Topic: SMALL GRAIN 11 Controls Grain Size, Grain Number and Grain Yield in Rice

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Today’s discussion

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ORIGINAL ARTICLE

SMALL GRAIN 11 Controls Grain Size, Grain Number and Grain Yield in Rice

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Background

- The big picture – what is the societal or socioeconomical problem(s) to be solved?

- Rice Grains

- Grain size
  - What is it?
  - Why is this important?

Let’s go through the Introduction!
Rice is one of the most important cereal crops and the main food source of the global population.
Rice yield component

- Yield components: structures of the rice plant that directly translate into yield.
  - The number of panicles per given area
  - The number of spikelets (potential) grains per panicle
  - The percent of filled grains per panicle
  - The weight of each grain.

Grain weight

- Grain weight is positively associated with grain size, which is determined by grain length, grain width, and grain thickness.
Factors regulating grain size

- Previously discovered QTL
  - GS3: grain length and grain weight
  - qGL3/GL3.1: grain length
  - GW2: grain width and weight
  - qSW5/GW5: grain width
  - Etc.

- Most are involved with either cell proliferation or cell expansion process.
The Novelty : let’s get back to the introduction!

“To further understand the molecular mechanisms that determine grain size, we have previously isolated small grain mutants (smg) in rice (Duan et al., 2014). Here we report that smg11 is a new allele of DWARF2 (D2), which encodes a cytochrome P450 (CYP90D2) involved in brassinosteroid (BR) biosynthetic pathway (Hong et al., 2005). Brassinosteroids play important roles in plant growth and development. Several studies show that genes involved in BR signaling and BR biosynthetic pathways influence seed size in Arabidopsis and rice (Zuo and Li, 2014; Li and Li, 2015, 2016).”
What is the biological question(s) being asked?

Let's brainstorm and write on the board!
What approach was chosen to address the question?

- Scope of the study
  - What was the plant used?
    - What genotypes were used?
  - What was the study approach?
  - What traits were characterized?
    - Were they molecular, cellular, biochemical, physiological or morphological?
What is the hypothesis?

Let’s brainstorm and write on the board!
What are the techniques used and what type(s) of data generated?

Let’s go through the M&M!
What are the techniques used and what type(s) of data generated?

- Method 1: Morphological analysis of smg11 grains

Fig. 1: The smg11 mutant produces small grains. a Mature paddy rice grains of KYJ and smg11. b Brown rice grains of KYJ and smg11. c The average length of KYJ and smg11 grains. d The average width of KYJ and smg11 grains. e The 1000-grain weight of KYJ and smg11. Values c-e are given as mean±SD. *P < 0.05; **P < 0.01 compared with the wild type by Student’s t-test. Bars: 2 mm in a and b.
What is the expected outcome?

Let’s brainstorm!
What are the techniques used and what type(s) of data generated?

- Method 1: Morphological analysis of smg11 mutant

- The smg11 mutant had smaller grains, and lower 1000-grain weight compared to WT.
What are the techniques used and what type(s) of data generated?

- **Method 2:**
  Morphological analysis of *smg11* panicles
What is the expected outcome?

Let’s brainstorm!
What are the techniques used and what type(s) of data generated?

- **Method 2:** Morphological analysis of *smg11* panicles

  *smg11* formed dense and erect panicles due to a decrease in the length of panicle axis and increases in the secondary panicle branch number and grain number per panicle.
What are the techniques used and what type(s) of data generated?

- Method 3: Cell expansion analysis by SEM & Gene expression analysis.
What is the expected outcome?

Let’s brainstorm!
What are the techniques used and what type(s) of data generated?

- **Method 3: Cell expansion analysis by SEM & Gene expression analysis**

  - The small grain phenotype of *smg11* mainly results from the reduced cell expansion in spikelet hulls.
  - *SMG11* regulates grain size by influencing expression of grain size genes involved in the regulation of cell expansion.
What are the techniques used and what type(s) of data generated?

- **Method 4:**
  Identification of smg11 mutation via MutMap approach & genetic complementation analysis.
What is the expected outcome?

Let's brainstorm!
What are the techniques used and what type(s) of data generated?

Method 4: Identification of \( smg11 \) mutation via MutMap approach & genetic complementation analysis.

- MutMap showed that LOC_Os01g10040 is a good candidate gene for \( SMG11 \).
What are the techniques used and what type(s) of data generated?

- Method 4: Identification of smg11 mutation via MutMap approach & genetic complementation analysis

- Transgenic plants containing LOC_Os01g10040 showed WT phenotypes.
What are the techniques used and what type(s) of data generated?

- Method 5: Gene expression analysis of BR-related genes
What is the expected outcome?

Let’s brainstorm!
What are the techniques used and what type(s) of data generated?

- Method 5: Gene expression analysis of BR-related genes

It is plausible that the mutation in *SMG11/D2* might decrease BR signaling or responses by repressing expression of BR signaling genes (e.g. *OsBRI1* and *BU1*), resulting in small grains.
What are the techniques used and what type(s) of data generated?

- **Method 6**: Overexpression of \textit{SMG11}.

\textit{Fig. 6} Overexpression of D2/\textit{SMG11} increases grain size due to large cells in spikelet hulls. \textbf{a, b} Grains of ZH11, \textit{pActin:SMG11\#1}, and \textit{pActin:SMG11\#2} and \textit{pActin:SMG11\#3}. \textit{pActin:SMG11\#1} is ZH11 transformed with \textit{pActin:SMG11}. \textbf{c, d} SEM analysis of the outer surface of ZH11 \textit{c} and \textit{pActin:SMG11\#2} \textit{d} lemma. \textbf{e, f} SEM analysis of the inner surface of ZH11 and \textit{pActin:SMG11\#2} lemma. \textbf{g} Grain length. \textbf{h} Grain width. \textbf{i} 1000-grain weight. \textbf{j} Expression levels of \textit{SMG11/D2} in ZH11 and \textit{pActin:SMG11\#2} and \textit{pActin:SMG11\#3} lemma. \textbf{k} The average length of outer epidermal cells in ZH11 and \textit{pActin:SMG11\#2} lemma. \textbf{l} The average width of outer epidermal cells in ZH11 and \textit{pActin:SMG11\#2} lemma. \textbf{m} The average width of inner epidermal cells in ZH11. Values \textbf{g-n} are given as mean ± SD. *P < 0.05, **P < 0.01 compared with ZH11 by Student's t-test. Bars: 2 mm in \textbf{a-b} 100 μm in \textbf{c-f}.
What is the expected outcome?

Let’s brainstorm!
What are the techniques used and what type(s) of data generated?

- Method 6: Overexpression of *SMG11*.

- Overexpression of *SMG11* promotes grain growth by increasing cell expansion in spikelet hulls.
What are the key findings?

Let’s brainstorm and write on the board!
Importance for crop production

- The effect of $D2/SMG11$ on grain yield depends on its expression levels.

- “Our findings define the functions of $D2/SMG11$ in grain size and grain yield, suggesting that an optimized expression of $D2/SMG11$ is a promising approach to improve grain yield in rice.”
Is the experimental design/workflow suitable to prove the hypothesis?

Let’s brainstorm!
Did the key findings address or prove the hypothesis?

Let’s brainstorm!
What else can be done to further strengthen the work/study?

Let’s brainstorm!
Q&A

ANY QUESTIONS?
15 mins to go...
Fill in the discussion assessment form!

- What is the main idea of the study?

- Summarize the findings and state whether the findings address the scientific and/or societal questions/problems.

- Do you like this article? Why?