

## **A SEMINAR PAPER ON**

### **Utilization of Wild Species for Genetic Improvement of Crops**

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#### **Course Instructors**

**1. Dr. A. K. M. Aminul Islam**

**Professor, BSMRAU**

**2. Dr. Md. MizanurRahman**

**Professor, BSMRAU**

**3. Dr. Md. SanaullahBiswas**

**Associate Professor, BSMRAU**

**4. Dr. Dinesh Chandra Saha**

**Associate Professor, BSMRAU**

#### **Major Professor**

**Dr. Md. Golam Rasul**

**Professor,**

**Department of Genetics and Plant  
Breeding, BSMRAU**

#### **SUBMITTED BY**

**HasnaJamaly**

**MS Student**

**Reg. No.: 15-05-3564**

**Department of Genetics and Plant Breeding**

**BANGABANDHU SHEIKH MUJIBUR RAHMAN AGRICULTURAL UNIVERSITY**

**SALNA, GAZIPUR 1706**

# **Utilization of Wild Species for Genetic Improvement of Crops**

## **ABSTRACT**

Variation in plant population is very important for plant breeders. Wild species as genetic resources has a great role in genetic variation. By using wild species in breeding programme high yield, high quality and quantity, extension of adoption ability to biotic and abiotic stress can be obtained. This will lead to objective, to assure sustainable crop production and to ensure conservation of genetic diversity. Some beneficial trait like resistance capacity and cytoplasmic male sterility have been exploited from wild species to cultivated crops. Wild species have been used for crop improvement like rice, wheat, maize, vegetables etc. As there is some limitation to use wild species, some approaches were made to enhance the utilization of wild species for genetic improvement of crops and conservation strategy has been made for further utilization in future.

**Key words:** Genetic resources, Biotic and abiotic stress, Cytoplasmic male sterility, genetic improvement, Conservation.

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# CHAPTER 1

## INTRODUCTION

The wild species of crop plants is important source of genetic resources for refining agricultural production and also for maintaining sustainable agro-ecosystems. Their rich set of useful traits that can be introduced into crop plants by crossing.

Wild species differ from cultivated crops in a number of important ways which greatly affect strategies for their collection, conservation and utilisation. The effects of the differences between wild and cultivated species upon sampling strategies have been described in detail by (Marshall and Brown, 1983) and upon conservation by (Frankel and Soule, 1981).

Crop domestication and improvement can be described as a procedure of successive rounds of selection that ultimately results in the isolation of genetic diversity valuable to agriculture from ancestral wild species. These successive rounds of selection have resulted in the crops that feed the world today, but at the cost of reducing their genetic variation, leaving them with less allelic range than their wild ancestors and other crop wild relatives (CWR) (Ross-Ibarra et al., 2007; van Heerwardenet *al.*, 2011). This is often referred to as “domestication bottleneck” (Hammer, 1984; Tanksley and McCouch, 1997).

Wild species are found in natural ecosystems. They incline to contain greater genetic variation than crops because they have not passed through the genetic bottleneck of domestication; therefore, they provide a reservoir of genetic variation for improving crops and thereby it's anobvious choice for meeting contemporary food security demands.

The significance of wild species as a critical resource for future food security has not been fully recognized despite their potential as gene donors for crop improvement was clearly recognized much early in the 1920s and 1930s by the renowned Russian plant geneticist Nicolai Vavilov. Climate change is predicted to bring about increased global temperature, along with associated carbon dioxide (CO<sub>2</sub>) increase, altered pattern of rainfall and salinity, emergence of new pest strains and diseases (Tester and Langridge, 2010). The timing and pattern of rainfall is also predicted to change although uncertainty exists about the expected degree of changes. These predicted climatic changes are expected to have fairly widespread impacts on agriculture for example, rice flowers show increased sterility at high temperatures, maize is very sensitive to drought at the time of flowering, wheat senescence starts earlier and

faster under warmer conditions etc (Lobellet *al.*,2012). To meet these challenges, plant breeders need all the genetic diversity available in the form of germplasm, landraces and wild species. Some of the genetic diversity may be found in landraces, traditional/farmer's varieties that are still being cultivated by farmers around the world. However, a much wider spectrum of biodiversity is found in wild plant species that are closely related to domesticated crops. They are of key importance to breeding efforts that help in adopting to climate change. There are about 10 000 to 80 000 comestible plants on earth, but only 29 species account for 90% of our food products. Considering its rich spare of plant genetic resources, Bangladesh is no better off in the use plant genetic resources, if not worse off. The country needs to give an crucial attention towards conserving its reserve of genetic resources, which are on a rapid wane, not only for future but also for their immediate use in crop improvement, for use as fuel and fibre, for nutrition and medecine. What is a wild plant today can generate to be an important plant tomorrow with our new knowledge about its essential value in food and nutrition, in medicare, its new use through new processing technology; the contributions that plant genetic resources make in keeping a sound environment and in sustaining the ecosystem not withstanding (Razzaque and Hossain, 2007).

**Objective:**

- To assure sustainable crop production.
- To ensure conservation of genetic variation.

## **CHAPTER 2**

### **MATERIALS AND METHOD**

The seminar paper is absolutely a review paper. Therefore, no specific methods of studies are followed to prepare this paper. All the information and data collected from secondary sources. The title is selected with the consultations of my major professor. The seminar paper has been prepared by reciting different books, journals, booklets proceeding and consultancy report which are available in libraries of BSMRAU and internet. Some information is also collected from the website of BARI, BRRI and some private agricultural organizations. Maximum necessary supports have been taken from internet searching. Finally, this seminar paper was prepared with the consultation of my respective major professor and honourable seminar course instructors.

## CHAPTER 3

### REVIEW OF FINDINGS

Plant genetic resources are the reflection of total genetic diversity which include the landraces, primitive forms, weed races and most specially wild species. In future we have to depend on wild species and wild relatives for their broad genetic base. Crops are often improved or better protected by using genes from wild species (Ulukan, 2011). Wild species as genetic resources can be used in breeding programs to produce new crops and new uses for existing crops, to meet breeding objectives for sustainability of crop production, and to ensure the entire world's people benefit from crop improvement through enhanced food security and quality. The key to thriving crop improvement is a continued supply of genetic variability and beneficial traits contained in this diversity (Heslop-Harrison, 2002). The process of introducing genetic diversity from wild species into cultivars for food security requires a significant amount of time, resources, and human capacity. It is a long process, starting in the wild, where genetic resource experts, botanists, and taxonomists locate, identify, and collect propagating material. This then passes through the hands of genebank curators for conservation and characterization; geneticists, agronomists, and pathologists for further characterization and evaluation, trait and gene discovery, and validation; and finally pre-breeders, or germplasm enhancement programs, and breeders for variety development. These products then feed into seed systems (both formal and informal) and eventually end up in farmers' fields (Dempewolf *et al.*, 2012).

#### **3.1 Beneficial Traits from Wild Species to Crop Gene Pools**

##### **3.1.1 Resistance to biotic stresses**

Pests and diseases are the main causes of low productivity in cultivated plants. For biotic stresses, resistance is either not available in cultivated species or is available only at very low levels. On the contrary, very high levels of resistance to pests and diseases have been reported in many wild relatives of cultivated species, and in some case attempts to transfer this resistance have been successful. Some wild species that carry biotic stress resistant gene are mentioned in Table 1.

**Table 1. Representatives of some important plant wild species carrying traits of biotic stress resistance**

Species	Trait	Genes	Utilization	Reference
<i>Agropyronelongatum</i>	rust resistance	<i>Lr24</i>	marker validation in wheat for leaf rust resistance	(Gupta <i>et al.</i> , 2006)
<i>Avenabarbarata</i>	crown rust resistance	<i>Pc39, Pc45</i> and <i>Pc94</i> genes	Seedling resistance	(Cabral and Park, 2014)
<i>Elymusrepens</i>	<i>Fusarium</i> head blight resistance	Not assigned	Wheat introgression line production	(Zeng <i>et al.</i> , 2013)
<i>Haynaldiavillosa</i>	powdery mildew resistance	Serine/threonine kinase gene <i>Stpk-V</i> on <i>Pm21</i> locus	Transferred to to wheat for <i>Pm</i> resistant line development	(Cao <i>et al.</i> , 2011)
<i>Triticummonococcum</i>	powdery mildew resistance	<i>Pm1</i>	Mapping of <i>Pm</i> resistance markers	(Yao <i>et al.</i> , 2007)

### 3.1.2 Tolerance to abiotic stresses

Drought, salinity, acidic soils, phosphorous deficiency, and variation in temperature are the major abiotic stresses contributing to the significant loss of production in cereal and legume crops. Many wild relatives have shown high levels of tolerance to these stresses, and some genes conferring these stress tolerances have been successfully transferred into cultivated species. Some wild species that are carrying abiotic stress tolerant gene are given below in Table 2

**Table 2. Representatives of some important plant wild species carrying traits of abiotic stress**

Species	Trait	Genes	Utilization	Reference
<i>Aegilopsunia risfata</i>	aluminum tolerance	ALMT1	Producing 3A, 3B, 3D wheat substitution lines	(Miller <i>et al.</i> , 1997)
<i>Spartina alterniflora</i>	salt tolerance	SaSce9	Salt tolerance after transferringArabidops is	(Karan and Subudhi, 2012)
<i>Triticummon ococcum</i>	heat tolerance	Heat shock protein (HSP) gene	Controlling thermal tolerance	(Vierling and Nguyen, 1992)
<i>Phleumprate nse</i>	freezing tolerance	fructosyltransferae (FST) genes	Fructan accumulation for winter hardiness	(Yoshida and Tamura, 2011)
<i>Brachypodiu mdistachyon</i>	drought tolerance	sucrose synthase gene, glucose- 1phosphate adenyltransferae gene	Acting as an osmoportectan sugar biosynthesis	(Verelstet <i>al.</i> , 2013)

### 3.1.3 Cytoplasmic male sterility

Cytoplasmic male sterility (CMS) is a maternally inherited trait that prevents plants from producing normal pollen and is used as a tool to generate large-scale commercial F1 hybrid seeds in many crops. This scheme has been more often used for developing commercial hybrids in cross-pollinated crops (maize, sorghum, and pearl millet) to exploit hybrid vigor. Additional CMS sources and fertility restorer genes have been desirable since the Southern corn leaf blight (Bipolarismaydis) disease epidemic of the 1970s, which was precipitated by the wide-scale use of cms-T cytoplasm in the United States (Holley and Goodman, 1989). There are a few examples exist that demonstrate the potential of wild species as sources of cytoplasmic male sterility and nuclear restorer genes. CMS lines having cytoplasm from the wild relative *Oryza sativa* f. *spontanea* have been used widely for production of commercial hybrids in China (Yuan, 1993). In legumes, interspecific crosses between *Glycine max* and *G.*

soja have given rise to a cytoplasmic-nuclear male sterile line and its maintainer (Dwivedi *et al.*, 2008).

### 3.2 Wild Species for Crop Improvement

#### 3.2.1 Rice

Bacterial leaf blight caused by *Xanthomonasoryzaepv. oryzae* has been one of the most widely distributed and devastating rice disease worldwide. In 1990, the transfer of Xa21 gene from wild rice (*Oryzalongistaminata*) for resistance to bacterial blight in IR72 started the systematic use of wild rice gene pool. Wild rice, *Oryzarufipogon* has been utilized for blast resistant gene, Pi33 introgression into rice variety IR64, which in the most used rice blast resistant variety (Balliniet *al.*, 2007). Many more unique traits such as weed competitiveness, drought tolerance and ability to grow under low input conditions has been transmitted from *O. glaberrima* to *O. sativa* and combined with high yield to develop NERICA (New Rice for Africa), which is high yielding, drought, pest resistant and adjusted to the growing conditions of West Africa (Sarla and MallikarjunaSwamy, 2005). Apart from these there more valuable genes present in wild species of rice which can be transferred in cultivated rice variety, these are given below in Table 3.

**Table 3. Progress in the transfer of agronomically important genes from wild *Oryza* species into cultivated rice at IRRI**

Trait	Donor species
Grassy stunt resistance	<i>O. nivara</i>
Brown plant hopper resistance	<i>O. officinalis</i> ; <i>O. minuta</i> ; <i>O. latifolia</i> ; <i>O. australiensis</i>
White-backed plant hopper resistance	<i>O. officinalis</i>
Cytoplasmic male sterility	<i>O. perennis</i> <i>O. glumaepatula</i>
Tungro resistance	<i>O. rufipogon</i>

(Source: Brar, 2005)

#### 3.2.2 Wheat

*Triticumdicocoides* has been found to be a rich source for *Fusarium* head blight resistance which is one of the finest known member in wild emmer wheat family (Oliver *et al.*, 2007). Krugmanet *al.* (2011) highlighted the significance of *Triticumturgidum ssp. dicocoides* for drought tolerance genes, metabolites and high protein content gene. Sohailiet *al.* (2011) have reported that diploid wheat progenitors *Aegilopstauschii* for drought and salt tolerance in wheat and *Aegilopscrassa* utilized for greater physiological performance under water scarcity. *Aegilopstauschii* show resistance to Hessian fly, *Aegilopsgeniculata* for powdery

mildew resistance and also for barley yellow dwarf virus resistance, *Aegilopsvariabilis* show nematode resistance that have contributed towards wheat production improvement (Yumurtaci, 2015).

### **3.2.3 Maize**

Blight resistant genes transmitted from wild relative of Mexican maize (*Tripsacum dactyloides* L.) into commercial corn lines is a well-known achievement story which resolute corn blight of U.S.A. and Prischmann *et al.* (2009) introduced genes from *Tripsacum dactyloides* into cultivated corn for resistance to rootworm.

### **3.2.4 Brassicas**

Sexual incompatibility barriers between different Brassica species make gene introgression difficult from crop wild relatives into cultivars. However, these barriers have been overcome by using somatic hybridization via protoplast fusion. Wild black mustard (*Brassica nigra*) signifies wild gene reservoir to improve cultivated Brassicas against several pathogens. Interspecific allopolyploids between *B. fruticulosa*, *B. nigra* and *B. rapa* facilitate the use of wild relatives in Brassicas as bridge species (Chen *et al.*, 2011).

### **3.2.5 Sunflower and Sesame**

The wild species of sunflower, *Helianthus argophyllus* is used for tolerance to drought stress in sunflower and *Helianthus paradoxus* for tolerance to salinity (Miller and Seiler, 2003). Gene sources have been identified in *Sesamum laciniatum* resistant to leaf phyllode, *S. malabaricum*, *S. mulyanum* and *S. alatum* resistant to powdery mildew.

### **3.2.6 Pulses**

Among wild species of pulses, *Vignatibolata*, *V. mungo* var. *sylvestris*, *V. radiata* var. *sublobata* have provided resistance to yellow mosaic virus. *V. vexillata* has high protein and resistance to cowpea pod sucking bug and bruchids and it is crossable with *V. unguiculata* and *V. radaita*. Cytoplasmic male sterile systems were established for pigeon pea manipulating the cross-pollination mechanism and using wild *Cajanus* species (Mallikarjuna *et al.*, 2012).

### **3.2.7 Vegetables**

The wild relatives of vegetable crops constitute an increasingly important resource for improving vegetable production and critical resource in ensuring food security. Late blight caused by the *Phytophthora infestans* is the most important disease of potato production worldwide as exemplified by the Irish potato famine in the mid-nineteenth century. Late blight resistance genes were introgressed from the wild species *Solanum demissum*, *S. stoloniferum* and the cultivated *S. tuberosum* ssp. *andigena* and *S. phureja* into

common potato in different parts of the world (Bradshaw *et al.*, 2006). Similarly in tomato, more than 40 resistance genes have been derived from *Solanum pennellii* var. *pennellii*, *S. cheesmanii*, *S. peruvianum* and *S. pimpinellifolium* for traits such as better soluble solid content, fruit color, and adaptation to harvesting (Rick and Chetelat, 1995). Among cucurbits, wild *Cucumis ficifolius* exhibited absolute resistance to cucumber green mottle mosaic virus, *Fusarium* wilt and high level resistance to downy mildew.

**Table 4. Crop wild species in different vegetable crops utilized for their genetic improvement**

Vegetable crop	Wild species	Important traits	References
Tomato	<i>Solanum</i>	Bacterial wilt,	Hanson <i>et al.</i> , 1998;
	<i>pimpinellifolium</i>	Bacterial spot,	Yang and Francis., 2007
	<i>S. peruvianum</i>	Tomato leaf curl virus,	Kasrawi, 1989;
	<i>S. pimpinellifolium</i>	High lycopene	Pilowsky and Cohen, 1990;
	<i>S. chilense</i>	content,	Zamir <i>et al.</i> , 1994
	<i>S. habrochaites</i>	Salt tolerance.	Hanson <i>et al.</i> , 2000
	<i>S. pimpinellifolium</i>		Fernández-Ruiz <i>et al.</i> , 2002
Brinjal	<i>Solanum linnaeanum</i>	<i>Verticillium</i> wilt,	Liu <i>et al.</i> , 2015;
	<i>S. torvum</i> ,	Powdery mildew,	Bubici <i>et al.</i> , 2008
	<i>S. sisymbriifolium</i>	Bacterial wilt,	Behera and Singh, 2002
	<i>S. indicum</i> ,	Fruit and Shoot Borer,	Isshiki and Kawajiri, 2002
	<i>S. violaceum</i> ,	Male sterility	
	<i>S. aethiopicum</i> ,		
	<i>S. incanum</i>		
Cucumber	<i>Cucumis hystrix</i>	Gummy stem blight,	Chen <i>et al.</i> , 2008
	<i>C. metuliferous</i>	Downy mildew, Cucumber mosaic virus (CMV-C), Zucchini yellow mosaic virus (ZYMV)	Norton <i>et al.</i> , 1980

### **3.3 Limitation to use of wild species**

There are two major problems that limit the use of wild species . First, because wild relatives are generally more difficult to maintain and to regenerate, so they have been neglected. The second problem is that basic information to aid the handling and use of accessions is often lacking. Descriptor lists designed for cultivated species may not apply. A thorough biosystematics understanding of the pattern of genetic variation, both nuclear and cytoplasmic, is needed to rationalize the testing and breeding of wild material (Brown and Marshall, 1986).

Hybrid inviability and sterility is often discussed in reviews (Stalker, 1980) is the failure to get progeny or subsequent generations from attempted crosses. In Glycine, hybrids between soybean and perennial Australian Glycine earlier frustrated by inviability (Ladizinsky *et al.*, 1979), were eventually obtained first at the tetraploid level (Broue *et al.*, 1982; Newell and Hymowitz, 1982) and second, at the diploid level (Grant *et al.*, 1986) by embryo culture. These hybrid plants are perennial and sterile. Colchicine doubling of the chromosome number has so far failed to restore their fertility.

A major limiting factor in the use of wild relatives is the accurate delineation of attributes which are present in wild species and which it would be beneficial to transfer. Recognition of desirable characters comes from familiarity with the current breeding objectives, a knowledge of what is already available in the cultivated species, and what attributes the wild relatives possess, as well as the imagination to perceive new options. It is concluded that phenotypic evaluations of wild species should be critically considered to determine whether sources of the trait are already plentiful in the cultivated gene pool, and whether the trait is likely to show marked pleiotropy or epistasis when transferred (Brown and Marshall, 1986).

### **3.4 Approaches to enhance utilization of wild species in crop improvement**

Prebreeding is a key step in linking the valuable traits of wild species to modern variety development by providing breeders with wild genetic diversity in a more immediately usable form. Prebreeding is a useful ways to gain desirable trait for crop improvement (Dempewolf *et al.*, 2017)

#### **3.4.1 Using cloned genes from wild species to produce transgenics:**

Many wild species with desirable genes are either totally cross-incompatible with cultivated species or require complex bridge crossing and/or embryo rescue techniques for crosses to be successful. In practice this results in a long struggle to incorporate and retain desirable genes while eradicating linkage drag and deleterious genes from the wild accession. Traditional backcross breeding can be used for this process but is generally a tedious, time-consuming,

Molecular cloning and subsequent transfer through transformation has been suggested as the method of choice to overcome the problems associated with direct introgression. One notable transfer of a wild species gene through transgenesis to a set of cultivars is for bacterial blight, which is one of the most destructive diseases of rice. In this case, the broad-spectrum resistance gene Xa21 from *Oryzalongistaminata* (Khush *et al.*, 1990) was cloned through a map-based approach (Song *et al.*, 1995) and transferred through Agrobacterium-mediated transformation to five rice cultivars (Zhai *et al.*, 2000) and a widely used hybrid restorer line in China (Zhai *et al.*, 2001). In this case the transgenic lines displayed high levels of broad-spectrum resistance to the disease and maintained elite agronomic traits of the parents. Clearly, the transgenic approach can accelerate the introgression of the new alleles from wild relatives to crop species compared to conventional breeding, which in many cases can be a slower and less precise method due to linkage drag. The use of transgenic transfer of wild species genes could therefore increase the genetic diversity available for crop improvement.

#### **3.4.2 Marker-aided introgression**

Molecular marker-based genetic linkage maps have delivered a method to monitor and simplify interspecific gene transfer and to mitigate linkage drag, thus improving the prospects for fruitful introgression of desirable genes from wild species. It has been concluded that by combining wild species crosses with molecular genetic linkage maps, it could be possible to identify and selectively introgress new alleles from wild species that normally were not considered to be sources of useful variation. Expanding on this, Tanksley and Nelson (1996) suggested advanced backcross and quantitative trait loci (QTL) analysis as an efficient breeding methodology for the simultaneous discovery and transfer of valuable QTL from unadapted germplasm into elite breeding lines. Using this breeding scheme, unique wild gene introgressions for improved fruit yield, size, weight, shape, and firmness were transferred into cultivated tomato (Fulton *et al.*, 1997; Bernacchi *et al.*, 1998).

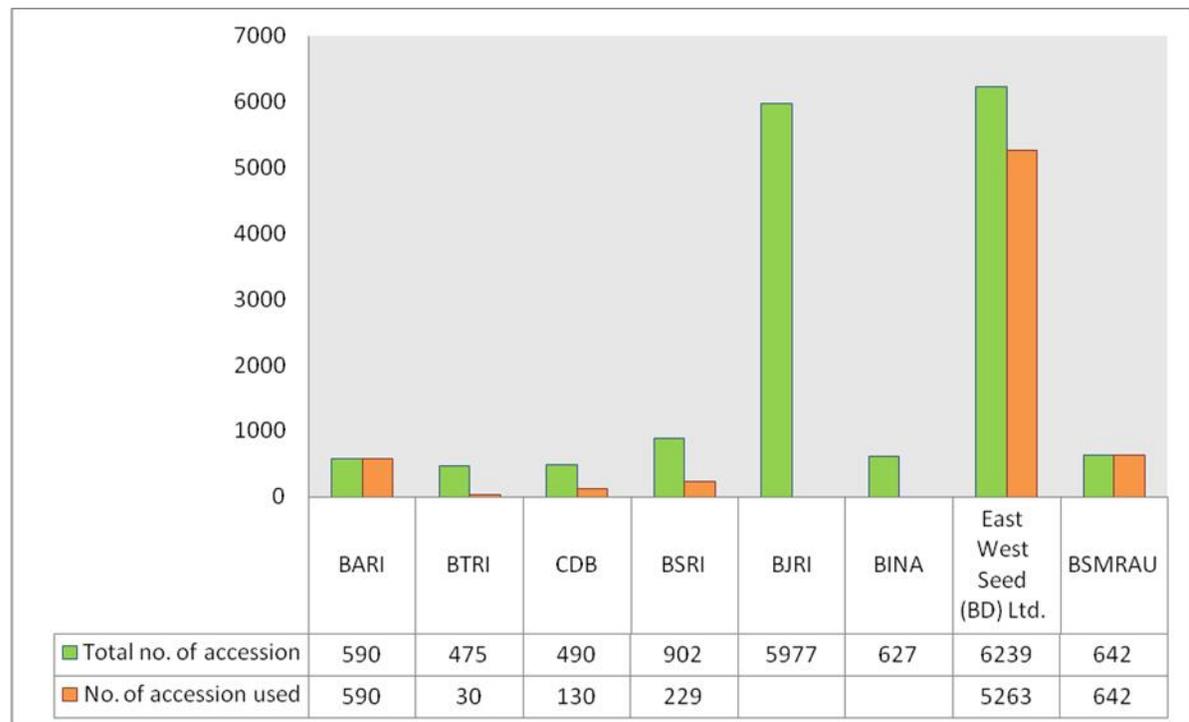
#### **3.4.3 Developing exotic genetic libraries**

In addition to providing a resource for the discovery and characterization of genes that underlie traits of agricultural value, (Zamir, 2001) highlighted the immediate utility of the introgression lines for the enhancement of agricultural productivity of modern crop varieties and that the exotic libraries should consist of a set of lines, each of which carries a single, defined chromosome segment that originates from a donor species in an otherwise uniform elite genetic background and that provides systematic coverage of the entire genome. Once such permanent genetic resources have been generated for diverse donor accessions, they can be screened for multiple phenotypic characteristics to identify alleles of economic

importance. Then materials will be readily available to other researchers interested in using the exotic genetic libraries in applied genomics and plant breeding.

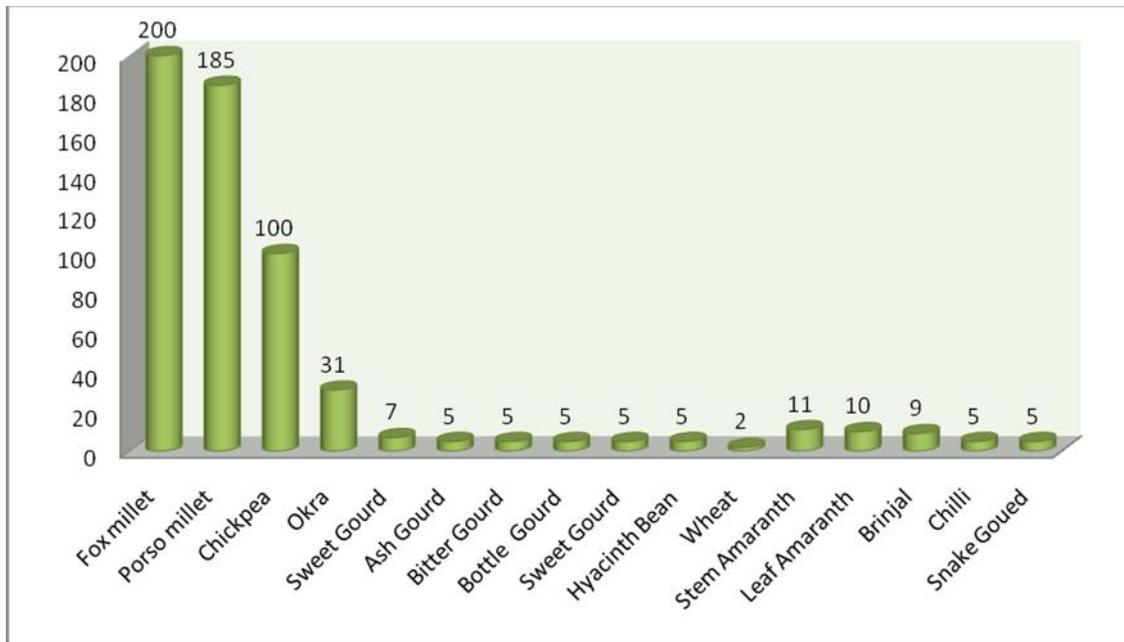
### 3.5 Status of the Use of Plant Genetic Resources in Bangladesh

Characterization and evaluation work is still in preliminary phases in Bangladesh. Studies on core collections should be emphasized. However many organization have used number of germplasm for breeding, seed multiplication like the Bangladesh Agricultural Research Institute(BARI) has 590 accessions, Bangladesh Tea Research Institute (BTRI) has used about 30, Cotton Development Board (CDB) has utilized about 130 accessions, Bangladesh Sugarcane Research Institute (BSRI) 229, Bangladesh Jute Research Institute (BJRI) 2915, East West Seed (Bd) Limited Bangladesh 5263 and Bangabandhu Sheikh MujiburRahman Agricultural University (BSMRAU) has used 547 accessions (Razzaque and Hossain, 2007).

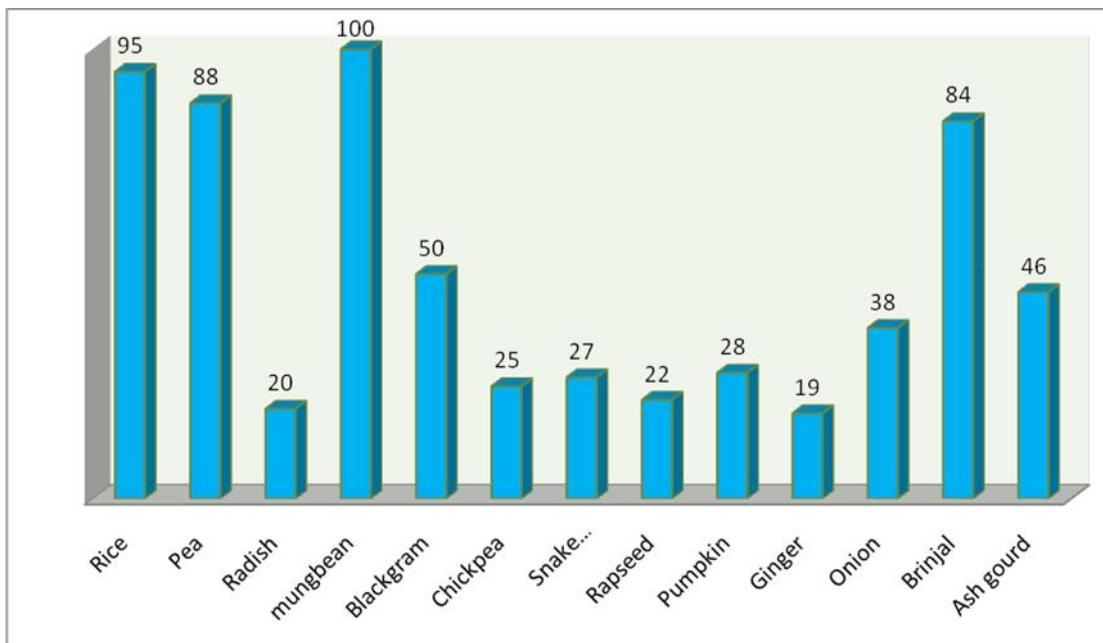


**Fig 1. Use of plant genetic resources by different stakeholder organizations.** (Source: Razzaque and Hossain, 2007).

BARI and BSMRAU have used some genetic resources of different crops for breeding purpose and for seed enhancement to conserve the resources, these are presented through Fig 2. and Fig 3. respectively.



**Fig 2. No. of accessions of different crops used by BARI.** (Source: Razzaque and Hossain, 2007).



**Fig 3. No. of accessions of different crops used by BSMRAU.** (Source: Razzaque and Hossain, 2007).

### 3.6 Plant Biodiversity Conservation Strategies

Management of plant biodiversity needs a well programmed massive evaluation of extended territorial lands. So far, extinction of many plant species including agronomically important crops may cause irreplaceable resource problem. The international framework for crop wild relative conservation strategy covers in situ as well as ex situ collections. Major ex situ conservation methods are i) Seed genebanks, ii) Field genebanks, iii) Tissue culture, iv) Cryopreservation, v) Pollen storage, vi) Botanic Gardens. However, ex situ conservation needs more financial support and seed viability testing, it is accepted as a convenient way for preserving inheritance of plant species for long years. Major and minor crop genetic resources are under the pressure of genetic erosion and this turnover seriously degrades the important crop gene pool (Khoury *et al.*, 2014). In the different regions of the world, there are several institutes and research centers working at national and international level. They work as providers of important cultivars, landraces and crop wild relatives. For example, in CIMMYT (El Batan, Mexico), there is a large collection of maize seeds collected from 64 different countries including landraces, wild relatives of maize (*Teosinte and Tripsacum*). Moreover, United States of Department of Agricultural (USDA) Service is one of the fundamental collection centers for major crops and their close relatives. Also, there is a large ex situ seed conservation facility that was active as Turkish Seed Gene Bank and supported by Ministry of Food, Agriculture, and Livestock of Turkey. In this collection, wild wheat relatives and landraces reserved approximately 10% of all collection (Ozbek, 2014). In 2010, The Global Partnership for Plant Conservation Strategy released an updated conservation plan for threatened plant species. There are different precautions released by this international association that implies monitoring of plant resources, maximizing the capacity of target nations, supporting new partnerships between countries, assisting the development of effective plant conservation methods and attract the public attention. There is a separate seed storage center (Svalbard Global Seed Vault) working as a reservoir service for future food security. According to the data obtained from the last updates (Yumurtaci, 2015), this seed vault holds more than 820,000 seed samples covering staple food crops and their wild progenitors. This center supports to the conservation of valuable seed sources with a partnership by accepting seeds from all over the world, and samples are strictly protected under the material security rules. These actions with future strategic conservation plans will be strengthen the seed banking and sustainable conservation of valuable plant materials.

## **CHAPTER 4**

### **CONCLUSION**

- Crop wild species supports the genetic improvement of crops in several ways by transferring the desirable gene into cultivated crop and make the crop resistant against the biotic and abiotic stress and also by exploiting cytoplasmic male sterility trait into cultivated species. Utilization of wild species can overcome the challenges arising from pest emergence, climate change to ensure sustainable crop production.
- For maintain genetic variability it is essential to conserve the wild species as an important part of genetic resources. Evaluation and phenotypic characterization of wild species should be done for efficient conservation and also for easy assessment of desirable trait which is to be transferred into cultivated species.

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