Int.J.Curr.Microbiol.App.Sci (2024) *13*(02): 102-114

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 Volume 13 Number 2 (2024)
Journal homepage: http://www.ijcmas.com

Original Research Article https://doi.org/10.20546/ijcmas.2024.1302.015

Microbial Technology Based Sustainable Pigeon Pea Crop Management under Environmental Stress

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Keywords

Pigeon pea, environmental stress, crop productivity, nodule, microbial technology

Article Info

Received:
20 December 2023
Accepted:
31 January 2024
Available Online:
10 February 2024

ABSTRACT

The Pigeon pea (*Cajanus cajan*), a perennial legume crop belonging to the family *Fabaceae*, has been affected by multiple abiotic and biotic constraints in recent decades. The Pigeon pea legume provides multiple nutrient source legumes for human foods. Crop productivity worldwide has reduced due to unbeatable alterations and un-rhythmic environmental change. Nutrients, light, agrochemicals, temperature, water, and heavy metals are commonly reported environmental constraints in the last few years that adversely influenced legume Pigeon pea plant health and harvest efficiency worldwide. The excessive application of agrochemicals in agricultural fields poses grave threats to soil fertility and led to land degradation worldwide. Leguminous plants have the remarkable ability to work with special nodule-living bacteria in their roots and to gather or fix atmospheric nitrogen. Through this phenomenal process, inert nitrogen gas is taken from the inexhaustible supply in the air and used by plants to build amino acids and proteins essential to life. Because nitrogen fertiliser is the most expensive input for food production, the biological nitrogen fixation (BNF) approach is a very attractive alternative to expensive nitrogen chemical fertilisers. This review encompasses an in-depth analysis of environmentally friendly disease management practises including integrated pest and disease management approaches, biological control methods, and the use of resistant cultivars. Recent advancements in microbial fertilizer technology have opened new avenues of augmentation in stress agricultural productivity. Thus, in this article, we will explore recent advancements in legume growth that support microbial technology under stress environments.

Introduction

Health is a great achievement for every person. Protein plays an important role in a healthy diet. In India, agriculture is the main source of all types of food consumption such as pulses, cereals, vegetables, spices, oils, etc. Pulses are widely cultivated in India, especially by small-holding farmers. These are low-input crops because of their ability to assimilate atmospheric nitrogen (Krishna *et al.,* 2010). Pulse cultivation also contributes to the improvement of soil fertility and subsequently the productivity of non-leguminous crops in rotation (Robertson *et al.,* 2001). Equally important is their role in the diet of the people, particularly the rural people, who can -not afford expensive animal protein products to meet their dietary needs of essential amino acids. Pulses are high in protein, low in fat and sodium, cholesterol-free, and an excellent source of both soluble and insoluble fibres as well as complex carbohydrates, vitamins, folate, and minerals, especially calcium (Ca), phosphorous (P), iron (Fe), and magnesium (Mg) (Odeny, 2007). Pulses efficiently complement cereal-rich foods to make wholesome meals by balancing the amino acid and micronutrient content of the diet. No wonder they are called 'poor man meat'. Presently, pulses are grown on approximately 67 million hectares with 61 million tonnes of production worldwide. In India, the latest estimates for 2007-08 indicate that the production of pulses in the country is 15.1 million tonnes from an area of 24.45 million hectares (Ministry of Agriculture, 2009). Despite being the largest producer in the world with a 25% share in global production (MoEF & CC, 2009), India imports over 2.0 million tonnes of pulses every year to meet its domestic requirements. The major pulses cultivated and consumed in India are Chickpea, Pigeon pea, Moong bean, Urd bean, Lentil, and field pea (Ranjekar, 2003) contributing 39, 21, 10, 7 and 5%, respectively, to the total production of pulses in the country (MoEF & CC, 2009).

Nutritional properties of the Pigeon pea

India's second most important pulse crop is *Cajanus cajan* (L.) Millsp. Botanical term for Pigeon pea. It also has many other traditional names as Red Gram/ Tur/Arhar. Belonging to the Fabales order, the *Fabaceae* family has a subfamily called Faboideae. In botanical terms, *Cajanus cajan* plants have vascular glands on their leaves, calyx, and pods that secrete a sticky substance (Hurbusa *et al.,* 2022).

Medicinal properties

In India, all foods have medicinal properties. Herbal remedies gradually lost use in favour of synthetic medications. Nonetheless, according to estimates from the World Health Organization, 80% of people globally, especially those from developing and underdeveloped nations, still receive some portion of their main medical treatment from herbal remedies (Vardhini and Haq, 2014). Pigeon pea is a great fodder crop and is used to treat various disorders. In Indian states, this crop is used in many ways. In Bangladesh, Garotribes use it as a diabetes cure (Pal *et al.,* 2011) and as an energising source. In Trinidad and Tobago, the leaves are part of the red gramme to prevent food poisoning cold infection, and constipation (Lens, 2007). In other countries, the Chinese use *Cajanus cajan* leaves as a folk medicine cure to staunch blood, as an analgesic, and to kill parasites. Along with the leaf, other parts of plant seeds and vegetative stems are used to treat gingivitis, stomatitis, and as a toothbrush (stem portion), (Ganeshan, 2008). It is also a traditional medicine in eastern Rajasthan as fresh juice and boiled leaves are used orally to prevent the effect of intoxication and as a laxative, a paste of leaf is also applied to treat oral ulcers and inflammations, (Upadhyay *et al.,* 2010). Pigeon pea seeds and leaves are used as dressings for the induction of lactation (Pal *et al.,* 2011).

Genomic structure of the Pigeon pea

The environment maintains all crop genomic structures along with their bio-physio-chemical properties. A significant orphan crop, Pigeon pea *(Cajanus cajan)* is mostly farmed by smallholder farmers in Africa and India. The first pigeon pea pangenome, derived mostly from 89 accessions in India and Philippines (Zhao *et al.,* 2020). A draft genome sequence for pigeon peas was produced in 2012 and is being used for genetic improvement of this crop. The variable genome contributes to species diversity and provides functions that are not essential but may provide a selective advantage under certain conditions, including resistance to biotic and abiotic stresses (Saxena *et al.,* 2008). In 2017, in a larger composite pool of 1000 accessions. In 2017, low-coverage whole-genome sequencing was completed on 292 Pigeon pea accessions, which represent 95% of the overall genetic variation found in a huge combined collection of 1000 accessions encompassing the wide geographic spread of the pigeon pea. Sequencing data from the reference cultivar and 89 accessions with >9.5x coverage sequencing data were used to build a pan-genome for pigeon peas and to identify the presence/absence of genes in these accessions, (Varshney *et al.,* 2017). The Pan genome derived from these accessions has 55,51A significant orphan crop, Pigeon pea is mostly farmed by smallholder farmers in Africa and India. The first Pigeon pea pangenome, derived mostly from 89 accessions in India and the Philippines (Zhao *et al.,* 2020). 2 genes, 13.41% of which show PAV in the accessions studied, and 225 SNPs linked to nine traits. Twenty-one of the 225 SNPs were repeated in various years and places, demonstrating that Pigeon pea yield is heavily influenced by the environment (Zhao *et al.,* 2020). The polymorphic survey of a set of Pigeon pea accessions has also indicated a lack of genetic diversity within the cultivated gene pool (Kumar *et al.,* 2018). Wild Pigeon pea species are reservoirs of many useful genes and hold great potential for crop improvement. The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) gene bank is responsible for collecting, conserving, and distributing Pigeon pea germplasm comprising land races, modern cultivars, genetic stocks, mutants, and wild Pigeon pea species. It holds over 13,200 accessions of cultivated pigeon pea and 555 accessions belonging to 66 species of six genera in the genus *Cajanus* from 74 countries (Upadhyaya *et al.,* 2013). This germplasm collection based on the cross-ability relationship between cultivated and wild Pigeon peas has been grouped into three gene pools (Sharma *et al.,* 2017).

Production and Consumption

Pigeon pea is a major grain legume crop ranked sixth in area and production globally (Fu *et al.,* 2008). It is an important source of protein in human diets and is used in dhal and as a green vegetable. According to FAO (2017) statistics, the estimated globally sown Pigeon pea area now stands at over 7.03 m ha, with a production of 4.89 m t and an average yield of 695 kg/ha. The crop is well adapted to rain-fed areas of India (5.60 m ha), Myanmar (0.6 m ha), Kenya (0.28 m ha), and Tanzania (0.25 m ha). In all these countries, Pigeon pea is intercropped either with cereals such as sorghum (*Sorghum bicolour*), pearl millet (*Pennisetum glaucum*), and maize (*Zea mays*) or legumes such as soybean (*Glycine max*), mung bean (*Vigna radiata*), and urd bean (*Vigna mungo*).

India is the principal pigeon pea-growing country, accounting for approximately 90% of the world's production (Singh *et al.,* 2019). Next to Chick pea, Pigeon pea is the second most important pulse crop in India. It is mainly cultivated in Maharashtra, Karnataka, Madhya Pradesh, Andhra Pradesh, Uttar Pradesh, Gujarat, Jharkhand, Orissa, and Tamil Nadu (Figure 2). The ranking of yield showed that U.P. has 4th position with 3rd Gujarat and 2nd Maharashtra. The top state of India in Pigeon pea production is Karnataka. Approximately 98% of the total cultivation area of Pigeon pea is occupied by these 10 states in the country. Maharashtra is the largest producer of Pigeon pea with a production area of 10.51 lakh ha and an average productivity of 6.03 quintal per ha. In Karnataka, it is grown in an area of approximately 1.1 million ha with a production of 0.73 million tonnes and a productivity of 665 kg/ha (DES, 2018).

Pigeon Pea as source of nutritious food

In rain-fed agricultural circumstances, pulse crops (PP) are the most essential food element with the lowest costs. Additionally, in conventional cereal-based diets, PP is the most important source of additional protein to bridge the gap in nutrition in the tropics and subtropics (Belete Kuraz Abebe, 2022). Pigeon pea regarded as a lifeline of subsistence farming in tropical and subtropical regions, (Saxena *et al.,* 2010). The range of nutrient contents obtained were: dry matter 86.6%-88.0%, crude protein 19.0%–21.7%, crude fat 1.2%–1.3%, crude fibre 9.8%–13.0%, and ash 3.9%–4.3%. Mineral ranges (mg/100 g dry matter) were as follows: K 1845-1941, P 163-293, Ca 120-167, Mg 113-127, Na 11.3-12.0, Zn 7.2-8.2, Fe 2.5-4.7, and Cu 1.6-1.8. There were no significant differences in Na levels among the six varieties ($p>0.05$). For the other components, varietal differences ($p<0.05$) were observed. The values obtained for dry matter, crude protein, fat, ash, Ca, Cu, Fe, and Mg were similar to those in Pigeon pea grown elsewhere, whereas those for crude fibre and Zn were higher. This crop would positively contribute to protein in the diet and the diversification of agricultural produce (Amarteifio *et al.,* 2002).

Major components

Most protein found within pulse seeds is in the form of storage proteins classified as globulins, albumins, and glutelins (Roy *et al.,* 2010). Globulins make up approximately 65% of the total protein in Pigeon pea. Globulins are soluble in salt-water solutions and represent approximately 70% of the total protein in pulses; albumins are soluble in water and account for 10-20% of the total protein in pulses; and glutelins are soluble in dilute acid and base and account for 10-20% of the total protein in pulse seeds. Globulins found in selected Cucurbitaceae seeds exhibited significant antihyperglycemic activity (Teugwa *et al.,* 2013). The lysine content in pulse seeds is high compared with that in cereal crops and grains such as rice. Its domination in legumes is pivotal in providing the essential amino acids required for proper human nutrition (Duranti, 2006). Protein isolates from plant origin have enormous potential and prospects in the food industry for nutritive and physicochemical properties and are cost-effective.

Nutritional and functional analysis of the protein isolates obtained using different extraction techniques had promising results for their superior quality and possible use in food products (Adenekan *et al.,* 2018). The solubility of proteins and their functionalities are affected by extraction conditions, solvent type, and heat treatment. Carbohydrates account for 55%–65% of dry matter in Pigeon pea, including starch and non-starch polysaccharides. Due to poor digestibility compared with cereal starch, legume starches promote slow and moderate postprandial glucose and insulin responses and have a low glycemic index due to higher amylose content than cereals (Sajilata *et al.,* 2006). Legumes contain a large amount of starch and fibres that are resistant to digestion in the small intestine and pass into the large intestine for bacterial fermentation to produce short-chain fatty acids (Chung *et al.,* 2008).

Minor components

Other than the major components such as protein and carbohydrates, there are minor components consisting of pigeon peas that exhibit bioactive effects. There is little information available regarding the phytochemical profiling of small molecules in Pigeon pea seeds. Phytochemicals are chemicals produced by plants through primary or secondary metabolism. Campos-Vega *et al.,* (2010) summarised the minor components of pulses, including phenolic compounds, enzyme inhibitors, lectins, fatty acids, phytosterol phytic acid, and saponins. In current studies, most of the so-called anti-nutrients (such as tannins, saponins, and phytic acids) have been found to have health-promoting properties if used properly (Bawadi *et al.,* 2005). Some bioactive substances are sensitive to processing conditions; for example, enzyme inhibitors and lectins have little effect after cooking. Among the many bioactive substances in pulses, the most extensively investigated compounds include phenolic compounds, phytic acid, and saponins (Marathe *et al.,* 2011).

Factors affecting the growth of pigeon pea crop health and production

Abiotic stresses

Throughout their life cycle, Pigeon peas are subject to a variety of abiotic stresses, including those related to moisture (waterlogging or drought), temperature, photoperiod, and minerals (salinity or acidity). Waterlogging stress causes morphological, physiological, and biochemical changes in pigeon peas that change the cells' underlying processes (Kumar *et al.,* 2020). Because Pigeon pea is typically farmed as a crop supplied by rainfall, moisture stress is prevalent among these challenges. Crop failure is frequently caused by temperature extremes (too high or too low) during the reproductive stage in the northwest and north eastern regions of India (Choudhary *et al.,* 2011). The growth and development of cover crops are influenced by environmental variables such as light intensity, temperature, rainfall, and soil fertility. Soil-incorporated residues from cover crops improve soil organic matter, which in turn improves soil fertility as well as its physical, chemical, and biological properties, thereby restoring soil productivity. The grade of photosynthetic photon flux density produced in artificial shade differs significantly from that produced in the field under shade trees. Different degrees of blue and red light are received and/or transmitted depending on the properties of the upper storey tree canopy, which might significantly affect under storey cover crop growth and net photosynthesis compared with cover crops cultivated under artificial light. The following findings are based on the responses of cover crops cultivated in artificially shaded conditions (Baligar *et al.,* 2008).

Photoperiod (sunlight duration)

Pigeon pea is a photosensitive and thermosensitive crop. It is grown in places where the day duration ranges from 11 to 14 h and there are significant temperature fluctuations owing to variances in height and latitude. According to Silim *et al.,* (2007) studied, results indicated that the two long-duration genotypes, 'ICEAP 00040' and 'T 7', were the most sensitive to photoperiod variation, with flowering rate reduced by 0.001 d-1 per hour increase in day length, while the extra-short duration genotype, 'ICPL 90011', was the least sensitive. Carberry *et al.,* (2001) discovered that when day length in the photoperiod-inductive phase exceeded a crucial value, flowering in short-duration pigeon pea cultivars was delayed by up to 100 days. Cultivars with medium and long durations responded to photoperiod by delaying flowering by more than 150 days.

Weather (rainy and post rainy season)

In India, waterlogging is one of the most serious constraints for crop production and productivity, where approximately 8.5 MHA of arable land is prone to this problem. Out of the total (3.9 MHA) area under pigeon pea, approximately 1.1 MHA is affected by excess soil moisture, causing an annual loss of 25-30% (Sultana, 2010).

Soil Nutrient

An uneven fertilization schedule and the availability of soil nutrients are two of the other factors causing low pigeon pea productivity. The farming community currently applies organic manures without considering the balanced and sufficient amount of nutrients needed for pulse crops, which leads to the appearance of several nutrient shortages and the degradation of soil physical qualities (Singh *et al.,* 2019).

pH

The pH of the soil ranged from 5.09 (strongly acidic) to 6.77 (slightly acidic), the EC of the soil was 0.047–0.14 dS/m (low), the soil OC level was 1.6%–2.42% (moderate), total N was 0.12%–0.23% (low to moderate), available phosphorus content was 6.82–13.52 mg/kg (low to moderate), and the CEC value of the soil was 14.8–23 (moderate). Except for Abela Abaya, all of the locations had sandy clay loam soil texture (Anjulo *et al.,* 2021).

Heavy Metals

Heavy metals are essential components of environmental matrices that include both imperative and non-obligatory variables. Heavy metal-polluted soil contaminants have become more common as geogenic and industrial activities have increased. Heavy metals as Cadmium (Cd) is a highly toxic heavy metal that contaminates soil and adversely affects plant growth, resulting in decreased crop production.

The objective of this study was to determine the effect of Cd on germination and early seedling growth of *Cajanus cajan*. Seeds placed on sterilized filter paper were exposed to varying concentrations of Cd solutions (20, 60, 100, 200 and 400 ppm) prepared using anhydrous $CdCl_2$ under laboratory conditions.

Increasing concentrations of $CdCl_2$ significantly reduced the germination percentage, root length, shoot length, fresh weight, and dry weight compared with the control (Swapna *et al.,* 2016). Gandhi *et al.,* (2020) performed a series of tests to optimise the effects of heavy metals on Pigeon pea seeds under various concentrations of Cu, Pb, Mn, and Ba, and found significant changes in germination and other physiological operations. However, compared with other heavy metals, the results of his study showed Cu and Pb are the most effective pollutants and deteriorate properties of Pigeon pea.

Salinity

Soil salinity affects pigeon pea plants through osmotic stress and interference with the uptake of mineral nutrients. However, these stresses have a drastic impact on the productivity of Pigeon peas (Choudhary *et al.,* 2011). Salinity tolerance was measured by Karajol and Naik (2011). During germination, 11 genotypes of Pigeon peas were tested at doses of 0, 100, 125, 150, 175, 200 and 250 mM NaCl.

Salinity did not affect the germination percentage although it did delay germination at 250 mM in all accessions to various degrees. White-seeded varieties like 'WRP 1', 'GS 1', and 'TS 3' appeared to be more salt-resistant than red- or black-seeded cultivars like 'Black tur', 'Asha', and 'Bennur Local', which were deemed highly vulnerable to salt stress based on their germination rate and final germination percentage.

Soil Pollution and Contamination

The Pigeon pea is capable of producing abundant harvests of seeds rich in protein with values around 21 to 25% (Mula *et al.,* 2010), even in low fertility soils, being adapted to high temperatures and drought conditions (Akande *et al.,* 2010). Pigeon peas can survive quite well in degraded soils and tolerate water stress (Odeny, 2007).

Waste from the mining, chemical, and steel processing industries, as well as other connected industries, are the most common source of soil pollution (Gandhi *et al.,* 2015).

Biotic Stress

Numerous biological diseases drastically affected pigeon pea as *wilt*, sterility mosaic virus, blight, and pests as pod borer, pod fly in the field, and bruchids in the field and storage are among the principal biotic stress. When compared with conventional management strategies for biotic stressors, the results of on-farm testing demonstrated a considerable influence on seed production, net profit, and benefit-cost ratio.

Table.1 Nutritional composition of Pigeonpea (Kunyunga *et al.,* 2013)

S. No.	Proximity	Value/1 Cup, 154 g
1	Water	101.46 g
2	Energy	209 Kcal
3	Energy	876 kJ
4	Protein	11.09 g
5	Total fat (lipid)	2.53 g
6	Ash	2.16 g
7	Carbohydrate	36.78 g
8	Total dietary fibre	7.9 g
9	Total Sugars	4.62 g
10	Calories	209 kcal
11	Fat	22.77 kcal

(g= gram, kJ=Kilo Jule, kcal= kilocalorie)

Table.2 Mineral properties of Pigeonpea (Singh *et al.,* 2016)

S. No.	Minerals	Value (Unit)	S. No.	Vitamins (water soluble)	Value (Unit)
1	Calcium, Ca	65 mg	1	Vitamin B1 (Thiamine)	0.616 mg
2	Iron, Fe	2.46 mg	2	Vitamin B2 (Riboflavin)	0.262 mg
3	Magnesium, Mg	105 mg	3	Vitamin B3 (Niacin)	3.388 mg
4	Phosphorus, P	196 mg	4	Vitamin B5 (Pantothenic acid)	1.047 mg
5	Potassium, K	850 mg	5	Vitamin B6 (Pyridoxine)	0.105 mg
6	Sodium, Na	8 mg	6	Vitamin B9 (Folate)	266 µg
7	Zinc, Zn	1.6 mg	7	Folate, food	266 µg
8	Copper, Cu	0.206 mg	8	Folate, DEF	266 µg
9	Manganese, Mn	0.884 mg	9	Choline	70.5 mg
10	Selenium, Se	2.3 µg	10	Vitamin C (Ascorbic acid)	60.1 mg

(mg=milligram; µg= microgram)

Figure.1 Nutritional benefits of Pigeon pea

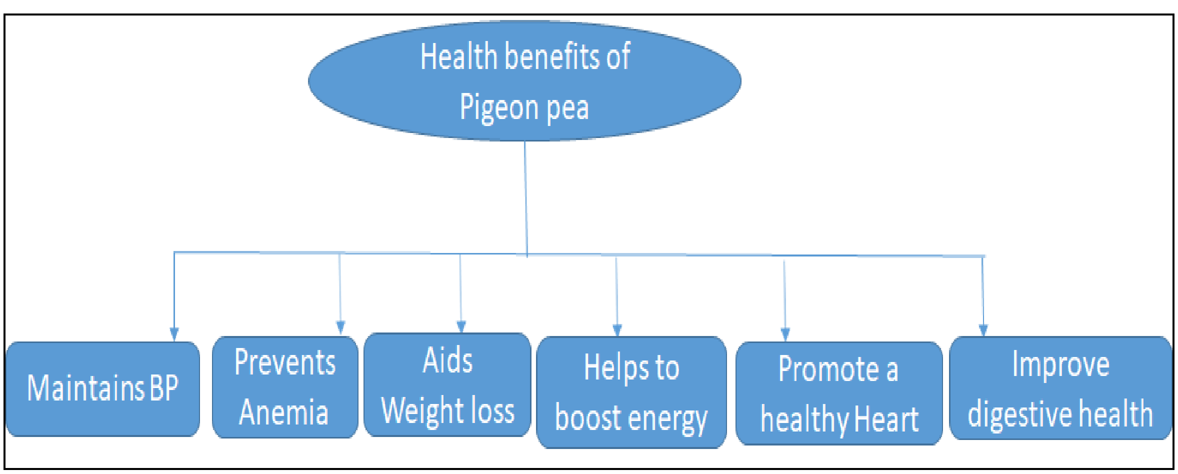


Table.3 Chemical properties of Pigeonpea (Singh *et al.,* 2016)

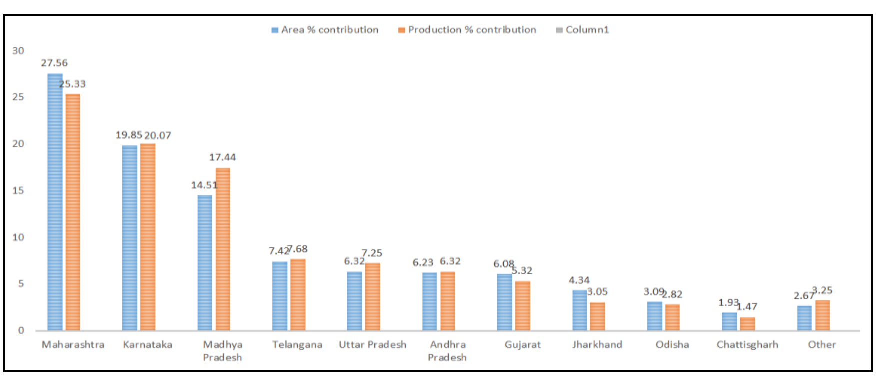
S. No.	Lipids	Value (Unit)	S. No.	Vitamins	Value (Unit)
1	Fatty acids, total saturated	0.545 g	1	Fat-soluble Vitamins	0.616 mg
2	Palmitic acid 16:00 (Hexadecanoic acid)	0.507 g	2	Vitamin A, RAE	5 µg
3	Stearic acid 18:00 (Octadecanoic acid)	0.038 g	3	Vitamin A, IU	103 IU
4	Fatty acids, total monounsaturated	0.02 g	4	Beta Carotene	62 µg
5	Oleic acid 18:1 (octadecenoic acid)	0.02 g	5	Lutein + zeaxanthin	293 µg
6	Fatty acids, total polyunsaturated	1.344 g	6	Vitamin E (alpha-tocopherol)	0.6 mg
7	Linoleic acid 18:2 (octadecadienoic acid)	1.286 g	7	Vitamin K (phylloquinone)	37 µg
8	Linolenic acid 18:3 (Octadecatrienoic acid)	0.059 g	8	Folate, DEF	266 µg

(g=gram; µg= microgram)

Table.4 Microbes contamination of Pigeonpea

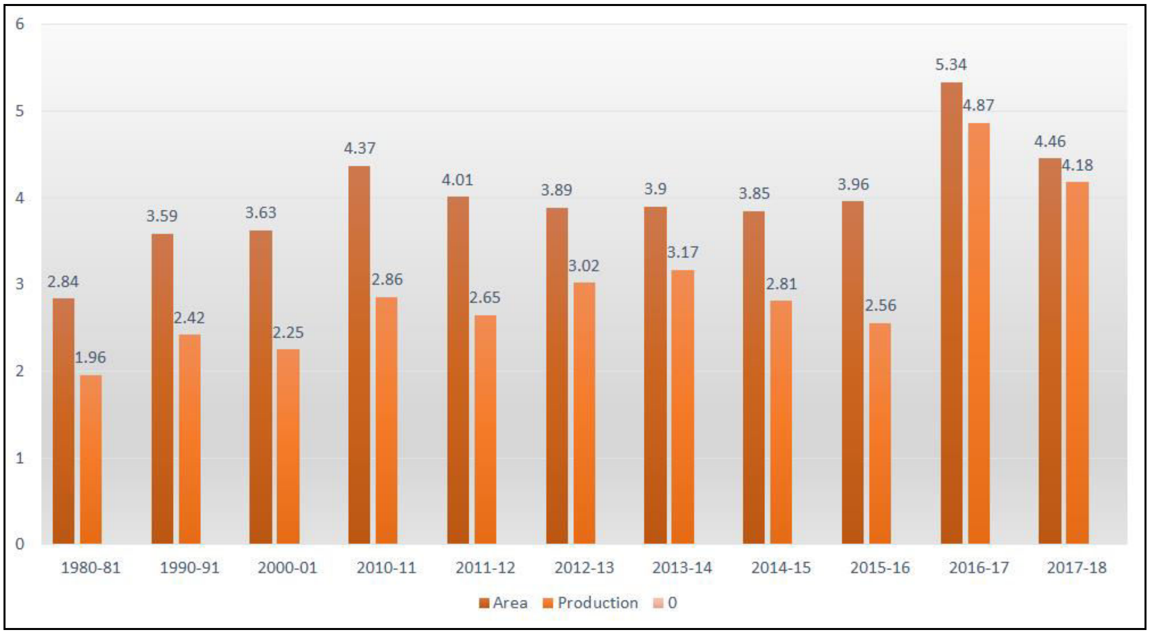
S. No.	Disease	Organisms
1	Fusarium wilt	*Fusarium sp.*
2	Dry root rot	*Rhizoctonia bataticola*
3	Alternaria leaf spot	*Alternaria alternate*
4	Powdery mildew	*Leveillula Taurica*
5	Pigeon pea sterility mosaic	*Pigeonpea sterility mosaic*
6	Mung bean yellow mosaic virus	*Redgram yellow mosaic*
7	Phytophthora Blight/Stem Blight	*Phytophthora drechsleri* f. sp. cajani
8	Wilt	*Fusarium oxysporum* f. sp. udum
9	Canker	*Diplodia cajani*
10	Bacterial leaf spot and stem canker	*Xanthomonas campestris* pv. Cajani
11	Viral Disease Sterility Mosaic	Sterility mosaic virus

Figure.2 Total area and production coverage of major states of India, of pulses (area lakh/ha and production lakh/tons).



(Source: DES, Ministry of Agri. & FW (DAC & FW), Govt. of India; 2017-18- IIIrdAdv. Est.)

Figure.3 Total production from 1990 to 2018 years of major states of India



(Source: DES, Ministry of Agri. & FW (DAC & FW), Govt. of India; 2017-18*- IIIrdAdv. Est)

Among the biotic management methods, weed management had the highest incremental cost (Rs. 2,974 ha^{-1}) whereas pod borer management had the lowest (Rs.798 ha^{-1}) compared with existing practises (Singh, 2001). The pod borer is the most dangerous pest on the planet. A wide variety of insect infestations occur in eastern Africa, causes most serious disease is *Fusarium wilt* (*Fusarium udum*). Birajdar *et al.,* (2018) investigated the diversity of *wilt*-causing *Fusarium* species using morphological analysis and genetic markers. The 20 primers used in the RAPD series, in which only 8 primers were polymorphic, showed 20%-55% genetic diversity among the isolates of *Fusarium* species, which were isolates from Pigeon pea root samples in the Maharashtra and Karnataka growing regions. Some examples have been illustrated in Table 4.

Microbes as potential tool to mitigate abiotic and biotic stress induced negative impact on Pigeon pea

Since "Hiltner" concept of rhizosphere in year 1904, the most research findings have been reported on soil-plant-microbe interactions under different environmental conditions led to positive findings. Efficient microbes as single population and in consortia inoculum effectively deals in resource accessibility, plant health development and resilience to different stresses (Hong *et al.,* 2022). The multilateral microbial communications with plants in soils, water and air determines its survival and life cycle dogma (Trivedi *et al.,* 2022). Climatic fluctuations and anthropogenic sources insistently led to stress environment and ruined the capacity of establishing beneficial soils interactions and finest yield peak (Vimal and Singh, 2020). Plant root exudates develop ubiquitous microbial associations and benefited plants under multiple abiotic and biotic stress managements.

The microbe efficiently encounters abiotic and biotic calamities with different supportive mechanisms as antibiosis and competition, phytohormones production, ACC deaminase, VOCs, siderophore, antibiotics, vitamins, organic acids and hydrolytic enzymes production traits (Vimal *et al.,* 2022) in different crops. The microbial community structure facilitated soils with transformation and translocation of vital growth nutrients and enriched bio-availability of sufficient nutritional supplies to legumes crops (Hong *et al.,* 2022).

In Pigeon pea, two diseases are of prime importance. These are *Fusarium wilt* and sterility mosaic, and a third disease, called *Phytophthora* blight, is also on the increase, but its incidence is limited to poorly drained fields. In most of the Pigeon pea growing areas, both *wilt* and sterility mosaic diseases are prevalent and cause severe damage each year. Therefore, breeding involves resistance to both diseases simultaneously, and several genotypes with high levels of resistance are available. Saxena *et al.,* (2012) reported a dominant gene for resistance to *wilt*, which will be very useful in breeding *wilt*-resistant hybrids. This is because hybrids involving both resistant × resistant and resistant × susceptible parental lines will exhibit resistance to this disease.

Bacterial isolates were tested against the fungal pathogen *Fusarium udum*, which is known to infect the susceptible type of Pigeon pea that is widely grown in India, for an environmentally friendly and long-term treatment of this disease. *In vitro* and *in vivo* investigations were conducted to evaluate the antifungal activity of these bacterial isolates.

Pseudomonas and *Bacillus* sp. isolates were isolated from Pigeon pea field soil. Five *Pseudomonas* spp. isolates (Pf05, Pf14, Pf19, Pf23, Pf25) and four *Bacillus* spp. isolates (Bc01, Bc09, Bc14, Bc20) were identified as promising biocontrol agents against *Fusarium wilt* (Rana *et al.,* 2014). A new mucolytic strain, *Pantoea dispersa*, was tested against the fungus *Fusarium udum*, which is known to infect the susceptible Pigeon pea (T-15-15), which is widely grown in India. In both pot and field experiments, the efficacy of *P. dispersa* as a biocontrol agent was compared with that of the chemical fungicide Bavistin and the antifungal biocontrol agent *Trichoderma* Monitor WP. *P. dispersa* inhibits the growth of *F. udum In vitro*. When compared with the chemical fungicide Bavistin and antifungal biocontrol agent *Trichoderma* Monitor WP treatments, *P. dispersa-treated* pigeon pea (T-15-15) seeds demonstrated a higher percentage of seed germination and lower *wilt* incidence in a pot experiment. Furthermore, the root, shoot, and growth lengths were all determined to be greater (Maisuria *et al.,* 2008).

Pigeon pea and cowpeas towards the *G. fasciculatum* show high susceptibility due to a large area of the root's cortical tissue in both hosts prohibiting the entry of invaders as root-knot nematodes or root *wilt* soil-borne fungi to a limited range. The Pigeon pea plant was chosen for subsequent trials based on maximum root colonisation in which four substrates were evaluated for the multiplication of roots. *G. fasciculatum* in the same plant's roots. Experiments to find the best non-chemical and more environmentally friendly substrate for the growth of *G. fasciculatum* FYM and Karaj oilseed are two natural media. Both alone and with others, cake was attempted (Goswami *et al.,* 2007). *Solani Fusarium* (Mart). Sacc. is a pathogenic fungus that causes *wilt*ing. Basher *et al.,* (2012) isolated, five distinct isolates of *F. solani*, subjected to RAPD-PCR-based genetic diversity analysis in terms of DNA polymorphism. V3 (*Lycopersicum esculentum Mill*.) and V5 *(Solanum melongena* L.) isolates of *F. solani* exhibited 78.2 % similarity. Isolates V1 (*Lens esculentum* L.) and V2 (*Acacia* sp.) shared 74.2 % of their sequences. Isolates (V1 and V2) and (V3 and V5) had 65.5% sequence similarity. Isolate V4 (*Gladiolus* sp.) produced findings that were 70.3% comparable. A UPGMA dendrogram and percentage similarity table validated the genetic diversity pattern among *F. solani* isolates (Bashir *et al.,* 2012). Varshney *et al.,* (2012) studied several markers for the improvement of legume crops for advanced agriculture techniques along with next-generation sequencing in the advancement of crop genotypes. There are many genetic resources in the form of markers and mapping, including SSR markers, transcript assembly and SNP markers, DArt markers, cost-effective SNP genotyping platforms, genetic and transcript maps, trait mapping, and molecular breeding.

Next generation promising studies for controlling stress incidence and disease

A group of 36 elite-grown pigeon pea genotypes with varying levels of resistance to *Fusarium wilt* were studied for genetic diversity and simple sequence repeat indicators associated with *Fusarium wilt* resistance. A total of 59 alleles were amplified using twenty-four polymorphic sequence repeat markers across these genotypes, with an average high polymorphism information content score of 0.52.

According to their *Fusarium wilt* reactivity, UPGMA and PCA cluster analyses classified the 36 Pigeon pea genotypes into two primary clusters. Six simple sequence repeat markers were found to be strongly linked with *Fusarium wilt* resistance using Kruskal-Wallis ANOVA and simple regression analysis. The percentage of phenotypic variance that these markers explained ranged from 23.7 % to 56.4%. The goal of this research was to determine if pre-screened SSR markers can be employed in genetic diversity analyses and if they have a link to disease resistance (Singh *et al.,* 2013).

Disease-resistance genes are important components of the plant immune system. In a study by Zheng *et al.,* (2016), adopted a strong pipeline and recognised an aggregate of 4,217 R-qualities in the genomes of seven sequenced vegetable species. An emotional variety of R-qualities with primary differences demonstrated a fast birth-and-death rate during R-quality advancement in vegetables. The quantity of R-qualities fleetingly extended and then immediately contracted after entire genome duplications, which implied that R-qualities were touchy to ensuing di- fluidization.

R proteins with a curled loop (CC) area are more conserved than others in vegetables. In the interim, different types of vegetable R proteins with just a couple of average spaces were exposed to higher rates of misfortune during development. Even though R-qualities advanced rapidly in vegetables, they would in general go through refining choices rather than positive choices during advancement. In addition, taming occasions in a few vegetable animal varieties were specially chosen for the qualities directly associated with the plant-microorganism communication pathway while stifling those R-qualities with low event rates.

Future legume farming and farmers

The development of "seed village," in which all farmers in a village are motivated to plant advanced genotype of pigeon pea, was developed to address this difficulty in seed production and maintain the genomic purity of the released varieties (Saxena *et al.,* 2006). Dutta *et al.,* (2011) studied Pigeon pea production based on early maturation, high production, large seed, flood tolerance, resistance to pod borers, fast cooking time, and grain taste. Farmers select early maturing cultivars because they want a quick return on their investment, many harvests in a season, to minimize Pigeon pea competition with intercropped species, and to reduce the amount of yield lost to water shortages at the end of the season. Most Pigeon pea producers preserved seeds for the season's planting. Several other crops in under developed nations have also been observed. Several farmers conserved seeds for the following planting season, and only a few farmers bought seeds (Mula *et al.,* 2010).

Future prospects

- The next key objective is to develop mapping populations employing identified genetic resources for trait mapping and marker-assisted breeding. The ideal genotypes for creating a mapping population should be genetically diversified and have a contrasting phenotype for the characteristic of interest.
- The availability of large-scale genetic data and cost-effective genotyping tools, as well as the possibility to outsource genotyping work, are expected to speed up trait mapping for additional essential traits in legume crops. This will increase the adoption of molecular breeding for enhancing agricultural production of these legume crops eventually.
- Farmers who are interested in intercropping may be supplied with pulse seed mini kits. Farmers should be trained and production technologies should be demonstrated in the field by KVKs at the district level.

Acknowledgement

Shraddha Singh wants to express her sincere gratitude to Head of the Department, Professor Rubina Lawrence and *Ph.D.* Guide, Ebenezer Jeyakumar, Associate Professor for their valuable insights, review, editing and mentorship during the preparation of this review paper. All authors are thankful to Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh for infrastructure facilities to conduct this study.

Author Contribution

Shraddha Singh: Investigation, formal analysis, writing—original draft. Rubina Lawrence: Validation, methodology, writing—reviewing. Ebenezer Jeyakumar:—Formal analysis, writing—review and editing.

Data Availability

The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations

Research Funding: Not applicable

Ethical Approval: Not applicable.

Consent to Participate: Not applicable.

Consent to Publish: Not applicable.

Conflict of Interest: The authors declare no competing interests.

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How to cite this article:

Shraddha Singh, Rubina Lawrence and Ebenezer Jeyakumar. 2024. Microbial Technology Based Sustainable Pigeon Pea Crop Management under Environmental Stress. *Int.J.Curr.Microbiol.App.Sci.* 13(2): 102-114.
doi: https://doi.org/10.20546/ijcmas.2024.1302.015