



# From the archives: A rice grain size regulatory module, GWAS of primary plant metabolism, and promoter trapping of polarity markers

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## October 2021: A regulatory module controlling grain size in rice

Since ancient times, humans have produced food by sowing seeds harvested from plants with favorable characteristics. Primitive farmers selected cereal species showing altered plant architecture and seed morphology that facilitated plant cultivation and boosted grain production. Thus, a compact growth habit together with increased seed size marked the evolution of wild grasses into domesticated cereals.

In rice, the QTL for seed width on chromosome 5 (*qSW5*) was one of the first domestication traits to be characterized: cultivated varieties show a deletion in *qSW5* that causes an increase in the number of cells in the lemma (the outer glume of the rice flower), resulting in a dramatic increase in seed size (Shomura et al., 2008). In the last decade, additional factors controlling grain length and width have been identified, including the histone H4 acetyltransferase GRAIN WEIGHT 6a (GW6a; Song et al., 2015).

Gao et al. (2021) discovered that GW6a physically interacts with HOMOLOG OF DA1 ON RICE CHROMOSOME 3 (HDR3)—a protein with ubiquitin-binding activity that stabilizes the GW6a protein levels by delaying its degradation. As a result, enhanced acetyltransferase activity leads to higher expression of target genes involved in the determination of grain morphology. GW6a and HDR3 positively regulate seed size and weight. Plants over-accumulating GW6a or HDR3 produce larger and heavier grains (see Figure), mainly by altering cell proliferation in lemmas. Therefore, GW6a and HDR3 represent good candidates for

further genetic improvements of high-yielding rice varieties for modern farmers.

## October 2017: GWAS of primary plant metabolism

During the life of a plant, primary metabolism supplies the structural components that sustain growth as well as specialized molecules that support the response to a wide range of stresses. Thus, central metabolism must be tightly regulated by a complex network integrating both developmental and environmental cues.

To dissect the regulatory mechanisms controlling primary metabolism in Arabidopsis, Fusari et al. (2017) performed a Genome-Wide Association Study (GWAS) using a panel of 349 diverse accessions in two experimental conditions. The authors identified interesting cis-QTL (mapping to structural genes) and trans-QTL (mapping to regulatory genes). They also provided evidence that natural genetic variation represented in the panel was largely associated with phenotypic variation observed in the accessions, with a large effect of polymorphisms detected in cis-QTL on enzyme abundance and activity. The authors studied in detail a QTL that affects the activity of six enzymes and found significant changes in multiple traits in a loss-of-function mutant of the ACCELERATED CELL DEATH6 (*ACD6*) gene. Interestingly, *ACD6* turned out to be a key player in keeping the balance between growth and defense through coordination of central metabolism. This study reinforces the relevance of GWAS in the dissection of the genetic basis of important traits in plants. Soon, the integration of big data obtained by multi-omics approaches using Artificial Intelligence could



**Figure** HDR3 functions upstream of GW6A to regulate grain size and weight. Mature grains of *hdr3-1*, *GW6a-OE-1*, and *hdr3-1/GW6a-OE-1*. Reprinted from Gao et al. (2021), Figure 6A.

be a critical step in crop breeding programs aimed at generating plant varieties that better adapt to stressful environments (Harfouche et al., 2019).

### October 1997: Promoter trapping IDs polarity markers

One of the most fascinating topics in developmental biology is the study of how a globular embryo generates a complex multicellular organism formed of different organs with specialized functions. In general, the development of complex organisms such as seed plants follows four main axes: apical–basal, central–peripheral, adaxial–abaxial, and proximal–distal. The apical–basal axis is established during embryogenesis, with the formation of the shoot and root apical meristems that will give rise to all above and below ground organs of the developing plant.

In the early days of *Arabidopsis* research, genetic studies employed mutants with polarity defects to decipher the regulation of axial development. To investigate apical–basal patterning, Topping and Lindsey (1997) screened a population of transgenic plants previously obtained using the promoter trap strategy (random insertion of a promoter-less  $\beta$ -glucuronidase [*GUS*] gene) and identified reporter lines showing *GUS* activity in specific positions along the apical–basal axis. Among the selected marker lines, *POLARIS* (*PLS*) was specifically visualized in the root apex of embryos and seedlings. Given that *PLS*–*GUS* activity was detected in a mutant defective in root meristem formation, the authors proposed that *PLS* might function in the polar organization of the root, likely by interacting with auxins and cytokinins.

Almost 10 years later, the same group discovered that *PLS* encodes a small peptide involved in modulating cell division and expansion in developing roots through crosstalk with ethylene and auxin pathways (Chilley et al., 2006). More recently, a combined empirical and computational approach

defined a model that integrates *PLS* and components of hormone signaling pathways in root patterning (Moore et al., 2015).

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