

mRNA Transcript Expression in the Ear Shoot Apical Meristem and Correlation with Yield

A Translational Genomics Experiment
Utilizing Next-Generation
Sequencing Technology
And the B73 Genome Reference
Sequence

GENETIC MATERIALS

Four homozygous lines: Ex-PVP Accessions

(1) LH1

(2) PHG39

(3) LH123HT

(4) PHG84

Six F_1 Hybrids

Six F_2 Families

Twelve Reciprocal BC1 Families: A^*B/A ; A^*B/B

EXPERIMENTAL DESIGN

Sampling	Phenotyping
BC1	BC1
Parents	Parents
BC1'	BC1'
F ₁	F ₁
F ₂	F ₂

Rep 2

Phenotyping	Sampling
F ₂	F ₂
F ₁	F ₁
Parents	Parents
BC1'	BC1'
BC1	BC1

Rep 3

Sampling	Phenotyping
Parents	Parents
F ₂	F ₂
BC1'	BC1'
BC1	BC1
F ₁	F ₁

Rep 1

GENETIC MODEL

Genotypic Value by Generation

- $F_1: \gamma_{uv} = 1.00\beta_1 + 0.50\alpha_u + 0.50\alpha_v + 1.00\delta_{uv} + 0.25\alpha\alpha_{uv} + \xi_{uv};$
- $F_2: \gamma_{uv\ominus} = 1.00\beta_2 + 0.50\alpha_u + 0.50\alpha_v + 0.50\delta_{uv} + 0.25\alpha\alpha_{uv} + \xi_{uv\ominus};$
- $BC1: \gamma_{uv.u} = 1.00\beta_3 + 0.75\alpha_u + 0.25\alpha_v + 0.50\delta_{uv} + 0.1875\alpha\alpha_{uv} + \xi_{uv.u};$
- $BC1': \gamma_{uv.v} = 1.00\beta_4 + 0.25\alpha_u + 0.75\alpha_v + 0.50\delta_{uv} + 0.1875\alpha\alpha_{uv} + \xi_{uv.v};$
- Parent u: $\gamma_u = 1.00\beta_5 + 1.00\alpha_u + \xi_u;$
- Parent v: $\gamma_v = 1.00\beta_5 + 1.00\alpha_v + \xi_v;$
- β_j = effect attributable to generation j;
- α_u = additive effect of line u;
- α_v = additive effect of line v;
- δ_{uv} = dominance effect of line u * line v;
- $\alpha\alpha_{uv}$ = intergametic epistatic effect of line u * line v;
- ξ_{uv} = residual genetic effect.
- We focus on genotypic value of the F_1 s even though genetic parameters are estimated from all generations.

EAR TRAIT PRINCIPAL COMPONENTS

Genotypic Variation All Non-Additive

Trait	PC1 (KPR)	PC2	PC3	PC4	PC5
Kernels per Row	0.41336	-0.08237	0.84068	-0.13904	-0.31014
Cob Length	0.41515	-0.27390	-0.41113	-0.73539	-0.16246
Cob Weight	0.39445	-0.57872	0.02820	0.32264	0.60552
Grain Fill	0.42503	-0.11827	-0.31814	0.47400	-0.46176
Ear Weight	0.40339	0.50367	-0.14800	0.27287	-0.13984
Grain Weight	0.39723	0.56179	0.01757	-0.19142	0.52724
Eigenvalue	26.96989	2.31529	0.52409	0.16375	0.02698
% Variance	89.90	7.72	1.75	0.55	0.09

Tissue Sampling, Sequencing, and Bioinformatics

- Ten 1mm inflorescence meristem tips were sampled per plot (9AM-12noon). Sample date recorded for all tips.
- Excised tips were frozen in liquid N.
- RNA Extracted and sample sent to National Center for Genomic Resources, Santa Fe NM, for sequencing.
- Polyadenylated RNA isolated, reverse transcribed, and cDNA amplified.
- 36-bp reads generated by Illumina™ Genome Analyzer II instrument.
- Reads aligned to maizesequence.org 4a.53 version of the B73 maize genome.

Frequency distribution of false discovery rates in tests for significant genetic variation across 30,208 genes. Nearly all significant genotypic variation is additive.

FDR Range	Genotypic Value	Additive	Dominance	Additive x Additive Epistasis	Residual Genetic
FDR<=0.001	8,112	7,267	2	6	42
0.001<FDR<=0.01	3,051	3,351	8	7	240
0.01<FDR<=0.05	3,282	3,633	3	13	619
0.05<FDR<=0.10	1,730	2,011	0	10	633
0.10<FDR<=0.20	2,409	2,448	43	59	1,194
0.20<FDR<=1.00	11,624	11,498	30,152	30,113	27,480
%<=FDR(0.20)	61.5	61.9	0.2	0.3	9.0

Observed and expected frequencies of genes with significant genotypic transcript variation at the $\alpha \leq 0.05$.

	Observed	Expected	Prob>Chi-Square
Genes Varying in Transcript Expression $\alpha \leq 0.05$	16,017	1,510	<0.001

Observed and expected frequencies of genes with significant genotypic transcript variation at the $\alpha \leq 0.05$ level and significant Spearman rank correlation with the KPR component at the $\alpha \leq 0.0404$ level. Empirical Spearman correlation coefficient distribution is discrete, not continuous.

	Observed	Expected	Prob>Chi-Square
Genes Varying in Transcript Expression $\alpha \leq 0.05$; And correlated with KPR component $\alpha \leq 0.0404$	845	647	<0.001

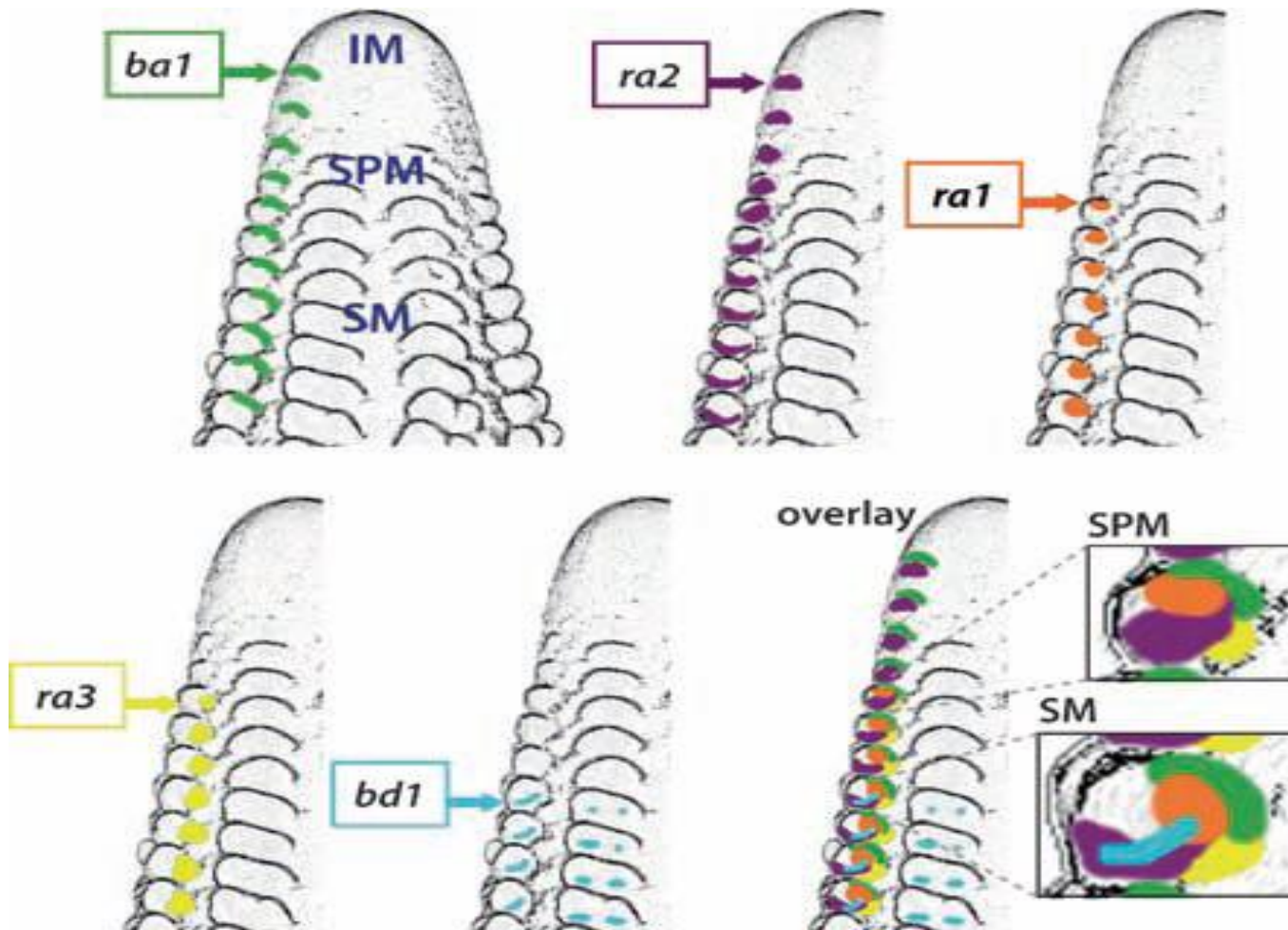
Summary of functional categorization of significant genotypic variation in transcript expression and association with variation in genotypic variation in ear KPR phenotype.

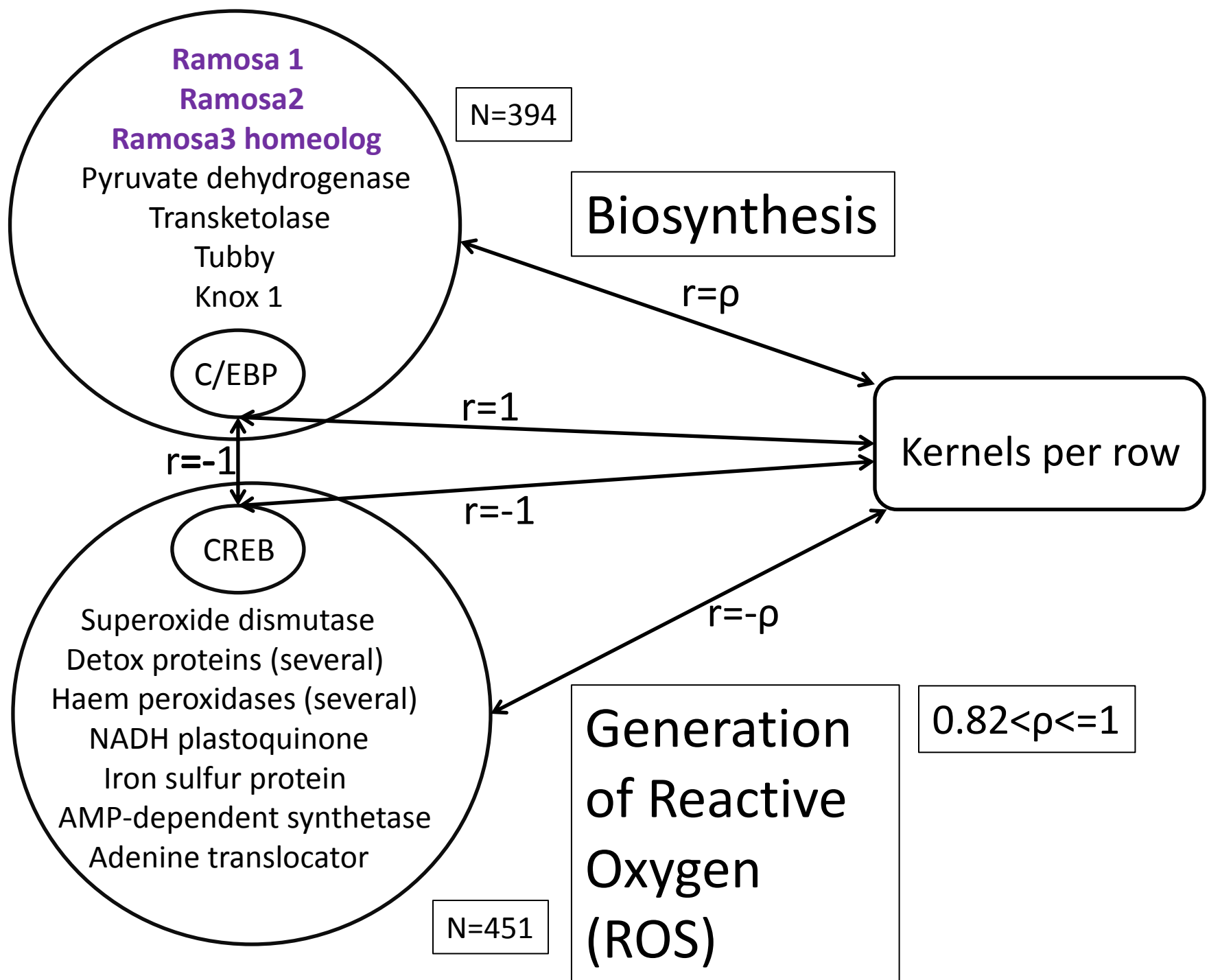
Functional Category	Over-Representation of Significant Genotypic Variation in Transcript Expression	Over-Representation of Significant Spearman Correlation with KPR Component
STRESS RESPONSE	NO (Under represented)	NO
OXIDO-REDUCTASE	NO	YES
TRANSCRIPTION FACTORS	NO	YES
SUGAR	NO	YES
LIPIDS	NO	YES
PYRUVATE	YES	YES
AMINO ACID	YES	YES
TRANSPORT	YES	YES
TRANSLATION	YES	NO
ATP	YES	NO
HEAT SHOCK (ATP BINDING)	YES	NO
NAD/NADH	YES	NO
PHOSPHORYLATION	YES	NO
SIGNAL TRANSDUCTION	YES	NO

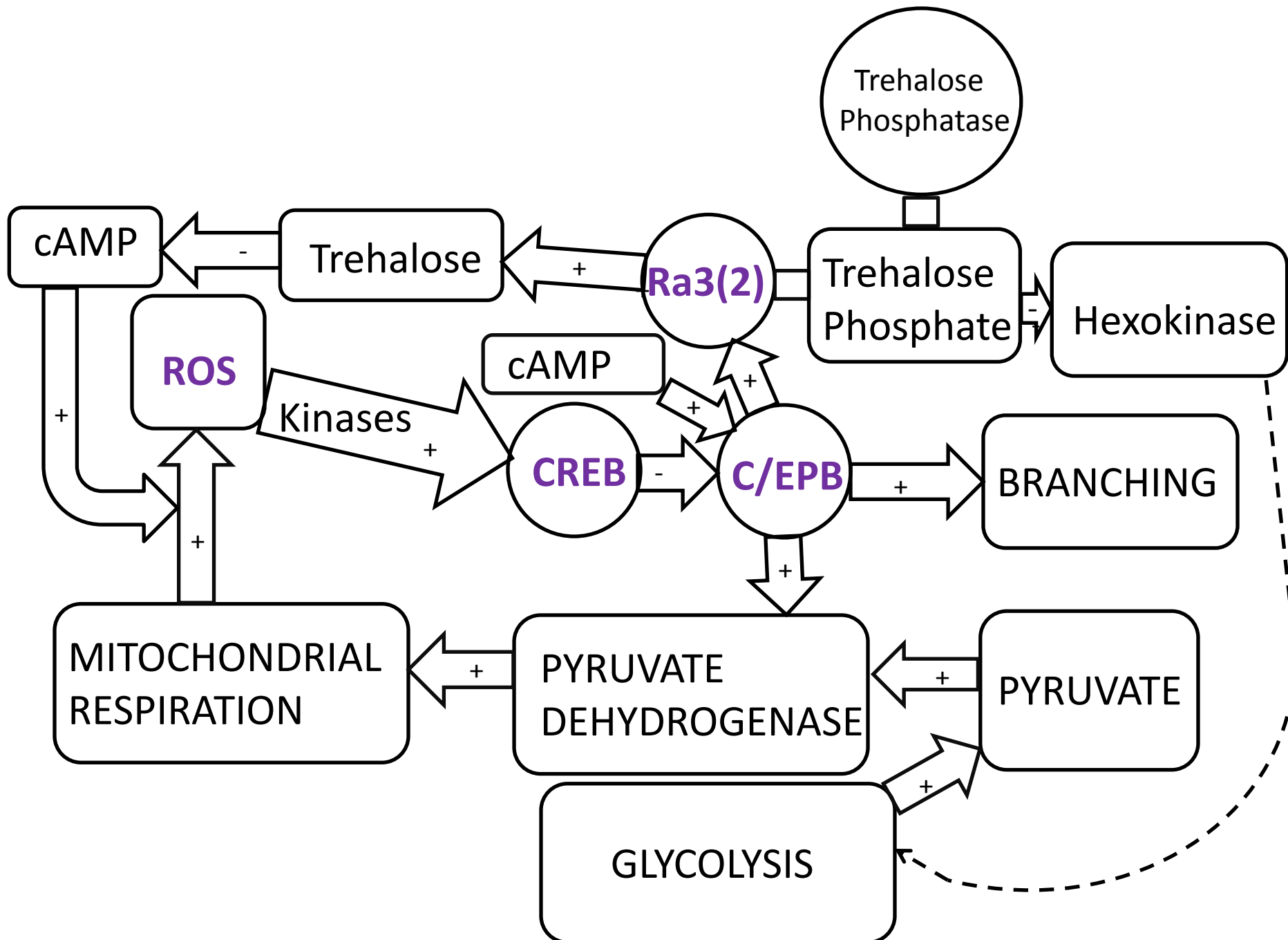
**Significance Level of Genotypic Variation in Gene Expression
And Rank Correlation with Genotypic Variation in the
Kernels Per Row Component of the Mature Ear**

Gene	Genotypic Expression Variation FDR	Rank Correlation Of Expression with Kernels Per Row Component
Ramosa 1- C2H2 Zinc Finger Transcription Factor	0.0100	0.9429
Ramosa 2 –Lateral Organ Boundary Transcription Factor	0.0173	0.9429
Ramosa 3 homeolog-Trehalose Phosphatase – Chromosome 2	0.0008	1.0000
Ramosa 3 –Trehalose Phosphatase – Chromosome 7	0.0006	0.3134
C/EPB – CCAAT Enhancer Binding Transcription Factor	<.0001	1.0000
CREB – cAMP Response Element Binding Protein	<.0001	-1.0000

Gene Expression in Early Ear-Shoot Development







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QUESTIONS & COMMENTS

