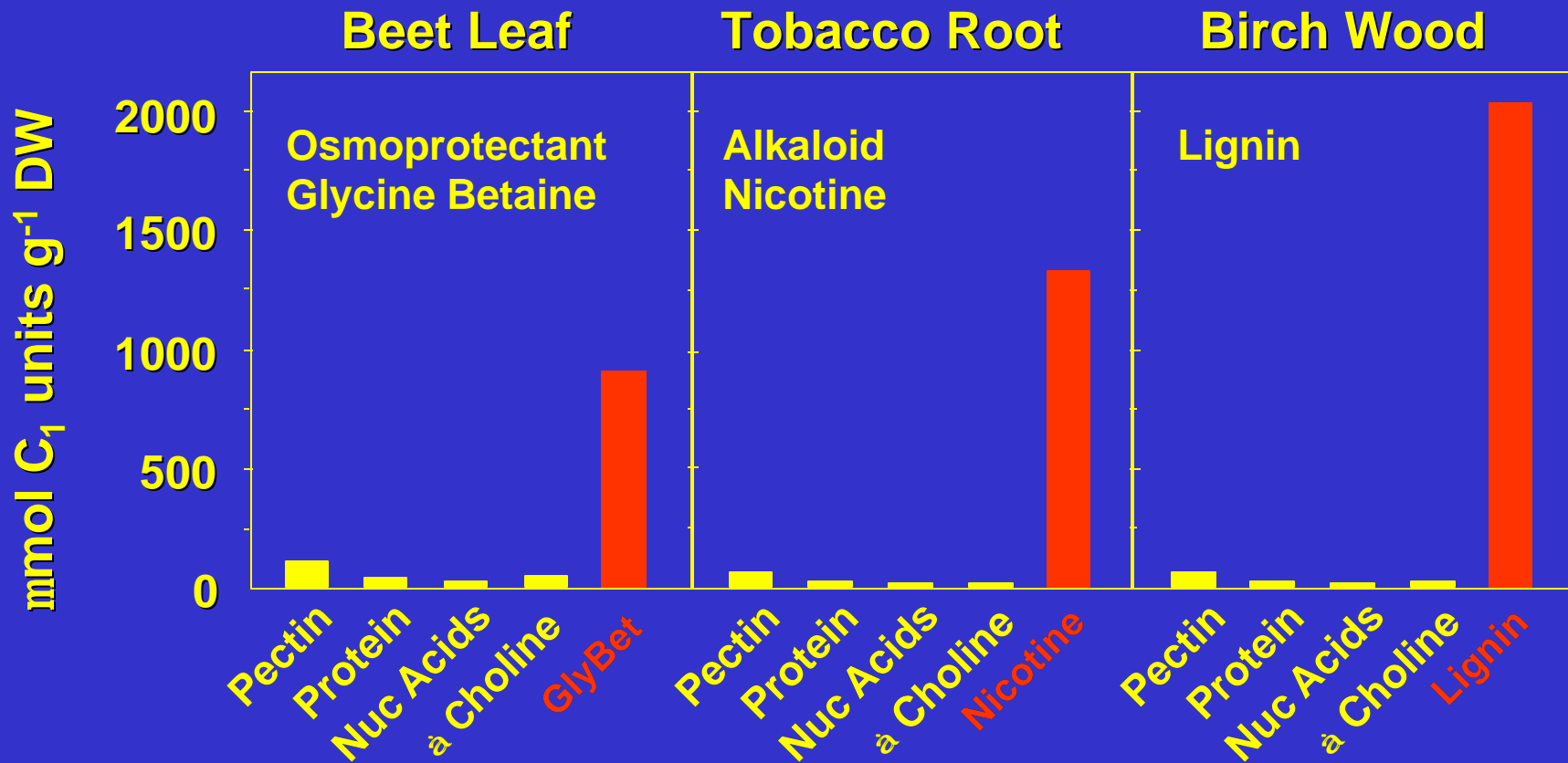


**Caffeine**  
(alkaloid)



**Syringyl lignin**

# The scale of C<sub>1</sub> demands in plants



# Engineering Questions

- **System response to  $C_1$  demand - or  $^-$  ?**
  - **Metabolic flux**
  - **Gene Expression**
- **Enzymes exerting major flux control ?**
- **Relative importance of  $C_1$  sources ?**
- **More pathways ? Compartmentation ?**



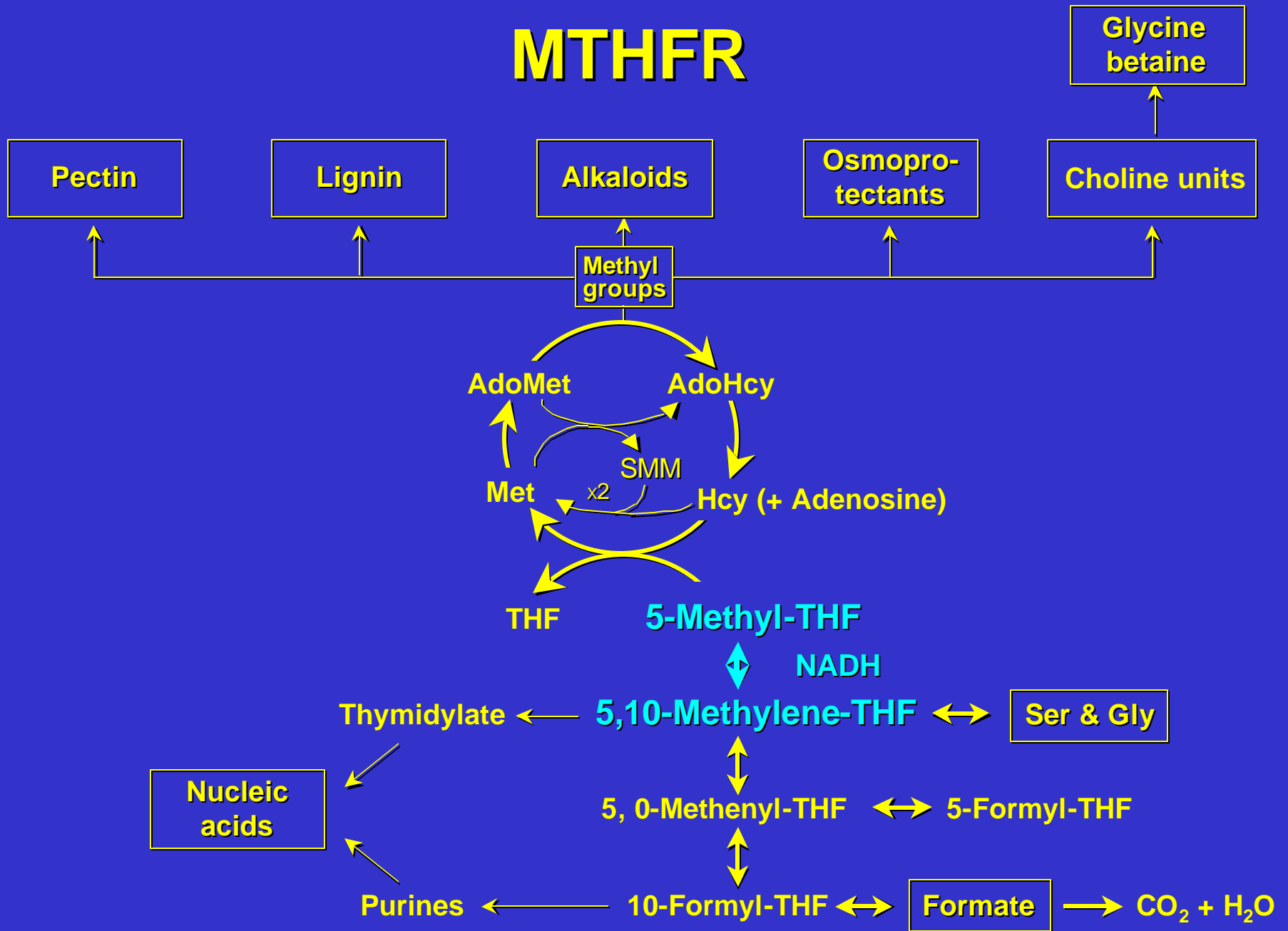
# Engineering Objectives (Tobacco and maize)

- Essential preliminary cloning, build DNA arrays
  - MTHFR de novo
  - » 20 genes by homology
- Raise or lower  $C_1$  demand and supply
  - Antisense/sense
  - Mutants
- Measure fluxes (MS, NMR, radiolabeling, MFA/  
modeling) & gene expression (DNA arrays)

## Progress (Years 1 & 2)

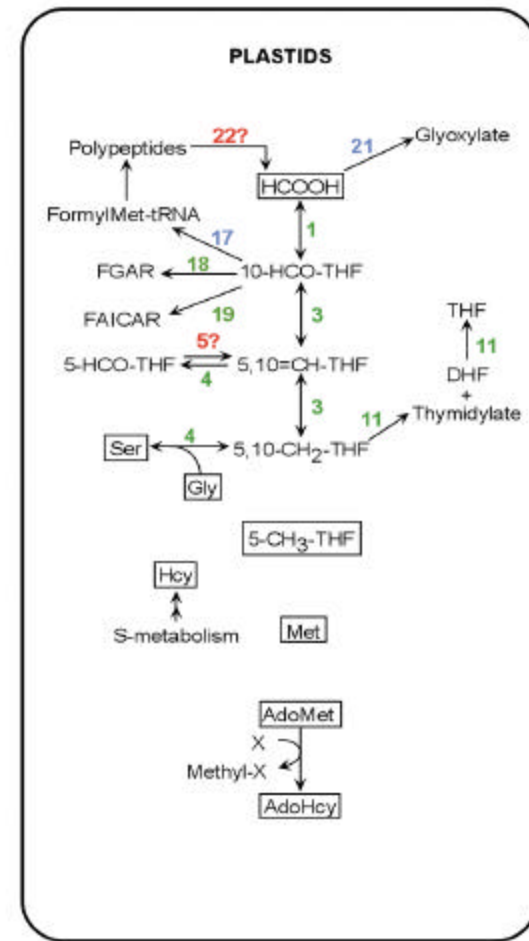
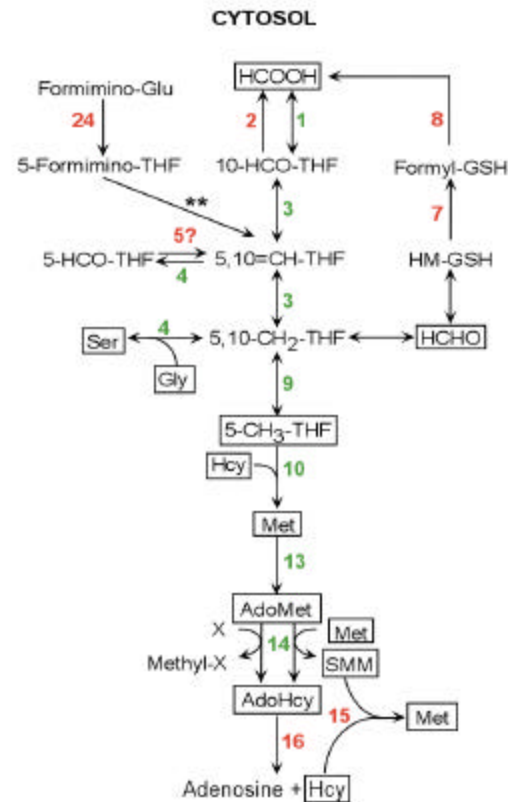
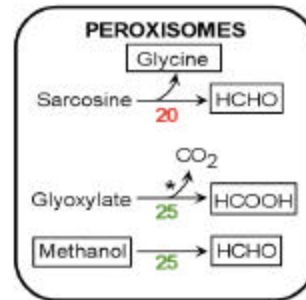
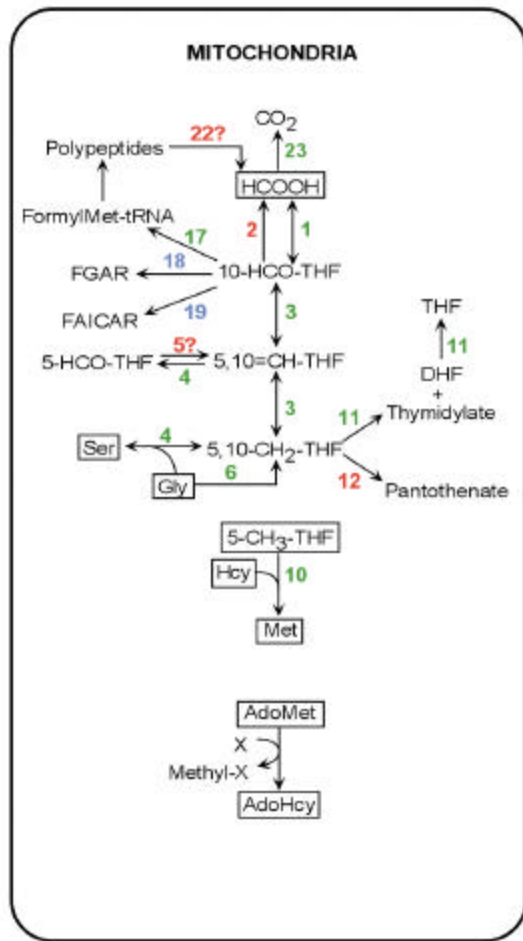
- **Methylene-THF reductase**
- **Genomics & pathway discovery**
- **Development of transgenics/mutants**
- **Engineering glycine betaine synthesis;  
labeling & modeling (tobacco)**
- **Maize C<sub>1</sub> DNA arrays & labeling in wildtype  
& glycine betaine-deficient mutant lines**

# MTHFR

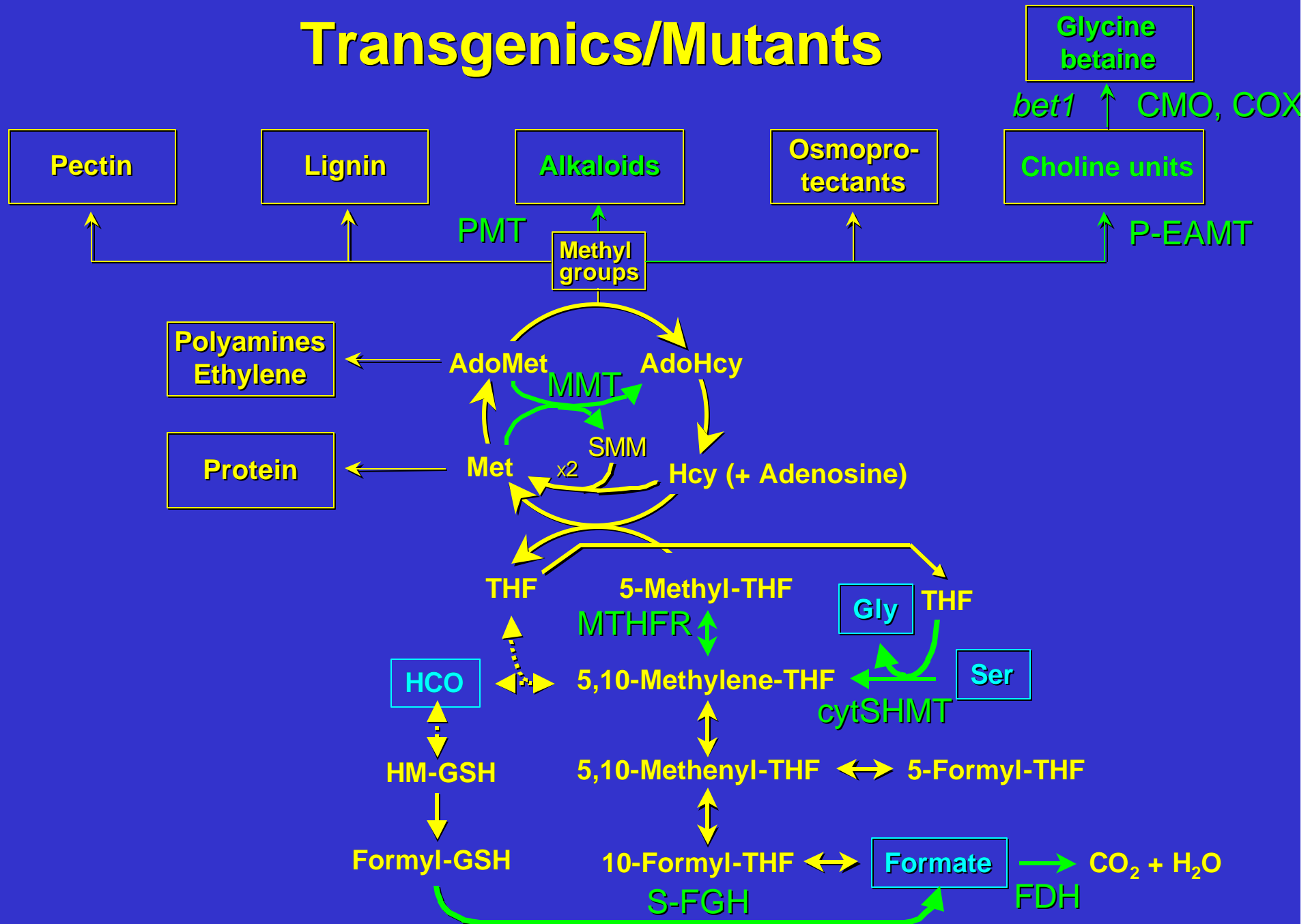


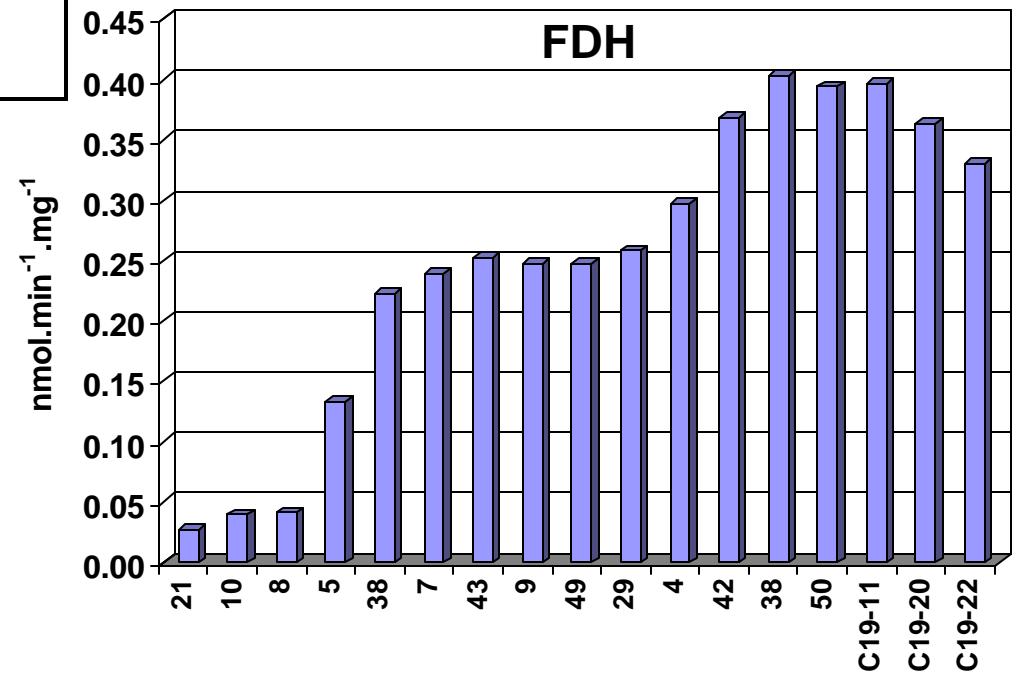
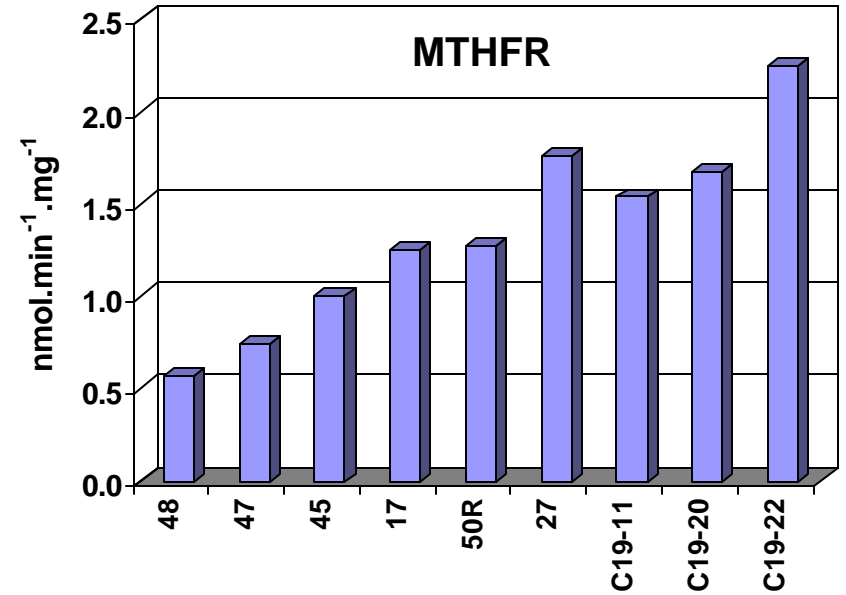
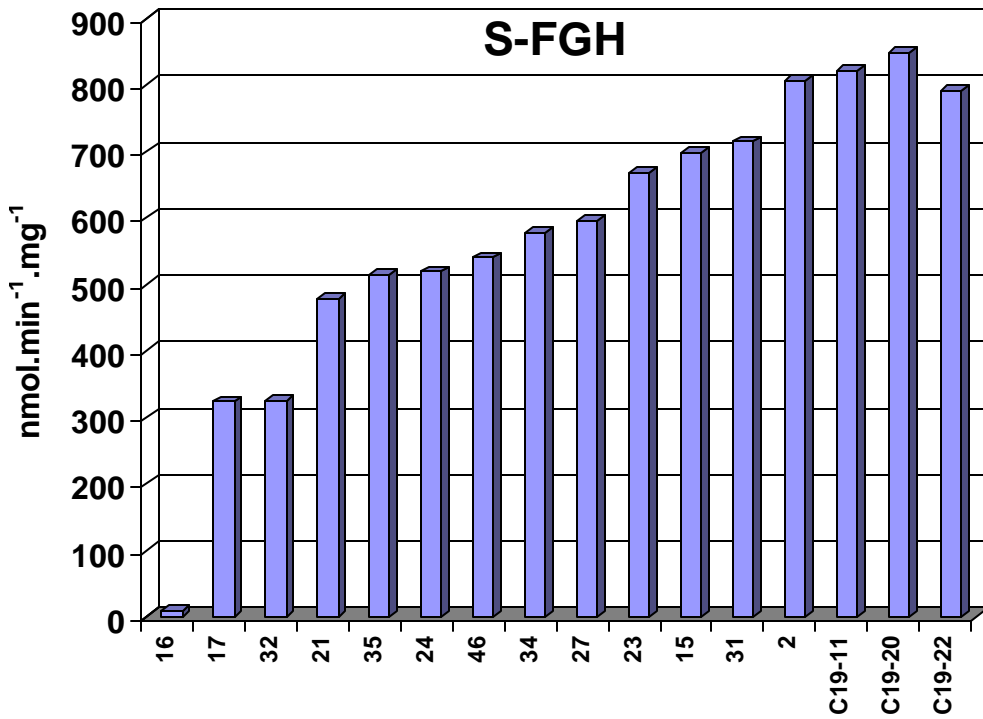
# Genomics & pathway discovery; compartmentation

from *TIPS* Review (Hanson, Gage, Shachar-Hill)



# Transgenics/Mutants

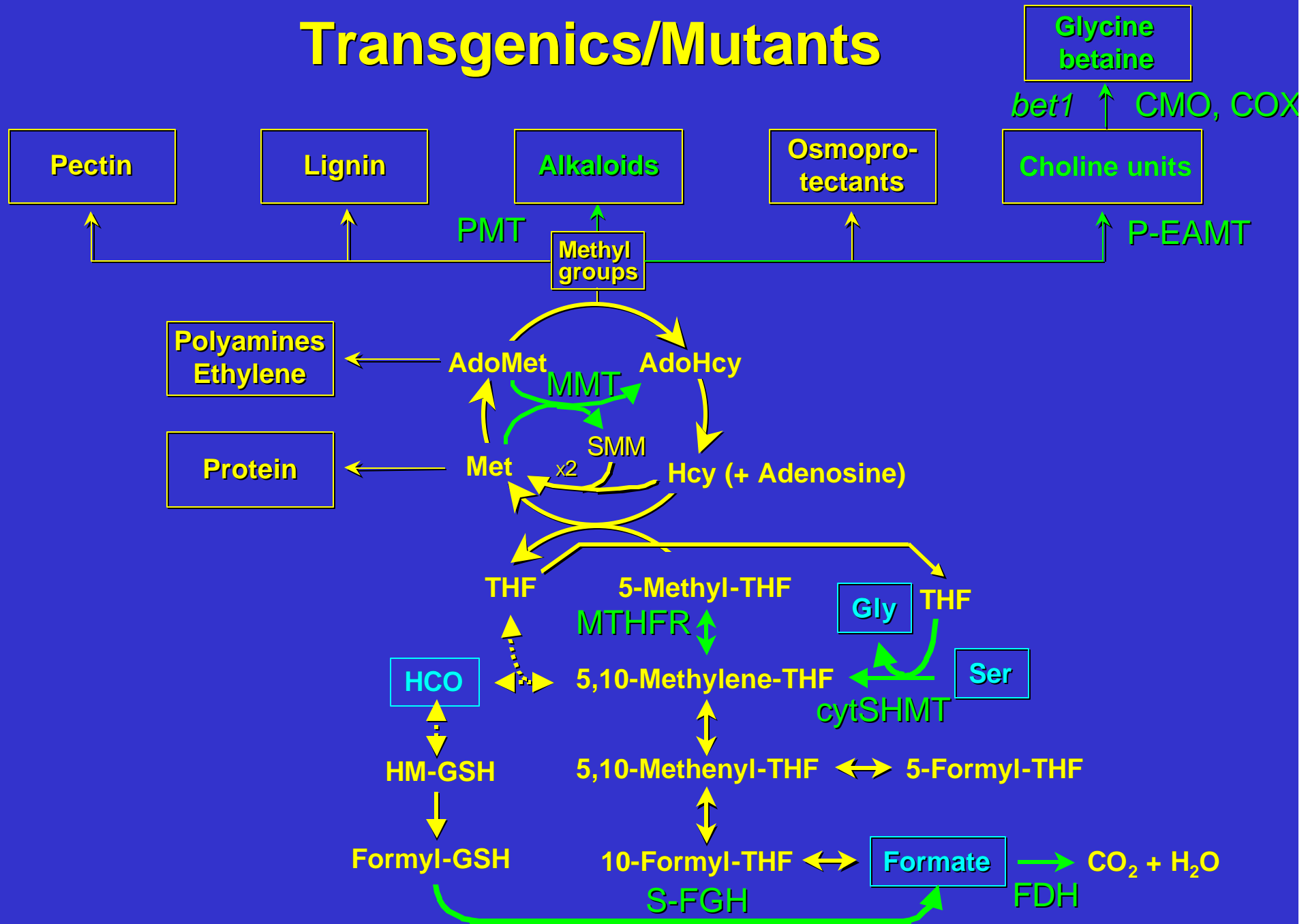




**Mean enzyme activities of different tobacco clones expressing antisense FDH, MTHFR or S-FGH**

**(Sanja Roje & A.D. Hanson, U. FL)**

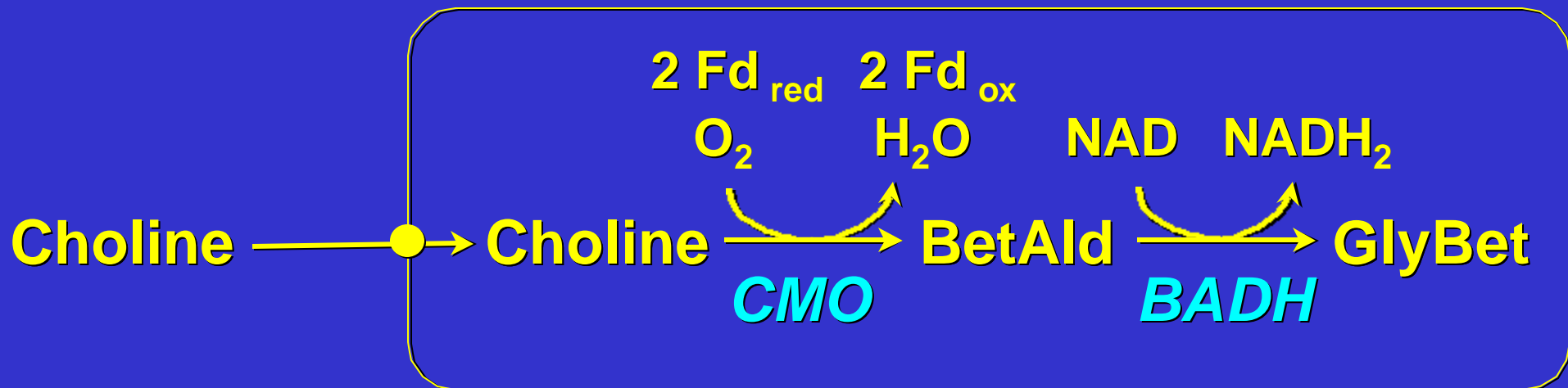
# Transgenics/Mutants



# Glycine betaine synthesis

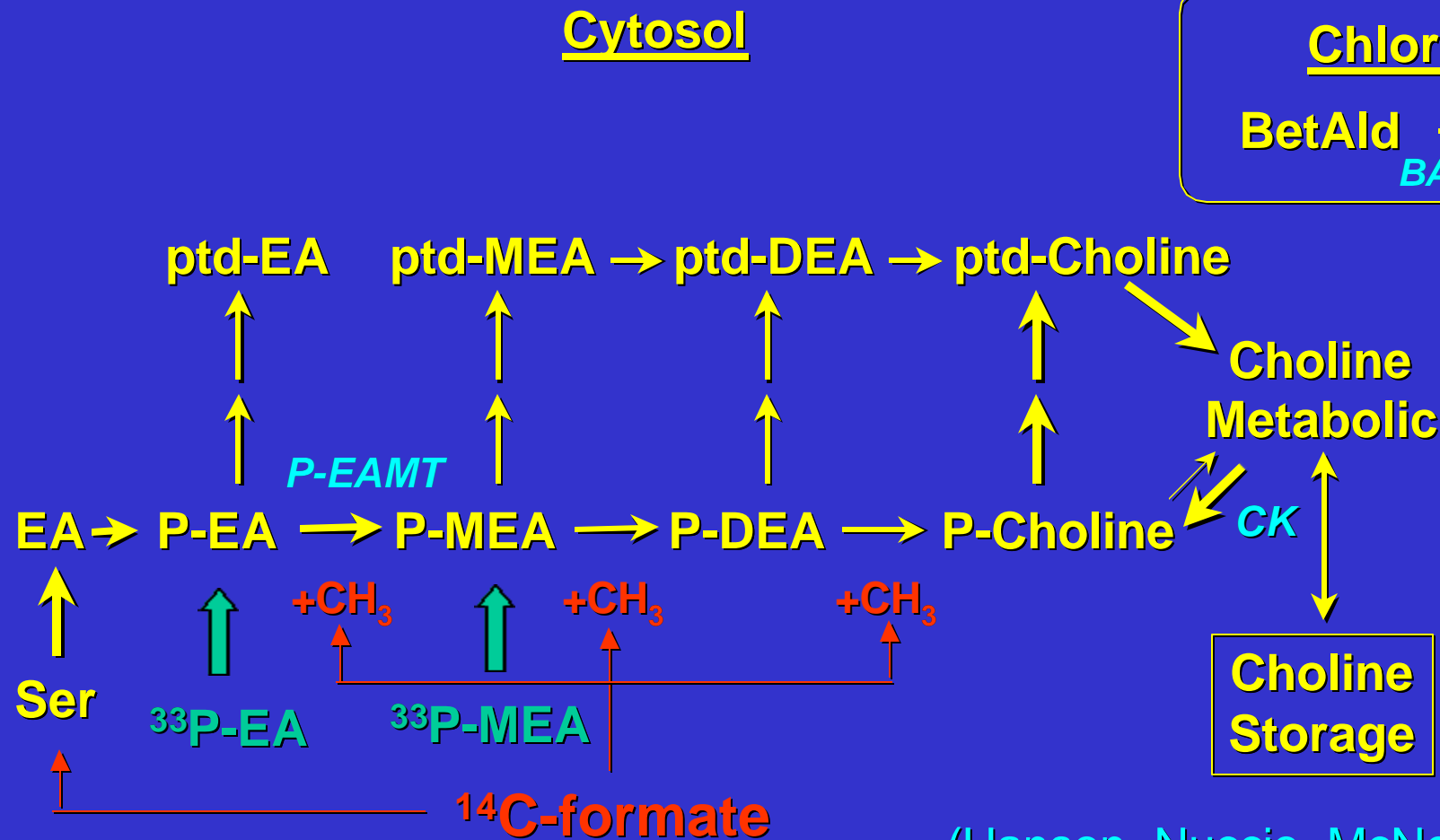
*Cytosol*

*Chloroplast*





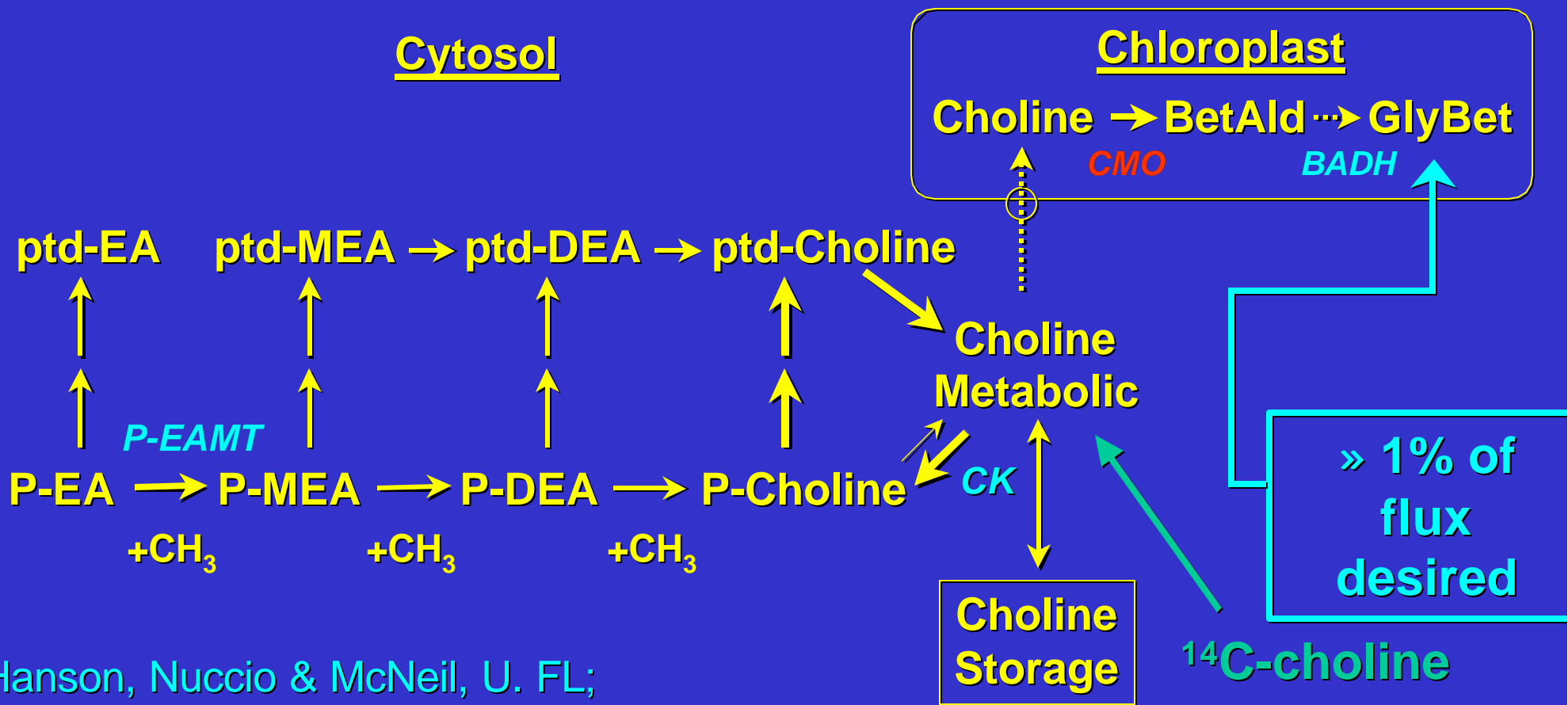
# Engineering glycine betaine synthesis Wild-type tobacco



(Hanson, Nuccio, McNeil, U. FL;  
Rhodes, Purdue; Shachar-Hill, NMSU)

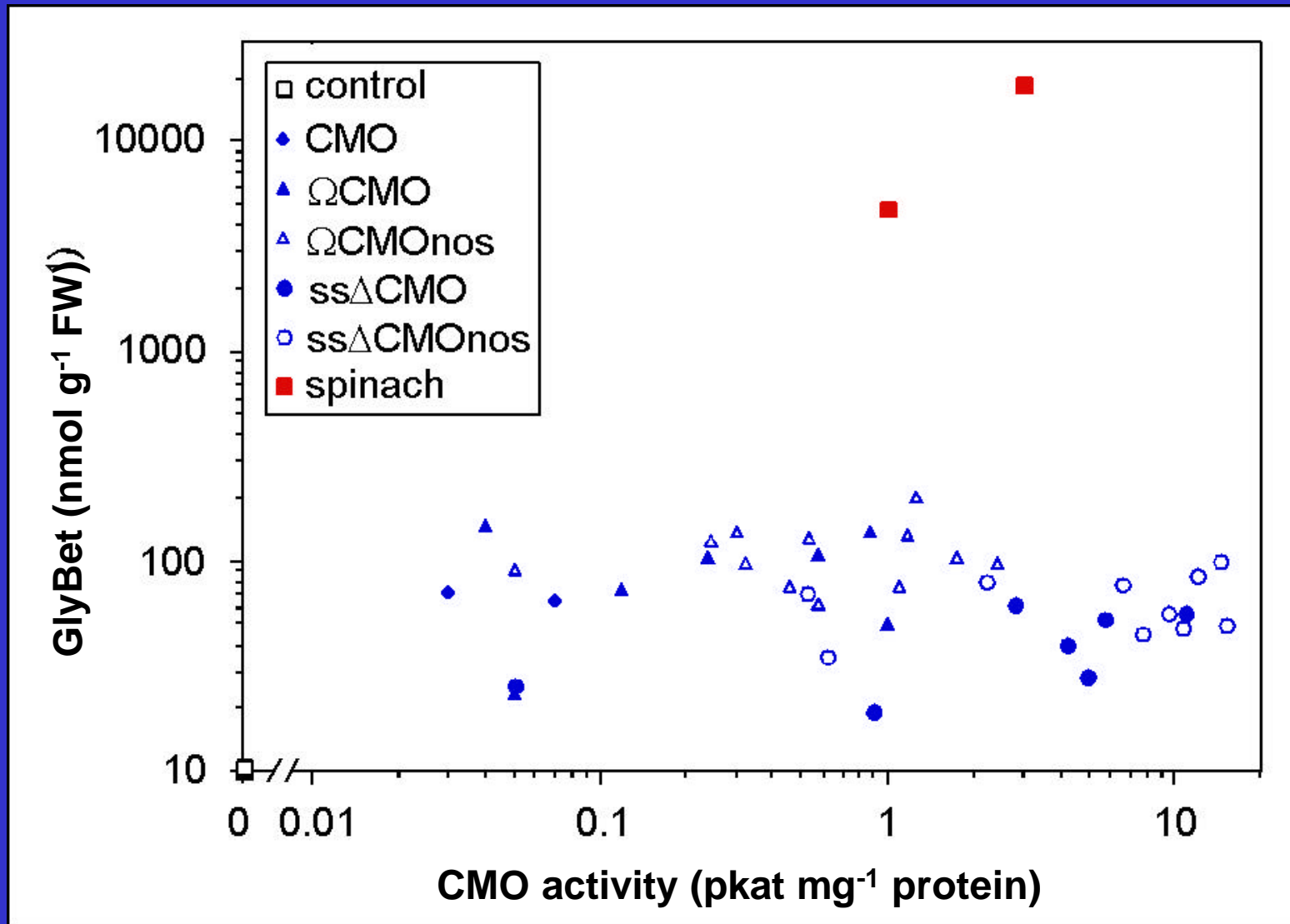
# Engineering glycine betaine synthesis Transgenic tobacco

## Chloroplastic expression of CMO



(Hanson, Nuccio & McNeil, U. FL;  
Rhodes, Purdue; Shachar-Hill, NMSU)

# CMO Expression & [GlyBet] in Tobacco

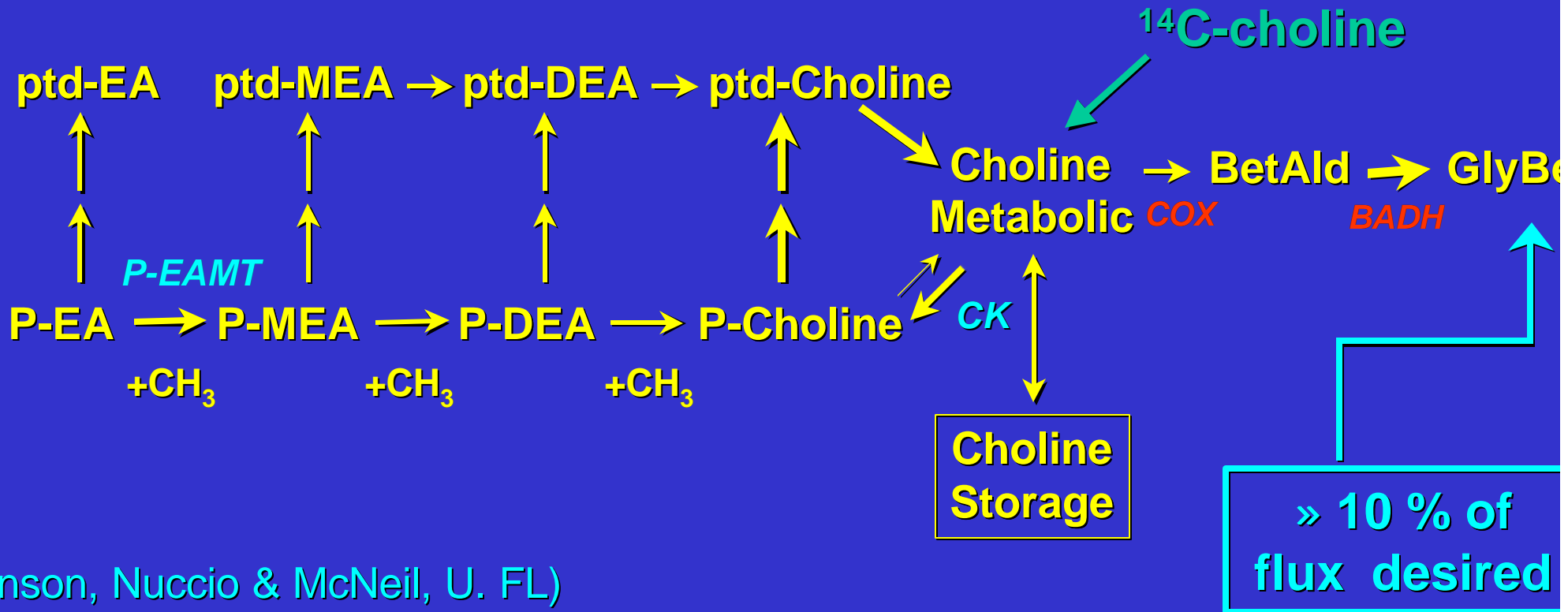


(Hanson, Nuccio & McNeil, U. F)

# Engineering glycine betaine synthesis Transgenic tobacco

Cytosol

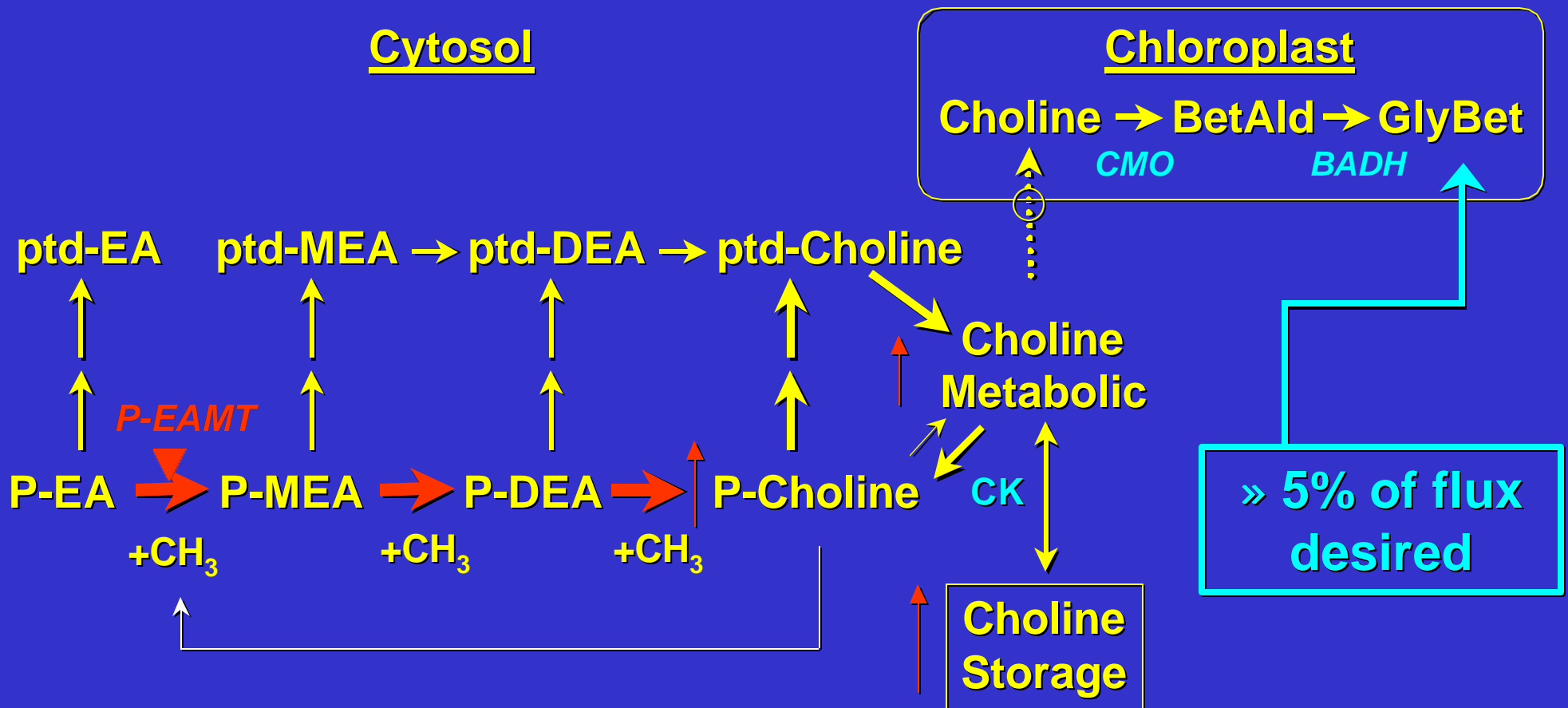
Cytosolic expression  
of COX + BADH



anson, Nuccio & McNeil, U. FL)

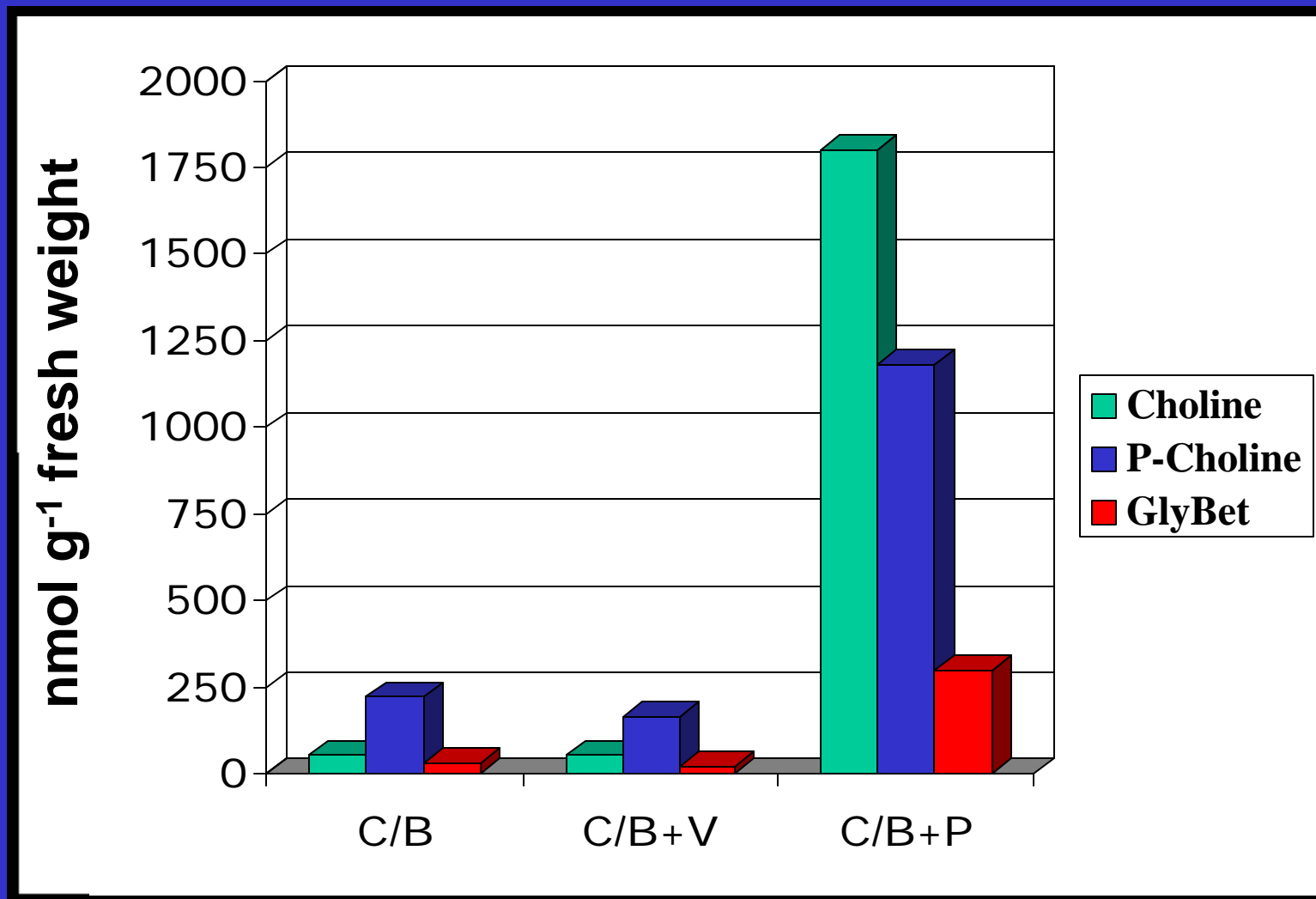
# Engineering glycine betaine synthesis

## Transgenic tobacco - overexpression of P-EAMT



(Hanson, Nuccio & McNeil, U. FL)

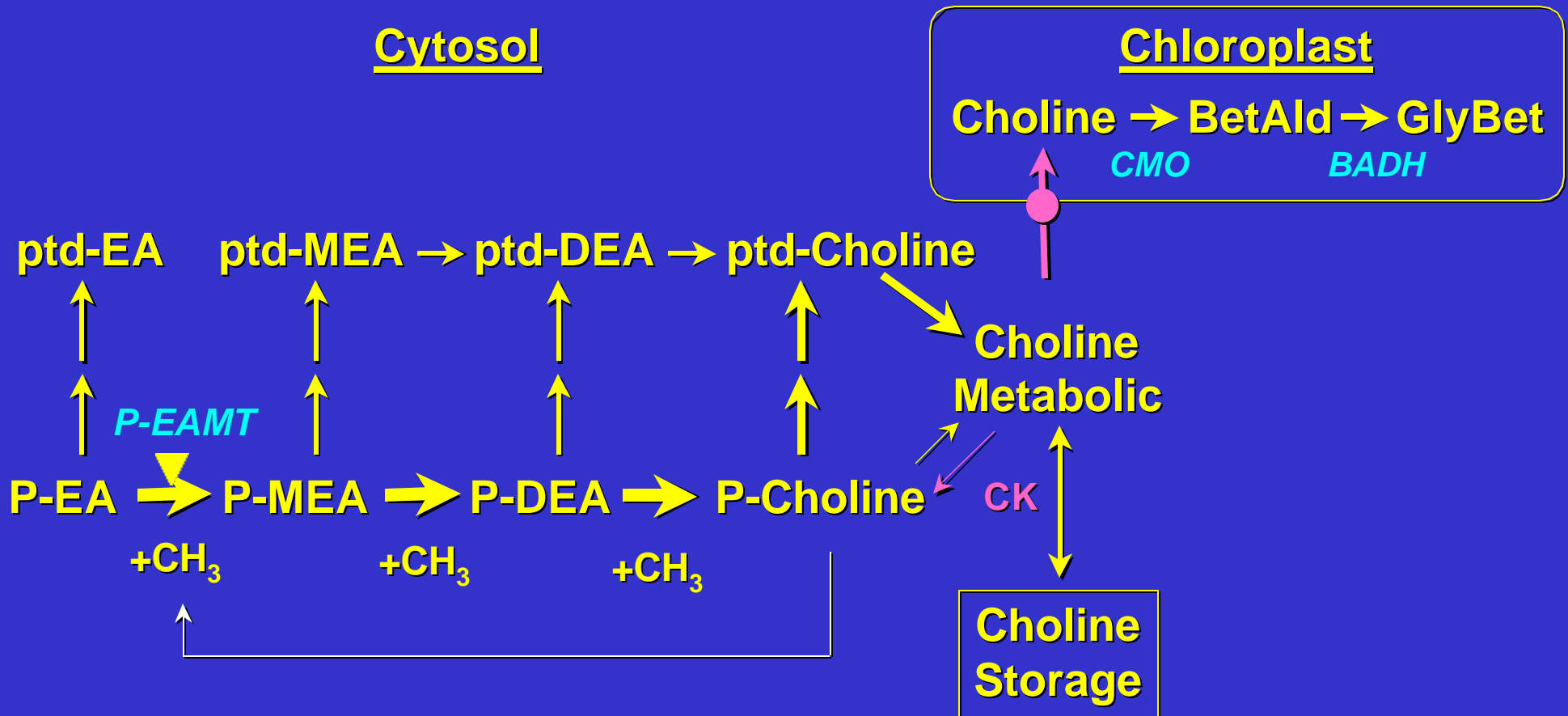
# CMO<sup>+</sup> BADH<sup>+</sup> PEAMT<sup>+</sup> Transgenics



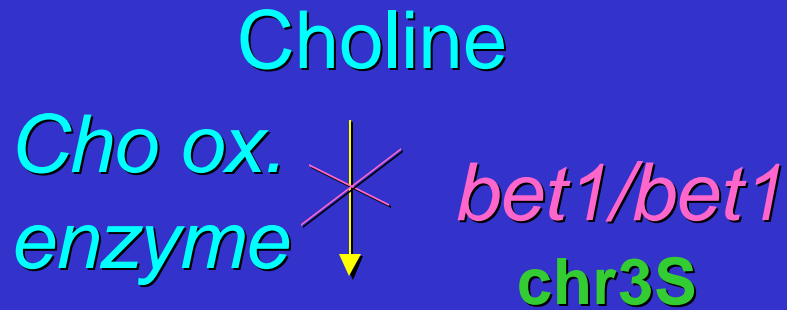
(Hanson, Nuccio & McNeil, U. FL)

# Engineering glycine betaine synthesis

## Transgenic tobacco - future targets

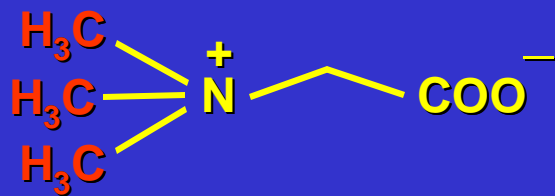


# Maize betaine genes



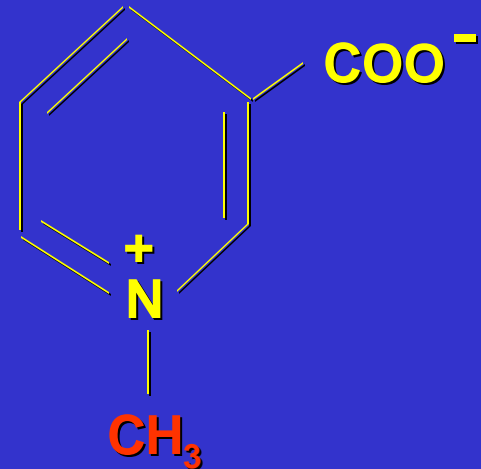
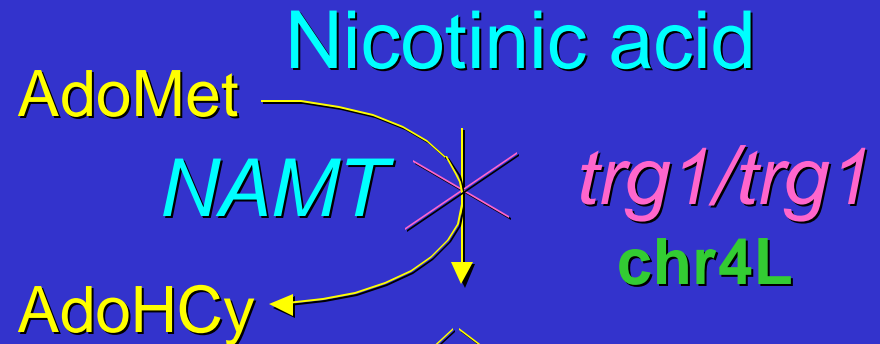
BetAld

*BADH*



Glycine betaine

$M+H^+ = 118$



Nicotinic acid  
betaine (trigonelline)

$M+H^+ = 138$



ion

# PD-MS of Maize Betaines

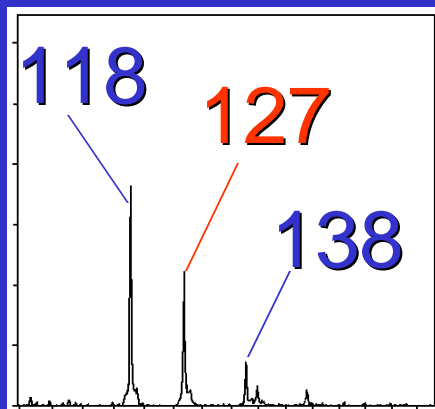
*Bet1/Bet1*  
*Trg1/Trg1*  
leaf

*bet1/bet1*  
*Trg1/Trg1*  
leaf

127 = d<sub>9</sub>-GB  
internal std.

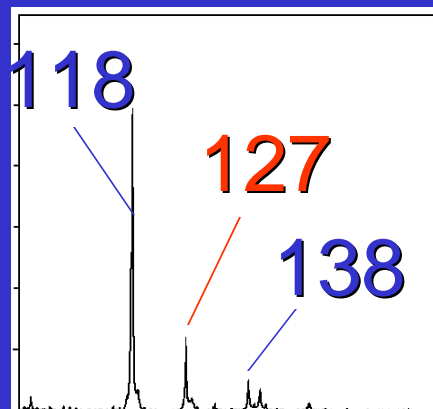
P o s i t i v e

0 mM NaCl



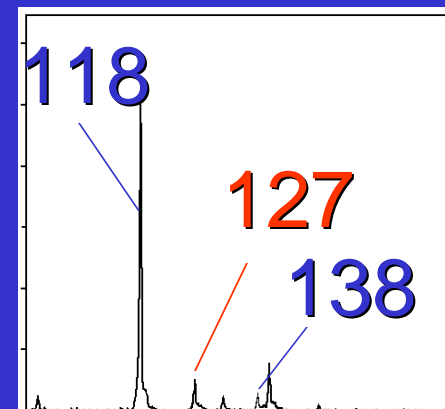
m/z

150 mM NaCl  
3 days

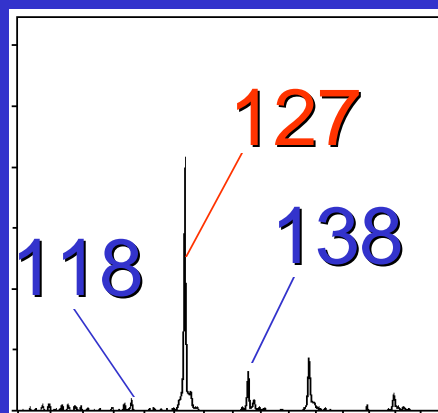


m/z

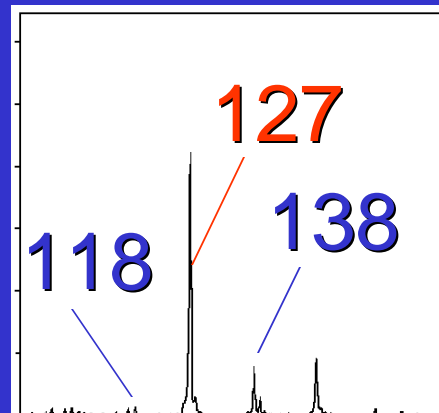
150 mM NaCl  
7 days



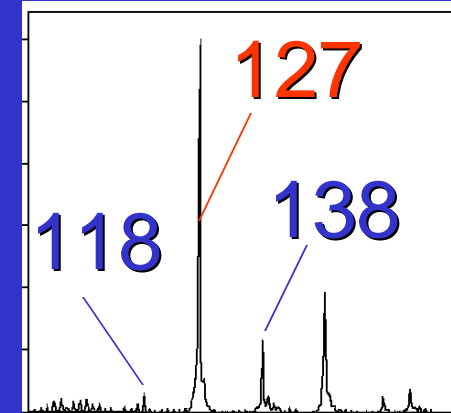
m/z



m/z



m/z



m/z

(Greg Peel & D. Rhodes, Purdu

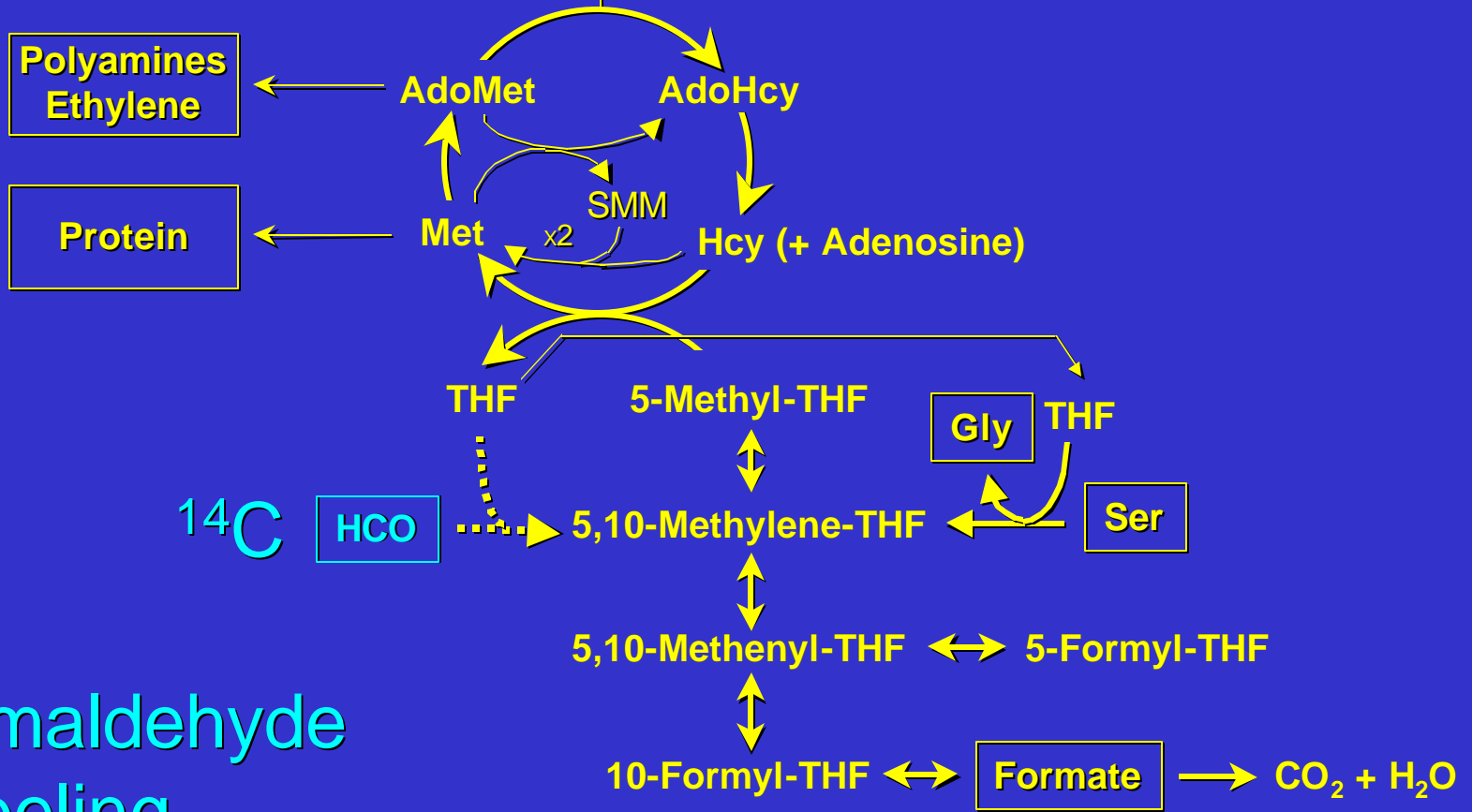
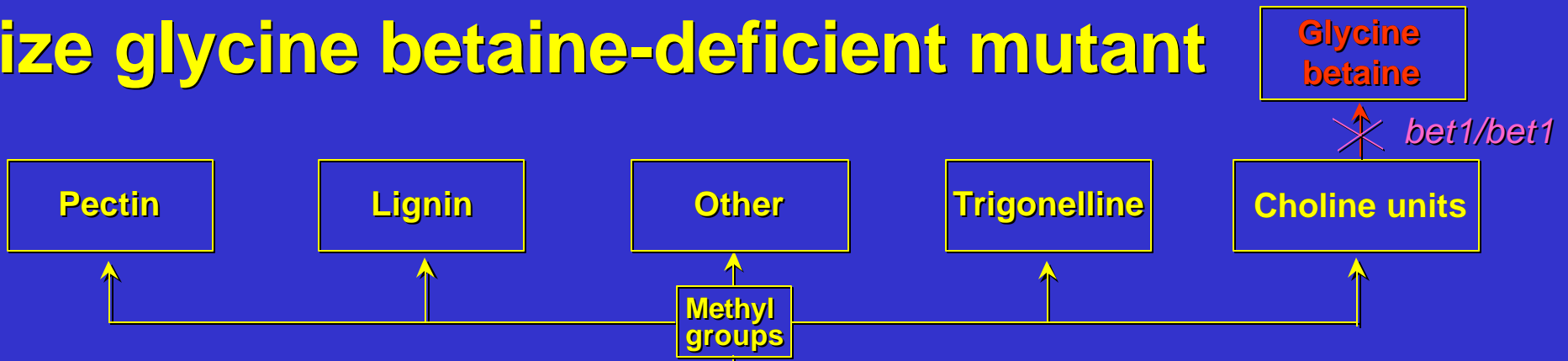
# Maize metabolite pool sizes

			Glycine betaine	Choline	P-Choline
			nmol/gFw	nmol/gFw	nmol/gFw
<i>Bet1/Bet1</i>	L	Control	3047	754	100
		Salinized *	9518	988	48
	R	Control	9	271	61
		Salinized *	7	298	25
<i>bet1/bet1</i>	L	Control	6	1245	596
		Salinized *	6	1335	402
	R	Control	4	421	39
		Salinized *	2	315	53

Peel & Rhodes, Purdue)

\* 3 days at 150 mM NaCl

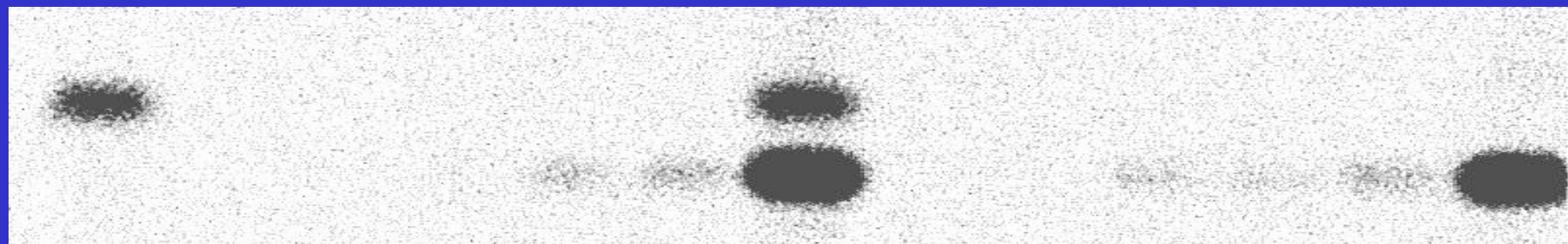
# Maize glycine betaine-deficient mutant



<sup>14</sup>C-Formaldehyde labeling

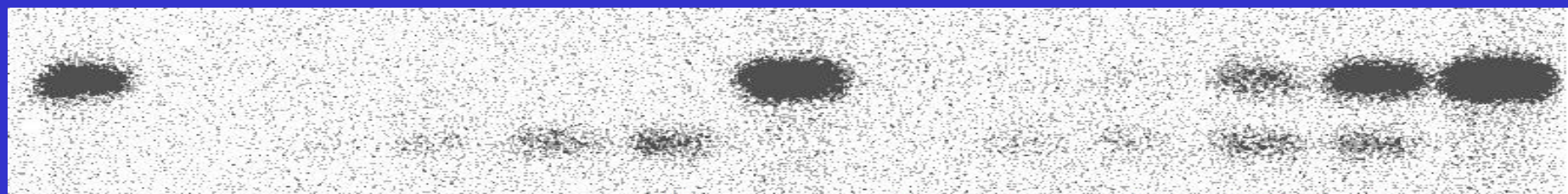
# Maize leaf betaine fraction; $^{14}\text{C}$ -formaldehyde labeled

*bet1/bet1* Control, Non-salinized *Bet1/Bet1*



**GB** 0 30 60 120 240 **GB +** 0 30 60 120 240 **Trg**  
**std** **Time (min)** **std** **Time (min)** **std**

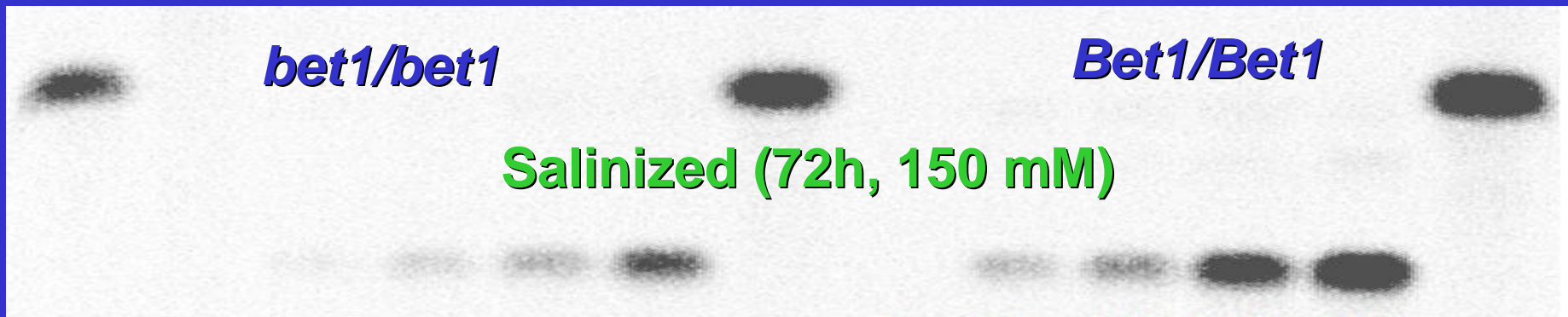
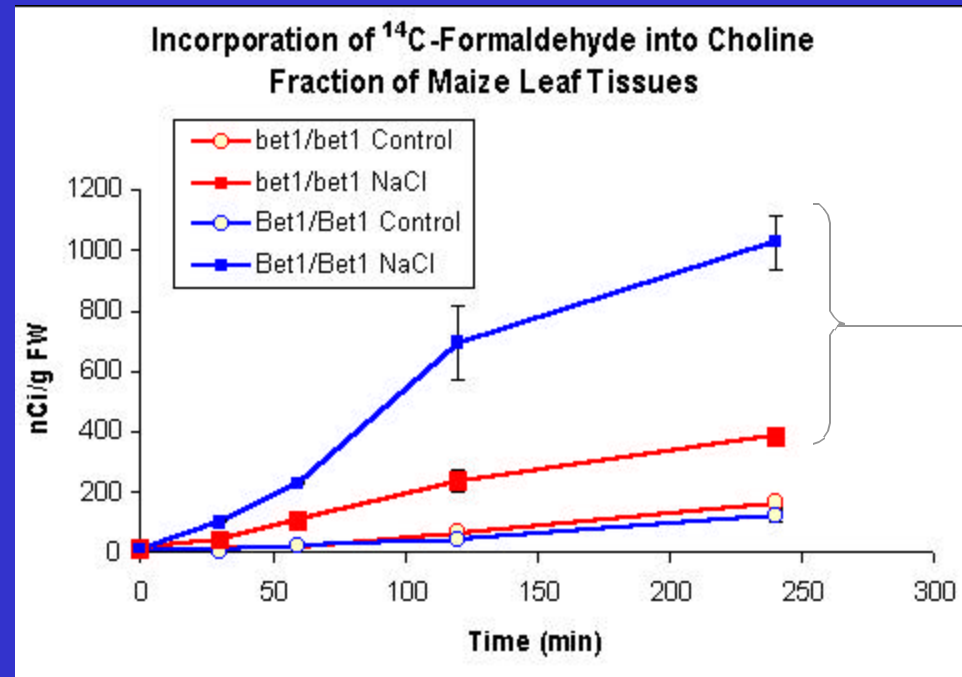
*bet1/bet1* Salinized (72h, 150 mM) *Bet1/Bet1*



**GB** 0 30 60 120 240 **GB** 0 30 60 120 240 **GB**  
**std** **Time (min)** **std** **Time (min)** **std**

# Maize leaf base fraction; $^{14}\text{C}$ -formaldehyde labeled

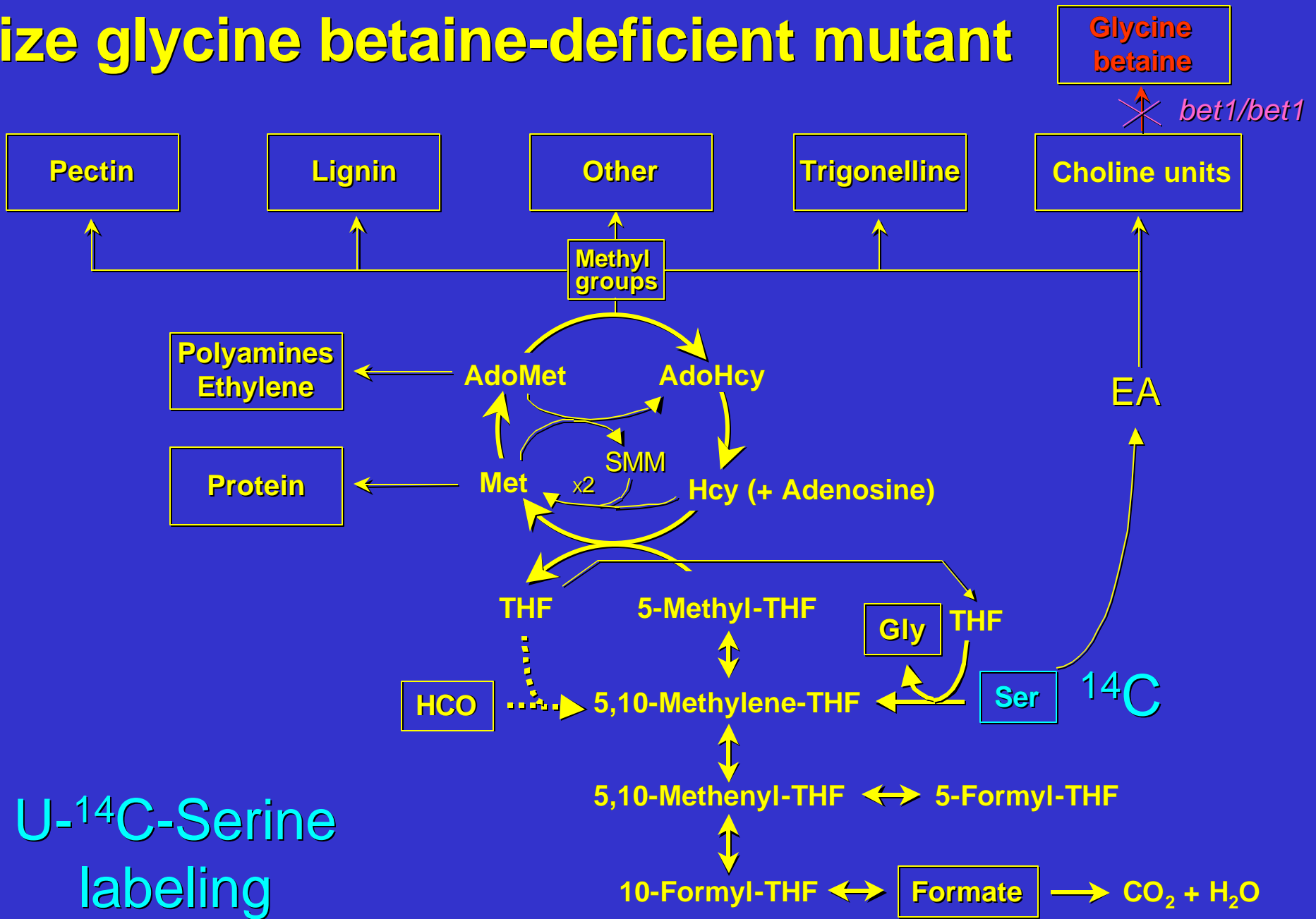
(Greg Peel, Purdue)



**GB**    **0**    **30**    **60**    **120**    **240**    **GB**  
**std**                      **Time (min)**

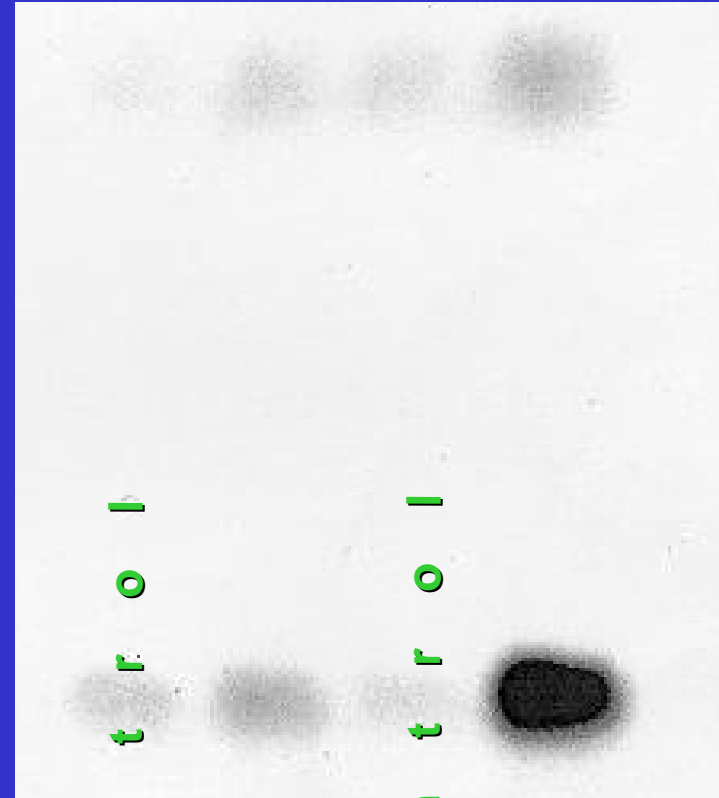
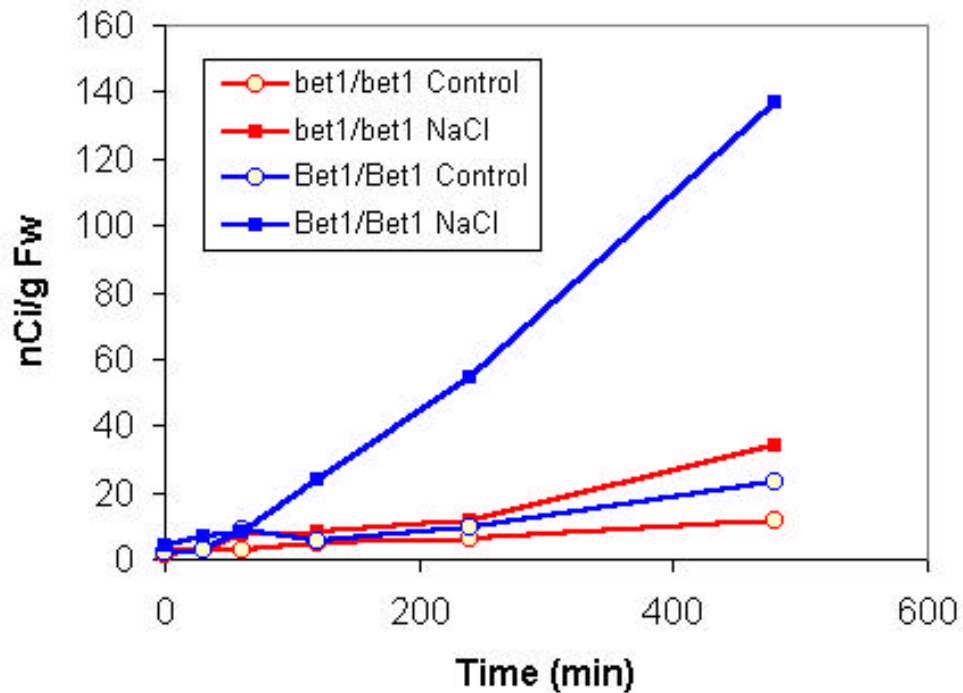
**GB**    **0**    **30**    **60**    **120**    **240**    **GB**  
**std**                      **Time (min)**

# Maize glycine betaine-deficient mutant



U-<sup>14</sup>C-Serine labeling

### Choline + Ethanamine



**Maize leaf base  
fraction; U-<sup>14</sup>C-serine  
labeled  
(Greg Peel, Purdue)**

**(480 min)**

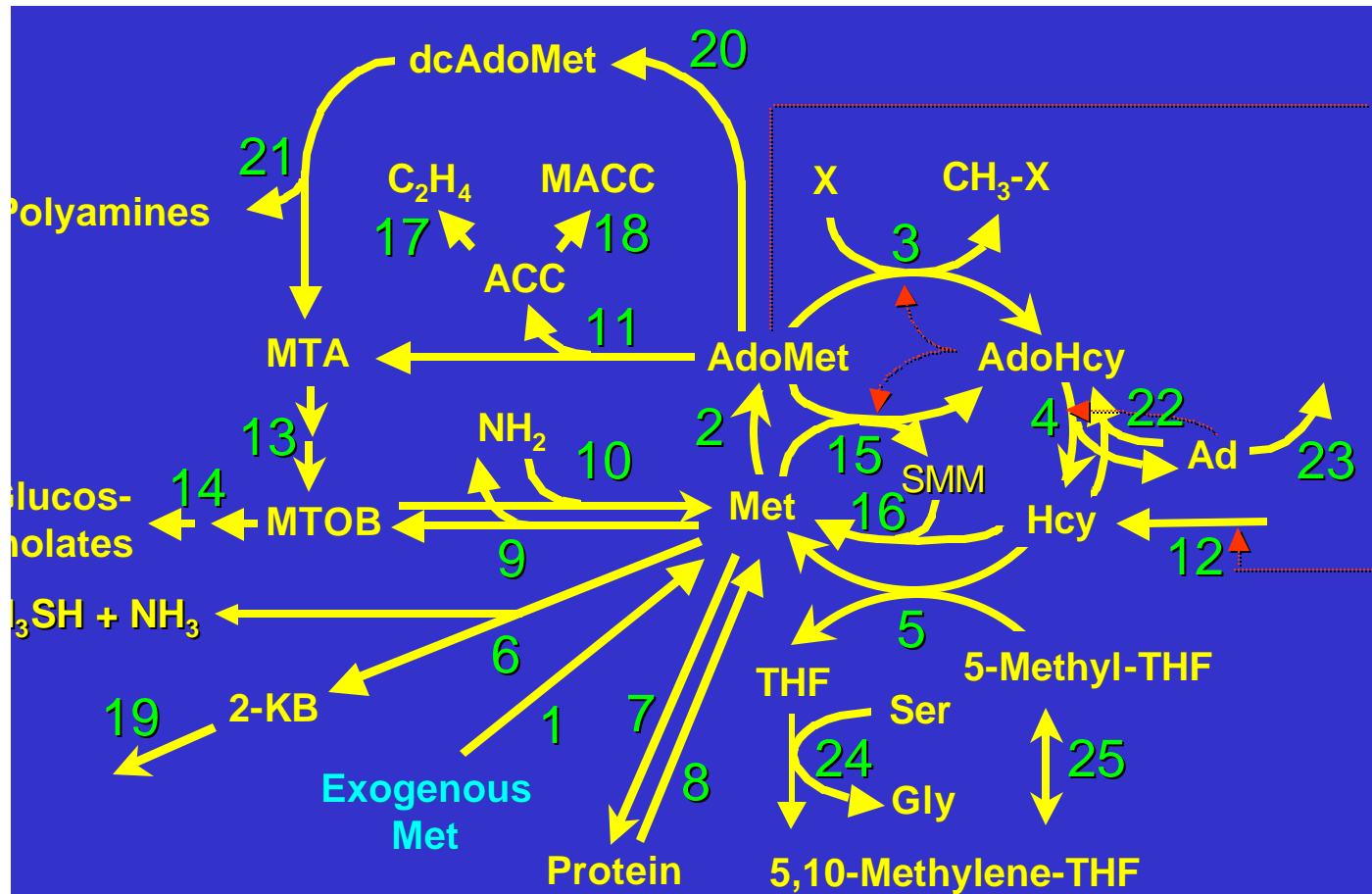
control Salinized control Salinized

*bet1/bet1* *Bet1/Bet1*

# Maize DNA arrays (Hong Wang, U. AZ)

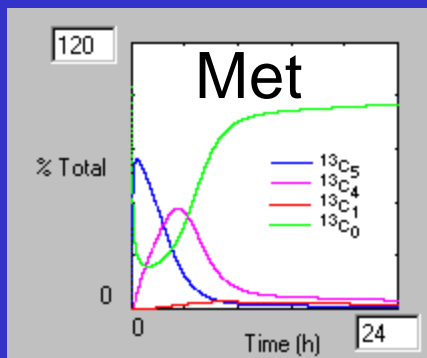
<i>Bet1/Bet1</i> (GB) and <i>bet1/bet1</i> (gb) leaf comparison	GB/gb	GB/gb	GB/gb
Transcript	0hr	6hr	72hr
Methionine adenosyltransferase (cytosol)	1.07	1.01	1.13
S-Adenosyl-L-homocysteine hydrolase (cytosol)	1.07	0.71	0.94
Methionine synthase (cytosol)	1.10	0.94	1.01
Methylene-THF reductase (NADH) (cytosol)	1.07	0.89	1.35
Methylene-THF dehydrogenase/cyclohydrogenase 1 (cytosol)	1.05	1.07	0.87
Methylene-THF dehydrogenase/cyclohydrogenase 2 (cytosol)	0.97	1.22	0.96
Methylene-THF dehydrogenase/cyclohydrogenase 3 (mitochondrion)	0.93	1.10	1.03
Formate-tetrahydrofolate ligase (cytosol)	1.21	0.90	0.94
Serine hydroxymethyltransferase (mitochondrion)	1.15	1.00	0.88
Glycine cleavage system P-protein (mitochondrion)	1.25	1.17	1.32
Glycine cleavage system H-protein (mitochondrion)	1.00	1.06	1.00
Glycine cleavage system T-protein (mitochondrion)	1.01	1.21	1.08
Formate dehydrogenase (cytosol)	1.03	1.01	1.42
Methionine S-methyltransferase (cytosol)	1.27	1.19	0.86
S-Adenosylmethionine decarboxylase (cytosol)	1.11	1.51	1.63
ACC synthase (cytosol)	0.95	1.21	0.86
Cystathionine gamma-synthase (cytosol)	1.10	0.89	0.95
Adenosine kinase (cytosol)	0.89	1.31	1.08
Betaine aldehyde dehydrogenase (BADH) (plastid)	1.13	0.98	1.13
Glutathione-dependent formaldehyde dehydrogenase (cytosol)	0.99	0.86	0.90
S-Formyl glutathione hydrolase (cytosol)	1.01	0.93	0.93
5,10-Methenyl-THF synthetase (cytosol)	1.14	0.86	0.88



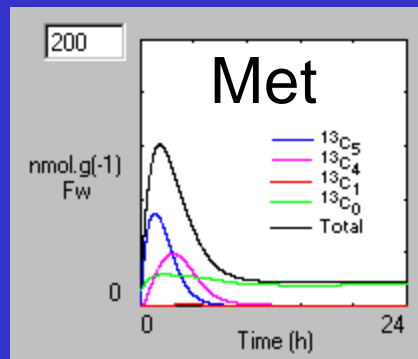


**Kinetic Modeling**  
*e.g. simulation of metabolism of a pulse of <sup>13</sup>C<sub>5</sub>-Met*

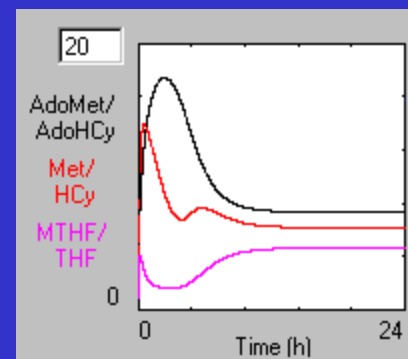
(Rhodes, Purdue)



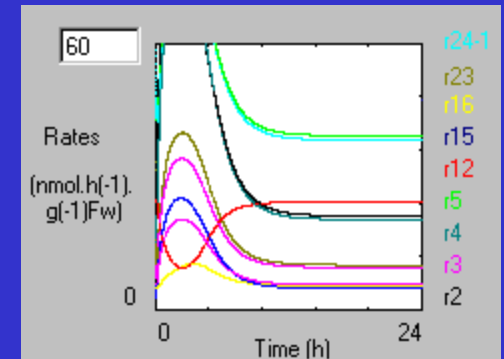
Isotopomer %



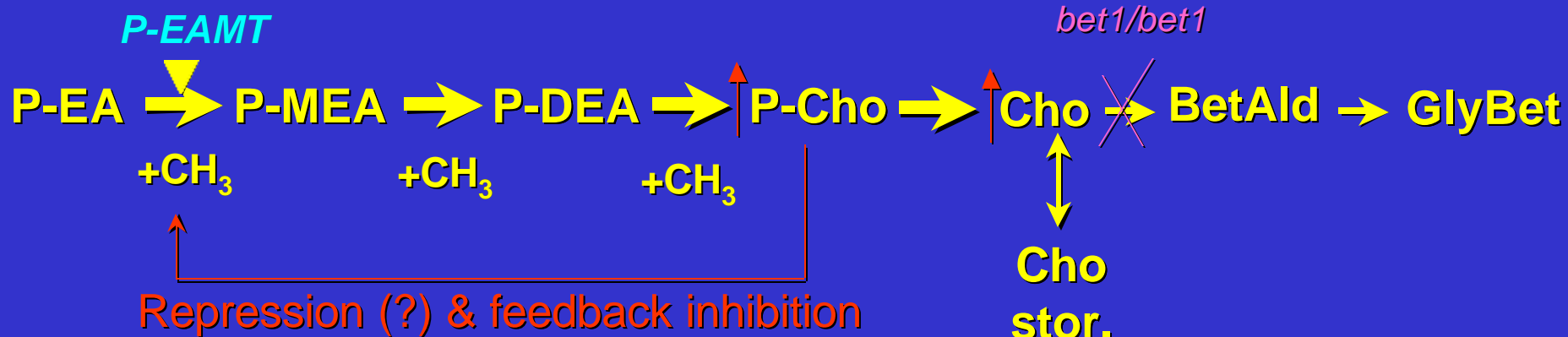
Pool sizes



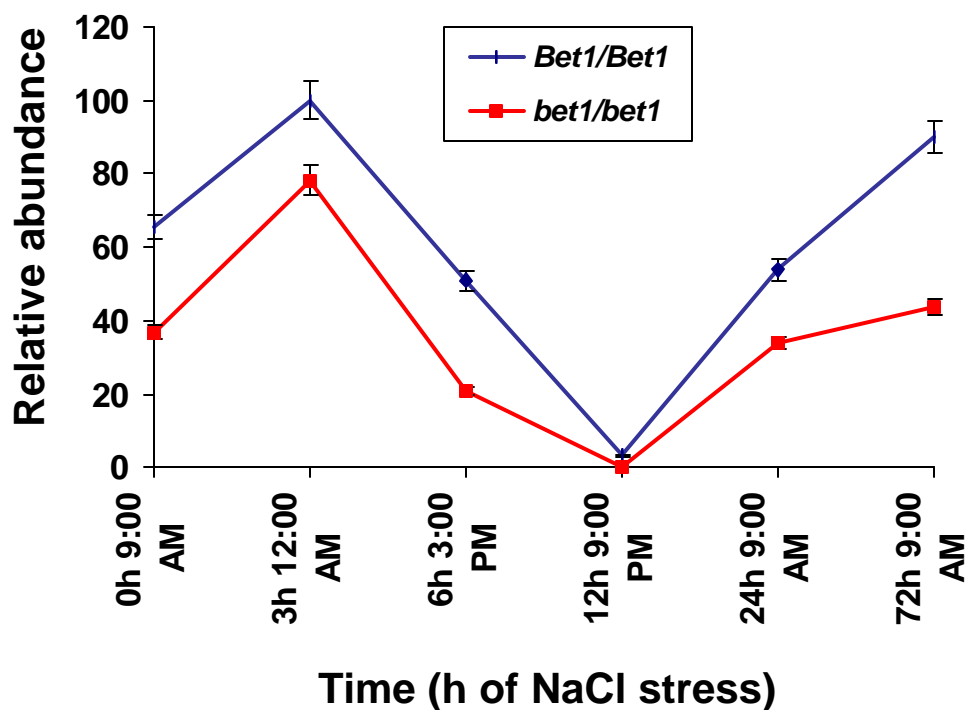
Metabolite ratios



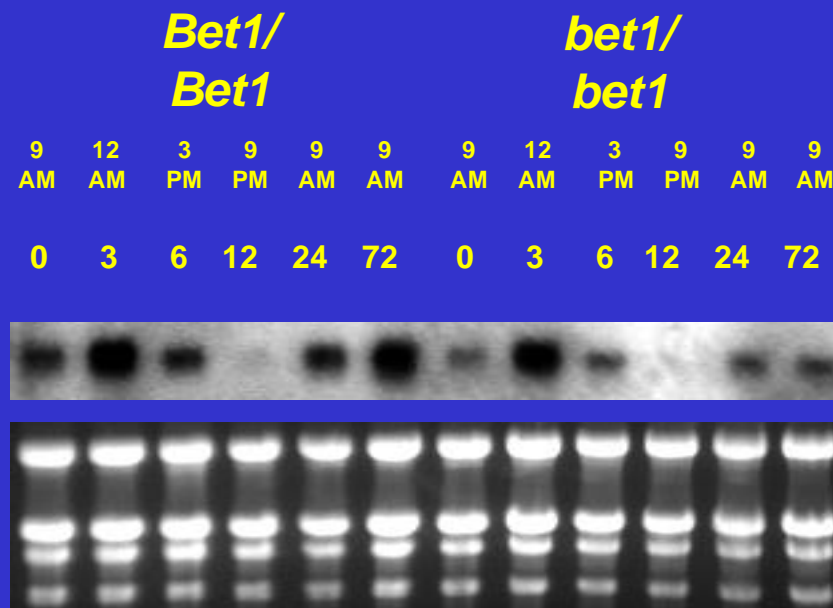
Rates



**P-EAMT Transcript Abundance in Maize Leaves**

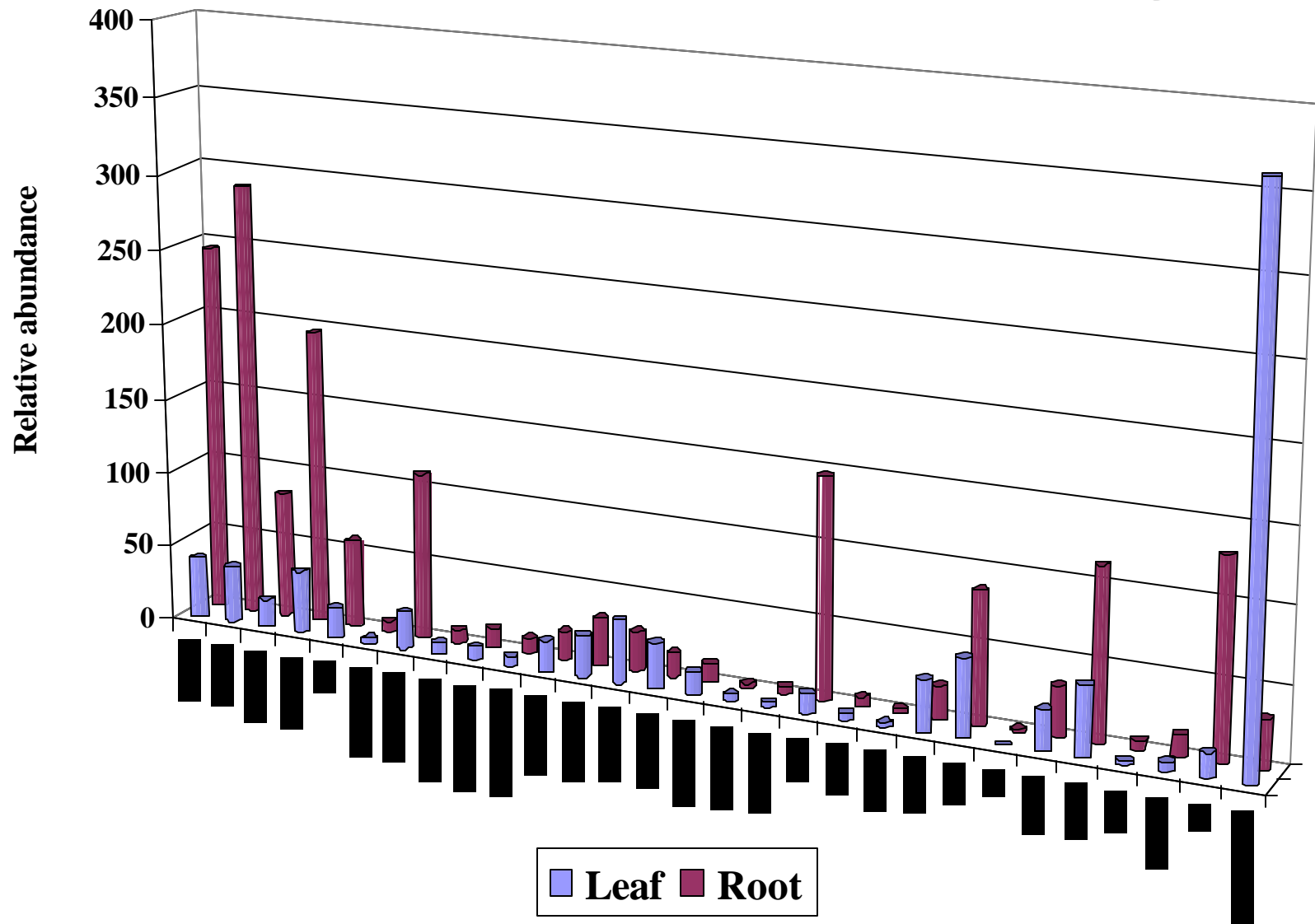


**P-EAMT Leaves**



(Hong Wang, U. AZ)

# Maize DNA arrays



(Hong Wang, U. AZ)

# Publications

- *J Biol Chem* - MTHFR cloning & characterization
- *TIPS* - Invited C<sub>1</sub> metab & engineering review (genomics)
- *J Biol Chem* - MS approach to SMM cycle \* \*
- *Plant Physiol* - Modeling of choline metabolism \* \*
- *Plant Physiol* - Engineering/modeling GlyBet synth. (CMO) \* \*
- *Metab Engin* - Engineering/modeling GlyBet synth. (CMO, COX + BADH) \* \*
- *Annu Rev Plant Physiol Plant Mol Biol* - Invited C<sub>1</sub> review
- *Plant J* - Fluxes via transmethylation & SMM cycles in Arabidopsis \* \*
- *Annu Rev Plant Physiol Plant Mol Biol* - Invited NMR review
- *Metab Engin* - Invited review on modeling of plant pathways
- *Metab Engin* - Invited review on ME of plant osmolytes
- *Plant Physiol* - Microarray & labeling data for maize; *Bet1/Bet1* cf. *bet1/bet1*

\* MS or modeling supported by C<sub>1</sub> grant; \* NSF; \* USDA

# Outreach - Workshops, Websites

- **Zia Symposium III - January 2000, NMSU**  
Hands-on computer sessions, 60 participants
- **ASPP Annual Meeting - July 2000, San Diego**  
Minisymposium on models in metabolic research & eng  
Hands-on computer sessions, 60 participants
- **Plant Biochemistry Summer Course - July 2001, Pullman**
- **Metabolic modeling website**  
<http://www.hort.purdue.edu/cfpesp/models/models.htm>
- **C<sub>1</sub> Project website (data, materials, protocols)**  
<http://www.hos.ufl.edu/meteng/1Cpage1.html>