

SNPeffect: Identifying Functional Roles of SNPs using Metabolic Networks

Background

- Leveraging the tremendous natural variation in poplar species to design tailored feedstocks necessitates an understanding of the genotype-to-phenotype relationships

Approach

- Integrate heterogeneous metabolomics, transcriptomics, phenomics, and proteomics datasets using metabolic models were used as the scaffold
- Explain changes in growth rate, and differential metabolite and enzyme levels, as the outcome of one or more SNPs in the coding regions of the genotype

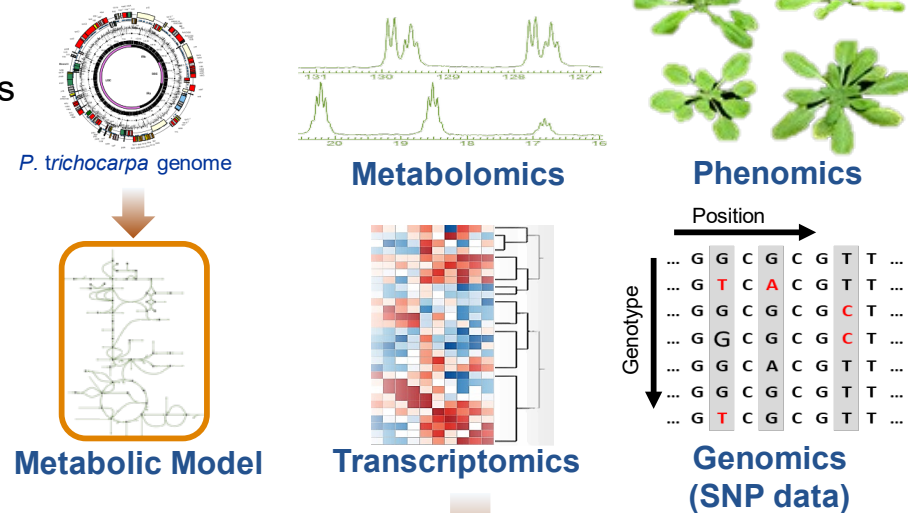
Outcome

- Identified functional SNPs (~4k) from >80k present in poplar metabolic genes
- Quantitative estimates of the effect of a SNP on metabolic reaction flux
- Provided Mechanistic interpretation of the deciphered genotype-to-phenotype relations

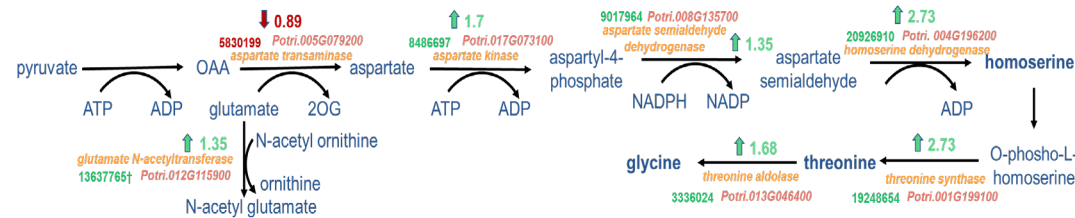
Significance

- SNPeffect is immune to the confounding effects caused by population structure and multiple-testing
- Resultant SNP hits are being used as priors in genomic selection to increase signal-to-noise ratio
- SNPeffect meta-analysis can be used to evaluate and explain GWAS hits

SNPeffect Inputs



SNPeffect Outputs



SNP position (chrom)	MAF	Gene	Predicted SNP Role	Experimental Evidence of Growth-Related Phenotype
10453399 (13)	0.24	4CL	Activating	Transgenic poplar with downregulated 4CL show reduced growth in field trials
2121750 (8)	0.39	PAL	Activating	PAL overexpression reduced growth in field trials