

Novel approaches for integration of physiology, genomics and breeding for drought resistance improvement in rice

Rachid Serraj¹, Dongcheng Liu, Hong He, Reena Sellamuthu, Somayanda Impa, Jill Cairns, Glenn Dimayuga and Rolly Torres

¹ International Rice Research Institute, DAPO 7777, Metro Manila, Philippines, www.irri.org, Email: R.Serraj@cgiar.org

Abstract

Rice yields in drought-prone rainfed areas remain globally low and unstable. An important goal for food security in drought-affected and water scarce environments is thus to reduce yield gaps between experimental plots and farmers' fields. Increased crop yield and water productivity require the optimization of the physiological processes involved in the most critical stages of plant responses to soil drying and dehydration avoidance mechanisms. New high-throughput and precise drought phenotyping methodologies are now being used under both field and controlled conditions, using the Fraction of Transpirable Soil Water (FTSW) as soil moisture co-variable for capturing the dynamics of plant growth responses to water deficits. This allows large-scale and consistent evaluation of potential drought resistant donors. Large collections of rice germplasm, including wild relatives, hybrids and mutant lines are screened for drought resistance traits. Genetic sources of drought resistance have been identified at IRRI for all major rice agro-ecosystems and some of the associated traits have been characterized. The identification and physiological characterization of QTLs for performance under drought stress across environments is currently a major focus. This approach provides a powerful tool to dissect the genetic basis of drought resistance. If validated with accurate phenotyping and properly integrated in marker-assisted selection programs, it will accelerate the development of drought resistant genotypes. Multidisciplinary research, integrating physiology with breeding, simulation modeling, and molecular genetics will realize the potential of these approaches and increase the efficiency of crop improvement in drought-prone environments.

Media summary

The development of new high throughput drought phenotyping methodologies and multidisciplinary research that integrates crop physiology with breeding and molecular genetics will realize the potential of these approaches and increase the efficiency of rice crop improvement in drought-prone environments.

Key Words

Water deficit, rice, crop improvement, FTSW, phenotyping

Introduction

The variation of rice production in rainfed areas is closely related to total annual rainfall, but, even when the total is adequate, shortages at critical periods such as flowering stage greatly reduce productivity, resulting in severe economic losses (Bernier et al., 2008). Rice yields in drought-prone rainfed systems remain as low as 1.0 to 2.0 t/ha, and unstable due to erratic and unpredictable rainfall. With current and predicted water-scarcity scenarios, irrigation has only limited potential to alleviate drought problems in rainfed rice-growing systems (O'Toole 2004). It is therefore critical that both agronomic and genetic management strategies focus on efficient use of available soil

moisture for crop establishment, growth, and yield. Recent progress made in rice genomics must be matched with a better understanding of drought physiological mechanisms and their relationship to varietal performance in drought-affected farmers' fields. Identification of donors, QTL mapping and use of QTL/genes affecting performance under stress in marker-aided breeding, and screening of improved varieties in multi-location trials all depend on the development of repeatable, low-cost, high-throughput phenotyping procedures that reliably characterize genetic variation for drought resistance and its major component traits. Therefore, special efforts are now being made for the conceptualization, design, and management of phenotyping programs for drought resistance, to maximize the identification of donors, QTLs, and breeding lines that can be used in the improvement of yield stability in the drought-prone target environments.

Plant water use and drought adaptive responses

Plant responses to soil water deficits can be typically described as a sequence of three successive stages of soil drying (Serraj and Sinclair, 2002):

- *Stage I*: water is freely available in the soil and transpiration is not limited by soil moisture.
- *Stage II*: the rate of water uptake no longer matches potential transpiration rate. Stomatal conductance declines, limiting the transpiration rate to a level similar to that of soil water uptake, and resulting in the maintenance of plant water balance.
- *Stage III*: plants are no longer able to limit transpiration through stomatal conductance; they must then resort to other mechanisms of drought adaptation for survival.

The physiological processes contributing to crop yield, including leaf tissue expansion, transpiration, photosynthetic rate, and growth, start to be down-regulated late in stage I or early in stage II of soil drying (Serraj et al., 1999). At the end of stage II, these growth-supporting processes have effectively reached zero and no further net growth occurs in the plants. The focus of stage III is mostly on survival, which can be critical in natural dry-land ecosystems, but has little relevance to increasing/stabilizing crop yield in most agricultural situations. Thus, increased crop yields and water productivity require the optimization of the physiological processes involved in the critical stages (mainly stage II) of plant response to soil drying (Serraj and Sinclair, 2002).

A new framework for high-throughput and precise phenotyping

Progressive water deficit influences many physiological processes such as transpiration, photosynthesis or leaf expansion. These physiological processes are inhibited when soil moisture available for transpiration (Fraction of Transpirable Soil Water, FTSW) decreases to values in the range of 40-50%, with a trend that appears to be consistent across a wide range of environments and genotypes (Sadras & Milroy 1996). We developed a drought phenotyping platform, using FTSW as a soil moisture co-variable under controlled environmental conditions, for monitoring and comparing the dynamics of genotypes responses to progressive soil drying. This technique has been expanded to the field (upland), where soil moisture profiles are monitored in parallel with plant water status and leaf gas exchange measurements. Plant water status is monitored using infra-red thermal imaging for large-scale canopy temperature measurements at the plot level (Serraj and Cairns, 2006). The integration of these field-based methods with carbon isotope discrimination, detailed measurements of plant growth and development parameters and yield components allows the development of high-throughput, field-based and precise drought phenotyping. This framework is now being used on a large-scale on the IRRI experimental farm for detailed evaluation of potential drought resistant donors and large number of lines identified by drought breeding

programs. Using FTSW as the stress covariable, on-station field experiments can also be integrated with controlled environment experiments and multi-location drought trials.

Dynamics and genetic basis of tissue growth and spikelet sterility under drought

We recently evaluated genotypic variation of transpiration and leaf growth responses to soil water deficit under controlled and field conditions. The relationship between relative transpiration and soil drying, as measured by FTSW, were well described by linear-plateau functions that allowed the determination of the soil-water thresholds at which transpiration of drought-stressed plants began to decrease compared to the well-watered treatment. FTSW soil-water thresholds varied significantly among genotypes, suggesting a link between the kinetics of transpiration response to water deficits, leaf gas exchange and plant growth parameters under drought.

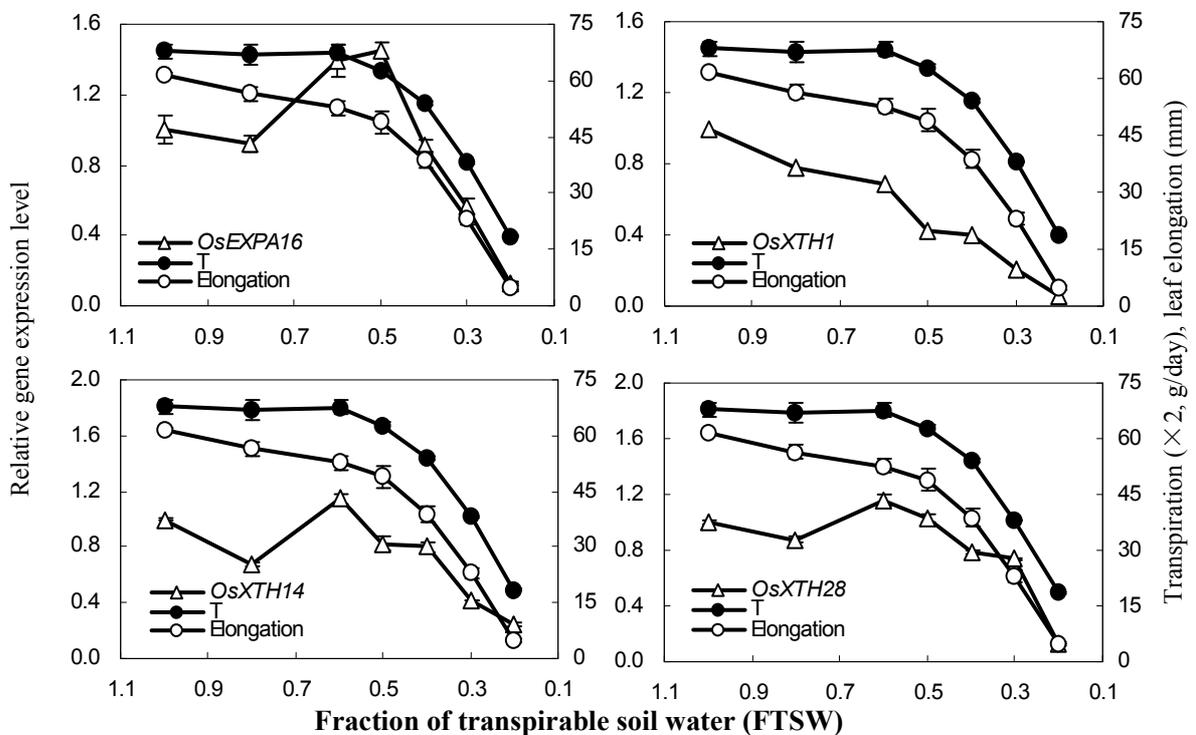


Figure 1. Responses of leaf elongation, transpiration and relative expression of one expansin and three XTH genes along with FTSW in the rice variety IR64. The elongation (white circle) of leaf 7 was measured with the new emerged leaf in 16 hours, and the transpiration (T, black circle) at the stage of leaf 7 was measured in 24 hours in the phytotron. Relative expression level (white triangle) of each gene (*OsEXPA16*, *OsXTH1*, *OsXTH14*, and *OsXTH28*) was measured by real-time reverse transcription (RT)-PCR (1= expression data from the well-watered control, FTSW=1.0) in the elongating zone (3cm) of leaf 7. Data are means (\pm SE) of at least 3 replicates.

We used the FTSW dry-down phenotyping approach for analyzing gene expression and stress-response mechanisms of leaf elongation rate (LER). Transpiration and stomatal conductance both declined with increasing soil moisture deficit. However, there was a significant interaction of stress intensity with greater reduction in stomatal conductance than transpiration during severe stress (FTSW = 0.3 and below). LER was highly sensitive to water deficit, declining at a higher FTSW

threshold value than transpiration and stomatal conductance (data not shown). Expression profiles of expansin and XTH genes were determined in the leaf elongating zone at specific soil water deficits. Four genes, *OsEXPA16*, *OsXTH1*, *OsXTH14*, and *OsXTH28* showed similar changes in expression and consistent association with changes in leaf elongation (Fig.1). Work is under way to profile large-scale expression of LER and QTL mapping of leaf and root growth under drought in controlled and field conditions.

A similar phenotyping framework has been used to analyze the physiological mechanisms and genetic basis of spikelet sterility and grain failure under reproductive-stage drought. Drought-induced spikelet sterility and inhibition of panicle exertion in rice was recently related to the inhibition of peduncle elongation and the down-regulation of cell-wall invertase genes (Ji et al., 2005). The physiological response of peduncle elongation rate to drought stress and the genetic variability of this trait have been recently analyzed in a set of diverse rice parental lines using the FTSW soil dry-down. Strong correlations were found between peduncle elongation rate, spikelet sterility and yield under drought. QTL mapping for these traits is now underway in both upland and rainfed lowland field conditions.

Conclusion: strategy for drought resistance improvement

It is now well accepted that the complexity of drought can only be tackled with a holistic approach integrating plant breeding with physiological dissection of the resistance traits and molecular genetic tools together with agronomic practices that lead to better conservation and use of soil moisture and matching crop genotypes with the environment.

References

- Bernier J, Atlin GN, Serraj R, Kumar A, Spaner D. 2008. Breeding upland rice for drought resistance (A Review). *J Sci Food Agric.* (in press).
- Ji XM, Raveendran M, Oane R, Ismail A, Lafitte HR, Bruskiwich R, Cheng SH and Bennett J. 2005. Tissue-specific expression and drought responsiveness of cell-wall invertase genes of rice at flowering. *Plant Mol Biol.* 59:945–964
- O’Toole JC. 2004. Rice and water: The Final Frontier. First International Conference on Rice for the Future. 31 August- 2 Sept 2004, Bangkok, Thailand
- Sadras V.O, Milroy S.P. (1996) Soil-water thresholds for the responses of leaf expansion and gas exchange. *Field Crops Research* 47, 253–266
- Serraj R, Allen HL, Sinclair TR. 1999. Soybean leaf growth and gas exchange response to drought under carbon dioxide enrichment. *Global Change Biol.* 5: 283-292.
- Serraj R, Sinclair TR. 2002. Osmolyte accumulation: can it really help increase crop yield under drought conditions? *Plant Cell & Environ.* 25: 335-341.
- Serraj R, Cairns JE. 2006. Diagnosing Drought. *Rice Today* 5(3): 32-33.