

## A REVIEW

# Role of microsatellite markers in molecular diversity analysis of rice bean (*Vigna umbellata*)

Deepanshi Rathore, Monika, Monika Bajpai and Nidhi Varshney<sup>1</sup>

Department of Biotechnology, Faculty of Life Sciences, Institute of Applied Medicines and Research, Ghaziabad, (U.P.) India (Email: monisingh6666@gmail.com)

<sup>1</sup>National Institute of Plant Genome Research, New Delhi, India

Email : deepanshi.rathore1996@gmail.com

**Article Info :** Received : 08.02.2020; Accepted : 28.03.2020

Over the last few decades, the use of molecular markers has played very important role in rice breeding and genetics. Rice bean is a multipurpose, less utilized crop accepted to be tamed in the Myanmar-Thailand locale of Asia. It is believed to be a potential nutritive fodder legume. Among various types of molecular markers, microsatellites (SSRs) have been widely in used due to several advantages over other markers. These markers are appropriated all through the genome, high number of allelic variety at every locus, incredibly polymorphic just as being species-explicit and co-predominant; they have become an ever increasing number of critical hereditary markers in rice reproducing programmes. In spite of the fact that there has been next to no exploration or exceptionally less distributed writing on rice bean with respect to its genetic diversity, the aim of this review is to summarize the current knowledge concerning the linkage of microsatellite markers to rice bean which is regarded as minor food and is mainly grown for human consumption, though it is additionally utilized for roughage and green manure. Rice bean has an ability to give balance diet to the domesticated animals and to continue under wide scope of climatic condition in any case, more spotlight is required on this harvest for greater prominence as a potential vegetable yield.

**Key words :** Rice bean, Molecular markers, Microsatellite markers (SSR), Molecular diversity

**How to cite this paper :** Rathore, Deepanshi, Monika, Bajpai, Monika and Varshney, Nidhi (2020). Role of microsatellite markers in molecular diversity analysis of rice bean (*Vigna umbellata*). *Asian J. Bio. Sci.*, 15 (1) : 15-20. DOI : 10.15740/HAS/AJBS/15.1/15-20. Copyright @ 2020: Hind Agri-Horticultural Society.

## INTRODUCTION

Rice bean [*Vigna umbellata* (Thunb) Ohwi and Ohashi] is a less abused grain vegetable developed fundamentally in Nepal, Bhutan, North East India upto Myanmar, Southern China, Northern Thailand, Laos, Vietnam, Indonesia and East Timor. In India, rice bean is principally developed in the North-Eastern slopes, which is a hotspot for natural decent variety. *Vigna umbellata* is a dicot plant has a place with a family Fabaceae. It for the most part called rice bean and grown largely under rainfed conditions in a mixed farming or intercropping

system with sorghum, maize, or cowpea, it is in the principle become under moving cultivation and utilized as vegetable, beat, matured heartbeat, roughage and medication. In parts of Southeast Asia, rice bean exists as a complex with its wild structure from which it isn't systematically notable and with which it can shape fruitful hybrids (Seehalak *et al.*, 2006). This harvest is viewed as a minor food and grub crop in Nepal and northern India (Dahiphale *et al.*, 2017). This minor heartbeat has been minimal contemplated, yet its profitable development and plentiful cases demonstrates that it has a high return potential as a vegetable (green units), grain and search

crop (Smartt, 1991).

Rice bean is thought to be domesticated from a wild form *V. umbellata var gracilis*, which is a cross rich type. These wild categories have been portrayed to happen in normal and upset natural surroundings and are of indefinite, photoperiod-delicate, openly stretching, twining plant types with little seeds. Most rice bean landraces refined in North Eastern India are like these wild sorts. In an investigation of the hereditary qualities of taming of rice bean, Isemura *et al.* (2010) educated that there is high collinearity between adzuki bean and rice bean in the request for molecular markers. Similarity in the training qualities between the genome of the two species was likewise detailed in a similar report. They presumed that the world class qualities of rice bean hold incredible potential for its improvement as well as its associated species.

Notwithstanding, improvement and use of rice bean through customary or molecular rearing despite everything linger behind different harvests like cowpea and mung bean in the class *Vigna*.

*Vigna umbellata* is a short-lived perennial legume commonly grown as an annual. It has a very flexible habit as it is erect, semi-erect or twining. It is commonly 30-100 cm in height, but can grow upto 200 cm (Ecoport, 2014). The stems are branched and finely haired. The leaves are trifoliolate with whole, 6-9 cm long flyers. The blossoms conceived on 5-10 cm long axillary racemes. The natural products are barrel shaped, 7.5-12.5 cm long Unit. Rice bean seeds are truly factor in shading, from greenish-yellow to dark through yellow, earthy coloured. Yellow-tanish types are accounted for to be the most nutritious. The red type gives its normal name to the grain in a few dialects, for instance in Chinese-red small bean, (Ecoport, 2014).

Rice bean is an adaptable vegetable, every so often considered as dismissed and underutilized (Joshi *et al.*, 2008). In any case, however, less significant than *Vigna unguiculata* (cowpea), *Vigna angularis* (adzuki bean) and *Vigna radiate* (mung bean), rice bean is a locally important donor to human nourishment in parts of India and South-East Asia.

All pieces of the rice bean plant are edible and utilized in cookery arrangements. Rice bean is a N-fixing vegetable that advances the N status of the soil, along these lines giving N to the accompanying harvest. Its taproot beneficially affects soil structure and when furrowed in, returns natural issue and N to the soil. Rice

bean began from Indochina and was potentially trained in Thailand and neighboring districts (Tomooka *et al.*, 2011). It is found normally in focal China, India and in the Indochinese Promontory. It was acquainted to Egypt, toward the East Bank of Africa and to the Islands of the Indian Sea. It is presently refined in tropical Asia, Fiji, Australia, tropical Africa, the Indian Ocean Islands just as in the Americas (USA, Honduras, Brazil and Mexico) (Rajerison, 2006; Van Oers, 1989 and Khadka and Acharya, 2009). In the center slopes of Nepal, rice bean is developed along rice bunds and patio edges (Khadka and Acharya, 2009). Rice bean is a quick summer-growing legume start from ocean level upto elevations of 1500m in Assam and 2000 m in the slopes of the Himalayas (Khadka and Acharya, 2009). Rice bean needs a short day length to items seeds. It is developed on a broad scope of soils checking shallow, barren or corrupted soils. Incredible soil ripeness may defer unit development and lessen seed yield (Khadka and Acharya, 2009). *Vigna umbellata* is an adaptable vegetable that can develop in muggy subtropical to warm and cool mild atmospheres. It is very much co-ordinated to zones with yearly precipitation running from 1000 to 1500 mm however, it is likewise similarly tolerant of drought. It does better in areas where average temperatures range from 18 to 30°C, tolerates 10-40°C but does not survive frost (Ecoport, 2014 and Rajerison, 2006). It chooses full light and its growth can be vulnerable if it is inter cropped with a tall acquaintance crop that outshines it, such as maize (Khadka and Acharya, 2009).

The Asiatic *Vigna* species have a place with the sub-variety *Ceratotropis*, a genuinely extraordinary and homogeneous gathering, basically limited to Asia, having chromosome number of  $2n = 22$  (aside from *V. glabrescens*,  $2n = 44$ ). There are seven developed species inside the sub-sort, including mung bean or green gram, dark gram or urad bean and moth bean just as various wild species. Fake crosses have been made between *V. mungo* and *V. umbellata* to deliver improved mung bean assortments (Singh *et al.*, 2006). There are three pretty much optional genetic supplies inside the gathering: rice bean is closer to *V. angularis* than to different species, being in the *Angulares* gathering (Kaga *et al.*, 1996 and Tomooka *et al.*, 2003). In India, rice bean is planted in February and Walk for reap during summer and in July and August for collect in December (Khanal *et al.*, 2009 and Oommen *et al.*,

2002). It very well may be planted alone in little fields or close to bunds of rice terraces. Rice bean profits by being planted between lines of a tall grain, for example, maize or sorghum that it can use for rising. Rice bean is a solid plant that is impervious to numerous irritations and maladies and it needn't bother with manure or exceptional consideration during development. Rice bean ordinarily develops in 120-150 days in the wake of planting yet may perhaps require additional time at higher elevations. Seeds are collected when 75 per cent of the units turn earthy coloured. Reaping is best done in the first part of the day or late evening to diminish the danger of warmth initiated breaking.

### Molecular marker:

It has been indicated that molecular markers are generally significant and useful asset for germplasm assessment, hereditary decent variety examination, quality mapping and marker-helped choice (MAS) for crop improvement. Not withstanding, genomic investigations of this yield has lingered behind that of other vegetable harvests, for example, soybean, basic bean, mung bean and adzuki bean because of the absence of polymorphic DNA sub-molecular markers. Until this point, there are relatively few molecular markers revealed for rice bean and truth be told, not very many of them, for example, RFLP, RAPD, AFLP and ISSR have been accounted for in rice bean. A number of factors ought to be considered while choosing from the several molecular markers:

- Marker system availability
- Difficulty of the technique and time investment
- Estimated polymorphism levels within the study population
- Quantity and quality of available DNA available
- Transferability among laboratories, populations, pedigrees and species
- The size and structure of the population to be studied
- Obtainability of skilled workers and equipment
- Cost per data-point and funding availability
- Method of marker inheritance and the type of genetic information needed in the population. In most areas of molecular genetics, microsatellites are now the marker of choice.

### Micro-satellites (SSRs):

Simple sequence repeats (SSRs) or microsatellites are themes of short couple repeats that may fluctuate

in the recurrent units at a given locus. SSRs have explicit preferences over different markers as they happen much of the time and arbitrarily in all eukaryotic DNA, are multiallelic and are agreeable to both manual scoring and computerization. SSRs have been utilized in decent variety investigation, hereditary loyalty examination, quality mapping and species identification and linkage examination. The term microsatellite was first instituted by Litt and Luty (1989). Microsatellites are basic tedious themes containing of 1 to 6 base sets and they can be found in both coding and non-coding areas. The transformation pace of this kind of hereditary marker has been esteemed to be somewhere in the range of 10-2 and 10-4 per age. SSRs are a preeminent decision for enlarge the extent of the markers accessible to these species specialists in light of their liberality, high polymorphism, co-predominance, reproducibility and transferability to related vegetables species. As contrast with genomic SSRs, genic SSRs are situated in the coding area of the genome and have some common favourable circumstances. For a model, they are in progressively preserved coding locales of the genome and the age of genic SSR markers is equivalently simple and reasonable, and profoundly transferable to related taxa. Due to these points of interest, genic SSRs have been created and utilized in many plant species.

There are looks into being led on related vigna species. Thirteen SSR markers created for adzuki bean, which have been appropriated over its 11 chromosomes, were utilized to evaluate the hereditary decent variety of rice bean. Forty-seven SSR markers produced for mung bean indicated dependable banding and polymorphisms were utilized to examine the hereditary assorted variety of 230 rice bean increases. The quantity of SSR markers utilized in rice bean so far is less than those revealed for different vegetables, for example, mung bean, adzuki bean, normal bean, chickpea, pigeonpea and soybean.

Genetic diversity concentrates with a set number of increases from China, Nepal and Thailand have been accounted for before. Wang *et al.* (2004, 2012 and 2015) considered hereditary assorted variety in 230 promotions of rice bean gathered from 12 areas of China utilizing mung bean SSRs. They detailed a bunched at this point summed up circulation of the promotions proposing a wide trade of germplasm over

the territories. In any case, the most extensive investigation so far with a wide scope of developed and wild rice bean increases is by Tian *et al.* (2013), They examined 472 promotions (developed and wild) from 16 Asian nations and detailed high quality decent variety (>0.5) in the South and South East Asian promotions. In every one of these examinations, number of Indian germplasm was immaterial. Muthusamy *et al.* (2008) examined hereditary assorted variety in 10 rice bean germplasm gathered from Meghalaya, a North Eastern Himalayan province of India and detailed high hereditary decent variety. Investigations of hereditary assorted variety with an impressive number of germplasm from Indian Himalayan area, where rice bean is chiefly developed, has not been led.

### **Analysis of genetic diversity:**

An away from of the degrees of hereditary variety inside the accessible germplasms has been considered as a significant factor for any viable hereditary improvement and hybridization programmes. Molecular marker strategies are presently all around perceived as an intend to survey genetic variation inside characteristic populaces and germplasm assortments. The decision of the most suitable molecular markers for the investigation of hereditary variety relies basically upon the basis of the exploration what's more, hereditary structure of the species. Quick and exact distinguishing proof of plant genotype is significant in any plant reproducing system and basic for assurance of restrictive germplasm. molecular markers are valuable device for distinguishing proof of hereditary variety and genotyping in cultivars. Countless near evaluations have been completed to recognize the most dependable marker innovation for genotyping of cultivars high allelic assorted variety and germline soundness of microsatellite (SSR) markers makes them better over the discretionary preliminary based markers and their convenience in cultivar distinguishing proof has been archived in an enormous number of vegetatively engendered crops. In any case, SSR markers are most certainly not reasonable to recognize the variety inside cultivars and consequently encourage the utilization of locus-explicit microsatellite markers.

### **Examination of phlogeny and developmental connections:**

Morphological and topographical varieties framed

the premise of prior hypothesis of advancement. With the progression in molecular science, similarity of hereditary structure of characteristic populace turns out to be clear and gives data on time scale and sort of hereditary variety related with species disparity. RFLP markers have demonstrated their adequacy in transformative science by deducing the connection between hexaploid genome ( $2n = 42$ , AABBDD) of bread wheat and its predecessors. Transposon components are likewise valuable in such manner and have been effectively applied in rice and wheat for recognizing the cultivars having close hereditary foundations. The effortlessness and cost adequacy make the PCR-based markers better over the RFLPs and transposons are right now being utilized in recognition of hereditary variety and phylogenetic investigation.

### **Germplasm preservation and management:**

Information on existing hereditary variety inside the germplasm also, common populace is basic for arranging of *in situ* and *ex situ* preservation procedures. The data on hereditary variety in characteristic populaces of wild species can likewise help to choose the topographical regions with the most extreme hereditary variety. Data dependent on molecular markers is promising and frequently utilized by protection scientists to reinforce preservation hereditary qualities. Molecular markers can investigate the hereditary variety among the populace in regular stands and furthermore help in planning proficient systems for ideal examining from the current variety. The improvement of center assortments from the enormous germplasm is significant for any administration activities. Molecular markers are valuable in identifying the copies among the center assortment and along these lines expanding the administration proficiency. When the center assortment is distinguished. Molecular markers are utilized to screen and protect the hereditary variety and along these lines diminishing the odds of hereditary disintegration. Genome-specific repetitive DNA sequence (SSRs) broadly utilized because of their high changeability among the person of an animal groups and rigid PCR condition.

### **Conclusion:**

The researches stated above clearly indicate that rice bean legume is less explored area of research till now. The future research should be carried out on rice

bean and its genetic diversity using molecular markers as the legume do have great potential.

## LITERATURE CITED

- Dahiphale, A.V., Singh, U.P., Kashyap, Sanjeev Kumar, Kumar, Sandeep and Singh, Hari (2017).** Precise nitrogen management: Away forward for enhancing resources use efficiency and productivity of direct seeded rice: A review. *Internation J. Chemical Studies*, **5** (6) : 1485-1493.
- Isemura T., Kaga, A., Tomooka, N., Shimizu, T. and Vaughan, D.A. (2010).** The genetics of domestication of rice bean, *Vigna umbellata*. *Ann. Bot.*, **106** : 927–944. DOI: 10.1093/aob/mcq188.
- Joshi, K.D., Bhanduri, B., Gautam, R., Bajracharya, J. and Hollington, P.B. (2008).** Rice bean: A multi-purpose underutilized legume. pp. 234–248, In: J. Smartt and N. Haq (Eds), *New crops and uses: their role in a rapidly changing world*. International Centre for Underutilized Crops.
- Kaga, A., Tomooka, N., Egawa, Y., Hosaka, K. and Kamijima, O. (1996).** Species relationships in the subgenus *Ceratotropis* (genus *Vigna*) as revealed by RAPD analysis. *Euphytica*, **88** : 17-24.
- Khadka, K. and Acharya, B.D. (2009).** *Cultivation practices of rice bean* (Pokhara, Nepal: Local Initiatives for Biodiversity, Research and Development (LI-BIRD), pp.31.
- Khanal, A. R., Khadka, K., Poudel, I., Joshi, K. D. and Hollington, P. (2009).** Report on farmers' local knowledge associated with the production, utilization and diversity of rice bean (*Vigna umbellata*) in Nepal. 2009; In: *The Rice Bean Network: Farmers indigenous knowledge of rice bean in Nepal* (report N°4), EC. 6th FP, Project no. 032055, FOSRIN (Food Security through Rice Bean Research in India and Nepal).
- Litt, M. and Luty, J. A. (1989).** A hypervariable microsatellite revealed by *in vitro* amplification of a dinucleotide repeat within the cardiac muscle actin gene. *American J. Human Genet.*, **44** : 397–401.
- Oommen, S. K. Oommen and Sumabai, D. L. (2002).** *Rice bean- potential fodder crop*. The Hindu. Sci. Tech., online ed. India's Nat. Newspaper.
- Rajerison, R. (2006).** *Vigna umbellata* (Thunb.) Ohwi and H. Ohashi. In: *PROTA 1: Cereals and Pulses*, M. Brink and G. Belay, Eds. (Wageningen, The Netherlands: PROTA).
- Seehalak, W., Tomooka, N., Waranyuwat, A., Thipyapong, P., Laosuwan, P., Kaga, A. and Vaughan, D.A. (2006).** Genetic diversity of the *Vigna* germplasm from Thailand and neighboring regions revealed by AFLP analysis. *Genet. Resour. Crop Evol.*, **53**: 1043–1059.
- Singh, S., Kundu, S.S., Negi, A.S. and Singh, P.N. (2006).** Cowpea (*Vigna unguiculata*) legume grains as protein source in the ration of growing sheep. *Small Ruminant Research*, **64** (3): 247– 254. DOI: 10.1016/j.smallrumres.2005.04.022.
- Smartt, J. (1991).** *Evolution and genetic resources* (Editor). In grain legumes. Cambridge University, Press, UK. pp. 140–175.
- Tian, J., Isemura, T., Kaga, A., Vaughan, D.A. and Tomooka, N. (2013).** Genetic diversity of the rice bean (*Vigna umbellata*) genepool as assessed by SSR markers. *Genome.*, **56** (12) : 717–727. doi: 10.1139/gen-2013-0118 PMID: 24433207.
- Tomooka, N., Kaga, A., Vaughan, D.A. and Jayasuriya, A.H.M. (2003).** Advances in understanding the genus *Vigna* subgenus *Ceratotropis* In: AHM Jayasuriya and DA Vaughan (eds) *Conservation and use of crop wild relatives*. Proceedings of the joint Department of Agriculture, Sri Lanka and National Institute of Agrobiological Science, Japan Workshop held on 3 February, 2003.
- Tomooka, N., Kaga, A., Isemura, T. and Vaughan, D.A. (2011).** *Vigna*. In: Chittaranjan Kole (Ed.) *Wild Crop Relatives: Genomic and Breeding Resources Legume Crops and Forages*. NY: Springer, pp. 291– 311.
- Van Oers, C.C.C.M. (1989).** *Vigna umbellata* (Thunb.) Ohwi and Ohashi. Record from Proseabase, L.J.G. Van der Maesen and S. Somaatmadja, eds. (Bogor, Indonesia: PROSEA (Plant Resources of South – East Asia) Foundation).
- Wang, L.X., Cheng, X.Z., Wang, S.H. and Tian, J. (2012).** Analysis of an applied core collection of adzuki bean germplasm by using SSR markers. *J. Integr. Agr.*, **11** (10): 1601–1609.
- Wang, L. X., Chen, H., Bai, P., Wu, J., Wang, S., Blair, M., and Cheng, X.Z. (2015).** The transferability and

Deepanshi Rathore, Monika, Monika Bajpai and Nidhi Varshney

polymorphism of mung bean SSR markers in rice bean germplasm. *Mol Breeding*, **35** (77): 1–10.

azuki bean [*Vigna angularis* (Willd.) Ohwi and Ohashi]. *Theor. Appl. Genet.*, **109** (2): 352–360. PMID: 15014881.

**Wang, X.W., Kaga, A., Tomooka, N. and Vaughan, D.A. (2004).**

The development of SSR markers by a new method in plants and their application to gene flow studies in

■ **Webliography**

Ecoport (2014). *Ecoport database*. Ecoport.

15<sup>th</sup>  
Year  
★★★★★ of Excellence ★★★★★