ISSN: 2582-6980

JUNE 2022

AGRI MIRROR FUTURE INDIA

AIASA Agriculture Magazine

A Voice for Agriculture

Volume 03 | Issue 05

aiasanewdelhi aiasa5 AIASA https://aiasa.org.in/?page_id=2851

A Voice for Agriculture

AGRI MIRROR : FUTURE INDIA

Volume 03 | Issue 05 | JUNE 2022

Article Id: 225-228

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ALLELOPATHY: AN IMPORTANT TOOL IN WEED MANAGEMENT

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Introduction

Weed is an undesirable and unwanted plant, harmful to living organisms, aggressive and invasive in nature which will compete with crop for nutrients, light, space and water leads to decline crop yield by 45-90 %. Hence, weed becomes the most severe and widespread biological constraint to agricultural production and cause serious damage in cropped and non-cropped lands. Herbicides have become a boon to farmers in areas where the labour availability is limited and wages are high. The use of herbicides has been increasing in India enormously in the last few decades which is impacting enormously on the soil health due to chemical and residual effect of the active ingredient even though chemical herbicide is the effective and timely management option in this present day cultivation, environmental concern is also very important for the sustainable future and healthy soil. The best method to avoid use of these chemical herbicides is use of natural herbicides. Many plants and several microorganisms ensure their survival by naturally competing with other organisms by producing a wide array of phytotoxic chemicals that could be effectively used by man as herbicides.

Allelopathy

The term allelopathy derives from two Greek words *allelon* which means "of each other", and *pathos* means "to suffer". The term allelopathy was first defined by Hans Molisch in 1937 to indicate effects resulted from biochemical substances transferred from plant to plant. Allelopathy is a form of interaction both positive and negative in between the organisms that is due to the action of chemical substance referred as allelochemicals. Allelopathy defined as "the chemical interactions between plant and plant or plants and microorganisms, leading either positive or negative effects on the performance of neighbours" or "one plant species effects on another plant species or organisms by releasing chemicals into the soil and air environment".

Allelopathy is a phenomenon in which one organism release biochemical that influences the growth, survival, development and reproduction of other organisms. Released biochemicals are called as allelochemicals and which have good or lethal effects on targeted organisms. Phytochemicals produced by plant species into the surrounding environment reduced emergence and expansion of surrounding plants by altering their metabolism activity such as respiration, enzyme synthesis, photosynthesis, mineral ion uptake, protein and nucleic acid synthesis refers as allelopathy. Allelopathy has both competitive and defensive characteristics in many invasive plants.

Difference between herbicides and use of Allelopathy as tool of Bio herbicide

HERBICIDES	
SYNTHETIC HERBICIDES	**BIO-HERBICIDES**
▪ Kill the plant	▪ Suppress growth of weeds
▪ Non target toxicity	▪ No threat of toxicity
▪ Human health hazards	▪ No health hazards
▪ Some are non-biodegradable	▪ Biodegradable
▪ Cause pollution	▪ Environmental friendly
▪ Promote genetic resistance	▪ No threat of resistance development
▪ Bad intercropping impacts	▪ Promote new intercropping system

Types of Allelopathy

1. True allelopathy

Allelochemicals are toxic to their original form in which it produced in environment.

2. Functional allelopathy

Allelochemicals are non-toxic to plant at initial form, when it released in to environment but after transformation by microorganisms in to another form it become toxic.

3. Alloallelopathy

It is chemical coactions between the two different species. Allelochemicals which are released by one species harmful to other species and does not affecting on its source.

4. Autoallelopathy

It is chemical co-action within the same species. Allelochemicals released by one species harmful to itself.

5. Concurrent/ direct allelopathy

Types of allelopathy in which released toxic from living species directly affect on surrounding species. It is also known as 'living plant effect'.

6. Residual allelopathy

It is allelopathic effect due to the residues decomposition of previous crop or plant on succeeding crop or plant.

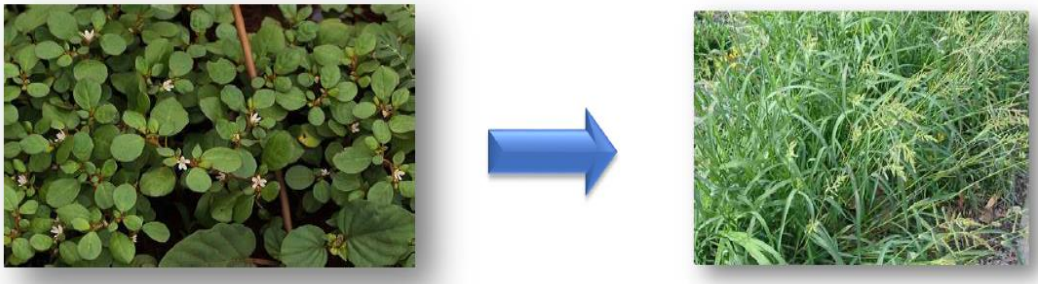
Types of Allelopathic interactions

1. Allelopathic effect of weed on crop

Avena fatua in Wheat field

Wild oat plants may produce toxic substances i.e scopoletin (7-hydroxy-6-methoxycoumarin) and vanillic acid (4-hydroxy-3-methoxybenzoic acid) that suppress the growth and development of desirable species, thus accounting for severe yield loss in infested wheat fields.

2. Allelopathic effect of weed on weed



Trianthema portulacastrum extracts increased soluble protein, amylase and total phenol that suppress the growth and development of desirable species of *Echinochloa colonum*.

3. Allelopathic effect of crop on weed

The importance of sorghum allelopathy as an ecological tool in managing weeds, highlighting the most recent advances in the allelochemicals (benzoic acid, p-hydroxybenzoic acid, vanillic acid, ferulic acid, chlorogenic acid, m-coumaric acid, p-coumaric acid, gallic acid, caffeic acid, p-hydroxibenzaldehyde, dhurrin, sorgoleone, m-hydroxybenzoic acid and protocatechuic acid,) present in sorghum, their modes of action, and their fate in the ecosystem.

4. Allelopathic effect of crop on crop

Residual allelopathic effect (Chlorogenic acid as allelochemical) of Sunflower on Potato tuber. Sunflowers have allelopathic chemicals that is, they give off toxins (terpenes and various phenolic compounds) from all their parts (roots, leaves, stems, flowers, seeds, etc.) that impede (Residual effect) the growth of other plants or even kill them.

Classification of allelochemicals

- ✓ Aliphatic compounds
- ✓ Unsaturated Lactones
- ✓ Fatty acid and Lipid
- ✓ Cyanogenic glucosides
- ✓ Terpenoids
- ✓ Aromatic Compounds

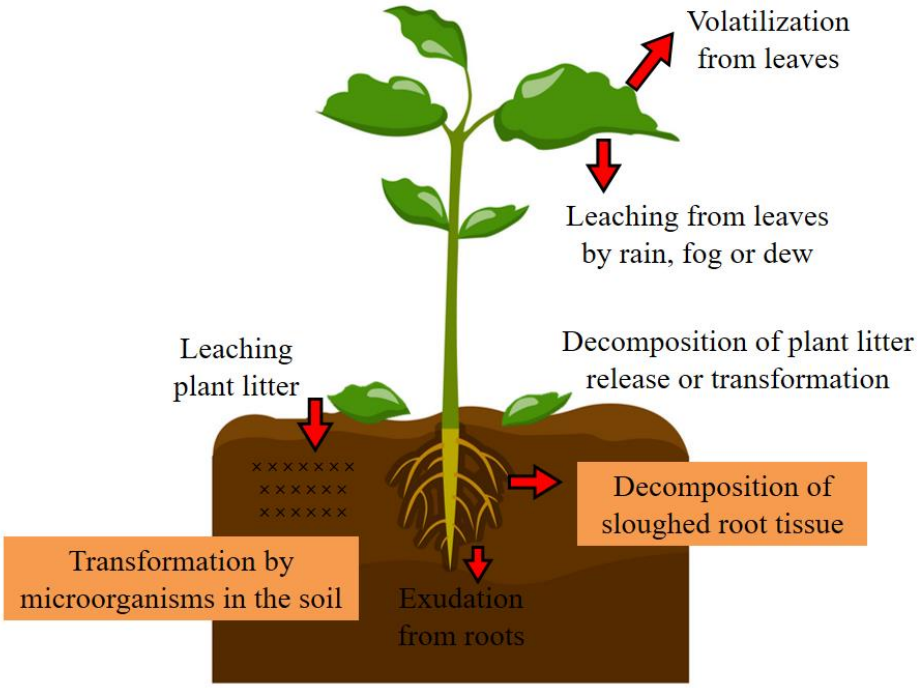


Fig. 1: Fate of allelochemicals in plant and soil environment

Allelochemicals are compounds released by one **plant** or **plant** residues that may have a negative or positive effect on other **plant**. The chemicals released from the plant leaves will be subjected to volatilization due to high atmospheric temperature and more leaching of the component due to rain, fog or dew. When the plant leaves get mature and fall on the soil get leached into soil through transformation by several microorganisms and decomposition of leaf litter occur. The chemicals released from the plant roots will gets directly enter into soil environment and also through the decomposition of the sloughed root tissues (Fig. 1).

Conclusion

The main aim behind allelopathy research is utilization of founded allelopathic effects to increase agricultural production, reduction in cost of pesticides, stop degradation of environment and furnish proper sustainable practices of weed management and sustainable development of agricultural production as well as ecological systems. The efficacy of these allelopathic extracts can be enhanced in combination with reduced rates of herbicides for managing weeds in field crops.

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AGRI MIRROR : FUTURE INDIA
ISSN: 2582-6980

Article Id: 226

ERI SILKWORM REARING IN TAMIL NADU

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Ericulture

Four types of silk are commercially exploited in India. Apart from the marvellous mulberry silk, which is quite popular the world over, there are a few other varieties that are equally attractive. They are collectively termed as Vanya silk or non-mulberry silk comprising of tasar, eri and muga. The eri silkworm is the only vanya species, is completely domesticated and reared indoor throughout the year. This is the multivoltine insect completing at least five to six years in a year and polyphagous in nature. The word "Eri" is derived from Sanskrit term Erranda which refers to castor plant, *Ricinus communis*., the primary food plant or eri silkworms. Eri silk is also known as *Endi* or *Errandi* in India. The wooly white silk is often referred to as *Ahimsa silk* or the *fabric of peace* as the process does not involve the killing of the silkworm. The eri shares about 65 % of total vanya silk production in the country. The states like Assam, Andhra Pradesh, Tamil Nadu, West Bengal, Arunachal Pradesh, Manipur, Meghalaya, Nagaland, Odisha, Madhya Pradesh and Uttar Pradesh are the major eri silk producing states.

Status of Ericulture in India

Nearly two lakh families are directly or indirectly associated with ericulture, where involvement of women is about 65 per cent and involvement of weaker section of the society is 52.4 per cent. The silk produced by eri silkworm is considered as the third most important silk in the world after mulberry and Chinese Tasar.

Ericulture as an additional income generating avocation has presently spread over to some non-traditional states of India. Besides Assam, it is cultivated in Meghalaya, Nagaland, Manipur, Mizoram and Arunachal Pradesh. Further, at present, it is spreading to different non-traditional states like, Andhra Pradesh, Tamil Nadu, Karnataka, Gujarat, Jharkhand and Chhattisgarh. The current production of eri silk is 6952 MT in India. Particularly in Tamil Nadu, the districts like Krishnagiri, Dharmapuri and Salem are cultivating eri silkworm rearing.

Host plants of Eri silkworm

Eri silkworm is a polyphagous insect and feeds on a wide range of host plants. Castor is considered as the primary food plant, since it is all time suitable for rearing of eri silkworm irrespective of seasons. Castor, the most preferred host plant is abundantly found in natural forests in plains and hilly areas. Eri host plants are interchangeable at rearing during scarcity of one host. In the East and West Garo Hills district of Meghalaya and Tamil Nadu, tapioca is cultivated for tubers in which the foliage can be used for rearing silkworms which gives additional income to the farmers.

Food plant of Eri silkworm

Eco races and Strains of Eri silkworm

25 ecoraces of eri silkworm are characterized collected from different parts of North Eastern region of India, *viz*., Borduar, Titabar, Khanapara, Mendipathar, Dhanubhanga Kokrajhar, Nongpoh, Diphu, Borpeta, Imphal, Inao, Mukokchung etc. and in Tamil Nadu, Commercial C2 breed and Borduar are practiced by farmers.

Eri silkworm has six homozygous strains classified on the basis of larval colour and body markings, namely, Yellow Plain (YP), Yellow Spotted (YS), Yellow Zebra (YZ), Greenish Blue Plain (GBP), Greenish Blue Spotted (GBS), Greenish Blue Zebra (GBZ). These strains produce different attractive coloured cocoon, i.e., white, creamish white, deep brick red and light brick red.

Eri Silkworm rearing

Young age silkworm rearing/ Early stage rearing

First to third instar rearing is called young age rearing. Young age silkworm rearing is also known as "Chawki rearing." Tray rearing is recommended for young age rearing. The young age (I-III instars) silkworm rearing is conducted either in the wooden trays of 50 cm x 60 cm x 5 cm size or in bamboo tray (of 70 cm dia.). Higher temperature from 26-28°C and relative humidity ranged 85-90 % are ideal conditions for young age rearing. Sufficient tender (glossy), fresh and nutritive leaves should be provided to young age larvae. The young age worms are very delicate and should be handled with utmost care.

Late age silkworm rearing

Late age worms consist of fourth and fifth instars which need ideal conditions of temperature ranged 24-26°C and relative humidity ranged 70-80 % during rearing conditions. The late age worms consume 80-85 % leaves supplied during the entire larval period. In late age eri silkworm rearing two methods of rearing are adopted.

Early stage rearing **Late age silkworm rearing**

1. Bunch rearing

In bunch rearing method, about 10-12 castor leaves are tied together to make a bundle and hung vertically on a horizontal bamboo/wire/string support. Then the worms are allowed to feed on the tied leaves. The foliage is changed by keeping fresh bunch near the exhausted one and the worms crawl over the new one. Just below the hanging bunches, bamboo mat or tray is kept on the floor so that the worms which fall down are not contaminated with dust on the floor and can be picked-up and put on the bunches.

2. Tray rearing

In tray rearing method, the worms are reared providing the leaves on the tray. Trays are made up of either bamboo or wooden in different shapes and sizes. The shapes are round (bamboo made), square and rectangular (wooden). Bamboo trays of size 1.0 m diameter is more convenient to rear 10-15 dfls until 2nd / 3rd instar; while 600-700 worms can be reared up to 4th instar and 300 worms in the final instar which also provides sufficient space.

3. Platform rearing technique

This is new innovative rearing method of eri silkworm. The model platform rearing device for eri silkworm rearing consists of 3 nos. platforms each of 1 x 2 m size and made up of bamboo strips with sieve size of 1sq cm. Platforms are placed in 3 tier in bamboo rack of size l 2.2 x b 0.75 x h 1.60 m. Two nos. of such racks can be placed in a room floor area of 5.4 sq m. (1.2 x 4.5 m). Maximum of 1200 eri silkworms at 5th instar can be reared in each platform to accommodate 7200 silkworms by brushing 25- 30 dlfs.. To collect litters of silkworm, gunny cloth is to be fitted below each tier. The technology is found to be advantageous to accommodate almost double quantity of silkworms per unit against the traditional round bamboo try (1m diameter with capacity of 300 nos. 5th instar worms) rearing system

Matured worm collection and mounting

After completion of larval life span, the matured 5th stage larvae discarded its complete excreta consisting of liquid and semi-solid substances. Now the worms are ready for spinning cocoons. Before spinning, the worms stop feeding and become restlessly moving here and

there to search a suitable place for cocooning. The matured worms produce a hollow sound when it is rubbed gently between fingers. This is the time for picking the ripe worms and putting them on mountages.

Number of feeds and bed cleaning

Instar	Duration - Days	Temp. (^{0}C)	RH (%)	Feeds/day	Bed cleaning
I	3-4	26-28	80-90	4	I before moult
II	3-4	26-28	80-90	4	I before moult
III	3-4	26	80	5	Daily
IV	4-5	25-26	75-80	5	Daily
V	6-7	25-26	75-80	5	Daily

The commonly used mountages are chandraki, basket filled with dry leaves, jali (a bundle of dry leaves like mango, jack fruit, some ornamental plants, etc.) and gunny bag filled with dry leaves. The leaves should not be completely dried; semi-dried leaves are suitable for easy spinning. After keeping the optimum number of worms in the respective mountages, it is covered by newspaper or cloth to make support and calm and semi-dark, a suitable condition for cocooning is complete. Cocooning is completed in three days. The ideal condition for spinning is around 24-25°C temperature and 60-70 % relative humidity. While mounting, the optimum number of worms should be maintained per mountage, i.e., 300 worms per chandraki of 1.0 m diameter size.

Cocoon harvest

Cocoons should be harvested after 5-6 days of spinning in summer and 8-9 days in winter. The harvesting process is the best time of sorting of cocoons according to the quality. The cocoons should be sorted out into good, double, melted, stained, dead or inferior, cut or pierced cocoons. Good commercial cocoons should be shifted and dried perfectly after the harvest. Cocoons should be preserved carefully to protect from fungal infestation and attack from pest and predators. Eri cocoon are oval in shape and it is whitish and brick red colour.

White colour cocoon **Brick red colour cocoon**

AGRI MIRROR : FUTURE INDIA
ISSN: 2582-6980

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DOMESTICATION OF *VIGNA* SPECIES: EVOLUTION AND ADAPTATION

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Introduction

Plant domestication is one of the most important events in human history. It is a process in which wild plants evolve and adapt to agricultural conditions and human needs largely due to human selection. The genus *Vigna* is one of the major groups of legumes, used for many different purposes such as fodder, green manure, cover crops and high protein to one's diet. Comparable to all major legume such as chickpea, soybean and pea, *Vigna* species are still under many interventions. Plant domestication is one of basic tool to understand the foreground role of the crop.

Domestication Syndrome

Major cultivated crop and wild progenitors show many differentiated traits which are collectively termed as 'Domestication syndrome' (DS). The domestication syndrome refers to all modifications occurring in a crop plant when it becomes cultivated from the wild form and is therefore dependent on human intervention. Some of the most important syndrome traits include loss of seed dispersal, early flowering, increased size of the edible organs, and changes in plant architecture and organ coloration, and are the outcome of selection for adaptation to cultivated environments. The domestication syndrome traits for legume crops are generally common to all. The rate and the order in which the domestication of these traits occurred, however, differ somewhat. From the previous studies it been observed that few of the domestication traits such as pod shattering, flowering synchronization, plant architecture and seed dormancy are common, which are not only observed in legumes but in cereals too such as wheat and barley. The genetic control of domestication-related traits (DRTs) has been investigated in numerous crop species, including legumes, mainly by quantitative trait loci (QTL) mapping using crosses between cultivated and wild accessions. Increased knowledge of the genomic regions controlling DRTs is valuable to exploit wild germplasm efficiently for improving resistance to biotic and abiotic stresses and overall yield. Understanding the genetic basis underlying the domestication syndrome may be useful for exploiting genetic resources of wild plants for the improvement of crops. Most domestication-related traits are quantitative, thus plant domestication is typically studied using quantitative trait locus (QTL) mapping. The genus Vigna is an important taxon of leguminous plants and comprises about 100 species distributed in Asia, Africa, America, and Australia.

New Model Plant Species

Vigna species are claimed to be studied as the "new model plant species" because of their existence in the various harsh environments such as sandy soil, limestones, rocks, deserts

and wetland. *Vigna* species are diploid except *V. reflexo-pilosa* which is tertaploid (2n=4x=44). Within the genus *Vigna*, nine species have been, domesticated such as moth bean (Vigna aconitifolia), azudki bean (Vigna angularis), mungbean, blackgram, creole bean, bambara groundnut (Vigna subterranea), rice bean (Vigna umbellata), tuber cowpea and cowpea (Vigna unguiculata).

Domestication and Evolution

Domesticated related studies are conventionally targeted by the development of interspecific mapping population which revealed many domestication traits related Quantitative trait loci (QTL) such as in V. *angularis,V.mungu, V. radiata,V.umbellata* and *V,unguiculata.* To understand the difference caused during the slow evolving process of domestication, researchers highlighted many concepts which involve structural variations such as copy number variable (CNVs), presence absence variatation (PAVs), InDels, frameshift mutation, inversion, SNPs or duplication. Studies underlying previous studies and recent studies domestication is appeared to be affected by natural selection pressure initially later accompanied by the human selection that lead to post domestication variation (improvement) of the crop. Earlier QTL related studies revealed the potential loci conferring the differential trait among wild and cultivar. Therefore traits showing clear dichotomy are likely to be considered as domesticated traits. From the latest scientific interventions and high throughout sequencing technologies made genome sequencing possible, this revealed potential selection sweeps that had be either deleted or duplication under positive selection pressure. The genome sequencing and SNP genotyping platform has made genome sequencing possible for adzuki bean (Yang et al. 2015), mungbean (Kang et al. 2014) and cowpea (Lonardi et al. 2019). Genome expansion, polyploidization are major evolutionary processes that need to be explored. From the study by Kang et al. 2014 whole genome sequencing of cultivated accessions, wild relative mungbean (*V. radiata* var. sublobata) and *V.reflexo-pilosa* revealed 775,831 SNP and 98,590 InDel among wild and cultivated. Any protein changes underlying phenotypic differences between domesticated and wild should among these structural variations. On comparing the paralogous genes between mungbean and all other legume it is revealed that mungbean underwent the one whole genome duplication event. Speciation and domestication are substantial adaptation to various climatic conditions, farming practices such as ploughing and other anthropogenic activities. Organelle genome sequence such as of chloroplast and mitochondrial provide insight to the evolutionary relationship among species and other related clades such as Vigna accessions were closest to *Glycine*. Comparative analysis with *G. max* QTLs were characterized to provide important clues for the identification of mungbean QTLs such as seed size/germination and bruchid resistance QTL. Similarly, cowpea sequencing identified a unique inversion of 4.2mb on Vu03 chromosome among wild progenitor and cultivars. Major study on cowpea highlighted the nine traits potentially associated with the domestication which includes pod shattering, peduncle length, flower colour, days to flowering, seed weight, pod length, leaf width seed number per pod were discovered (Lo et al. 2018). Resistance to biotic and abiotic stress are novel genes which are found to abundant in the wild species than elite breeding lines, even in major legumes too. For

example soybean Rhg-1 loci conferring resistant to cyst nematode is controlled by CNV of the transcriptional regulator. The process of directly exploring wild causing intended manipulation in its genetic architecture to make quick way to domesticated crop is known as Denovo domestication. Recently attempted by Takahashi et al. 2019, tried domestication of wild species that are already tolerant to various kind of stress such as in *Vigna stipulacea*. This species has fast growth, short vegetative stage and broad resistance to pest and disease is treated with ethyl methanesulfonate (EMS) mutagenized population and obtained three mutants with reduced seed dormancy and one with reduced pod shattering. Denovo assembly of V. *Stipulacea* genome successfully identified SNP associated with dormancy. Therefore this was attempted in less time than conventional backcross breeding programs that took 5-6 years for successful introgression (98.7%) of the donor segment into the elite cultivar. Such novel approaches are better understood under the term speed breeding (SB). Whole genome resequencing methodologies which include pangenome at genus level will provide the better insight to domestication event in vigna genus and the potential sweeps will be discovered elucidated by earlier discovered domesticated traits by using QTL and GWAS. Domestication-related traits examined in the populations derived from a cross between cultivated mungbean and its presumed wild ancestor. Mungbean genetic linkage map is made for the identification of QTLs for domestication-related traits and other agronomically important characters. Genetic linkage maps of some mungbean have been constructed using RFLP, RAPD and SSR markers. These linkage maps have been used to map genes for azuki bean weevil resistance and seed color and to identify QTLs for seed weight, hard-sidedness, powdery mildew resistance and Cercospora leaf spot resistance. It will also be useful for the analysis of genome synteny among species within the genus **Vigna**.

The moth bean (*Vigna aconitifolia*), possibly the most primitive crop of the genus *Vigna*, is a highly drought and heat-resistant legume grown in arid areas. Moth bean domestication involved phenotypic changes, including reduction of seed dormancy and pod shattering, increased organ size, and earlier flowering and maturity. However, the genetics of the domestication process in moth bean is still not well known. A comparative genome analysis showed high genome synteny between moth bean and mungbean (*Vigna radiata*), adzuki bean (*Vigna angularis*), rice bean (*Vigna umbellata*), and yardlong bean (*Vigna unguiculata*). In total, 50 QTLs and 3 genes associated with 20 domestication-related traits were identified. Most of the QTLs belonged to five LGs (1, 2, 4, 7, 10). Key traits related to domestication such as seed dormancy and pod shattering were controlled by large-effect QTLs (PVE > 20%) with one or two minor QTLs, whereas all other traits were controlled by one–seven minor QTLs, apart from seed weight, which was controlled by one major and seven minor QTLs. These results suggest that a small number of mutations with large phenotypic effects have contributed to the domestication of the moth bean. Comparative analysis of QTLs with related *Vigna* crops revealed that there are several domestication-related large-effect QTLs that had not been used in moth bean domestication.

Conclusion

The various studies provides a basic genetic map and identified genome regions associated with domestication-related traits, which will be useful for the genetic improvement of the *Vigna* species. QTL mapping will also be useful for the analysis of genome synteny among species within the genus **Vigna**.

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AGRI MIRROR : FUTURE INDIA
ISSN: 2582-6980

Article Id: 227

SPEED BREEDING IN PULSES: AN OPPORTUNITY TO IMPROVE THE EFFICIENCY OF BREEDING PROGRAMS

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Introduction

Pulses are thought to be the most important component of a balanced diet. The estimated 9 billion global inhabitants by 2050 are considered to be the most crucial factor in the fight against hunger worldwide. Although they have been a resurgence in the past ten years as a means of addressing agricultural concerns all over the world, grain legumes, particularly pulse crops, can be utilized for addressing the human food and nutritional security. Breeders used a novel approach to research how to shorten the breeding cycle in order to increase the genetic gain from the crop.

The Idea of Speed Breeding

Rapid advances in breeding and research can be achieved through shorter breeding cycles (i.e., the time between crossing and the selection of progeny to use as parents for the next cross) and a reduction in the number of cycles needed to generate new varieties. In order to hasten the transition to the next breeding generation, speed breeding is a collection of approaches that involves changing the environmental conditions in which crop genotypes are developed. A growing technique used by plant breeders to create new cultivars quickly is speed breeding, also known as rapid plant breeding. In contrast to the 2-3 generations produced annually under typical glasshouse conditions, speed breeding can produce up to 4-6 generations annually. Speed breeding improves photosynthesis, which causes the crop to grow quickly. Compared to the conventional breeding method, this procedure produces the release of numerous generations of the same crop in a shorter amount of time. Speed breeding can be used to shorten generation time and to accelerate crop breeding and research programs including development of mapping populations, phenotyping adult plant traits, hasten backcrossing and pyramiding of traits, mutant studies and transformation.

Recent Developments

Speed breeding is a method that has recently been established in various crops. NASA's experiments to grow crops in space, using an enclosed chamber and an extended photoperiod, served as inspiration for the speed breeding idea. Speed breeding became the standard in cereal research efforts at the University of Queensland in Australia as a result of the possibility to generate adult wheat (*Triticum aestivum* L.) and barley (*Hordeum vulgare* L.) plants more quickly and enable faster selection and population development (Hickey et al. 2019). In order to boost the rate of photosynthesis, promote early flowering, and hasten plant growth, the

technique uses the best possible light quality, light intensity, day length, and temperature control. It is combined with annual seed harvesting to hasten generation time.

Crops including wheat, rice, and maize have experienced higher rates of genetic gain as a result of recent improvements in breeding techniques like as genetic engineering, genomic selection, and doubled-haploid technology (Hickey et al. 2017). Combining these technologies with speed breeding methods, which allow for rapid generation advancement by growing plant populations under carefully controlled photoperiod and temperature regimes to speed up their growth and development, can have an even greater impact (Li et al. 2018; Watson et al. 2018). The breeder's equation, a model of the anticipated change in a trait in response to selection, can be used to estimate the rate of genetic gain in a breeding operation (Lush 1943; Falconer and Mackay 1996; Lynch and Walsh 1998). The equation can be written as: $R = (\delta g \times i \times r)/L$, where R is the change in the trait mean per year, δg is the amount of genetic variation within the population, i is the selection intensity, r is the selection accuracy, and L is the length of the breeding cycle. Based on this equation, speed breeding protocols can improve genetic gain in crop improvement programs by increasing the number of plant generations cycled in one year, which can substantially reduce the length of the breeding cycle. This is particularly useful for crossing and line development prior to field evaluation.

Advantages and Applications

In order to increase the amount of variation in breeding populations and hasten the achievement of breeding objectives, speed breeding methods are particularly helpful for synchronising the flowering of domesticated and wild individuals in crop species. The following methods can be combined to create rapid cycling: improving the plant's environment for growth (such as plant density, photoperiod, and temperature); genetically engineering to target the flowering pathway; grafting young plants to mature rootstocks; using plant growth regulators; and collecting immature seeds (O'Connor et al. 2013; van Nocker and Gardiner 2014; Ceballos et al. 2017; Watson et al. 2018; Ghosh et al.

Crops are only now starting to profit from modern breeding methods, and the advantages are anticipated to outweigh the drawbacks (Varshney et al. 2012; Pazhamala et al. 2015; Kumar et al. 2016). Modern breeding techniques can be used with the aid of speed breeding protocols, which will help to overcome this constraint (O'Connor et al. 2013, Li et al. 2018). One such way is the quick generation of recombinant inbred lines in a speed breeding system. Many pulse crops, including chickpea, field pea, and peanut, have taken advantage of the photoperiod response by modifying it to produce more genetic gain in a shorter amount of time. In pulses, numerous speed breeding systems have been created. Here, we provide a summary of advancements across many species; Samineni et al. (2020) created a technique for growing chickpea in a glass house under artificial light without the addition of a growth regulator. According to this technique, a temperature-controlled glass house with working high-pressure lamps is needed to increase the photoperiod to 22 hours. This glass house provides for precise control of temperature, humidity, and lighting. Immature seeds were germinated at 20–23 days after flowering (DAF) to further shorten the generation cycle, and

the photoperiod was increased to encourage early flowering. Six accessions were employed, two from each of the three maturity groups—early, medium, and late. Each year, there were six or seven generations. Given that chickpea (Watson et al. 2018) is a cool-season legume, increasing light exposure to a full 22 hours per day led to an increase of 4-6 generations per year. Similar to groundnut, three more generations were produced annually (O'Connor et al. 2013). By using plant growth regulators like auxin and zeatin, in-vitro fast enhancement in lentil and faba bean increased the genetic gain. Pea efforts of a similar nature (Mobini et al. 2016). The potential pace of genetic gain will be increased by combining marker-assisted selection and genome editing techniques with speed breeding. Speed breeding via genomic selection, like in the case of wheat, has increased genetic gain (Voss-Fels et al. 2018). High-throughput phenotyping techniques, like unmanned aerial drones and field scan lasers, will improve breeding cycle observation, reducing manual error and producing quick, high-throughput results that may be used by machine learning algorithms afterwards. Because they complement cereals in terms of protein requirements, food pulse demand is rising. Pulses are a significant part of the human diet, supply animal feed, and restore soil fertility by biologically fixing nitrogen. Therefore, by speeding up breeding, improvements in food security are established early, preventing the detrimental effects of population under nutrition (Lenaerts et al. 2019). The fact that some of these crops are already a part of mainstream agri-food systems and need more affordable breeding programmes that can adapt swiftly to climatic or disease challenges explains the rising interest in these crops (Pazos-Navarro et al. 2017).

Conclusion

To accelerate the creation, testing, and commercial distribution of crop varieties, speed breeding must be combined with other breeding strategies and affordable high-throughput genotyping and phenotyping. Accelerating the creation and spread of better varieties will depend in particular on field testing and farmers' participation in the testing and evaluation of elite lines. The creation and adoption of better varieties will therefore be facilitated by thorough and reliable field testing in conjunction with client-oriented innovation that takes into account the full value chain (from seed suppliers to consumers).

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AGRI MIRROR : FUTURE INDIA
ISSN: 2582-6980

Article Id: 228

ALERT SERVICES IN FARM RESEARCH

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Conclusion

In years to come with climate change issues and price fluctuations in farm markets playing an important role in our farm research, the need of the hour is to effectively use research alert services to do more farm researches which are location specific and tailor made to meet our development needs and priorities in the near future. Our Policy Planners, Farm Professionals and Researchers need to integrate and work together in assisting, guiding and supporting our research system with more regional and location specific farm alerts to combat or mitigate climate change related farm challenges in the near future.

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