

Comparative transcriptome analysis identifies a positive regulator of wheat rust susceptibility that modulates amino acid metabolism

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In Brief

Wheat yellow rust and stem rust are two of the most economically damaging diseases of wheat worldwide. Identification of plant defense-related genes has traditionally relied on screening mutant populations, a process that is labor-intensive and time-consuming. Recent advances in transcriptome sequencing and improved genomic resources for many crop species can offer potential alternatives, accelerating the identification of novel, sometimes overlooked genetic regions that are important for plant immunity and pathogen ingress. In a new study by [Corredor-Moreno et al. \(2021\)](#), comparative transcriptome analysis resulted in the discovery of a positive regulator of wheat rust susceptibility that modulates amino acid metabolism.

Samples of different wheat varieties were sourced from multiple fields infected by the yellow rust pathogen (*Puccinia striiformis f.sp.tritici*, *Pst*) and were subjected to RNA-seq analysis. Samples from the same variety tend to group together within the phylogeny, demonstrating that this RNA-based approach can genetically define and separate varieties. Three wheat varieties (Oakley, Solstice, and Santiago) were selected based on their different susceptibility to *Pst*. The authors hypothesized that since plants of the same variety were collected from different environments and/or different developmental stages, the commonality between samples was their immune response to pathogen infection. Thus, genes involved in response to pathogen infection can be sorted out by co-expression cluster analysis (see figure). Among the biological processes that were significantly enriched across several important co-expression clusters, branched-chain amino-acid (BCAA) biosynthetic processes jumped out along with plant defense-related processes. The relationship between BCAAs and immunity

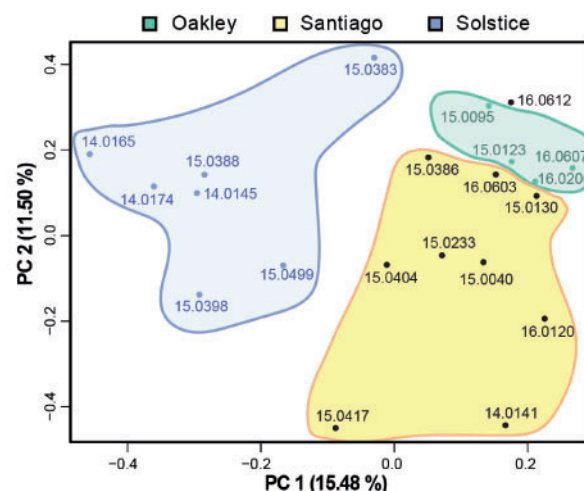


Figure RNA-seq analysis can be used to define the wheat variety in *Pst*-infected wheat. Principal component (PC) analysis of wheat gene expression profiles illustrates that samples group together by wheat variety, with two well-defined groups: (i) Solstice and (ii) Oakley and Santiago (blue, green and black font, respectively). (Reprinted from [Corredor-Moreno et al. \(2021\)](#) Figure 1C).

in cereal crops is largely unknown, although previous studies have shown that BCAAs serve as the precursors for glucosinolate, a well-known defense-related secondary metabolite found largely in Brassicaceae ([Sønderby et al., 2010](#); [Ishida et al., 2014](#)).

Using the co-expression cluster analysis combined with publicly available transcriptome data and qRT-PCR analysis carried out early during pathogen infection, the authors

focused on a mitochondrial BCAA aminotransferase 1 (*TaBCAT1*) as a key candidate gene whose expression levels could be tightly linked to disease progression. The authors created tetraploid wheat mutants with by TILLING (targeting local lesions in genomes) and *TaBCAT1*-silenced hexaploid plants by VIGS (virus-induced gene silencing). Disruption of *TaBCAT1* significantly reduced the plant's susceptibility to both yellow rust and stem rust (*Pgt*). *TaBCAT1* mutant plants had constitutively high levels of salicylic acid and high levels of expression of pathogenicity-related genes. In addition, mutation of *TaBCAT1* resulted in higher levels of BCAAs reflecting its likely role as a key enzyme in BCAA degradation. The levels of BCAA were also shown to tightly correlate with resistance against *Pst*. Thus, these results highlight a crucial, but previously under-

estimated role of BCAA metabolism in the defense response and potentially provide a new source of resistance against two of the most devastating diseases of wheat worldwide.

References

- Corredor-Moreno P, Minter F, Davey PE, Wegel E, Kular B, Brett P, Lewis CM, Morgan YML, Macías Pérez LA, Korolev AV, Hill L, Saunders DGO** (2021) The branched-chain amino acid aminotransferase *TaBCAT1* modulates amino acid metabolism and positively regulates wheat rust susceptibility. *Plant Cell* **33**: 1728–1747
- Ishida M, Hara M, Fukino N, Kakizaki T, Morimitsu Y** (2014) Glucosinolate metabolism, functionality and breeding for the improvement of Brassicaceae vegetables. *Breeding Sci* **64**: 48–59
- Sønderby IE, Geu-Flores F, Halkier BA** (2010) Biosynthesis of glucosinolates – gene discovery and beyond. *Trends Plant Sci* **15**: 283–290