IWYP International Wheat Yield Partnership
Research to Deliver Wheat for the Future

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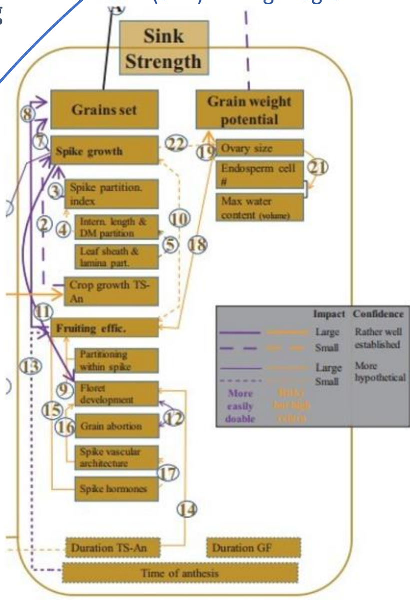
# Enhancing the Wheat Wiring Diagrams with More Genes and QTL

IWYP-associated scientists developed a framework for considering the traits and subtraits underpinning yield. These Wiring Diagrams (e.g., **Fig. 1**) were established based on the developmental biology of the wheat crop combined with the knowledge of the effects of genetic variation on specific developmental stages. The overall framework was defined at a high level, based on phenotypes and biochemical pathways that are visible, known or easily measured. Within and between the different defined stages of phenotypic development there are obviously huge numbers of biochemical steps within physiological networks, most of which are unknown. These steps are where genetic variation can influence crop development and downstream grain yield. Knowing more of these intermediate steps would provide more detailed and informative Wiring Diagrams and aid in linking QTL to specific steps, precise specification of haplotypes and identification of beneficial genetic variation. Thus, there is a need to incorporate more detail to enhance the utility of the Wiring Diagrams for application in breeding.

**Fig. 1**: Portion of Spike (sink) Wiring Diagram



Wiring Diagram References

- Nat. Food 3, 318-24, 2022
- JXB 74 (1), 40-71, 2023
- JXB 74 (1), 72-90, 2023

## Adding to the Information Database

Recent publications are beginning to provide much greater detail of the many genes underlying specific developmental steps. Lin et al. (Molecular Plant 17, 438-459, 2024) focused on wheat spike development, is a particularly pertinent example. The authors sought to define spike development in space and time by first defining the RNAs transcribed at each of the developmental stages. Amongst the large numbers of developmentally expressed genes, they chose to focus on transcription factors because these are likely to control downstream traits, including final yield. A pathway/regulatory network of transcription factors was hypothesized that drives spike formation. The roles of 36 of the 227 selected transcription factors active in spike development were verified by studying plants carrying mutations in their genes.

Such genes can now be mapped on to/underneath the Wiring Diagrams. Over time, as similar research projects are undertaken, the Wiring Diagrams can be underpinned with more of the genes that regulate the development of all tissues/organs/stages important in yield determination. Knowing such genes that influence yield determination makes it facile to assess whether variation in the genes has been selected during breeding. Lin et al. provide such examples. Known QTL can also be easily examined as to whether they lie at or near the identified genes. Where QTL are mapped close to variant candidate genes known to affect a particular developmental stage, it becomes simpler to find SNPs in the precise genes responsible for the QTL. Knowledge of such genes also aids selection of genes to be increased or reduced in expression by editing technologies, something necessary for widespread deployment of impactful gene editing.

## Accessing New Genetic Tools and Information

Lin et.al created a free and open access Wheat Spike Multi-Omic Database (https://39.98.48.156:8800/#/) for visualization of gene-centered data such as stage- specific expression, epigenetic landscapes, co-expression networks and the transcription networks underlying wheat spike development. The database also includes links to numerous spike developmental trait-related GWAS analyses and the KN9204 TILLING library. Such databases will surely be useful for augmenting the Wiring Diagrams and to those seeking to define and exploit the processes underlying the Wiring Diagrams as presently presented.