



Contents lists available at ScienceDirect

Plant Science

journal homepage: [www.elsevier.com/locate/plantsci](http://www.elsevier.com/locate/plantsci)



## The phenome analysis of mutant alleles in *Leucine-Rich Repeat Receptor-Like Kinase* genes in rice reveals new potential targets for stress tolerant cereals

Anne Dievart<sup>a,\*</sup>, Christophe Perin<sup>a</sup>, Judith Hirsch<sup>b</sup>, Mathilde Bettembourg<sup>a</sup>, Nadège Lanau<sup>a</sup>, Florence Artus<sup>a</sup>, Charlotte Bureau<sup>a</sup>, Nicolas Noel<sup>a</sup>, Gaétan Droc<sup>a</sup>, Matthieu Peyramard<sup>a</sup>, Serge Pereira<sup>b</sup>, Brigitte Courtois<sup>a</sup>, Jean-Benoit Morel<sup>b</sup>, Emmanuel Guiderdoni<sup>a</sup>

<sup>a</sup> CIRAD, UMR AGAP, 34398 Montpellier cedex 5, France

<sup>b</sup> INRA, UMR BGPI, INRA-CIRAD-SupAgro, TA 54/K, Campus International de Baillarguet, 34398 Montpellier cedex 5, France

### ARTICLE INFO

#### Article history:

Received 15 May 2015

Received in revised form 17 June 2015

Accepted 22 June 2015

Available online xxx

#### Keywords:

Abiotic stress

Mutant

LRR RLK

Rice

### ABSTRACT

Plants are constantly exposed to a variety of biotic and abiotic stresses that reduce their fitness and performance. At the molecular level, the perception of extracellular stimuli and the subsequent activation of defense responses require a complex interplay of signaling cascades, in which protein phosphorylation plays a central role. Several studies have shown that some members of the Leucine-Rich Repeat Receptor-Like Kinase (LRR-RLK) family are involved in stress and developmental pathways. We report here a systematic analysis of the role of the members of this gene family by mutant phenotyping in the monocotyledon model plant rice, *Oryza sativa*. We have then targeted 176 of the ~320 LRR-RLK genes (55.7%) and genotyped 288 mutant lines. Position of the insertion was confirmed in 128 lines corresponding to 100 LRR-RLK genes (31.6% of the entire family). All mutant lines harboring homozygous insertions have been screened for phenotypes under normal conditions and under various abiotic stresses. Mutant plants have been observed at several stages of growth, from seedlings in Petri dishes to flowering and grain filling under greenhouse conditions. Our results show that 37 of the LRR-RLK rice genes are potential targets for improvement especially in the generation of abiotic stress tolerant cereals.

© 2015 Z. Published by Elsevier Ireland Ltd. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

### 1. Introduction

Nowadays, rice of Asian origin (*Oryza sativa* L.) is the staple food for more than half of the human population. In less than 40 years, the world's population is predicted to reach 9 billion, raising the so-called "9-billion-people" issue [1]. For sustainable rice production in the years to come, a number of challenges need to be addressed by the entire rice community with the common goal of creating new elite rice varieties [2,3]. Large efforts have focused in the last years to complete sequencing of several *Oryza* genomes [4–10]. In functional genomics, the challenge is now to system-

atically assign a biological function to all genes in the genomes. To help in this task, the rice community worldwide has started to share efforts in the late 90's to produce insertion mutant collections required for gene functional analyses [11,12]. These mutant collections are available in several laboratories around the world: CSIRO in Australia [13], NIAS in Japan [14], OSTID in Europe [15], OTL in France [16], POSTECH [17] and PMBBRC [18] in Korea, RMD in China [19], TRIM in Taiwan [20], and UCD in USA [21]. These mutant collections contain insertion lines created with T-DNA, *Tos17*, *Ds*, and *dSpm* inserts mutagens and the engineered mutagens may additionally carry gene traps, enhancer traps and/or activation tags. They have been generated in different cultivars: Nipponbare (NB), DongJin (DJ), HwaYoung (HW), Zhonghua 11 (Z11), Zhonghua 15, Tainung 67 (TNG) and Kitaake. All these lines are listed based on their flanking sequence tags (FSTs) in two databases: RiceGE (<http://signal.salk.edu/cgi-bin/RiceGE>) and Ory-GenesDB (<http://orygenesdb.cirad.fr>). In total, ~225,000 FSTs are precisely positioned on the ssp. *japonica* cv. Nipponbare sequence

**Abbreviations:** LRR-RLK, leucine-rich repeat receptor-like kinase; MS, Murashige and Skoog medium; DJ, DongJin; HW, HwaYoung; Z11, Zhonghua 11; TNG, Tainung 67; FST, flanking sequence tag.

\* Corresponding author at: UMR AGAP, CIRAD, Avenue Agropolis, TA A 108/03, Bat 3, Bureau 51, 34398 Montpellier cedex 5, France.

E-mail address: [anne.dievart@cirad.fr](mailto:anne.dievart@cirad.fr) (A. Dievart).

<http://dx.doi.org/10.1016/j.plantsci.2015.06.019>

0168-9452/© 2015 Z. Published by Elsevier Ireland Ltd. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

**Table 1**  
List of LRR-RLK genes with known functions in rice.

Accession numbers	Names	Orthologous relationships described	Functions/comments	References
Os11g36180	Xa21		Resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i>	[61]
Os02g34790	Xoo-INDUCED KINASE 1 (XIK1)		Positively regulates XA21-mediated immunity	[62]
Os11g47000	Xa3/Xa26		Immune receptor playing the same role as Xa21	[63,64]
Os04g52780	Os FLAGELLIN SENSING 2 (OsFLS2)	AtFLS2	As in <i>Arabidopsis</i> mediates flagellin perception	[65]
Os01g52050	Os BRASSINOSTEROID INSENSITIVE 1 (OsBRI1)	AtBRI1	Cell elongation and cell division in shoot	[66]
Os09g12240	Os BRI1-LIKE 1 (OsBRL1)	AtBRL1	Cell elongation and cell division in shoot and root in conjunction with OsBRI1	[67]
Os08g25380	Os BRI1-LIKE 3 (OsBRL3)	AtBRL3	Cell elongation and cell division in shoot and root in conjunction with OsBRI1	[67]
Os06g50340	FLORAL ORGAN NUMBER 1 (FON1)	AtCLAVATA1 (AtCLV1)	Regulates floral meristem size	[68]
Os01g68870	MULTIPLE SPOROCTYTE 1 (MSP1)	At EXTRA SPOROGENOUS CELLS / EXCESS MICROSPOROCTYTES1 (EXS/EMS1)	Necessary to restrict the number of cells entering into male and female sporogenesis and to initiate anther wall formation	[55]
Os02g10100	MSP-LIKE 1 (MSL1)	At EXTRA SPOROGENOUS CELLS / EXCESS MICROSPOROCTYTES1 (EXS/EMS1)	Necessary to restrict the number of cells entering into male and female sporogenesis and to initiate anther wall formation in conjunction with MSP1	[69]
Os03g12730	BLAST RESISTANCE-RELATED (BRR1)	At BARELY ANY MERISTEM (BAM1 and BAM2)	Involved in blast resistance	[70]
Os03g50810	Os TRANSMEMBRANE KINASE (OsTMK)	four members of the TRANSMEMBRANE KINASE (TMK) subfamily	Role in plant growth	[71]
Os04g38480	Os SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE 2 (OsSERK2)	AtSERKs	Required for both Xa21, Xa3/Xa26 and FLS2 signaling and brassinosteroid-regulated plant growth	[72]
Os08g07760	Os SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE 1 (OsSERK1) also named Os BRI1-ASSOCIATED KINASE 1 (OsBAK1)	AtSERKs	Functions in rice development, affecting growth and angle of lamina joint; brassinosteroid signaling?	[73–75]
high degree of similarity but not identical to Os08g07760	BENZOTHIADIAZOLE-INDUCED SOMATIC EMBRYOGENESIS RECEPTOR KINASE 1 (BISERK1)	AtSERKs	Up-regulated upon <i>Magnaporthe</i> inoculation	[76]
Os08g34380	COMMISSURAL VEIN EXCESSIVE 1 (COE1)	AtSERKs	Responsible for commissural vein pattern formation in rice	[77]
Os02g14120	DEFECTIVE IN OUTER CELL LAYER SPECIFICATION 1 (DOCS1) also named OsSERK-like 4 (OsSERL4)		Involved in the proper development of root outer cell layers	[75,78,79]
Os02g40240	LEAF PANICLE 2 (LP2)		Negative regulator in drought response	[80,81]
Os02g12440	GAMMA-RAY INDUCED LRR-RLK 1 (GIRL1)		Highly induced by gamma irradiation, by several abiotic stresses (salt, osmotic, and heat), by hormonal treatment with salicylic acid or abscisic acid, but downregulated in response to jasmonic acid treatment	[82]
Os05g40770	OsRPK1		A salt-responding protein, whose expression is also induced by cold, drought, and abscisic acid; affects root architecture by negatively regulating polar transport and accumulation of auxin in roots	[83,84]
Os07g41140	RECEPTOR-LIKE PROTEIN KINASE 1 (RPK1)	AtRPK1	Overexpression of both <i>Arabidopsis</i> and rice RPK1 receptors induces a reduction in salt tolerance in <i>Arabidopsis</i> transgenic plants	[85,86]
Os06g03970	STRESS-INDUCED PROTEIN KINASE GENE 1 (OsSIK1)		Affects stomatal density in leaf epidermis and plays important roles in salt and drought stresses	[87]
Os04g48760	XIAO (“small” in Chinese)		Regulates brassinosteroid signaling and cell division	[88]
Os11g07225-like1 and Os11g07225-like2	25L1 and 25L2		Specific to wild <i>Oryza rufipogon</i> rice; responsible for the high temperature-dependent expression of hybrid weakness	[89]
Os02g05980	LEUCINE-RICH REPEAT RECEPTOR-LIKE KINASE 1 (LRK1)		Cluster of 8 genes; LRK1 present in Dongxiang wild rice, but absent in Guichao2; Overexpression of LRK1 improved quantitative yield components	[90]

Download English Version:

<https://daneshyari.com/en/article/8357327>

Download Persian Version:

<https://daneshyari.com/article/8357327>

[Daneshyari.com](https://daneshyari.com)