

W900

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**An Ethylene-Gibberellin Relay Co-opts the Green Revolution Gene to Allow Rice Adaptation to Submergence**

Takeshi Kuroha (Tohoku Univ.)  
Susan McCouch (Cornell Univ.)  
Moto Ashikari (Nagoya Univ.)

Deepwater rice field in Thailand



Water is essential for all living organisms, and plant lives around swamps and rivers has an advantage in terms of water availability

Excess water due to flooding has an adverse effect on the growth of most plants

**Deepwater response** (Tank was filled to the brim at the first day)

Non-Deepwater rice    **Deepwater rice**

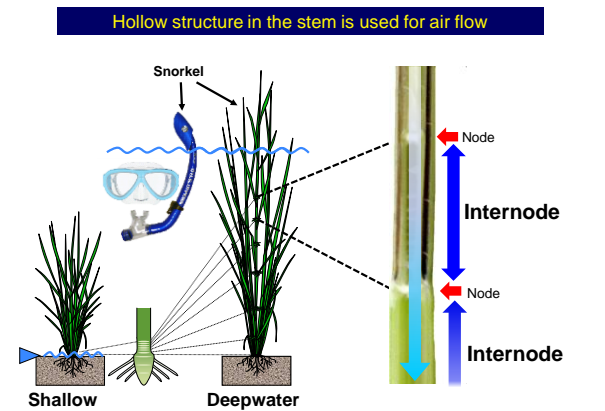
Hattori et al 2009 Nature

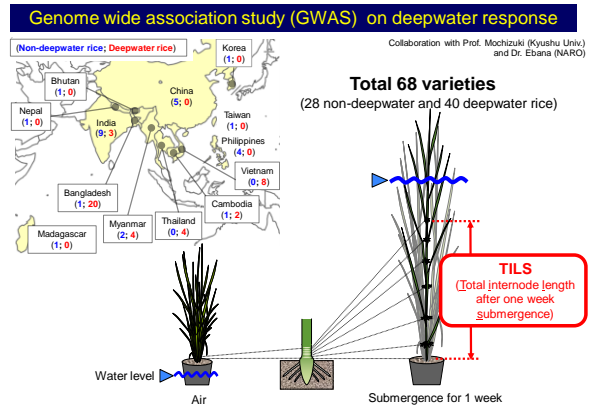
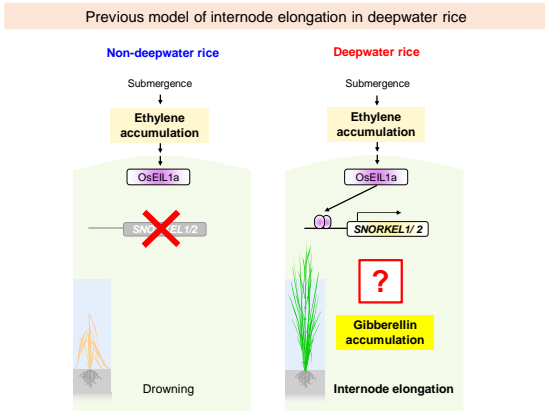
**Dry season**

**Rainy season**

**There are plants that can adapt to periodic flooding**

<http://angkorvat.jp>

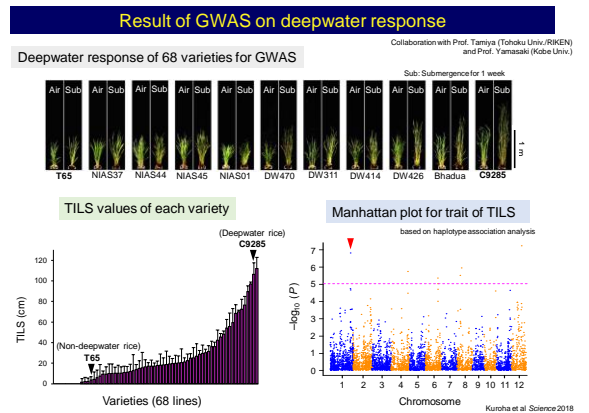
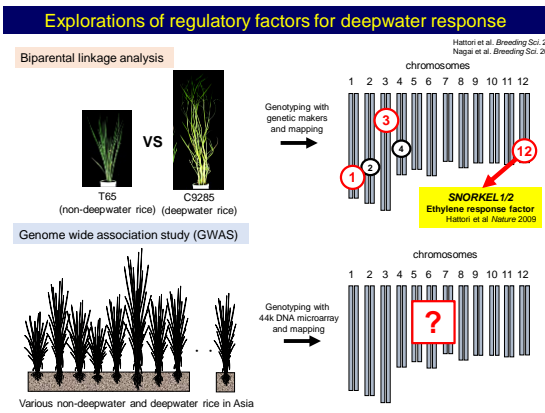
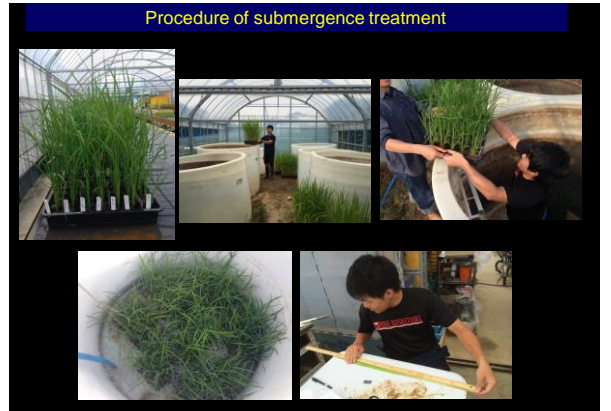


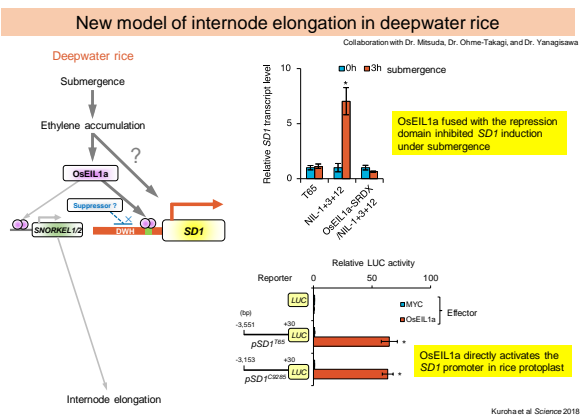
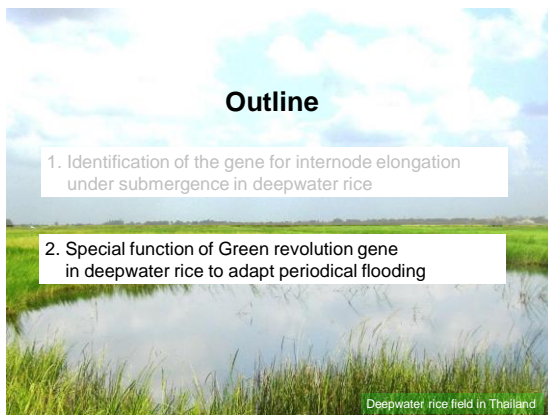
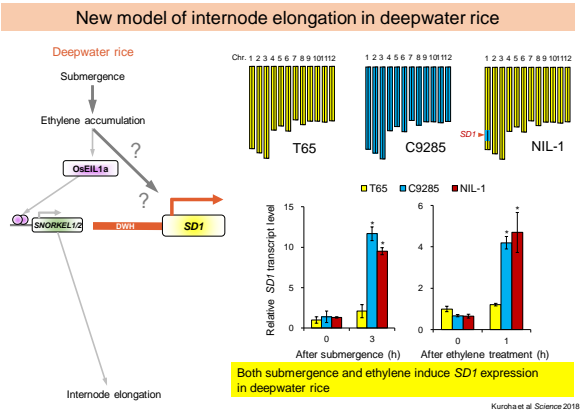
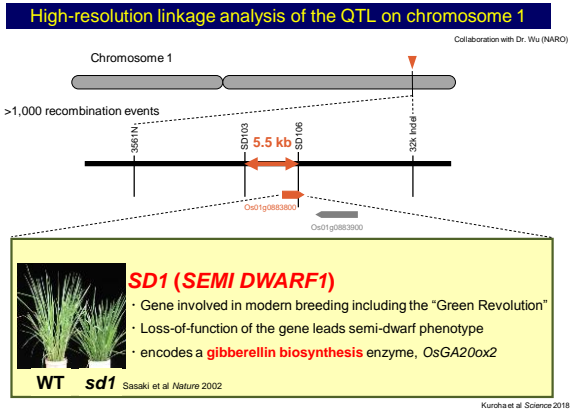
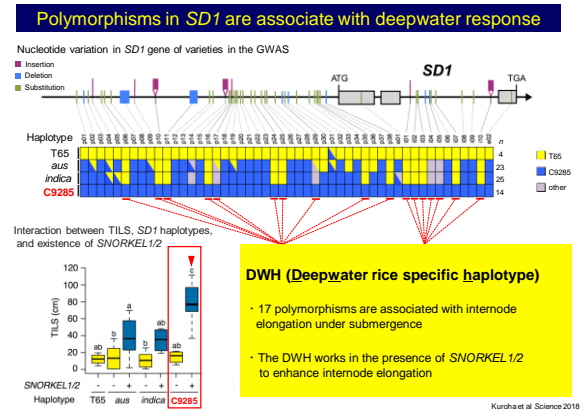
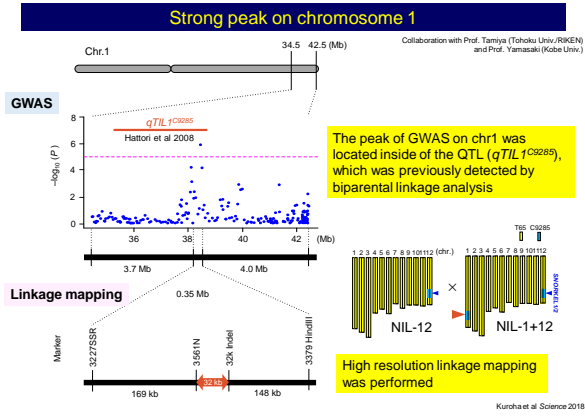


## Outline

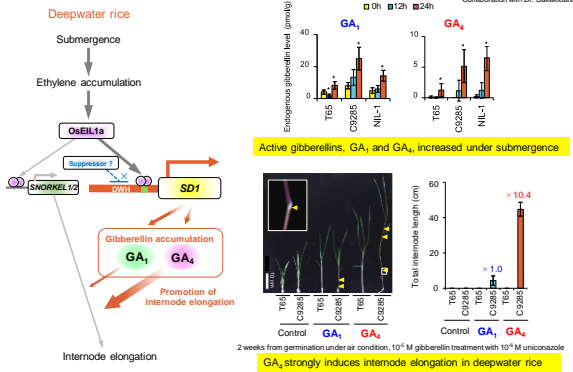
1. Identification of the gene for internode elongation under submergence in deepwater rice
2. Special function of Green revolution gene in deepwater rice to adapt periodical flooding

Deepwater rice field in Thailand

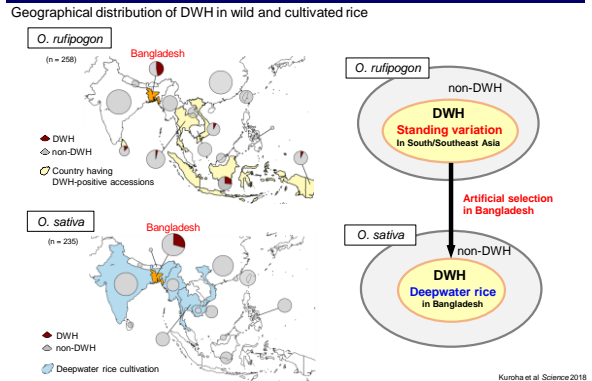




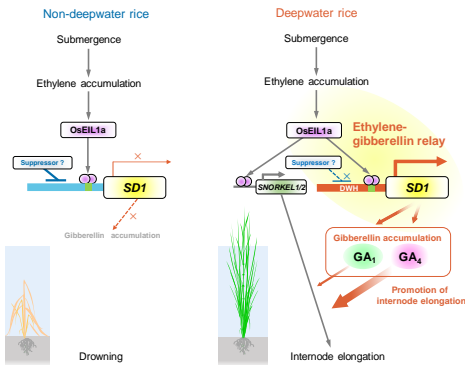
**New model of internode elongation in deepwater rice**



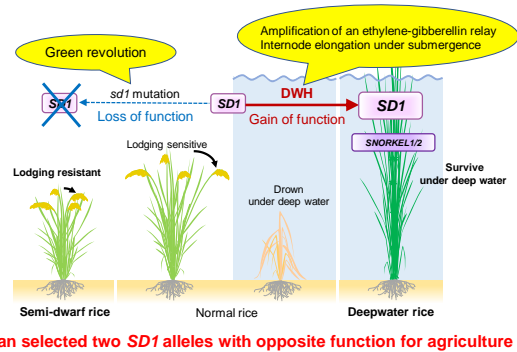
**Origin of the DWH**



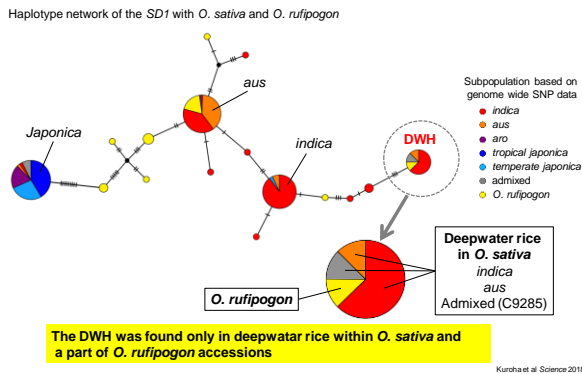
**New model of internode elongation in deepwater rice**



**Contribution of SD1 gene to rice breeding for two different purposes**



**Haplotype network of the SD1**



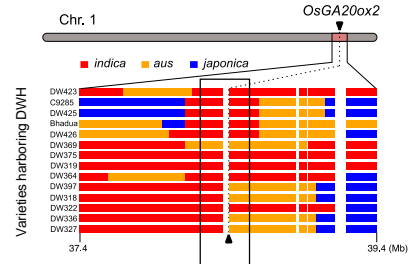
**Acknowledgement**

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|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <p><b>Nagoya Univ.</b><br/>Keisuke Nagai<br/>Rico Gamuyao<br/>(present: Johns Hopkins Univ. School of Medicine)</p> <p><b>Tomoyuki Furuta</b><br/>Masanari Nakamori<br/>Takuya Kitaoka<br/>Keita Adachi<br/>Anzu Minami<br/>Yoshinao Mori</p> <p>JST CREST<br/>JICA-JST SATREPS<br/>The Japan Advanced Plant Science Network<br/>The Canon Foundation<br/>MEXT/JSPS KAKENHI<br/>the NSF Graduate Research Fellowship<br/>USDA NIFA</p> | <p><b>Tohoku Univ.</b><br/>Shinjiro Yamaguchi<br/>(present: Kyoto Univ.)</p> <p>Kiyoshi Mashiguchi<br/>Yoshiya Seto<br/>(present: Meiji Univ.)</p> <p>Kazuhiro Nishitani<br/>Ryusuke Yokoyama</p> <p><b>Cornell Univ.</b><br/>Diane R. Wang<br/>(present: Univ. at Buffalo)</p> <p>植物環境突破力<br/>植物細胞観察の画像処理システム</p> | <p><b>Tohoku Univ. /RIKEN AIP</b><br/>Gen Tamiya</p> <p><b>Kyushu Univ.</b><br/>Toshihiro Mochizuki</p> <p><b>Univ. of Tokyo</b><br/>Shuichi Yanagisawa</p> <p><b>RIKEN CSRS/Nagoya Univ.</b><br/>Hitoshi Sakakibara</p> <p><b>RIKEN CSRS</b><br/>Mikiko Kojima</p> <p><b>Kobe Univ.</b><br/>Masanori Yamasaki</p> <p><b>NIAS</b><br/>Kaworu Ebana<br/>Jianzhong Wu</p> <p><b>AIST</b><br/>Masaru Ohme-Takagi<br/>(present: Saitama Univ.)<br/>Nobutaka Mitsuda</p> |
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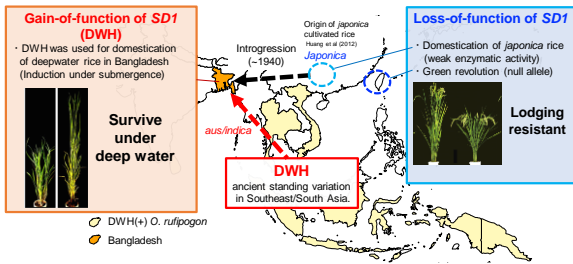
**Admixture analysis in *OsGA20ox2* region**

Admixture analysis using a subset of diverse non-admixed *O. sativa* as the reference panel (114 *Japonica*; 57 *aus*; 87 *indica*).



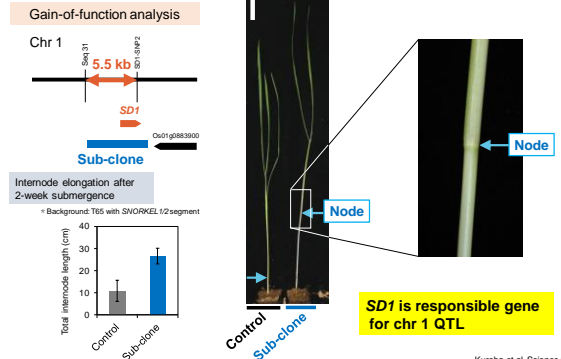
The DWH is associated with *indica* or *aus* subpopulations of *O. sativa*  
 The DWH was artificially selected for cultivation of *japonica* deepwater rice

**The evolutionary history and domestication of *SD1***



Human selected different alleles with opposite function of the same gene for agriculture history

**Responsible gene for chr 1 QTL. by linkage analysis**

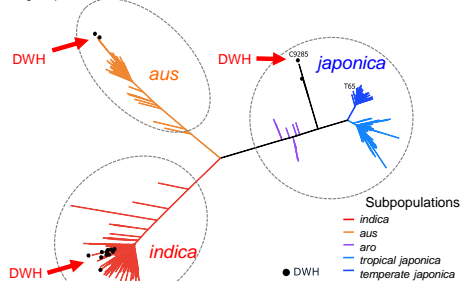


***SD1* is responsible gene for chr 1 QTL**

Kuroha et al Science 2018

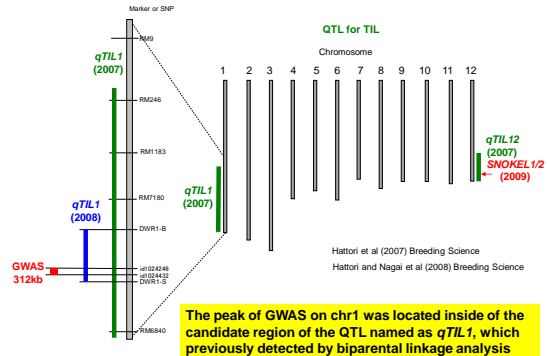
**Distance tree analysis of diverse *O. sativa* subpopulation**

Distance tree of 480 varieties of *Orizya sativa* including deepwater rice. Collaboration with Prof. McCouch (Cornell Univ).



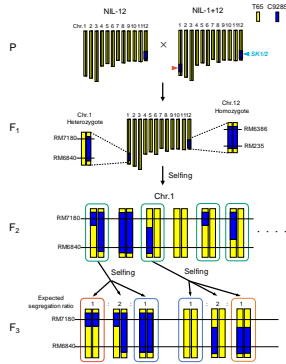
The DWH were present in only 14 Bangladesh deepwater rice varieties classified into *indica*, *aus*, or *japonica*.

**Chr1 QTL detected by biparental linkage analysis and GWAS**

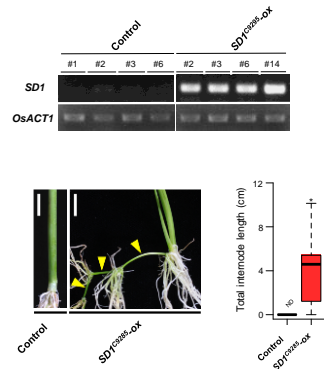


The peak of GWAS on chr1 was located inside of the candidate region of the QTL named as *qTIL1*, which previously detected by biparental linkage analysis.

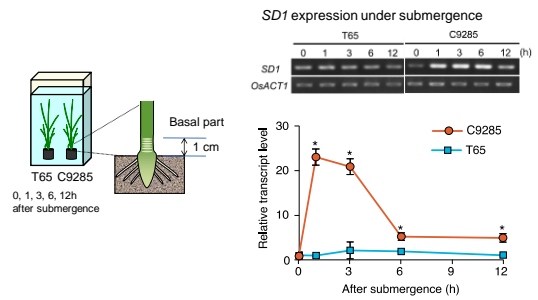
**Scheme for production of QTL mapping population on chromosome 1**



**Internode elongation by near-constitutive expression of the SD1 gene**



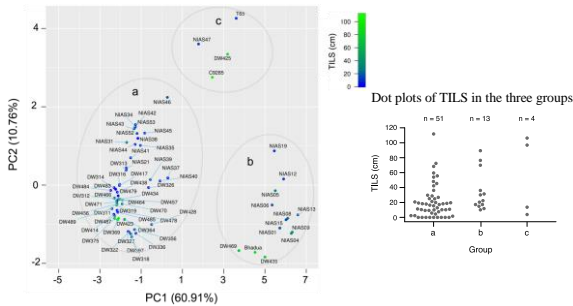
**Transcriptional regulation of SD1 under submergence treatment**



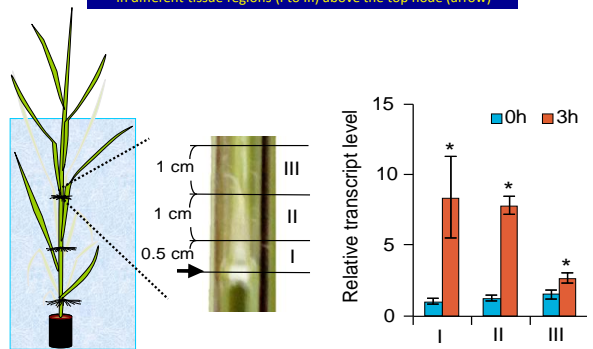
**Deepwater rice showed strong induction of SD1 expression under submergence treatment**

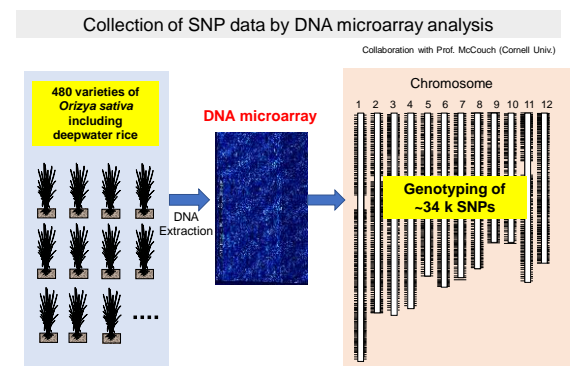
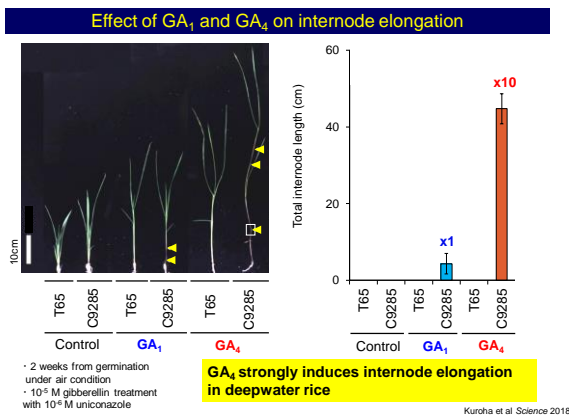
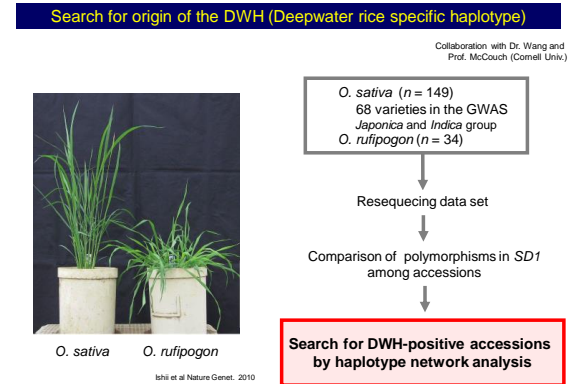
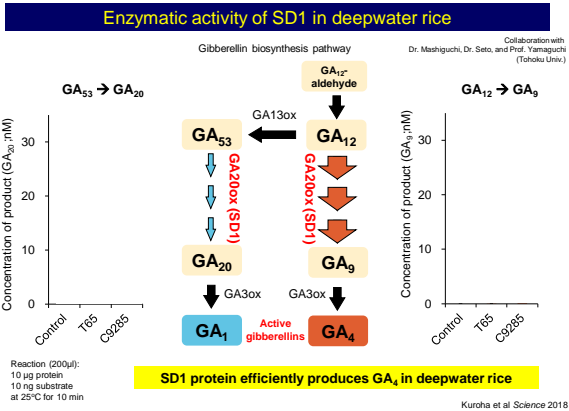
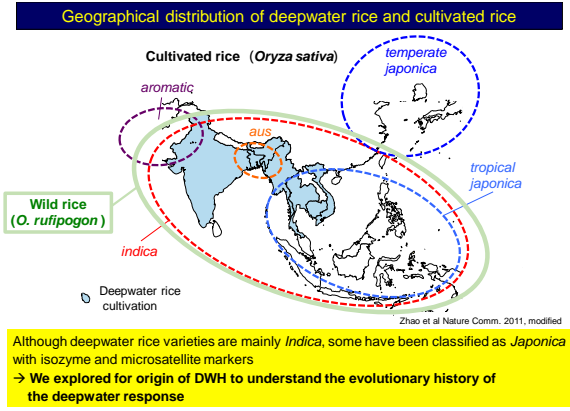
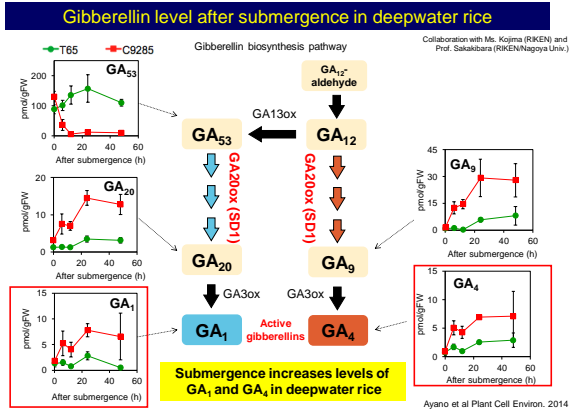
Kuroha et al Science 2018

**Principal component analysis (PCA) of the GWAS panel.**

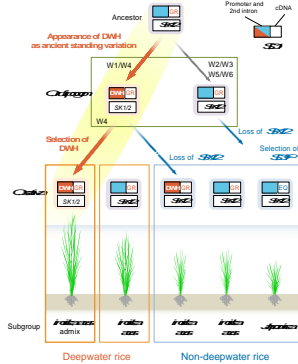


**Expression analysis of submergence-induced SD1 transcription in different tissue regions (I to III) above the top node (arrow)**

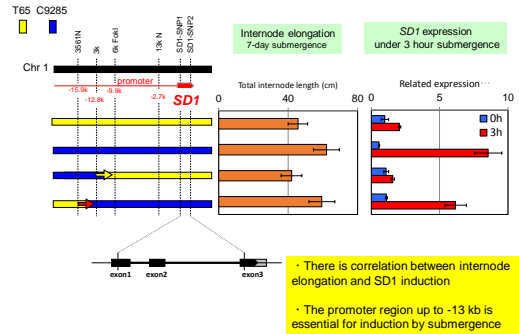




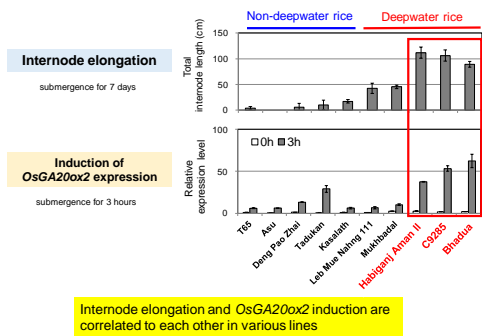
Evolutionary history of deepwater rice proposed in this study



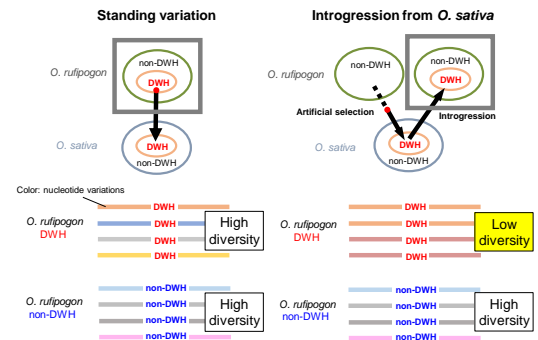
Interaction of internode elongation and SD1 induction in mapping lines



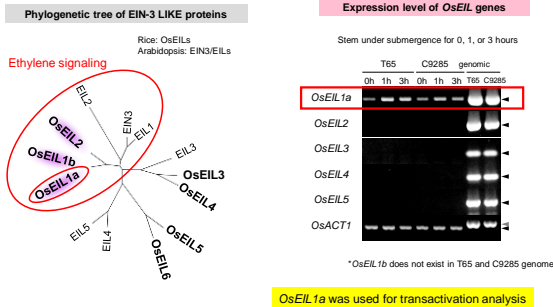
Relationship between internode elongation and OsGA20ox2 induction in various lines



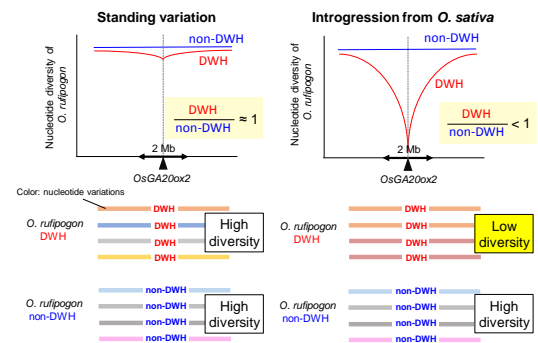
Evaluation of DWH in O. rufipogon



OsEIL1a is predominantly expressed in stem of deepwater rice



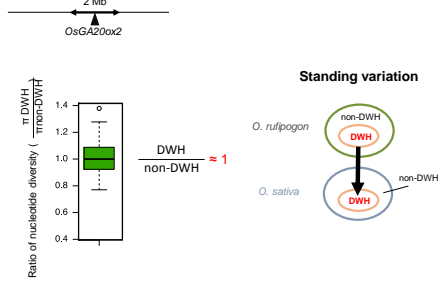
Evaluation of DWH in O. rufipogon





**DWH is ancient standing variation**

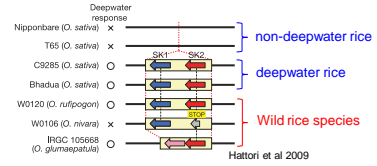
Nucleotide diversity of 2 Mb region on 108 accessions of *O. rufipogon* were compared.



**What is the evolutionary history of genes for deepwater response?**

**Evolutionary history of SNORKEL genes**

Wild rice species possess the *SNORKEL* genes, genes may have been acquired before or during wild rice species divergence.

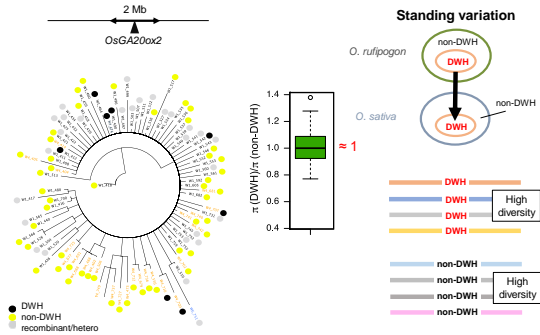


**What is the evolutionary history of the DWH in OsGA20ox2 ?**

Analysis on genome-wide relationships of DWH and globally diverse *O. sativa* and wild rice (*O. rufipogon*)

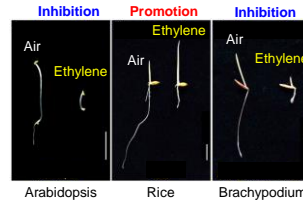
**DWH is ancient standing variation**

Nucleotide diversity of 2 Mb region on 108 accessions of *O. rufipogon* were analyzed.

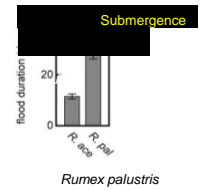


**Elongation of plant body for adaptation to flooding**

Elongation of coleoptile in rice seedlings under ethylene treatment in darkness

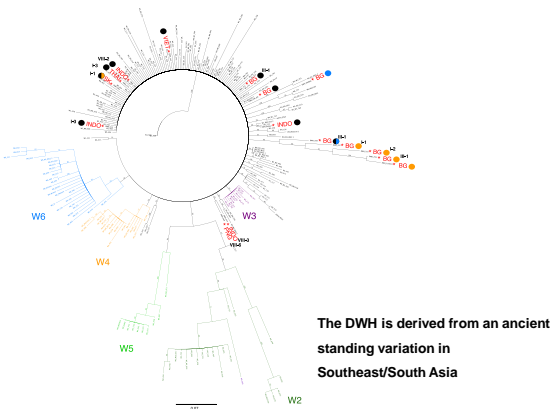


Submergence-induced petiole elongation in *Rumex palustris*



Yang et al 2015 Mol Plant

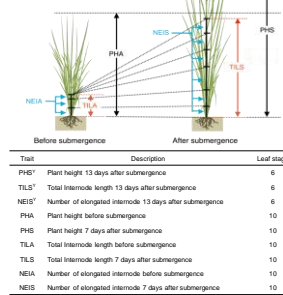
van Veen et al 2013 Plant Cell



The DWH is derived from an ancient standing variation in Southeast/South Asia

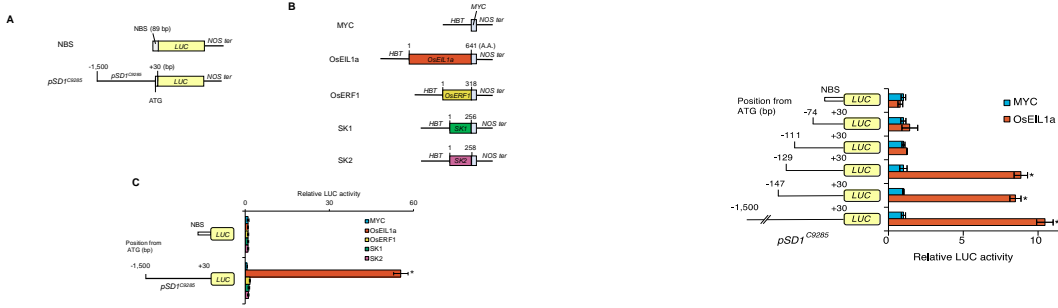
**6 leaf stage : 3 Traits**

**10 leaf stage : 6 Traits**

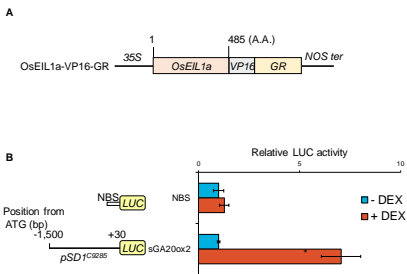


	PHI*	TLS*	NEIS*	PHA	PHS	TLS	NEA	NEIS
PHI*	1	0.74	0.73	0.26	0.26	0.26	0.71	0.71
TLS*	0.64	1	0.71	0.26	0.26	0.26	0.67	0.73
NEIS*	0.64	0.67	1	0.27	0.27	0.27	0.66	0.67
PHA	0.11	0.26	0.26	1	0.28	0.28	0.68	0.67
PHS	0.18	0.26	0.26	0.27	1	0.27	0.67	0.67
TLS	0.47	0.67	0.67	0.28	0.28	1	0.68	0.67
NEA	0.69	0.66	0.66	0.24	0.24	0.24	1	0.67
NEIS	0.67	0.65	0.65	0.26	0.26	0.26	0.64	1
NEI	0.41	0.54	0.54	0.18	0.18	0.18	0.65	0.65

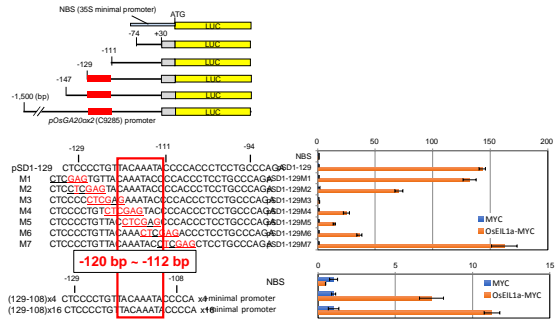
Transient assay for transactivation of SD1 promoter in rice mesophyll protoplast



Transactivation of SD1 promoter by chemical induction of OsEIL1a protein



cis-element for activation of OsGA20ox2 promoter by rice EIN3



cis-element is located in -120 bp to -112 bp region upstream of OsGA20ox2 gene

DNA binding domain of OsEIL1a protein for transactivation of SD1 promoter

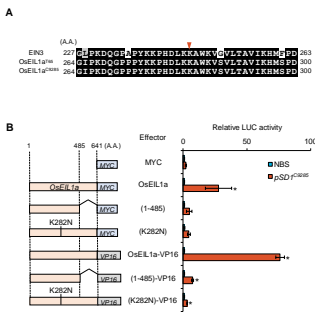
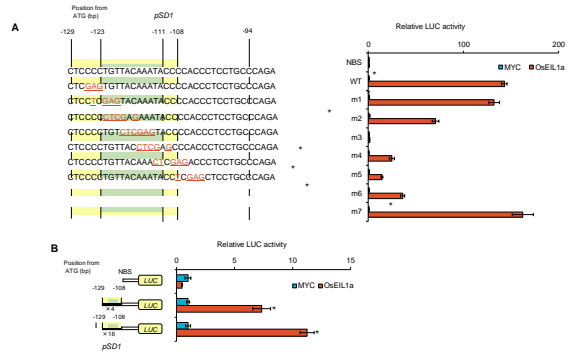
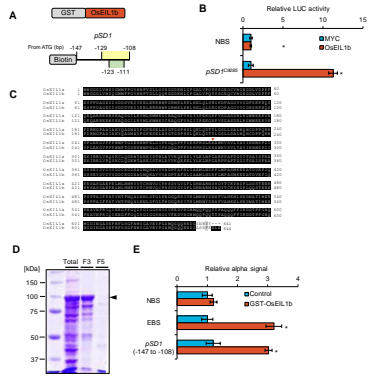


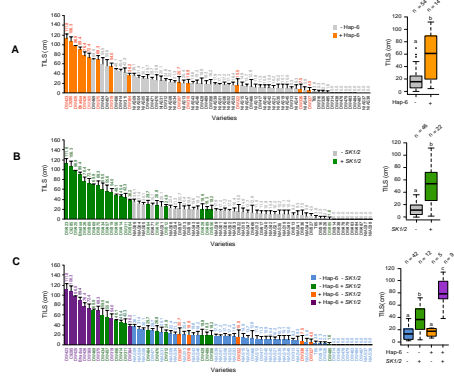
Fig. S27. cis-regulatory element for binding of OsEIL1a to the SD1 promoter.



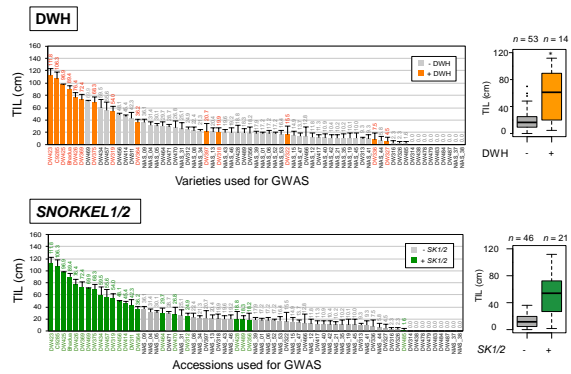
**Binding assay with OsEIL1b protein and *SD1* promoter *in vitro***



**Relationship between TILS value and Haplogroup 6 of *SD1* or presence/absence of *SK1/2* in the GWAS panel**



**Positive effect of both DWH and *SNORKEL 1/2* on TIL**



**Interaction between DWH and *SNORKEL 1/2* on TIL**

