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IN BRIEF

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

Gao et al. (2021).

<https://doi.org/10.1093/plcell/koab194>

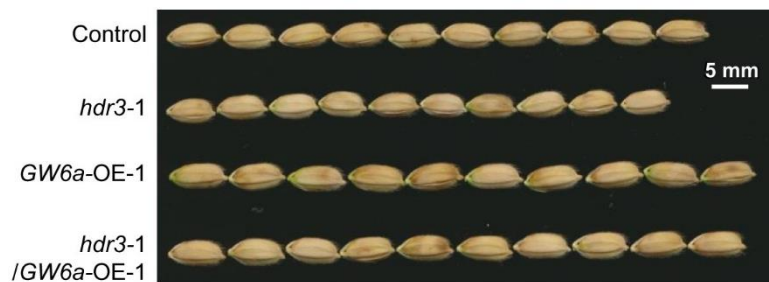


Figure 1. *HDR3* functions in a common genetic pathway with and upstream of *GW6a* to regulate grain size and weight. Mature grains of *hdr3-1*, *GW6a*-OE-1, and *hdr3-1/GW6a*-OE-1. Reprinted from Gao et al. (2021). Figure 6A.

Since ancient times, humans have produced their own food by sowing seeds they had harvested from plants with the most favourable characteristics. For example, primitive farmers selected cereal species showing altered plant architecture and seed morphology that not only facilitated plant cultivation but also boosted grain production. Precisely, 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 trait 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 remarkable 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. In fact, plants over-accumulating GW6a or HDR3 produce larger and heavier grains, mainly by altering cell proliferation in lemmas. Therefore, GW6a and HDR3 represent good candidates for the genetic improvement of high-yielding rice varieties for modern farmers.

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Song XJ, Kuroha T, Ayano M, Furuta T, Nagai K, Komeda N, Segami S, Miura K, Ogawa D, Kamura T, Suzuki T, Higashiyama T, Yamasaki M, Mori H, Inukai Y, Wu J, Kitano H, Sakakibara H, Jacobsen SE, and Ashikari M. (2015). Rare allele of a previously unidentified histone H4 acetyltransferase enhances grain weight, yield, and plant biomass in rice. *Proc Natl Acad Sci USA* **112**: 76–81

October 2017: GWAS of primary plant metabolism

Fusari et al. (2017). <https://doi.org/10.1105/tpc.17.00232>

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 able to integrate 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 largely associated with phenotypic variation observed in the accessions, with a bigger 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 by using Artificial Intelligence could be a critical step in crop breeding programs aimed at generating plant varieties that better adapt to stressful environments (**Harfouche et al., 2019**).

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Harfouche AL, Jacobson DA, Kainer D, Romero JC, Harfouche AH, Scarascia Mugnozza G, Moshelion M, Tuskan GA, Keurentjes JJB, Altman A (2019). Accelerating Climate Resilient Plant Breeding by Applying Next-Generation Artificial Intelligence. *Trends in Biotechnol.* **37(11)**:1217-1235.

October 1997: Promoter trapping IDs polarity markers

Topping and Lindsey (1997). <https://doi.org/10.1105/tpc.9.10.1713>

One of the most fascinating topics in development biology is to understand how a globular embryo generate a multicellular organism (formed of different organs with specialized functions). In general, the development of complex organisms such as seed plants follows four main axes (the apical-basal, the central to peripheral, the adaxial-abaxial, and the proximal to 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 further investigate apical-basal patterning, **Topping and Lindsey (1997)** screened a population of transgenic plants previously obtained by using the promoter trap strategy (i.e., random insertion of a promoter-less β -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 still detected in a mutant defective in root meristem formation, the authors proposed that PLS could function in the polar organization of the root likely by interacting with auxins and cytokinins.

Almost ten years later, the same group discovered that the *PLS* gene encodes a small peptide involved in the modulation of cell division and expansion in developing roots through crosstalk with ethylene and auxin pathways (**Chilley et al., 2006**). More recently, the combination of experimental data and computational approach defined a model that integrates the activity of PLS and components of hormone signaling pathways in root patterning (**Moore et al., 2015**).

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