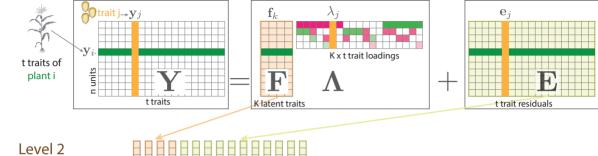
## 



secondary traits

M = K + t de-correlated traits

B Genomic Prediction applications

High-throughput phenotype data

focal trait

Independent LMMs



 $=\mathbf{X}\boldsymbol{eta}_m+\mathbf{Z}\mathbf{u}_m+\boldsymbol{\epsilon}_m$ 

Genetic

relatedness

Residuals

Blocks.

markers