

A SEMINAR PAPER ON
**Plant Genetic Resources: The Basis for Food Security and Sustainable
Agricultural Development**

Course Title: Seminar

Course Code: GPB 598

Term: Summer, 2018

Submitted to

Course Instructors

1. Dr. Md. Mizanur Rahman
Professor
2. Dr. A. K. M. Aminul Islam
Professor
3. Dr. Md. Rafiqul Islam
Professor
4. Dr. Dinesh Chandra Shaha
Assistant Professor

Major Professor

Dr. Nasrin Akter Ivy
Professor

Department of Genetics and Plant Breeding

Submitted by

Urmi Rani Shaha

MS Student

Reg. No.: 13-05-2983

Department of Genetics and Plant Breeding

BANGABANDHU SHEIKH MUJIBUR RAHMAN AGRICULTURAL UNIVERSITY
SALNA, GAZIPUR 1706

PLANT GENETIC RESOURCES: THE BASIS FOR FOOD SECURITY AND SUSTAINABLE AGRICULTURAL DEVELOPMENT

URMI RANI SHAHA

ABSTRACT

Plant genetic resources are the biological basis of food security. Plant Genetic Resources encompasses the diversity of genetic material in both traditional varieties and modern cultivars, as well as crop wild relatives and other wild plant species used as food. These resources serve as the plant breeder's most important raw materials and farmers most essential input. Some examples were found that PGR contributed to modern diets. Over 60 wild species were identified to have been used for the 13 crops, with over 100 beneficial traits having been derived from PGR. Today's bread wheat (*Triticum aestivum*) is developed from different wild relatives. Other major crops like rice, maize, potato is also derived from landraces or wild taxa. A major share of this productivity increase will have to come from the use of PGR to produce higher yielding, more nutritious, more stable and more eco-efficient crop varieties. Global awareness has grown for conservation of these valuable resources for the benefit of the society and for posterity. There are broadly 2 types of plant genetic resources conservation. These are *in-situ* conservation and *ex-situ* conservation. There are approx. 1723,378 genebanks in the world maintained by different organizations. In Bangladesh approximately 30,000 accession are preserved by different stakeholders. The total number of accessions conserved ex situ worldwide reaching 7.4 million.

Key words: In-situ, Ex-situ, Prebreeding, Wild relatives, Gene banks

TABLE OF CONTENTS

SUBJECTS	PAGE
ABSTRACT	i
TABLE OF CONTENTS	ii
LIST OF TABLES	iii
LIST OF FIGURES	iv
I. INTRODUCTION	1-3
II. MATERIALS AND METHOD	4
III. REVIEW AND DISCUSSION OF THE FINDINGS	5-21
IV. CONCLUSION	22
REFERENCES	23-25

LIST OF TABLES

NO.	TITLES OF TABLES	PAGE
1	Examples of nutrient composition within varieties	6
2	Summary of international flows of rice ancestors in selected countries	9
3	Important gene in wheat that were found in related species	10
4	Use of crop wild relatives in the past 20 years in released cultivars of 13 crops of international importance	13
5	Global germplasm holdings in terms of type of accession (mean percentage) for groups of crop	16
6	Collections of germplasm accessions of some major crops worldwide	17
7	CGIAR's germplasm holding	18
8	No. of accession held up by different stakeholders in Bangladesh up to 2011	21

LIST OF FIGURES

NO.	CAPTIONS OF FIGURES	PAGE
1	Number of undernourished people in the world at present	5
2	Confirmed and potential breeding uses of 10 crops with most breeding use citation in literature	7
3	Number of breeding uses in each year between 1930 and 2016 (black line) and scatter plot smoother (blue curve)	8
4	Contribution of <i>Tripsacum</i> to maize improvement	12
5	Growth in nationally designated protected areas (1928-2008)	14
6	Contribution of major crop group in total <i>ex-situ</i> collection	15
7	Ex situ holdings in major gene banks in the world	19
8	No. of accession used by different stakeholder organizations up to 2011	21

CHAPTER I

INTRODUCTION

Agriculture plays a key role in feeding millions and protective our natural resources and also the atmosphere. There's associate degree calculable 300,000 species of upper plants that represents the plant diversity. However, solely regarding 7000 species are domesticated and cultivated by humans over the century for food, fodder and feed. However solely 30 'feed the world', with the 3 major crops being maize (*Zea mays*), wheat (*Triticum aestivum*) and rice (*Oryza sativa*) (Wang, 2011). Nature has evolved a tremendous intra-specific genetic diversity in crop plants and their wild relatives. It's this diversity at inter specific species that enables for the cultivation of crops across completely different regions and in several things admire weather and soil conditions. These priceless and irreplaceable plant resources are referred to as plant genetic resources (PGR). Russian geneticist Nikolai Vavilov, considered by some as the father of plant genetic resources, realized the value of genetic variability for breeding and collected thousands of seeds during his extensive travels to establish one of the first gene banks (Ford-Lloyd and Jackson, 1986). The term genetic resources was coined by Otto Frankel and Erna Bennett (Frankel and Bennett, 1970). The utilization of plant genetic resources (PGR) in crop improvement, followed by adoption, cultivation and consumption or promoting of the improved cultivars by farmers, is utmost sustainable ways that to conserve valuable genetic resources for the long haul, and at constant time to extend agricultural production and food security. Plant Genetic Resources for Food and Agriculture is that the most significant resource for any country of the planet. Genetic resources will be defined as all materials that are available for improvement of a vascular plant species (Katna and Sood, 2015). PGR as the generative or vegetative propagating material of cultivated varieties (cultivars) in current use and new developed varieties, obsolete cultivars, primitive cultivars (landraces), wild and weed species, close to relatives of cultivated varieties and special genetic stocks as well as elite and current breeder's lines and mutants (Hammer and Yeklu, 2008). The primary use of plant genetic resources dates to over 10,000 years ago. When farmers selected from the genetic variation they found in wild plants to develop their crops. Plant genetic resources embrace all our agricultural crops and a few of their wild relatives as a result of they possess valuable traits. As human populations touched to totally different climates and ecosystems, taking the crops with them, the crops tailored to the new environments, developing, maybe, genetic traits providing tolerance to conditions like drought,

water logging, frost and extreme heat. These traits and therefore the physical property inherent in having wide genetic variability are necessary properties of plant genetic resources. Plant genetic diversity is vulnerable to “genetic erosion”, the loss of individual alleles/genes and of combinations of alleles/genes, such as those found in locally adapted landraces. Plant genetic diversity is prone to “genetic erosion”, the loss of individual alleles/genes and of mixtures of alleles/genes, admire those found in regionally tailored landraces. In step with Food and Agriculture Organization, replacement of native varieties by modern varieties leading to reduction of the light range of cultivars is that the main reason for genetic erosion. This is intensified by the elevation of new pests, weeds and diseases, environmental degradation, urbanization and land clearing. To abstain genetic erosion it necessary to conserve plant genetic resources properly. According to The State of Food Insecurity 2001 “Food security is a situation that exists when all people, at all times, have physical, social and economic access to sufficient, safe and nutritious food that meets their dietary needs and food preferences for an active and healthy life. PGRs are a strategic resource and lie at the heart of sustainable agriculture. PGR, the only source of plant genetic diversity, provides valuable traits needed for meeting the challenges of adapting crop varieties. An individual genotype with apparently good-for-nothing set of characters these days might suddenly become worthy tomorrow due to ever-changing weather conditions or outbreaks of disease. Therefore, it's been long accomplished that we tend to “conserve” all the diversity we've got. Conservation is the management, preservation and use of known genetic resources to meet the needs and aspiration of generation to come. There are broadly 2 types of plant genetic resources conservation. These are *in-situ* conservation and *ex-situ* conservation. The modern intensive agriculture entails uniformity and consequently contains a narrow genetic base. The modern intensive agriculture calls for uniformity and consequently has a narrow genetic base. In contrast, traditional agriculture had large number of diverse landraces. Bangladesh constitutes a large part of the South Asian Mega Centre of genetic diversity, sharing with India. The landscape of Bangladesh is the abode of some 5000 species of vascular plants (Khan, 1991). There are more than 500 species of medicinal plants, 130 species of fiber resources (both wild and cultivated), 18 species of bamboo. It is the secondary center of origin of major crops like rice, a number of vegetables like eggplant, the cucurbits, beans, fruits like jackfruit, banana, mango and citrus, spices like chili, ginger and turmeric, root crops like taros and yams, etc. Considering its wealthy reserve of plant genetic resources, Bangladesh isn't any more contented within the use plant genetic resources, if not worse off. Bangladesh needs to pay an imperative attention towards preserving its reserve of genetic resources, for posterity, for

their immediate use in crop improvement, to be used as fuel and fiber & for nutrition and Medicare. Global awareness has grown for conservation of these valuable resources for the benefit of the society and for posterity. To conserve the diversity found among species of cultivated plants, specialists set a technique that combines ex situ conservation (storing diversity in gene banks) with in situ on-farm conservation in matching agro-ecosystems for future accessibility to make sure food security and sustainable agriculture.

Objectives

- ✓ To review the role and contributions of plant genetic resources for food security and sustainable agricultural development.
- ✓ To highlight the status of plant genetic resources conservation and its utilization.

CHAPTER II

MATERIALS AND METHODS

This is as a whole, a review paper. All data and information are adopted as a secondary data. This review paper has compiled through an exclusive going through different books, booklets, articles, proceedings, thesis, Journals. For collecting recent information I visited different websites through internet. Valuable information and kind consideration has been received through personal contact with my honorable major professor and other resource personal. After collecting necessary information, it has been compiled and arranged chronologically for better understanding and clarification.

CHAPTER III

REVIEW OF FINDINGS

The majority of food-insecure and undernourished people live in rural areas. They are most numerous in Asia and Sub-Sahara Africa. Seven countries comprising Bangladesh, China, the Democratic Republic of the Congo, Ethiopia, India, Indonesia and Pakistan account for 65 % of the world's food insecure people. Although the number of undernourished people has dropped by over 20% since 1992 (216 million fewer than in 1990-92) today there are 815 million people who do not have enough to eat. This is more than the 795 million in 2014, although still down from about 900 million in 2000. 98% of the world's undernourished people live in developing countries. Comprising Asia: 519.6 million, Sub-Saharan Africa: 243.2 million, Latin America and the Caribbean: 42.5 million (figure 1). Despite a significant progress in domestic food grain production in recent decades approximately 25 percent of the population in Bangladesh remains food insecure and 36 percent of children younger than 5 years of age suffer from stunting or chronic malnutrition (FAO and UNICEF, 2018).

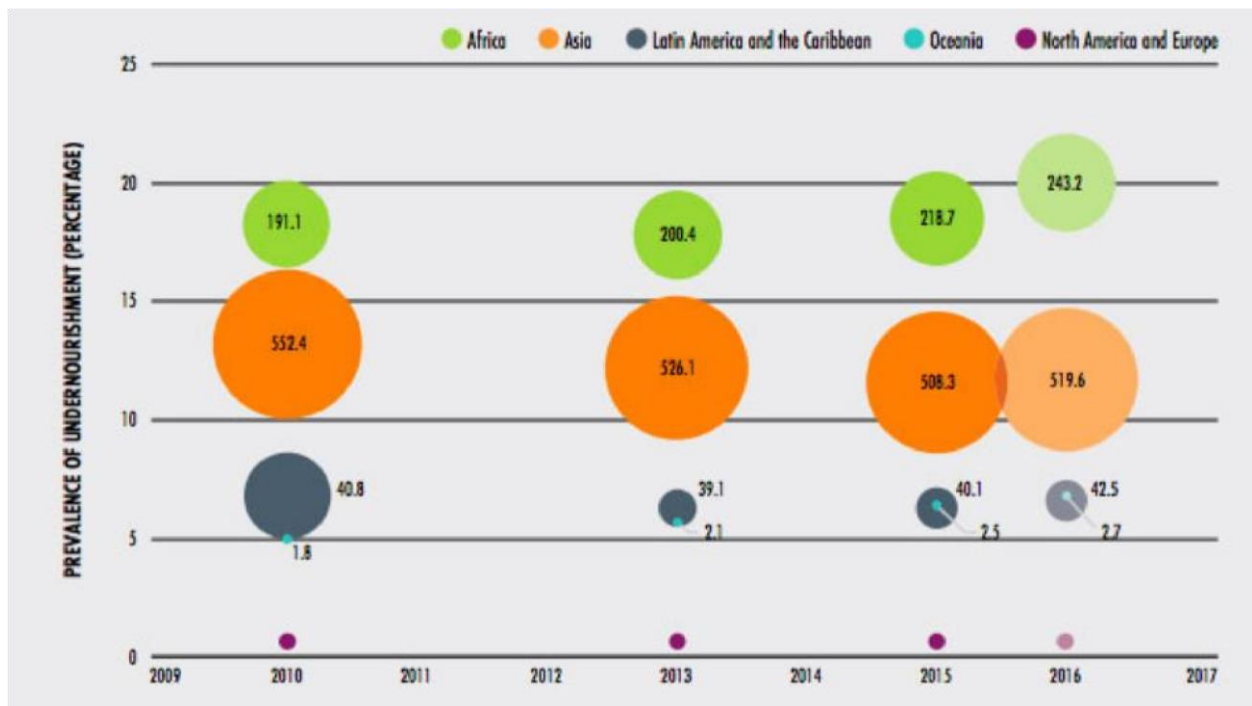


Figure 1. Number of undernourished people in the world at present.

(Source: Bruinsma, 2017)

The thousands of different crop varieties that have been developed over centuries by farmers and plant breeders, together with their wild relatives, carry the genes that will allow humanity to tailor its future plant food supply. The Food Pyramid shows that the groups of foods that should be consumed most to provide the body with protein, carbohydrates, vitamins and minerals are of plant origin, i.e. cereals and vegetables (table 1).

Table 1: Examples of nutrient composition within varieties

	Protein (g)	Fiber (g)	Iron (mg)	Vitamin C (mg)	BetaCarotenes (mcg)
Rice	5.6-14.6		0.7-6.4		
Potato	1.4-3.3	1.5-2.1	0.4-1.6	8-54	
Cassava	0.7-6.4	0.9-1.5	0.9-2.5	25-34	5-790
Sweet potato	1.3-2.1	0.7-3.9	0.6-14.0	24-35	100-23100
Taro	1.1-3.0	2.1-3.8	0.6-3.6	0-15	5-2040
Eggplant		9.0-19.0		50-129	
Mango	0.3-1.0	1.3-3.8	0.4-2.8	22-110	20-4320
Apricot	0.8-1.4	1.7-2.5	0.3-0.85	3.5-16.5	200-6939
Banana			0.1-1.6	2.5-17.5	42-2780

(Source: Burlingame *et al.*, 2009)

However, apart from energy intake nutrition is taken on new meaning in the 21st century. Emphasis is now given on foods which can promote well-being and health, and help to reduce the risk of diseases. Several terms are used to describe these bioactive compounds and the foods that contain them, e.g. phytochemicals, nutraceuticals or functional foods.

The extent of Crop Wild Relative (CRW) use varies widely among crops. Crops with long histories of breeding with their wild relatives continue to benefit the most from wild genetic diversity (figure 2). Rice (*Oryza sativa* L.), tomato (*Solanum lycopersicum* L.), and wheat in particular have sizable and well established prebreeding programs that focus specifically on CWR, leveraging advanced genomic tools and diverse characterization and evaluation data (Hajjar and Hodgkin, 2007; Kilian *et al.*, 2011; Nemeth *et al.*, 2015).

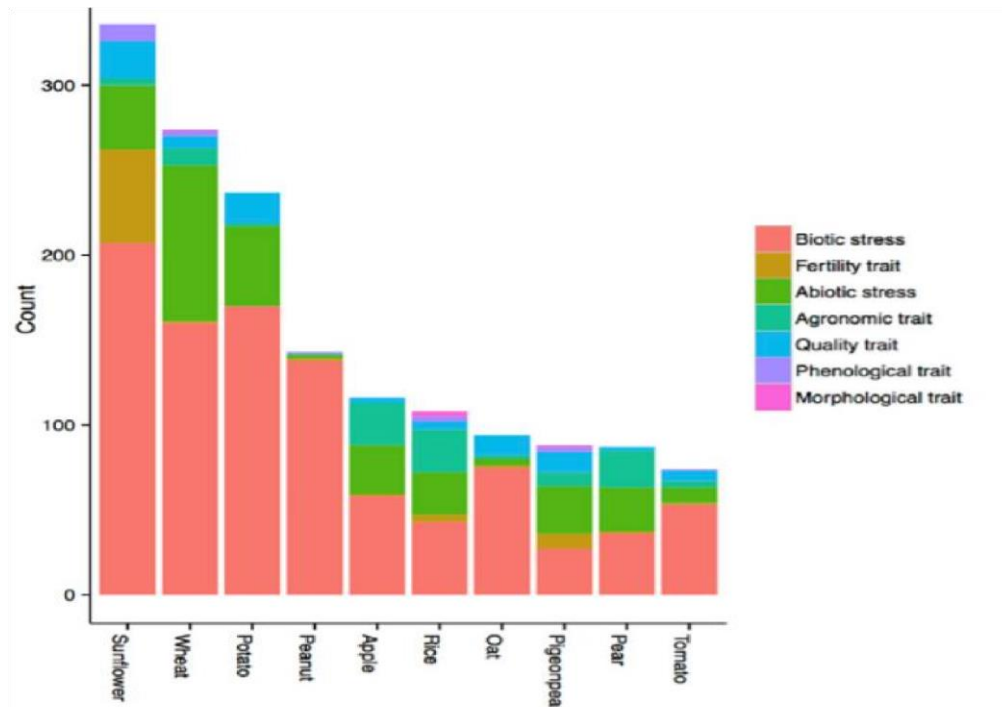


Figure 2: Confirmed and potential breeding uses of 10 crops with most breeding use citation in literature.

(Source: Hajjar and Hodgkin, 2007; Kilian *et al.*, 2011; Nemeth *et al.*, 2015).

As figure 2 clearly shows, sunflower (*Helianthus annuus* L.), wheat (*Triticum aestivum* L.), and potato (*Solanum tuberosum* L.) are the crops for which most breeding uses of CWR have been documented. For sunflower, the largest “use” category after biotic stresses are fertility traits, which is explained by the historically important role CWR have played in identifying sources for cytoplasmic-male sterility for the development of hybrid sunflowers. For wheat and potato, the abiotic stress categories appear to be particularly strong, indicating that, unlike for most other crops, CWR of potato and wheat appear to have been exploited quite significantly for abiotic stress resistances already.

For some crops, such as alfalfa (*Medicago sativa* L.), cassava, chickpea (*Cicer arietinum* L.), cowpea, finger millet, maize (*Zea mays* L.), and sweet potato, breeders have largely been able to find sufficient sources of resistance and variation for traits of interest within the domesticated gene pool. Wild species in each of these cases have been identified as potential sources for specific traits but are not sought by breeders for the widening of the genetic base of the crop per se. Even in the case of tomato, where the use of wild species in breeding is pervasive and most lines today host alleles from wild species.

The number of “use” references appears to be increasing over time, particularly since the turn of the century (figure 3). This indicates a trend towards an increased recognition in the scientific community of the value of these species. In 2011, the number of cited breeding uses peaked due to the release of the book series *Wild Crop Relatives: Genomic and Breeding Resources* (Dempewolf, 2017).

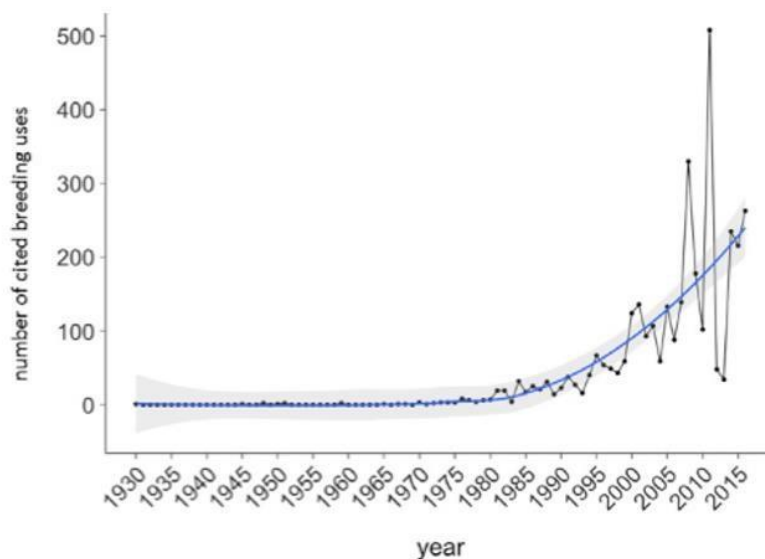


Figure 3: Number of breeding uses in each year between 1930 and 2016 (black line) and scatter plot smoother (blue curve).

(Source: Dempewolf, 2017).

In the following examples are given how plant diversity (can) contribute(s) to modern diets.

The development of rice varieties that are grown all over the world from the landraces. The landrace progenitor listed are for a country's commercially released varieties only; they do not include local landrace grown on a commercial basis by farmers (table 2).

Table 2: Summary of international flows of rice ancestors in selected countries

Country	Total landrace progenitors in all released varieties	Own landraces	Borrowed landraces
Bangladesh	233	4	229
Brazil	460	80	380
China	888	157	731
India	3917	1559	2358
Indonesia	463	43	420
Nepal	142	2	140
Nigeria	195	15	180
Pakistan	195	0	195
Philippines	518	34	484
Thailand	154	27	127
United States	325	219	106
Vietnam	517	20	497

(Source: Modified from Fowler and Hodgkin, 2004)

Contributions of Wheat Genetic Resources: Wheat belongs to the genus *Triticum*. *Triticum* arose from the cross (supposedly in nature) of two diploid wild grasses to produce tetraploid wheat, which today includes the many cultivated durum (pasta or macaroni) wheat's (*Triticum turgidum* L. var. Group *durum* Desf. $2n = 4x = 28$). Tetraploid wheat later crossed to diploid goat grass (*Triticum tauschii*) and gave rise to hexaploid, or bread wheat (*Triticum aestivum* L. $2n = 6x = 42$). There are hundreds of thousands of wild species, landraces, and local cultivars within the *Triticum* species that constitute the wheat's of the world. There are specific genes (table 3) that have made major impacts on wheat's can be directly traced to contributions from genetic resources.

Table 3: Important gene in wheat that were found in related species

Trait	Locus	Source
Disease resistance		
Leaf rust	Lr9	<i>Aegilops umbellulata</i>
	Lr18	<i>Triticum trimophaevii</i>
	Lr19	<i>Thinopyrum</i>
	Lr24	<i>Ag. elongatum</i>
	Lr25	<i>Secale cereal</i>
	Lr29	<i>Ag. elongatum</i>
	Lr32	<i>T. touschii</i>
Stem rust	Sr2	<i>T. turgidum</i>
	Sr22	<i>Triticum monococcum</i>
	Sr36	<i>Triticum trimophaevii</i>
Stripe rust	Yr15	<i>T. dicoccoides</i>
Powdery mildew	Pm12	<i>Aegilops speltoides</i>
	Pm21	<i>Haynaldia villosa</i>
	Pm25	<i>T. monococcum</i>
Wheat streak mosaic virus	Wsm1	<i>Ag. Elongatum</i>
Kernel bunt	Quantitative trait loci	<i>T. turgidum</i>
Pest resistance		
Hessian fly	H21	<i>S.cereale</i>
	H23, H24	<i>T. touschii</i>
	H27	<i>Aegilops ventricosa</i>
Cereal cyst nematode	Cre3	<i>T. touschii</i>
Quality traits		
Grain protein	Quantitative trait loci	<i>T. turgidum</i>
High protein		<i>T. dicoccoides</i>
Low molecular weight glutenins		<i>T. turgidum</i>

(Source: Sullivan, 2004)

Dwarfing Genes: “Norin 10,” a cultivar from Japan, provided two very important genes, Rht1 and Rht2 that resulted in the reduced height (or dwarf) wheat’s. Norin 10, in turn, inherited these genes originally from “Shiro Daruma,” a Japanese landrace (Foltz, 2009). The incorporation of the Rht1 and Rht2 genes into the new varieties that Borlaug ultimately was able to develop and deploy illustrated the difficulty of using genes from unadapted materials. But more importantly, it led to what is now been termed the “Green Revolution” (Pistorius, 1997; Sonnino, 2015). While it was originally thought that these genes contributed to higher production simply through reduced lodging via reduced height, it is now clear that they have other direct effects on yield via better nutrient uptake and tillering capacity (Pistorius, 1997; Esquinas-Alcázar, 2012).

Rust Resistance: Many of modern varieties have incorporated single major genes that convey resistance to specific races of the rust pathogen. Of >40 known genes for leaf rust resistance, 12 originated in species other than *T. aestivum* and *T. turgidum* while 20 of the 41 known genes for stem rust resistance originated in species other than *T. aestivum* and *T. turgidum* (Table 2) (Scarascia-Mugnozza and Perrino, 2002). Even among the genes originating from *T. aestivum*, many come from landraces.

Veery Wheat’s: Genetic resources have contributed more than single genes to crop improvement efforts. Perhaps the most important of these is the 1B/1R translocation that was identified as a simple transfer between rye and wheat in the former Soviet Union cultivar “Kaukaz.” The 1B/1R translocation, which carries a number of genes from rye, confers resistance to various diseases (fungal and viral pathogens) and adaptation to marginal environments. This translocation has been deemed so important that it has been incorporated into >60 wheat varieties, including the prominent Veery lines, that occupy >50% of all developing country wheat area, almost 40 million hectares (Scarascia- Mugnozza, 1995).

Yield Potential: Research at CIMMYT has led to the development of >600 new synthetic wheat’s, crosses between various durum wheat’s and *T. tauschii* accessions. Many of these crosses have produced rapid improvements in important characteristics, including disease resistance, abiotic stress tolerance, and yield.

Use of Genetic Resources in Maize Improvement

Although $\approx 50,000$ accessions of maize exist in germplasm banks around the world (Visser, 2010). While innumerable sources of exotic maize remain untapped for crop improvement, wild relatives are an excellent and robust source of novel characteristics have received notable attention. Of particular interest are the species of *Teosinte*, considered by some to be the most likely progenitor of domesticated maize (Sonnino, 2016), although the species has clearly differentiated into various races, species, plant habits (annual and perennial), and into two ploidy levels ($2n$ and $4n$). The specific genes and alleles that *Teosinte* could contribute to maize improvement. Also the species of *Tripsacum*, yet more distant relatives to maize, also offer promising potential. The genus consists of a number of species with varying levels of ploidy and a base chromosome number of 18. The species, contain a number of interesting genes (figure 4) benefits have been demonstrated for increased yield (Heinemann, 2007) and for disease resistance [an Ht gene derived from *Tripsacum floridanum* (Anthony and Ferroni, 2012)]. The characteristic of apomixes is found in many of the polyploid species of *Tripsacum* (Ruane *et al.*, 2016)

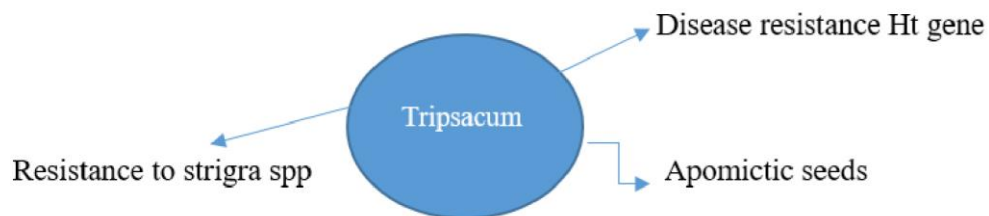


Figure 4: Contribution of *Tripsacum* to maize improvement.

(Source: modified from Ruane *et al.*, 2016)

In Africa, the parasitic weed *Striga* spp. is a significant pest of maize and other cereal crops. Some resistance has been found in certain *Teosinte* species and accessions. Recent efforts in screening a range of *Tripsacum* species have identified several promising accessions with near immunity to *Striga* infestation. Undoubtedly, *Teosinte* and *Tripsacum* represent significant untapped genetic resources for the improvement of maize. Over 60 wild species were identified to have been used for the 13 crops, with over 100 beneficial traits having been derived from them (table 4).

Table 4: Use of crop wild relatives in the past 20 years in released cultivars of 13 crops of international importance

Crop	Pest and disease resistance	Abiotic stress	Yield	Quality	Male sterility and restoration	Total no. of contributed traits
Cassava	+	-	-	+	-	3
Wheat	+++++++	-	+	+	-	9
Millet	+++ +	-	-	-	+	3
Rice	+++++++	+++	+	-	+	
Maize	+	-	-	-	-	2
Sunflower	+++	+	-	-	+	7
Lettuce	+++	-	-	-	-	2
Banana	++	-	-	-	-	2
Potato	+++++	-	-	-	-	12
Groundnut	+	-	-	-	-	1
Tomato	+++++++ ++	++	-	++	-	55
Barley	-	+	-	-	-	1
Chickpea	-	+	-	-	-	2

Plus signs indicate number of wild relatives that have contributed beneficial traits to crop varieties in each category of traits. Minus sign indicates wild relatives have not contributed beneficial traits in that category. Total number of individual traits obtained from wild species are indicated in the last column for each crop. (Source: Hajjar and Hodgkin, 2007)

Conservation of plant genetic resources

In situ conservation of crop wild relatives in protected areas

In situ conservation is often envisaged as taking place in protected areas or habitats (as opposed to ex situ conservation) and can either be targeted at species or the ecosystem in which they occur. It is a particularly important method of conservation for species that are difficult to conserve ex situ, such as many CWR.

The number of protected areas in the world has grown from approximately 56 000 in 1996 to about 70 000 in 2007 and the total area covered has expanded in the same period from 13 to 17.5 million km² (figure 5). This expansion is reflected at the national level with most countries reporting an increase in the total area protected.

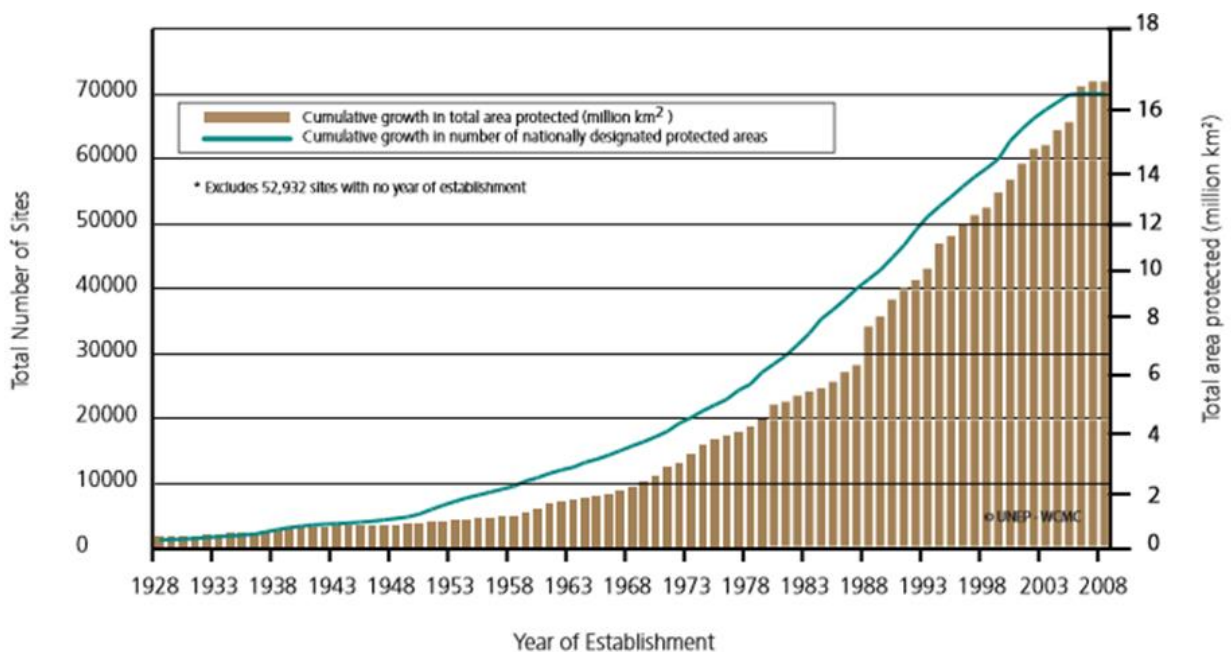


Figure 5: Growth in nationally designated protected areas (1928-2008).

(Source: Visser, 2010)

World ex situ collections of major crops

Figure 6 indicates that about 45 percent of all the accessions in the world's genebanks are cereals. The country reports confirm this. Food legumes are the next largest group, accounting for about 15 percent of all accessions while vegetables, fruits and forage crops each account for 6-9 percent of the total number of accessions maintained ex situ. Roots and tubers, as well as oil and fibre crops each account for 2-3 percent of the total (Allender, 2011).

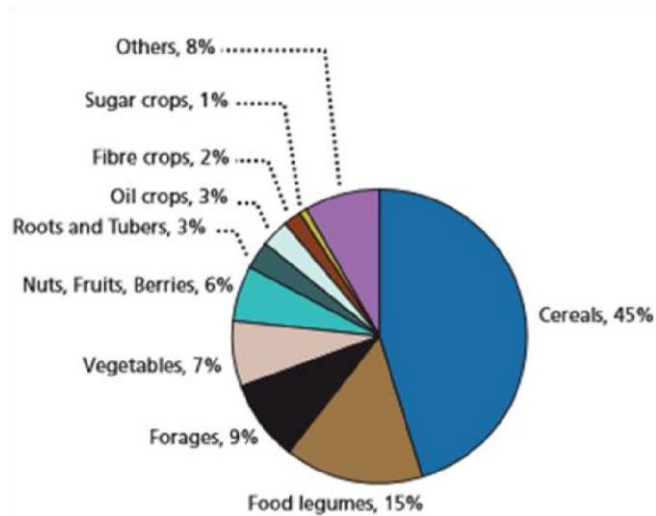


Figure 6: Contribution of major crop group in total ex-situ collection.

(Source: Allender, 2011)

Global germplasm holdings in terms of type of accession (mean percentage) for groups of crop indicates forages and industrial crops has a relatively high percentage of accessions that are wild relatives. The reverse is true for sugar crops, the majority of which are represented by advanced cultivars (table 5).

Table 5: Global germplasm holdings in terms of type of accession (mean percentage) for groups of crop

Commodity group	No. of accessions	% wild species	% Landraces	% Breeding materials	% Advanced cultivars	% Others
Cereals	3157578	5	29	15	8	43
Food legumes	1069897	4	32	7	9	49
Roots and tubers	204408	10	30	13	10	37
Vegetables	502889	5	22	8	14	51
Nuts, fruits and berries	423401	7	13	14	21	45
Oil crops	181752	7	22	14	11	47
Forages	651024	35	13	3	4	45
Sugar crops	63474	7	7	11	25	50
Fiber crops	169969	4	18	10	10	57
Medicinal, aromatic, spice and stimulant crops	160050	13	24	7	9	47
Industrial and ornamental plants	152325	46	1	2	4	47
Other	262993	29	4	2	2	64
Total/overall mean	6998760	10	24	11	9	46

(Source: Modified from Allender, 2011)

There are a lots of germplasm collection is done worldwide. Some major crops like rice, wheat, maize, barley, potato, sweet potato etc. is collected as germplasm (table 6).

Table 6: Collections of germplasm accessions of some major crops worldwide

Crop	Genus	Accession	Type of accession (%)				
			Total No.	WS	LR	BL	AC
Rice	<i>Oryza</i>	773 948	2	35	11	7	45
Wheat	<i>Triticum</i>	856168	4	24	20	13	39
Barley	<i>Hordeum</i>	466 531	5	23	17	8	47
Maize	<i>Zea</i>	327 932	1	33	21	4	42
Soybean	<i>Glycine</i>	229 944	6	17	7	13	56
Groundnut	<i>Arachis</i>	128435	3	31	10	4	52
Potato	<i>Solanum</i>	98 285	15	20	16	14	35
Sweet potato	<i>Ipomoea</i>	35 478	10	30	10	6	44
Tomato	<i>Lycopersicon</i>	83720	4	17	18	19	4
Capsicum	<i>Capsicum</i>	73 518	2	19	2	15	62
Cucurbita	<i>Cucurbita</i>	39583	2	32	4	6	56

WS: wild species. LR: landraces/old cultivars. BL: research materials/breeding lines. AC: advanced cultivars. OT: (others) the type is unknown or a mixture of two or more types.

(Source: Modified from Allender, 2011)

The materials in the CGIAR gene banks include traditional varieties and landraces, nondomesticated species, advanced cultivars, breeding lines, and genetic stocks (table 7). The effort required to assemble, document, and maintain these collections is enormous but well justified as the genetic diversity present in the gene banks represents a critical component in the world's fight against hunger. CIMMYT's newly established Genetic Resource Center contains \approx 120,000 accessions of wheat and 18,000 accessions of Latin American maize (of the 25,000–35,000 accessions in partner gene banks in Latin America). This represents the largest collection of these two important cereals.

Table 7: CGIAR's germplasm holding

Centre	Total holdings	Major species
CIAT	70,940	Cassava, phaseolus, rice
CIMMYT	136,637	Maize, wheat
CIP	13,911	Potato sweet potato
ICRAF	2,448	Agroforestry species
ICARDA	109,029	Lentil
ICRISAT	110,478	Chickpea, sorghum, groundnut
IITA	39,756	Yam, rice , maize, cassava
IPGRI	1,051	Banana, plantain
IRRI	13,470	Rice
WARDA	17,440	Rice
Total	595,806	

(Source: Avanzato and Vassallo, 2006)

Activities for the *ex situ* conservation of PGR are usually concentrated within germplasm/ gene banks, which handle collections of plant materials to maintain them alive and preserve their characteristics for appropriate use. There has been a far greater concern particularly in the last twenty-five years to collect widely the representative diversity in crop plants. The germplasm accessions assembled by the major genebanks in the world, which represent a sizeable part of the total world holdings for their respective crops. India rank first in *ex situ* holding that is approx. 32000 no. of accession followed by china. USA collected more than 25000 accession. Others countries like Russia, Japan, republic of Korea, Canada, Germany, Italy, Ethiopia, Hungary, Poland, Philippines holds a no. of accession and major genebanks (figure 7).

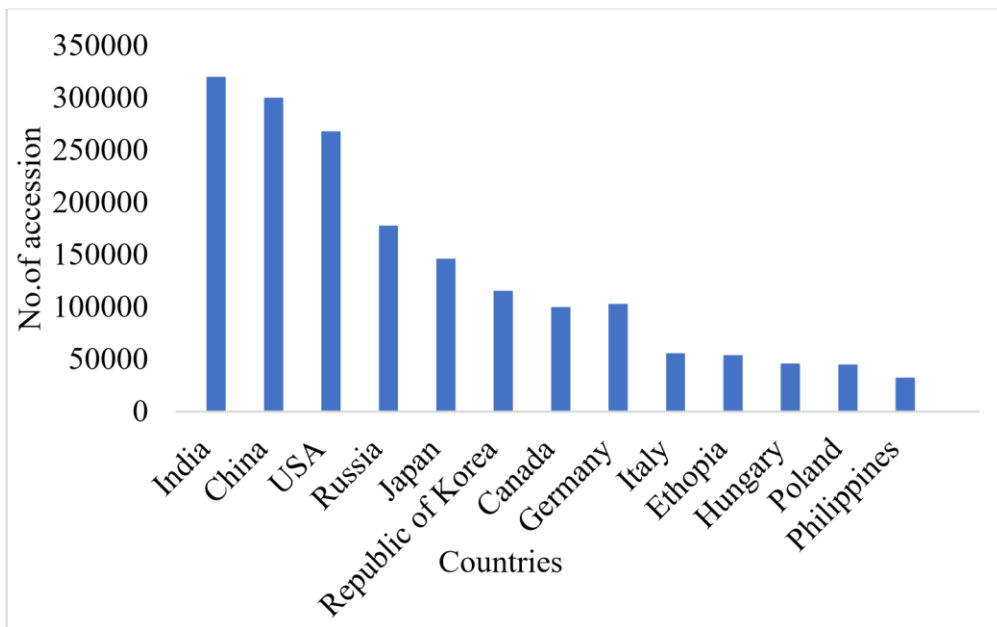


Figure 7: *Ex situ* holdings in major gene banks in the world.

(Source: Malik and Singh, 2006)

In Situ Conservation of Wild Crop Relatives and Wild Plants for Food Production in Bangladesh

The Bangladesh Agricultural Research Institute has identified two in situ locations (for pigeon pea and jackfruit), the Bangladesh Rice Research Institute has identified five in situ locations for wild rice and the Bangladesh Tea Research Institute has identified 100 Tea Estates as in situ locations of tea germplasm. For promoting in situ conservation of Wild Relatives of Crops and Wild Plants for food production, the major needs identified include: livelihood supporting species should be identified and their conservation promoted and regional approach in in situ conservation of PGR should be undertaken (Razzaque and Hossain, 2007).

Ex-situ conservation of plant genetic resources in Bangladesh

Ex situ programs/projects/ activities have been undertaken by stakeholder organizations. After 1996, Bangladesh Agricultural Research Institute undertook 3 exploration missions; Bangladesh Rice Research Institute undertook 6, East West Seed (Bd.) Ltd. undertook 8, Bangladesh Sugarcane Research Institute 4 missions, while Bangladesh Agricultural Research Institute, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Cotton Development Board and Bangladesh Tea Research Institute undertook one exploration mission each. Total germplasm collections (genebank plus field genebank) in different stakeholder organizations 27238 (table 8) (Razzaque and Hossain, 2007).

Characterization and evaluation work is still in preliminary phases in Bangladesh. Studies on core collections are yet to take off. However, the number of germplasm used for breeding by the Bangladesh Agricultural Research Institute was 791 accessions, Bangladesh Rice Research Institute about 6790 accessions, Bangladesh Tea Research Institute about 30, Cotton Development Board 130, Bangladesh Sugarcane Research Institute 229, Bangladesh Jute Research Institute 2,915, East West Seed (BD) Limited 5,263 and Bangabandhu Sheikh Mujibur Rahman Agricultural University used 547 (figure 8). This accessions are used for developing improved varieties through breeding program that are high yield potential with superior quality.

Table 8: No. of accession held up by different stakeholders in Bangladesh up to 2011

Organizations	Crops involved	Total no. of accession
BSMRAU	Various crop	642
BARI	Various crop	9368
BRRI	Rice	7290
BTRI	Tea	475
CDB	Cotton	467
BSRI	Sugar crops	1091
BJRI	Jute, kenaf, Mesta etc.	1666
Lal Teer Seed Limited	Various crop	6239
Total		27,238

(Source: Chowdhury, 2012)

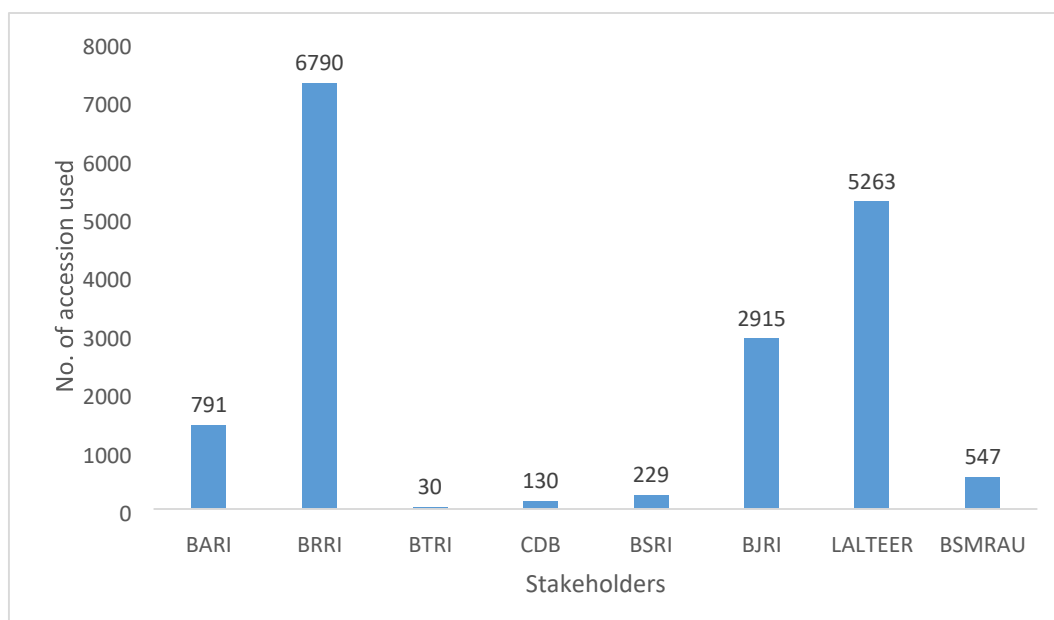


Figure 8: No. of accession used by different stakeholder organizations up to 2011.

(Source: Modified from Chowdhury, 2012.)

CHAPTER IV

CONCLUSIONS

- Plant genetic resources (PGR) are the basic materials that are essential for development of new crop varieties designed to combine high yield potential with superior quality, resistance to diseases and insect and also better adaptation to any stress condition. There are numerous ways to improve crops genetically, from traditional crossing and selection to the most recent gene transfer techniques. But all of these depend on the ability of plant breeders to assemble genes for the desired traits within new varieties. These new traits can be obtained from plant genetic resources. Plant genetic resources can contribute to achieve food security through providing elite gene to introgression in new varieties. In spite of advances in food production, food insecurity and malnutrition are still widespread. A 70 percent increase in world agricultural production over today's levels will be required to meet the food demands of the estimated 9.2 billion people in 2050. A major share of this productivity increase will have to come from the use of PGR to produce higher yielding, more nutritious, more stable and more eco-efficient crop varieties.
- Conservation of PGR directly benefits humanity. Countries that duly conserve their PGR can better face the challenges of socio economic development. There are approx. 1723,378 genebank in the world maintained by different organizations. In Bangladesh approximately 30,000 accession are preserved by different stakeholders. The total number of accessions conserved ex situ worldwide reaching 7.4 million. It is estimated that less than 30 percent of the total number of accessions are distinct.

REFERENCES

- Allender, C. (2011). The Second Report on the State of the World's Plant Genetic Resources for Food and Agriculture. *Experimental Agriculture*, 47(3), p. 574.
- Anthony, V. M., & Ferroni, M. (2012). Agricultural biotechnology and smallholder farmers in developing countries. *Current opinion in biotechnology*, 23(2), pp. 278-285.
- Avanzato, D., & Vassallo, I. (2006). Following almond footprints (*Amygdalus communis* L.): across Sicily cultivation and culture, folk and history, traditions and uses. International Society for Horticultural Science (ISHS).
- Bruinsma, J. (2017). *World agriculture: towards 2015/2030: an FAO study*. Routledge.
- Burlingame, B., Charrondiere, R., & Mouille, B. (2009). Food composition is fundamental to the cross-cutting initiative on biodiversity for food and nutrition. *Journal of Food Composition and Analysis*, 22(5), pp. 361-365.
- Dempewolf, H., Baute, G., Anderson, J., Kilian, B., Smith, C., & Guarino, L. (2017). Past and future use of wild relatives in crop breeding. *Crop Science*, 57(3), 1070-1082.
- FAO & UNICEF. (2018). WFP and WHO (2017) *The State of Food Security and Nutrition in the World 2017: Building Resilience for Peace and Food Security*.
- Foltz, J. D., & Azzam, A. (2009). Valuation and ownership of genetic resources in agriculture. *Public Policy in Food and Agriculture*; EOLSS Publishers: Paris, France, pp. 260-286.
- Ford-Lloyd, B., & Jackson, M. (1986). *Plant genetic resources: an introduction to their conservation and use*. Edward Arnold.
- Fowler, C., & Hodgkin, T. (2004). Plant genetic resources for food and agriculture: assessing global availability. *Annu. Rev. Environ. Resour.*, 29, 143-179.
- Frankel, O. H., & Bennett, E. (1970). *Genetic resources in plants-their exploration and conservation*. Genetic resources in plants-their exploration and conservation.

- Hajjar, R., & Hodgkin, T. (2007). The use of wild relatives in crop improvement: a survey of developments over the last 20 years. *Euphytica*, 156(1-2), pp. 1-13.
- Hammer, K., & Teklu, Y. (2008). Plant genetic resources: selected issues from genetic erosion to genetic engineering. *Journal of Agriculture and Rural Development in the Tropics and Subtropics (JARTS)*, 109(1), pp. 15-50.
- Heinemann, J. A. (2007). A typology of the effects of (trans) gene flow on the conservation and sustainable use of genetic resources.
- Katna, G., & Sood, V. K. (2015). Plant Genetic Resources, Traditional Knowledge and Their Use in Crop Improvement. In *Plant Genetic Resources and Traditional Knowledge for Food Security* pp. 23-38. Springer, Singapore.
- Khan, M. S. (1991). National Conservation Strategy of Bangladesh—Towards sustainable development: Genetic Resources in Bangladesh. Bangladesh Agricultural Research Council, IUCN, Dhaka, pp. 162-172.
- Kilian, B., Mammen, K., Millet, E., Sharma, R., Graner, A., Salamini, F. & Özkan, H. (2011). *Aegilops*. In *Wild crop relatives: genomic and breeding resources* pp.1-76. Springer Berlin Heidelberg.
- M K A Chowdhury, (2012). Conservation and Sustainable Use Plant Genetic Resources in Bangladesh, Bangladesh Agricultural Research council. pp. 100-103.
- Malik, S. S., & Singh, S. P. (2006). Role of plant genetic resources in sustainable agriculture. *Indian J Crop Sci*, 1(1-2), pp. 21-28.
- Meilleur, B. A., & Hodgkin, T. (2004). In situ conservation of crop wild relatives: status and trends. *Biodiversity & Conservation*, 13(4), pp. 663-684.
- Nemeth, C., Yang, C. Y., Kasprzak, P., Hubbart, S., Scholefield, D., Mehra, S. & King, J. (2015). Generation of amphidiploids from hybrids of wheat and related species from the genera *Aegilops*, *Secale*, *Thinopyrum*, and *Triticum* as a source of genetic variation for wheat improvement. *Genome*, 58(2), pp. 71-79.

- Noriega, I. L., Hilmi, A., & Esquinas-Alcázar, J. (2012). A brief history of the negotiations on the International Treaty on Plant Genetic Resources for Food and Agriculture. In *Crop Genetic Resources as a Global Commons* pp.147-161. Routledge.
- Pistorius, R. (1997). *Scientists, plants and politics: a history of the plant genetic resources movement*. Bioversity International.
- Pretty, J. (2006). *Agroecological approaches to agricultural development*.
- Razzaque, M. A., & Hossain, M. G. (2007). *Country Report on the State of Plant Genetic Resources for Food and Agriculture*. Bangladesh–Ministry of Agriculture p. 2.
- Ruane, J., Dargie, J. D., & Daly, C. (2016). *Proceedings of the FAO International Symposium on The Role of Agricultural Biotechnologies in Sustainable Food Systems and Nutrition*. FAO.
- Scarascia Mugnozza, G. T. (1995). *The protection of biodiversity and the conservation and use of genetic resources for food and agriculture: potential and perspectives*. Disertacion en Memoria de Frank L. McDougall (FAO).
- Sonnino, A. (2016). *Current and Potential Application of Biotechnology in Forestry: A Critical Review*. *Asian Biotechnology & Development Review*, 18(3).
- Sullivan, S. N. (2004). *Plant genetic resources and the law: past, present, and future*. *Plant physiology*, 135(1), pp. 10-15.
- Visser, L. (2010). *The state of diversity*. In *The Second Report on The Second Report on the State of the World's Plant Genetic Resources for Food and Agriculture* 3-22. FAO.
- Wang, S. M., & Zhang, Z. W. (2011). *The state of the world's plant genetic resources for food and agriculture*. *Journal of Plant Genetic Resources*, 12(3), 325-338