Development of salt-tolerant rice varieties through conventional and molecular breeding approaches

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Reason for the Award

The award recipient has conducted pioneering studies on improving salt-tolerance in rice through conventional and molecular breeding approaches and has produced diverse genetic mutations in the salt-tolerant rice varieties obtained through the breeding selection. Moreover, the awardee has made a significant contribution to identifying novel quantitative trait loci (QTLs) forsalinity tolerance at the reproductive stage in rice by using various mapping populations. This study was valued highly in terms of its efforts in producing varieties through the latest breeding approaches, leading to their registration and subsequent commercialization, and its potential effect in spreading these varieties to regions outside India under climate change.

Outline of Research Achievement

In India, around 6.73 million hectares (Mha) of lands are salt-affected, of which 3.77 and 2.96 Mha are sodic and saline, respectively. The productivity of rice under salt stress is very low, and it depends on the level and duration of salt stress. Rice occupies approximately 40.5% of the area in salt-affected soils, and the estimated production loss is about 22% in India. Krishnamurthy and his colleagues developed five salt-tolerant rice varieties (CSR46, CSR49, CSR52, CSR56, and CSR60) in different segments and three genetic stocks (CSR47, CSR51, and CSR53) for salt tolerance. He also produced and sold 754 quintals of breeder seeds and 1,224 quintals of truthfully labelled seeds of salt-tolerant rice varieties to seed-producing agencies and farmers. These rice varieties cover 1.6 Mha of salt-affected land annually in India. Salt-tolerant varieties have been adopted by land reclamation corporations, benefiting about 430,000 farmers. With the introduction of these salt-tolerant varieties, about 0.6 million tons of gypsum were saved, which would have cost about Rs.18M (around USD 250,000). Furthermore, he identified potential and novel donors for seedling and reproductive stage salt tolerance, which are being used in breeding programmes to develop new lines. He also identified novel quantitative trait loci (QTLs) for salinity and sodicity tolerance at reproductive stage using different bi-parental, multiparent advanced generation intercross (MAGIC), and association mapping populations. He successfully introgressed Saltol QTL into mega rice varieties, namely, Pusa44, PR114, and Sarjoo52, and he also focused on the introgression of spikelet fertility QTLs into Pusa44, PR114, and Sarjoo52 through marker-assisted backcross breeding (MABB). These salt-tolerant rice varieties have the potential to spread across salt-affected ecologies and could improve productivity, farm income, and livelihood security of resource-poor farmers in developing countries.

Main Publications:

(1) **S.L. Krishnamurthy**, P.C. Sharma, D.K. Sharma, K.T. Ravikiran, Y.P. Singh, V.K. Mishra, D. Burman, B. Maji, S. Mandal, S.K. Sarangi, R.K. Gautam, P.K. Singh, K.K. Manohara, B. C. Marandi, G. Padmavathi, P.B. Vanve, K. D. Patil, S. Thirumeni, O.P. Verma, A.H. Khan, S. Tiwari, S. Geetha, M. Shakila, R Gill, V.K. Yadav, S.K.B. Roy, M. Prakash, J. Bonifacio, A. Ismail, G.B. Gregorio & R.K. Singh. Identification of mega-environments and rice genotypes for general and specific adaptation to saline and alkaline stresses in India. *Scientific Reports* 7, 1-14. 2017.

(2) **S.L. Krishnamurthy,** R.K. Gautam, P.C. Sharma, D.K. Sharma. Effect of different salt stresses on agro-morphological traits and utilization of salt stress indices for reproductive stage salt tolerance in rice. *Field Crops Research* 190, 26-33. 2016.

(3) **S.L. Krishnamurthy,** P. Pundir, A.S. Warriach, Rathor S., B.M. Lokeshkumar, N.K. Singh and P.C. Sharma. Introgressed Saltol QTL Lines Improve the Salinity Tolerance in Rice at Seedling Stage. *Frontiers in Plant Science* 11:833. 2020.

Novel microbial tools to distinguish fecal pollution sources from livestock for effective agricultural watershed management

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Reason for the Award

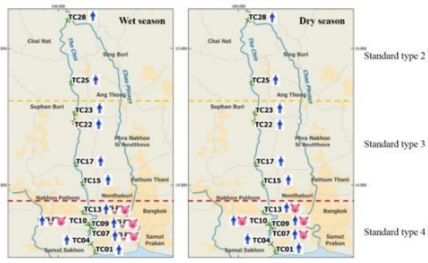
Using DNA-based detection techniques, including conventional PCR methods, the award recipient has developed fecal-derived microbial tracking markers and subsequently the rapid analysis method, utilizing and identified watershed pollution sources by examining bacteriophage DNAs. The awardee’s research established and clarified the actual sources of pollution in an agricultural basin in Thailand. This novel approach is highly valued as versatile tools that can be applied to solve agricultural as well as environmental management issues not only in Thailand but also in countries trying to control water pollution.

Outline of Research Achievement

Fecal contamination in freshwater has become a problem of increasing concern, particularly in agricultural watersheds where wastewater and surface runoff from livestock farming contribute to water pollution. Accurate wastewater source identification is crucial for effective agricultural watershed management and precise health risk assessment from pathogenic microbial contamination.

This research aimed to pinpoint fecal pollution sources from livestock farming (swine and cattle) and dense residential communities along the 325-km Tha Chin River located in Central Thailand. Microbial markers were developed and validated to specifically track contamination from swine and cattle origins using DNA of the bacterial order *Bacteroidales*, and from human communities using both the DNA of bacteriophage crAssphage and a culturable bacteriophage of *Enterococcus faecalis*. These microbial tools also revealed spatial and temporal patterns of contamination from different sources.

River site



Resulting pollution source maps

Cattle farm

Main Publications:

(1) Chyerochana, N., Kongprajug, A., Somnark, P., Kampaengthong, P. L., Mongkolsuk, S., & **Sirikanchana, K**. (2020). Distributions of enterococci and human-specific bacteriophages of enterococci in a tropical watershed. *International Journal of Hygiene and Environmental Health*, 226 (113482), 1–9.

(2) Kongprajug, A., Chyerochana, N., Somnark, P., Kampaengthong, P. L., Mongkolsuk, S., & **Sirikanchana, K**. (2019). Human and animal microbial source tracking in a tropical river with multiple land use activities. *International Journal of Hygiene and Environmental Health*, 222, 645–654.

(3) Somnark, P., Chyerochana, N., Mongkolsuk, S., & **Sirikanchana, K.** (2018). Performance evaluation of *Bacteroidales* genetic markers for human and animal microbial source tracking in tropical agricultural watersheds. *Environmental Pollution*, 236, 100–110.

Strengthening quality protein maize resilience and utilization as nutritious food and feed in rural areas of Zimbabwe

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Reason for the Award

In cooperation with farmers, the award recipient has developed F1 hybrid varieties of high-yielding, high-protein maize resistant to *Striga asiatica*, one of weeds. The awardee obtained successful results, not only in improving maize production but also in establishing business models in which the maize plant can be used as a nutritious food and livestock feed. We highly evaluated this study because it targeted challenges in real production cites with weed interference and its significant contribution to local economies in Zimbabwe.

Outline of Research Achievement

Maize is deficient in two essential amino acids, namely lysine and tryptophan, and thus most children in Zimbabwe suffer from protein energy malnutrition since poor families cannot afford alternative protein sources. Poor soil fertility problems coupled with frequent droughts are highly associated with the widespread occurrence of *Striga asiatica*, a parasitic weed that causes up to 100% yield loss. Together with rural farmers, Prof. Edmore Gasura and colleagues developed three high-yielding, drought-tolerant quality protein maize (QPM) varieties resistant to *Striga asiatica*. This maize yields ≥4 t/ha under heavy infestation by *Striga asiatica* and ≥10 t/ha under optimum conditions. This QPM is also rich in lysine and tryptophan, the essential amino acids frequently lacking in cereal diets. The team motivated >500 rural farmers after demonstrating the superiority of QPM by feeding it to their indigenous chickens. Indigenous chickens fed on QPM alone grew at the same rate as those fed on commercial feed and showed improved meat quality. The maize straw was used to grow oyster mushrooms as additional income and protein source for farmers. We established partnerships with the private sector (Mukushi Seeds), development agencies (Welt Hunger Hilfe and RUFORUM), and policy makers. We also trained >500 farmers through field days, trained three master's and six undergraduate students, produced six research articles, participated in three international conferences, and appeared in one newsletter article by the American Society of Agronomy.

Quality protein maize (resistant to *Striga asiatica*) under heavy infestation in the field

Indigenous chickens growing well after feeding on quality protein maize

Oyster mushrooms being grown using quality protein maize stover

Main Publications:

(1) **Gasura, Edmore**, Peter Setimela, Stanford Mabasa, Rwafa Rwafa, Susan Kageler, and Cacious Nyakurwa (2019). Response of IITA maize inbred lines bred for *Striga hermonthica* resistance to *Striga asiatica* and associated resistance mechanisms in southern Africa. *Euphytica* 215(10):151.

(2) Nyakurwa, Cacious Stanford, **Edmore Gasura**, Peter S. Setimela, Stanford Mabasa, Joyful Tatenda Rugare, and Simbarashe Mutsvanga (2018). Reaction of new Quality Protein Maize genotypes to *Striga asiatica*. *Crop Science* 58(3):1201-1218.

(3) Setimela, Peter Sekwane, **Edmore Gasura**, and Amsal Tarekegne (2017). Evaluation of grain yield and related agronomic traits of quality protein maize hybrids in Southern Africa. *Euphytica* 213(12):289.