

Biodiversity

REVIEW ARTICLE

Utilization of wild relatives of wheat, barley, maize and oat in developing abiotic and biotic stress tolerant new varieties

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Abstract

Dramatic changes in climatic conditions, exhibited as heat waves, water scarcity and heavy rains, continue to threaten crop quality and yield. Additionally, fungal-based plant pathogen booming is another reflection of climate change creating some potential risks for agricultural production of main staple crop species. Most of the abiotic and biotic stresses are under the control of complex traits. Moreover, a wide range of desirable quantitative characters in cultivated crops, such as disease resistance, might degenerate with time. Therefore, buffering crops against the large environmental changes is important for feeding the world's increasing population and requires implementation of effective food security strategies. Crop biodiversity plays a key role in the improvement of stress tolerant species and enables an extensive platform for identification of novel traits by using a range of molecular tools. This offers homozygous crop models for the traits of interest, prediction models related to the stress tolerance and genetic resources for the transformation of cultivated crops. This review provides an overview for application of different crop wild relatives and demonstrates their roles on development of stress tolerant plants. It also highlights the importance of global crop conservation and alternative plant species for future plant breeding.

Key words: Abiotic stress, Biodiversity, Biotic stress, Breeding, Molecular tools, Tolerance, Wild crops

Introduction

Since the beginning of agriculture, climate change and agricultural practices have been closely associated with crop domestication (Meyer et al., 2012). Moreover, genotype x environment (GxE) interaction is an important factor affecting both agricultural practices and crop yield. This parameter has become an effective starting point for researchers during the development of stress tolerant plants and enables comparative crop monitoring under different field regimes (Mohammed, 2009; Tester and Bacic, 2005).

During the domestication process, plants emerged as wild type, landraces and cultivated genotypes. Globally, crops have dispersed to various territories by animals, wind and floating in water and have created their next generations either

self or cross pollination, like wheat and maize, respectively. According to Tanno and Willcox (2006), residues of ancient crops emphasized a slow domestication process during crop cultivation. In the Old World, large seed formation has been used as a major selection criterion during harvest process (Fuller, 2007). More typically, reduced seed shattering, larger fruits instead of multiple and small sized ones, reduced branching with the increased seed number per plant, short germination periods without seed dormancy and self-incompatibility traits can be counted as preferred agronomic traits during crop domestication (Meyer et al., 2012).

In general, major abiotic or biotic factors cause domino effect on plant growth from germination stage to the grain filling. These stresses cause a mixture of massive external signals which determine the plant response to directly or indirectly defend plant survival (Tester and Bacic, 2005). Additionally, there are various mechanisms running under the programmed cell function along with genome re-arrangement. As the complex nature of plant cellular functions considered, one can guess the huge amount of regulatory pipelines that are constitutively opened or induced after

Received 06 February 2014; Revised 17 March 2014; Accepted 27 July 2014; Published Online 15 December 2014

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specific signals (Roy et al., 2014). Usually, shifts in sensing mechanisms, occurred under different stresses, create multi-stressed environment for plants that is not easy to cope with the negative effects of this new condition. Mittler (2006) suggested that understanding the responses of plants under the combination of different environmental stresses can reveal the stress related response mechanisms more effectively. This will allow researchers to solve antagonistic responses and triggering signal mechanisms under fluctuated stress conditions (Atkinson and Urwin, 2012).

According to Harlan (1976), breeding must be an ongoing work due to restriction of cultivation bottleneck that has negative pressure on crop production. In the field of plant research, simultaneous monitoring with non-invasive methods and genotype based sequencing are available new technics and enable detailed screening of individuals. In most of the cases, genome structure, type of stress and environmental variables help to define the suitable strategy for increasing the agronomical value of cultivated crops. The critical point is to improve the estimations about stress tolerant crop selection during these processes. So, we will need to build the feasible crop screening methods and effectively use the prevalent crop biodiversity. On the basis of the plant development, present technical advancements will enhance to make detailed evaluations for different type of plants and improve the efficiency of breeding.

Different Approaches for Sustainable Crop Improvement

In the middle of the 1900s, studies on the exploration of crop origins and their evaluation entered a rapid transition phase with the advancements in molecular biology techniques (Burger et al., 2008). In course of time, plant genetic studies merged with the tools of modern plant breeding have focussed on the genome structures and their associations with environment. A wide range of innovative infrastructures, such as genotype based sequencing and high resolution imaging, provide powerful opportunities to link conventional and modern techniques and facilitate rapid detection during complicated experiments for stress tolerant crop development (Visendi et al., 2013). Today, plant breeding is augmented by the emergence of genomic tools such as high-throughput phenotyping and bioinformatics. Hence, plant scientists started to mine more unknown species for capturing important traits and made them available for practical applications (Heslot et

al., 2013; Jannink et al., 2010). Thus, studies on identification of map-based evolutionary crop dispersion and selection of the most feasible samples from bi-parental or mixed populations aimed to enhance the genome based screening as a part of plant breeding. Hence, these dynamic simulations allowed us to understand the wild crop genomes and scaled up their importance on the development of stress tolerant varieties.

Obviously, mapping of economically important traits and mining polymorphic alleles in elite lines by using molecular markers like SNPs are important advancements on plant breeding. Concurrently, forward and reverse molecular genetic approaches are used to identify the trait of interest during stress tolerant plant breeding. Different molecular marker systems take roles on forward genetic approach that is based on capturing traits via using DNA or RNA, while reverse genetic focuses on in vitro expression of specific genes by using recombinant DNA technology. Mutation breeding, as reverse genetic method, is another promising tool for investigation of beneficial traits originated from wild plant species. Physical and chemical mutagens have been used to make new combination of alleles. With this method, mutated alleles can be used for the estimation of new resistant plant material after two generations. Today mutation breeding is used as an alternative method to transgenic breeding, and there are officially released crop mutant cultivars covering 261 barley, 172 wheat and 49 maize (FAO/IAEA Mutant varieties Database, <http://www.mvd.iaea.org>). As an example for mutation breeding, Njau et al. (2006) developed drought tolerant wheat genotype with a commercial name “Njoro BW1” that is agronomically grown in Kenya.

In plants, genetic imprinting of genes occurred after nucleic acid methylation has also significant role on crop evolution (Ikeda, 2009). The way of imprinting of a gene fully affects the plant stress response regulation and functional behavior of genome by keeping from generation to generation (Downen et al., 2012). In particular, intermingled genomes may have strong potentials on identification of stress tolerant plants. From this point of view, wild plants can cover our future breeding expectations by serving a set of useful gene regions (Malik and Singh, 2006). In addition, germplasm resources, including wild progenitors, have significant roles on the applied crop breeding research. Hence, genetic transferrability of crop collections deployed through international plant breeding programs might be effective on stress resistant genotype improvement.

One of the other plant breeding approaches is the construction of synthetic hybrids. Thus, gene transfer from wild progenitors may enhance tolerance level of a crop against to abiotic and biotic stresses. Utilizing hybridization based techniques might be accepted as linking tool between conventional and modern plant breeding without diminishing its importance. In this way, a set of hybrid genomes, merging product of cultivated and wild crop, present new genome formation for marker assisted selection. However, construction of this type of hybrids is labor sensitive, they can make contributions for surveying of stress related quantitatively inherited traits (Zaharieva et al., 2001; Whitford et al., 2013). But there are still limitations during gene transfer, for example, linkage drag obstacle causes miss pairing inductions for the desired part of alien chromosome, and wrong integration of an undesired region of genome is another problem (Kilian et al., 2011).

Across intra specific populations, phenological responses are controlled by phylogenetic plasticity. Thus plant phenology modelling may allow to improve further specific characteristics within and between species Especially, under rapidly changing climatic conditions, it is important to make true estimations on species and their genome potentials for high yield and highly adaptive characters (Wolkovich et al., 2014). Moreover, reduced polymorphism rates in the tested gene may provide a smooth estimation for the introgression of a selected trait that is going to be transferred from the wild progenitor after a serial procedure and selection can be performed among the individuals of these new developed crop sets (Mujeeb-Kazi et al., 2013). In this respect, studies indicate crop wild relatives as rich sources of having more purified and less complex capacity. Advances in omics technologies support the genome based plant research may be the elevators of this system (Mochida and Shinozaki, 2013). Particularly, next generation sequencing tools might be the candidates for surveying gene flow among important crop species.

As another strategy, hunting genes or gene regulated regions related to stress tolerance can be uniquely identified under specific stress conditions. Later, introducing these target regions into sensitive crops might be achieved via genetic engineering. Until now, releasing new crop species carrying wild or landrace based genome regions is still insufficient (Hajjar and Hodgkin, 2007). Apart from this, in wheat, one of the main reasons is the

infertile seed development that is mostly obtained after hybridization between diploid D genome and tetraploid BBAA genome. In addition, water usage in synthetic hexaploids is one to four times more than that of natural hexaploids and it causes a water use barrier in areas with rainfall scarcity. Some precautions could be taken into account by using fertility restoration genes. Although, the existence of some restorer lines is reported, the type of the donor plant has also effects on production of fertile genotypes. Seeds originated from these crosses have some phenological deficiencies, such as low chlorophyll content and subsequent grain yield (Kilian et al., 2011). Furthermore, surveying crops for agronomically important traits will be shaped through our commercial requirements. In this frame, future plant breeding studies will have to be covered with multiple approaches to maintain sustainable crop capacity.

Abiotic Stresses

Environmental stress factors can be divided into two subcategories before defining them as abiotic and biotic. From this point of view, attentions have focused on nutritional supporters called as fertilizers. At first, fertilizer usage associated with high yield. After, it is understood that excessively saturating soil with these synthetic growth enhancers can have negative side effects on yield and grain quality (Campbell et al., 2011). However, concentration of some nutritional compounds in soil may increase the defense potential of crop under moisture stress and herbivore attack. One of the risks in fertilizer usage is uncontrolled ion concentration changes. On the other hand, pesticides and herbicides lost their effectiveness due to the redevelopment of resistance. Under these circumstances, application of different kind of plant nutrition techniques alone may not be able to offer permanent solutions for plant growth recovery. These external interventions can be counted as minor stress factors and they can be the possible results of human-based efforts performed to gain more crop yield. Important abiotic stresses such as severe drought, heat, salinity, cold, flooding, UV etc. have occurred after major environmental changes.

Today's world stands at the edge of the new global environmental stage with its agricultural land and aquatic ecosystem property. Unfortunately, a serious breakdown in crop yield has been estimated as 40% by the year 2100 (IPCC, 2007). According to the FAO (2009) reports, both water and food requirements will increase the demands on crop production by the next two

decades. There are so many reports related to the future environmental stress handicaps that are so certain to be our challenges and will be placed on the critical corners of agriculture. Another problem is the severity and frequency of abiotic and biotic stressors which significantly cause grain yield losses in crops such as wheat, barley and maize (Lobell and Field, 2007). In addition, dependency to the alternative sources for clean energy requirement increased by the time. Therefore, crop production, especially for maize that is rich in cellulosic material, accelerated as a result of demands on biofuel consumption (Torney et al., 2007). This dependence lifted the total maize production into an important position and forced breeders to search for more feasible maize genotypes for biofuel production (Lorenz et al., 2009). Consequently, maize has exposed to a process that has a compel sharing between food and energy sectors. As it is given in maize production, increasing human population and decreasing agricultural areas are made the same impact on other important cereals that are used as our daily staple food.

Among abiotic stresses, salinity has become particularly widespread in many regions of the world and may cause serious salinization of more than 50% of all arable lands by the year 2050 (Bray et al., 2000). Furthermore, an increasing pressure to extend arable land is not optimal for the growth of major crops. Besides, irrigation practices have effects on leaf area index and grain yield. Especially, irrigation types also make perceptible changes on crop phenology. In reverse approach, uncontrolled irrigation can turn soil content into a salt rich form that is very toxic for plant growth and development (Munns and Tester, 2008). This is occurred because of wrong irrigation estimation for soil water requirement and unexpected evaporation rate increments by causing dry-land salinity during seasonal term. Salinity has three potential effects on plants: (i) lowering of the water potential, (ii) direct toxicity of any Na^+ and Cl^- absorbed and (iii) interference with the uptake of essential nutrients. Maintaining better nutrition with K^+ and Ca^{2+} , while limiting Na^+ uptake, is highly important trait contributing to high salt stress tolerance in plants. So, higher K^+/Na^+ or $\text{Ca}^{2+}/\text{Na}^+$ ratios are typical characteristics for salt-tolerant varieties, and they are used as a screening parameters for identification of salt-tolerant genotypes (Munns and Tester, 2008; Poustini and Siosemardeh, 2004). In many research groups, investigations dealing with the development of salt-tolerant varieties have concentrated on the uptake, transport, and accumulation of K^+ , Na^+ and Ca^{2+} in plants.

Under drought stress, accessible amount of external and internal water is important for continuous plant development. While external water content determines the rate of root water uptake, internal water potential plays a key role in ionic flow not only at individual cell level but also it affects the neighbour cells (Farooq et al., 2009). So, under extreme drought, plants usually prefer to close their stoma for preventing water loss and cells enter a balancing phase to provide a steady state osmotic potential. At the same time, there are variety of changes occurred in photosynthesis rate due to the increased amount of carbon-dioxide levels (Taub, 2010). Xerophytes have been accepted as indisputable drought tolerant plants and have natural physiological adaptation mechanism occurred with decreased leaf area, less stoma, root length. So, existing C_4 and Crassulacean acid metabolism (CAM) plants have the traits of water use efficiency under extreme drought and water scarcity (Taiz and Zeiger, 1998). From a different aspect, under different humidity conditions, canopy temperature is another important parameter to make concise decision about irrigation time. Also, it is used as a sign of plant water stress during shortage of rainfall. In principle, water use efficiency has been selected from crop wild relatives or highly adaptive domesticated ones (Condon et al., 2004).

Nowadays, serious global heating problem reported by Battisti and Naylor (2009) will be a drawback for future sustainable agriculture. With this foresight and rising temperature levels in all over the world, total cereal production will be started to decrease after the year 2030 (Tester and Langridge, 2010). In plants, acquisition of thermo-tolerance plays a key role on maintaining sufficient crop yield that is studied on desert conditioned plants during grain filling conditions (Porporato et al., 2003). An unbalanced heating temperature changes can negatively affect vegetative and generative plant growth stages. This is especially important in crops at anthesis stage and may be resulted as prolonged seed maturation (Giorno et al., 2013). Extreme cold and freezing stresses force the cell architecture to breakdown by making external water mobility inaccessible and transferring internal water into crystallized form respectively. In both situations, osmotic potential of cell changes due to the water and ionic unbalance. As a classical behaviour, cold stress sensitive plants have no ability to continue their growth under long-term cold or freezing temperatures and respond to cold by changing metabolite concentrations (Cramer et al., 2011). Chinnusamy et al. (2007) proposed some metabolites and antifreeze proteins

that protect cells from the negative effects of cold and freezing. On the other hand, these temperatures, without escaping out of range limits, are necessary for dormancy depended process before germination in winter cereals (Tester and Bacic, 2005).

Finally, ultraviolet (UV) rays and different radiation sources have also serious effects on whole plant populations. First impacts of UV observed on the upper part of plant organs as a result of defects that are occurred between the disulphide bonds of proteins. Thus, accordance with metabolite loses and irreversible DNA damages give harm to the other functional pathways. Also, exposure of plants to atmospheric ozone is another serious factor and cause global yield loses (Avnery et al., 2011).

Biotic Stresses

As a second major group, biotic stress factors can be classified into five independent groups in plants; virus, bacteria, fungi, insect and nematode-based diseases (Robert et al., 2001). Biotic stress factors can be detrimental to plant growth from seedling to the harvest phase. Vast majority of wild crops exhibit an innate immunity against the bacteria, fungi and viruses through chemical sensing of specific signals. As the severity and economic losses compared, fungi-based plant diseases are ranked on the top. Due to the polygenic nature, research on plant biotic stresses requires detailed implementation, such as metabolo-proteomics, to understand the plant resistance management system into plants. Studies, primarily focused on pathogen related diseases, suffer from extensive dissemination and re-development of pathogen resistance. Under pathogen attack, numerous responses observed at gene expression level could be controlled by DNA methylation, movement of transposable elements and alternative splicing. Thus, expression of several genes shows dependency to functional and structural regulation of target genome region. Previously, epidemics have showed unpredictable devastating effects of plant diseases. According to Strange and Scott (2005), there are two main points for ensuring healthy food production during plant disease infestation. Reduction of inoculum material and inhibition of virulence mechanisms maintained with promotion of crop genetic diversity can help to combat with the negative effects of plant diseases. So, pathogen resistant crop breeding has become an urgent issue in recent years (Atkinson and Urwin, 2012).

In the case of herbivory that alters the domestication process of wild progenitors,

development of herbivore resistant crops will be an important point for sustainable agriculture (Chaudhary, 2013). As an example, the effects of intra and interspecific competition in plants that is also under the control of herbivory resulted more tolerant wild perennial maize, *Zea diploperrenis*, against the stem boring damage rather than its wild annual, landraces and modern maize cultivars (Rosenthal and Welter, 1995). Insect and nematodes cause significant crop losses in grain yield that is estimated at 10-20% for major staple crops.

Up-dated anthropogenic scenarios indicate that Green House Gases will be scaled up to the alarming levels in the next seventy years and it is obvious that they will pose obstacles for agricultural production (IPCC 2007). Under varying conditions, previously non-dominant pathogens might be turned into harmful form and can lead to outbreaks. In the sum, producing crops as human food, livestock feed and energy supply, we need to seriously reconsider the climate change (Wheeler and von Braun, 2013) with the above mentioned stresses either uniquely or in a mixed pattern to provide cereal production sustainability.

Major Crop Progenitors and Environmental Stress Interaction

Wheat

Common wheat, containing allopolyploid genome structure (Shewry, 2009), is one of the oldest domesticated crops that was originated from a small region in Turkey (Feldman, 2001; Ozbek, 2014). In the recent article of Jaradat (2013), Fertile Crescent is defined as the place where the origin of wheat being stowed. This is firstly announced within “centers of domestication” reports of Vavilov’s research who dedicated himself to plant breeding (Vavilov, 1926). In the recent time, distribution of wild Triticeae tribe is well documented according to soil texture such as clay, loam, sandy soils and climate. Studies conducted to understand the spreading of wild relatives showed a great diversification map for Poaceae family members. Some species such as *Aegilops triuncialis*, exhibited an extended distribution from Europe to the Asia, while some others like *Aegilops searsii*, dominated in the specific parts of the Fertile Crescent. There is also large edge of geographic dispersion in the Middle-east, Turkey, North-eastern Africa and backyard of Western Asia where it is accepted as main lands for wild progenitors of wheat (Feldman, 2001; Kilian et al., 2011). As the last FAO reports (2011 and 2012) compared for

wheat, world total wheat production quantity has been decreased from 699.5 million tonnes to 671 million tonnes respectively, and wheat harvested areas also exhibited a downward slope with the values of 220.3 million hectares in 2011 and 215.5 million hectares in 2012 (<http://faostat3.fao.org>).

According to the previous reports, restriction of breeding bottleneck might be reversed via using wild progenitors (Redden, 2013). Traits related to high adaptation potential and survival capability under extreme conditions brought wild crops in an advantageous position. In this term, wheat wild relatives can accelerate this process at the point of identification of stress tolerance genes and associated regulatory regions. Thus, capturing a trait from crop wild relatives that is directly linked to stress response/defense mechanism will be more quickly achieved rather than cultivated one. In this way, conserved architecture of wild wheat genomes will serve as sources of ancient stable gene libraries (Tanksley and McCouch, 1997). Considering the wheat genome, einkorn wheat is known as diploid A genome progenitor and there is a non-completed argument for *Triticum urartu* and *Triticum monococcum* which is the real candidate progenitor of A genome. In this issue, core phylogenetic evidences conveyed the close neighbourhood by providing a clustered dendrogram analysis between these two main members (Brandolini et al., 2006). Now, the importance of A genome has affirmed as a result of *Triticum urartu* draft genome sequencing (Ling et al., 2013). In addition to the phylogenetic evaluation of wild emmer wheat (Ozkan et al., 2011), there are detailed studies explaining its master role on improvement of new hybrids and modern cultivars. In this case, Krugman et al., (2011) underlined the importance of *Triticum turgidum* ssp. *dicoccoides* specific some drought tolerance genes and metabolites. Same study reflected the gene expression induction of ABA signaling components and other hormone signaling factors at high levels in wild emmer wheat. Ieshisa et al. (2012) studied wild wheat D genome progenitor *Aegilops tauschii* together with synthetic hexaploid wheat, and detected a high level of gene expression induction for the components of ABA signaling pathway. In addition, accumulation of drought stress related key metabolites, such as glucose, trehalose, proline and glycine, exhibited valuable profiles in wild emmer wheat (Krugman et al., 2011). These metabolites are acted as promoters for enhancing tolerance mechanisms under salt stress (Munns and Tester, 2008). Rajendran et al. (2009) have reported interactions among Na⁺ exclusion, osmotic tolerance and Na⁺ tissue

tolerance in twelve different *Triticum monococcum* lines. Na⁺ is one of the key ions that exchanges during salt stress and high Na⁺ exclusion is correlated with higher salinity tolerance (Munns and Tester, 2008). However wild emmer wheat accepted as a valuable gene source for salt tolerance. Shavrukov et al. (2010) revealed a large physiological differences under salt stress for *Triticum dicoccoides* that is one of the best known member in wild emmer wheat family. This tetraploid relative of durum wheat has been found as rich gene source for *Fusarium* head blight resistance (Oliver et al., 2007). Also, an agronomically important tetraploid wild progenitor, *Triticum turgidum* var. *dicoccoides*, is a source of high protein content that is placed on wheat chromosome 6B Gpc-B1 region by controlling the zinc and iron movement through the seed before maturation (Distelfeld et al., 2006). Recently, a comparative study between wild emmer and cultivated wheat under salt stress has evidently demonstrated that the transcription factors, such as NAC2F, NAC8, DREB3A, MYB3R, and MYB2A, showed higher level of gene expression and it is supported to a clear correlation between salt tolerance and wild emmer wheat that is put forward the importance of this wild genome (Chen et al., 2013). In a different aspect, Kim et al. (2010) conducted a study to understand the genome x seed protein density interactions by using proteomic tool MALDI-TOF mass spectrometry. One of the convincing results was considerable amount of protein spots among A, B and D genome in wheat, and their functional ability annotated to important protein groups that were responsive under drought, cold and heat stress and pathogen attack related ones. With these features, each wheat genome carry important role on ensuring stress tolerance (Cenkci et al., 2008).

Among diploid wheat progenitors, evaluation of *Aegilops* (goat grass) species and their genomes under different environmental conditions can provide a variety of preferential gene sources due to their multi-environmental dispersion and growth availability (Baalbaki et al., 2006; Colmer et al., 2006; Valkoun, 2001). Common hexaploid wheat D genome progenitor *Aegilops tauschii* draft genome sequence has been published by Jia et al. (2013), indicating high adaptive traits are stacked on the specific genome regions of this crop. Harb et al. (2013) used three *Aegilops crassa* for the identification of changes in relative water content, chlorophyll content, chlorophyll fluorescence and biomass accumulation under drought conditions. Another diploid crop *Aegilops tauschii* is widely

distributed and contained well adapted species and it is used for drought and salt tolerant wheat improvement respectively (Dubcovsky et al., 1996; Sohail et al., 2011). In the past, efforts performed to produce stress adapted plants via hybridization based assays. Not only abiotic stress, but also biotic stress related mechanisms have been investigated at physiology and molecular level in different *Aegilops* species. To provide insect resistant alternative crop material, Suszkiw (2005) developed some new commercial spring wheat lines containing *Aegilops tauschii* Hessian fly resistance genes. In general, studies relevant to biotic stresses performed in cultivated crops and the number of studies conducted in wild crops are limited. Stoilova and Spetsov (2006) described powdery mildew resistance genes on the sixth chromosome of *Aegilops geniculata*. In another study, Schneider et al. (2008) reviewed rust resistance in *Aegilops speltoides*, Barloy et al. (2007) reported nematode (*Heterodera avenae*) resistance in *Aegilops variabilis*.

In addition, diploid A genome progenitor, *Triticum monococcum*, has been used to mark the traits related to resistance genes against to powdery mildew (Yao et al., 2007) and leaf rust (Sodkiewicz et al., 2008). Among biotic stresses, Russian wheat aphid (RWA) is considered as one of the harmful insect species for wheat and also other important staple crops such as barley. Since the first epidemic observed in USA, almost one billion dollar loss was caused by this insect. In Turkey, there was a big loss in wheat yield up to 60% in Konya due to the RWA (Elmali, 1998). Most of the RWA resistance genes have been located on D genome and attributes focused on D genome progenitor *Ae. tauschii*. Differently, Deol et al. (1995) investigated the resistance levels of some *Triticum monococcum* genotypes against to RWA and found two wild wheat accessions displaying equal resistance with bread wheat genotype (PI 372129) which was firstly identified as Dn4 gene (source of RWA resistance) carrier.

Rust pathogens are other sources of biotic stresses, and they are originated from different regions cause high amount of crop yield loss. Only in Asia, estimated yield loss in wheat could be 10% levels due to the non-controlled outbreaks of rust. As being a natural source of rust pathogen resistance, tetraploid wheat A and B genome progenitor *Triticum turgidum* var. *dicoccoides* often included in yellow rust resistant hexaploid wheat production (Chhuneja et al., 2008). Zaharieva et al., (2001) investigated *Aegilops geniculata* species for

Barley yellow dwarf virus resistance. In the past, Lagudah et al. (1993) examined the traits related to viral, nematode and fungal resistance among introgression wheat lines and underlined the D genome efficiency. One of the leaf rust resistance gene Lr21 and cereal cyst nematode disease-controlling locus Cre3 identified in *Aegilops tauschii* (Eastwood et al., 1994; Ling et al., 2004). Additionally, there are several wild progenitors maintaining leaf rust resistance such as *Aegilops geniculata* (Kuraparthi et al., 2007) and *Aegilops neglecta* (Marais et al., 2009).

Uncertain conditions and differential responses directly cause a pressure on individual or whole plant population. One of the feasible ways for core plant material selection is to follow the phenotypic responses and growth parameters under extreme and ordinary conditions. In this respect, different crosses and their subsequent lines have been produced for screening of particular traits either in the field or in glasshouse experiments. Hybrid wheat lines and recombinant inbred populations supported these approaches with measurable stress tolerant plants under salinity (Peleg et al., 2009). Also, hybridization of synthetic wheat hybrids with cultivated bread wheat plant may enable a set of tolerant plants (Mujeeb-Kazi et al., 2006). As an example, one cultivar that is produced via crossing the synthetic wheat with hexaploid bread wheat released with a commercial name taq 'Chuanmai 42' is publicly available. Harvest index results of this new bread wheat showed an increase in the amount of yield approximately at level of 20-35% in 2003 (CIMMYT, 2004).

Building specific wheat sets, either wild origin or hybridization based, needs systematically collected samples and multi-dimensional field screening of wheat mapping populations under different regimes. Today, discovery of PCR based molecular markers, such as simple sequence repeat (SSR), diversity array technology (DArT), amplified fragment length polymorphism (AFLP) and single nucleotide polymorphism (SNP) effectively provide novel contributions for establishing germplasm diversity and gene-trait relationship. Hence, high resolution mapping of genes from wild relatives and population mining will be possible with next generation breeding methods. All of these tools have been used to identify loci controlling preharvest sprouting tolerance and to deploy genes for drought and cold tolerance in wheat stem and stripe rust resistance and further more. At present, sequence-based genotyping methodologies have started to discover

new allelic diversity in crops. Thus, we will obtain more detailed data for wheat and its wild relatives.

Barley

As a wild ancestor of cultivated barley, *Hordeum spontaneum* has been distributed in diverse parts of the world from China (Zhang and Ding, 2007) to Mediterranean region (Harlan and Zohary, 1966). There are several phylogenetic studies through geographic variations of *Hordeum* species (Turpeinen et al., 2003; Wang et al., 2009). According to the FAO 2011 reports, world total production for barley was 133 million tonnes (<http://faostat3.fao.org>). Barley agricultural production is performed on wide range of environmental conditions. On the other hand, geographic distribution and emerging new isoforms of plant pathogens frequently depend on the temperature changes. So, there are several types of biotic stress factors found in the growing regions of barley. Especially, soil borne pathogenes like *Rhizoctonia*, cereal cyst nematodes cause a yield reduction and big economic loss in barley. *Cochliobolus sativus* is a causative of spot blotch disease and results with a yield loss of 30-40% for malting barley in USA (Liu and Friesen, 2010). For improving spot blotch resistant barley genotypes, adult plant resistance is preferred rather than developing race specific resistance. This is due to the rapid changes in temperature and its effects on releasing severe epidemics. In the center of the resistant plant breeding approach, genotyping is the first criterion and it is performed with the help of molecular tools such as molecular markers. Thus, marker assisted breeding leads the most important part of resistant/tolerant crop selection. Existence of a variety of next generation tools, such as SNP mining, can be designed to find out the agronomically important genes. Thus, more allelic variations can be screened by reducing the complexity of genomes. In barley, Illumina based SNP platforms have been developed to make true genotyping for resistant plant selection (Close et al., 2009) and wild barley characterization (Russell et al., 2014).

Wild barley populations are proposed as rich sources of important allelic variations of which were clustered in different sets of chromosomes by providing drought tolerance (Chen et al., 2009). As a specific example, Terra rosa type wild barley found as more drought tolerant than *Tabigha* type wild barley and these populations have high yield potential as a plus of stress tolerance (Ivancic et al., 2000). In addition to drought tolerance, barley is known as the most salt tolerant crop member, and

correlations between ionic and metabolomic profiles in response to salt stress (Figure 1) has investigated in wild and cultivated barley accessions (Wu et al., 2013). Comparative studies between cultivated and wild type barley accessions have been identified important genome regions related to aluminum tolerance (Cai et al., 2013). Moreover, Huang et al. (2013) have defined a regular population structure that is actively carrying distinguishable *Fusarium* resistant barley genotypes and Yun et al. (2006) reported an advanced backcross population that was constructed from the crosses between *Hordeum vulgare* subsp. *spontaneum* and the two-rowed malting barley cultivar for resistance to spot blotch, leaf blotch and leaf scald. Along with the development of molecular markers, germplasm mining initiated to identify stress tolerance genes. Lakew et al. (2013) have used to show the marker-drought stress tolerance associations in barley introgression lines, constructed with wild barley, via microsatellite and single nucleotide polymorphism markers. In wild barley, stress related defense gene diversity has been detected at higher level under biotic stress rather than abiotic stress (Fitzgerald et al., 2011).

Maize

Corn or maize is an about 95% cross-pollinated crop and the most domesticated monocot. It belongs to the Poaceae family and it is grown as a commercial row crop from as far 58°N latitude to 45°N latitude. Also it is one of the widely studied plants. There are several breeding objectives, such as grain yield, yield stability, agro-morphological traits and adoption to variable abiotic and biotic environmental conditions, for maize. Conventionally, creolization method, growing two distinct maize populations in adjacent farms, is routinely used to increase the genetic diversity in maize. This management system is specific to maize growers in Mexico and provides a well-established method for gene flow between commercial maize lines.

Recently, maize is being increasingly cultivated multi-purpose crop and will continue to play a leading role for shaping the future crop improvement systems (Lorenz et al., 2009). According to current FAO reports, maize production has been reported as 888 million tonnes in 2011 and 872 million tonnes in 2012 (<http://faostat3.fao.org>). Chaudhary et al. (2014) reported almost 110 diseases on the global basis caused by fungi, bacteria and viruses and 130 insect-pests. One of the unexpected southern corn leaf blight epidemic occurred in US in 1970 and

caused one billion dollar loss which is one of the biggest agro-economic disasters in the past. Advancements in maize genomics and breeding will have significant impacts on the lives of large proportion of the world's population. Especially, transgenic breeding is one of the plant breeding approaches that is preferred to perform sustainable corn production in many areas of the world. There are two main corn bore infestation diseases known as European corn borer (*Ostrinia nubilalis*) and Mediterranean corn borer (*Sesamia nonagrioides*). To prevent a sharp drop in corn production, genetically modified insect resistant corn varieties (Fig. 2) have been produced on 37 million hectares in 17 different countries for serving food and feed. By the same logic, *Bacillus thuringiensis* (Bt) transgenic corn, expressing different Cry1 proteins, has been generated against to Asian corn borer pathogen (He et al., 2003). Recently, Du et al. (2014) developed some transgenic insect resistant corn varieties carrying Cry1C gene.

According to the personal communication report of Hajjar and Hodgkin, (2007), some introgression initiatives in maize breeding

performed by introducing *Tripsacum* L. resistance genes, such as *Helminthosporium*, *Puccinia*, rootworm, drought and aluminum stress, into cultivated maize between the years of 1950-1980. After then, a lagging phase happened for maize cultivar development due to the enhanced field testing studies. Unfortunately, gene arrangements in wild maize progenitors have not reached to the expected levels. Instead of this, transgenic maize cultivars preferred to study the gene actions under several types of stress conditions (Amara et al., 2013).

Oat

The genus *Avena* L. belongs to the tribe Aveneae. Cultivated oat, containing ACD genomes, is commercially gained importance in the past decade due to its nutritional value. In 2012, total oat production occurred as 21 million tonnes in all over the world. According to the continent based reports, Europe is the biggest oat producer with 7.83 million tonnes and it is followed by US and Australia with 5.1 and 1.28 million tonnes respectively.

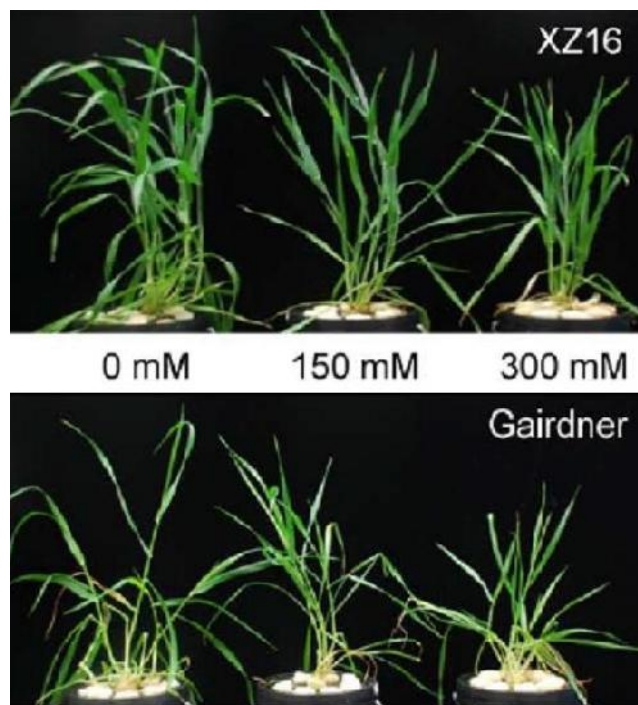


Figure 1. A comparative salt stress experiment under hydroponic culture in different barley genotypes, a-wild barley plants under salt stress, b-cultivated barley plants under salt stress (Source: Wu et al., 2013).



Figure 2. An overview of non-Bt maize (left) and Bt maize (right) after fungal infection (Source: Munkvold and Hellmich 2000, permission obtained from Plant Health Progress).

Avena has three different ploidy levels in the form of diploid, tetraploid and hexaploid like wheat (Loskutov, 2007). As it was listed in other wild crops, wild oat relatives are important for improving biotic and abiotic stress tolerant cultivated oat improvement (Zeller et al., 1998). Portyanko et al. (2001) reported conserved genome regions that were closely synthetic between hexaploid and diploid oat genomes. Cultivated hexaploid forms include *Avena sativa* and *Avena byzantina*, while *Avena abyssinica* identified as tetraploid and *Avena strigosa* found as diploid. *Avena* species are distributed mostly in the northern hemisphere and mainly around the Mediterranean Sea and the Canary Islands. Also, there are some endemic species like *A. canariensis* in the Canary Islands and *A. ventricosa* found in Cyprus. Different taxonomical classifications have been made according to the settlement and morphological characteristics (Legget and Thomas, 1995) and molecular markers (Wu et al., 2012). Due to the complex relationship between genetic and ecological factors, oat species showed a variation according to their geographical origin (Rezai and Frey, 1988). On the contrary, Runzhi et al., (2007) concluded that genetic diversity of wild oat in the broad spatial scale is not substantially changed by environment, agronomic practices or herbicide usage.

For a long time, *Avena* species have been accepted as soil weed contaminants by invading the agricultural production. Long-term weed management studies showed that weedy oat species can reduce the yield of important staple crops such as wheat, barley. In the field, if prior emergence of oat seeds occurs, yield loss is

happened at the rate of 0.42% for barley and 0.29% for wheat (O'Donovan et al., 1985). Wildeman (2004) claimed a non-competitive relationship between wild and cultivated oats under field and glasshouse conditions. This observation may be expressed as a defense mechanism in oat species survival and further studies may be conducted to examine the abiotic or biotic stress tolerant wild oat species of which show differences between genome structures and have the ability to live under extreme conditions. Studies on phylogenetic diversity testing in different oats performed for *Avena strigosa* and *A. barbata* (Cabral et al., 2013), multiple herbicide resistance (Lehnhoff et al., 2013), leaf rust resistance (Adhikari et al., 1999). Previously, Fennimore et al. (1999) studied seed dormancy regulation genes in wild oat (*Avena fatua* L.). According to Gallagher et al. (2013), drought and shading regimes had no effects on seed vigour of wild oat (*Avena fatua* L.). However, these stress factors have only reduced the dormancy period. Previously, declining the longevity of dormancy and seed property in the anthesis stage of wild oat (*Avena fatua*) confirmed by Sawhney and Naylor (1982).

Slender wild oat (*Avena barbata*) is a tetraploid wild relative of the cultivated oat (*Avena sativa*) and can survive under mesic and xeric environments. It is used as beneficial gene source for powdery mildew pathogen resistance after transferring resistance genes into the cultivated oat (Aung et al. 1977). Swarbreck et al. (2011) presented the available gene expression patterns of *A. barbata* root and leaf tissues under varying soil moisture. Previously, some important

biotic stress factors such as oat mosaic potyvirus, *Puccinia graminis* and some other abiotic stresses like drought have expanded the genetic basis of oat breeding. Oat, either existed wild or became cultivated, has been important food and feed stock. Since the beginning of 1990s, oat bran has been cited as its cholesterol lowering effect that was closely associated with beta glucan content. From the agronomic aspect, quality and seed purity offer uniform oat production which was strongly recommended for oat producers. In commercial oat production, threshold percentage for oat planted fields set as maximum 3%. Thus, sufficient grain yield can be obtained after harvest. In addition, improvement of milling quality has been prominent issue that is used as a selection criterion in oat breeding. As related to this action, grain yield, groat percentage and -glucan level are accepted as leading features in oat improvement studies (Yan et al., 2013). Breeding disease resistant, low water dependent and highly qualified oats will increase the value of this crop for end-users and describe a pivotal role for breeders at global level.

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 (CWR) 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). Along with this, systematic and molecular conservation techniques may provide reliable crop potential for sustainable capacity. Largely, climate change hinders the development of leaves and substantially cause immature ear emergence in crops. This physiological pressure simply cause a lower branching, decreased seed sets. Moreover, earthquakes, fire and urbanization reduce the number of evolving plant species and render their habitats. Collecting, preserving and refreshing various plant materials

should be planned in the frame of the germplasm management systems (Dempewolf 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 Europe, there is an association, Planta Europa Network, working for plant conservation security. 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.

In addition to the *ex situ* and *in situ* conservation centers that were established in several countries, there is a separate seed storage center (Svalbard Global Seed Vault) working as a reservoir service for future food security (Figure 3). According to the data obtained from the last updates (February, 2014), 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. One of the most important feature of this facility is no need to cooling due to the minus temperature levels in North Pole conditions. Thus, seeds are conserved at minimum cost and low risk in addition to traditional conservation centers and origin of places (<http://www.croptrust.org/>). These actions with future strategic conservation plans will be strengthen the seed banking and sustainable conservation of valuable plant materials.



Figure 3. An overview of Turkish Seed Bank conservation room. (Permission obtained from Dr. Kursad Ozbek)

Utilization of Useful Gene Sources From Alternative Crop Wild Relatives

Under the pressure of environmental stress and continuous agricultural practices, cultivated crops have been achieved to be our major food sources for centuries and they followed the way of natural selection by modifying their genomes through hundreds of crossing over. During the history of domestication, agricultural demands shaped the crop cultivation period and breeding of specific crop groups. This type of formation has never stayed behind the modern breeding efforts that were performed to obtain high yield and more resistant ones (Ozbek, 2014).

Today, powerful sequencing approaches have opened an important corridor for evaluating alternative crop genomes and attracted our attentions on different stress tolerance mechanisms with their wealthy metabolites that control strategic biochemical pathways under extreme conditions. Since the invention of model plant *Arabidopsis*, several studies on crop close relatives have been increased through the persistence of plant breeding efforts by serving new gene resources. For example, diploid wild grass *Brachypodium distachyon* has achieved to be escaped from genetic

bottleneck problem. As an advantage, *Brachypodium* has fully sequenced small genome size that is only 2% of the wheat (International *Brachypodium* Initiative, 2010). Recently, high phylogenetic similarity and syntenic maps promoted *Brachypodium* as a valuable plant model for wheat and barley (Mochida et al., 2013). Moreover, there was no report on negative effects of drought stress on growth and development of *Brachypodium distachyon* (Verelst et al., 2013). In addition to all, *Brachypodium* species have found as tolerant to other biotic and abiotic stresses that were compiled in the paper of Mochida and Schinozaki (2013).

Except *Brachypodium*, some forage and turf grasses growing on marginal areas may be alternative plant systems for suggesting new gene resources during improvement of abiotic and biotic stresses (Zhang et al., 2006). Another example, *Haynaldia villosa* (L.) is a wild relative species of common wheat that possesses many beneficial genes for improving resistance to powdery mildew, leaf and stem rusts, eyespot and wheat streak mosaic virus (WSMV) (Chen et al., 2002). According to Ladeiro (2012), genome potential of halophytes may be used to manage salt-

contaminated resources for further food requirements. Such halophytic relatives of barley, like sea barleygrass (*Hordeum marinum*) may have crucial effects on development of stress tolerant plants (Islam et al., 2007). *Hordeum marinum* is known as a provider line for oxidative stress defense with its reactive oxygen species (ROS) and superoxide dismutase (SOD) scavenging enzymes (Seckin et al., 2010). *Elytrigia elongata* is detected as more salt-tolerant plant than other species in Triticeae and it may be a potential source of tolerance genes for improving crops (Nevo and Chen 2010). Another crop wild relative, Sheepgrass, *Leymus chinensis* (Trin.) used for development of several stress resistant plants such

as wheat (Chen et al., 2005; Jiang et al., 1994) and *Arabidopsis* (Xianjun et al., 2011). In addition, as a desiccation model plant, *Sporobolus stapfianus* exemplifies an advanced stage of an evolutionary trend among desiccation tolerant plants (Gaff et al., 2009). *Agropyron* genus, consisting of important species such as *Agropyron cristatum*, is another reservoir for identification of stress tolerance related gene regions (Zhang, 2011). Thus, wild crop alternatives (Table 1) may be probable novel candidates to identify a QTL with dominant effects or to express the stress tolerance mechanisms in crops.

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

Species	Trait	Genes	Utilization	Reference
Abiotic stress				
<i>Aegilops uniarisfata</i>	aluminum tolerance	<i>ALMT1</i>	Producing 3A, 3B, 3D wheat substitution lines	Miller et al., 1997
<i>Agrostis stolonifera</i>	drought tolerance	-	QTL detection	Merewitz et al., 2014
<i>Agropyron cristatum</i>	drought and cold tolerance	Ascorbate and glutathione metabolism genes; 6-SFT	Antioxidant mechanism activation for drought tolerance; Fructan biosynthesis for cold tolerance	Shan and Liang 2010; Chatterton and Hardson 2003
<i>Brachypodium distachyon</i>	cold tolerance	ice recrystallization inhibition protein (<i>IRIP</i>) genes and C-repeat binding factor (<i>CBF3</i>) genes	Fructan accumulation under low temperature	Li et al., 2012
<i>Brachypodium distachyon</i>	drought tolerance	sucrose synthase gene, glucose-1-phosphate adenylyltransferase gene	Acting as an osmoportectan sugar biosynthesis	Verelst et al., 2013
<i>Elytrigia elongata</i>	salt tolerance	Not assigned	Salt tolerant wheatx <i>Elytrigia</i> amphiploid production	Colmer et al., 2006
<i>Hordeum marinum</i>	salt tolerance	Sodium transporter genes	Salt stolerant amphiploid production	Alamri et al., 2013
<i>Leymus chinensis</i>	salt tolerance	<i>LcDREB3a</i> transcription factor gene	induces expression of stress tolerance genes	Xianjun et al., 2011
<i>Salicornia brachiata</i>	salt tolerance	Vacuolar H ⁺ pyrophosphatase	Salt tolerant GM wheat	Roy et al., 2014
<i>Spartina alterniflora</i>	salt tolerance	<i>SaSce9</i>	Salt tolerance after transferring	Karan and Subudhi

<i>Sporobolus stapfianus</i>	drought tolerance	UDPglucose glucosyltransferase	Arabidopsis Leaf specific dessication gene survey	2012 Le et al., 2007
<i>Phleum pratense</i>	freezing tolerance	fructosyltransferase (FST) genes	Fructan accumulation for winter hardiness	Yoshida and Tamaura, 2011
<i>Triticum monococcum</i>	heat tolerance	Heat shock protein (HSP) gene	Controlling thermal tolerance	Vierling and. Nguyen 1992
<i>Triticum monococcum</i>	salt tolerance	<i>TmHKT1;5-A</i>	excluding sodium from the leaves,	James et al., 2011
Biotic stress				
<i>Agropyron elongatum</i>	rust resistance	<i>Lr24</i>	marker validation in wheat for leaf rust resistance	Gupta et al., 2006
<i>Avena barbarata</i>	crown rust resistance	<i>Pc39, Pc45</i> and <i>Pc94</i> genes	Seedling resistance	Cabral and Park, 2014
<i>Elymus repens</i>	<i>Fusarium</i> head blight resistance	Not assigned	Wheat introgression line production	Zeng et al., 2013
<i>Haynaldia villosa</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 et al., 2011
<i>Thinopyrum elongatum</i>	<i>Fusarium</i> head blight resistance	<i>FhbLoP</i>	FHB resistance	Chen et al., 2013
<i>Tripsacum dactyloides</i> L	corn root-worm resistance	Not assigned	Maizex <i>Tripsacum</i> introgression line production	Prischmann et al., 2009
<i>Triticum monococcum</i>	powdery mildew resistance	<i>Pm1</i>	Mapping of <i>Pm</i> resistance markers	Yao et al., 2007
<i>Leymus chinensis</i>	<i>Fusarium</i> head blight (FHB) resistance	<i>Fhb3</i>	FHB resistance in wheat- <i>Leymus</i> introgression lines	Qi et al., 2008

Conclusion

As multicellular organisms, plants always try to survive under variable conditions either sensing the upper part of soil or checking the subsoil for water and mineral support. In the former agricultural efforts, fertilizers, pesticides, herbicides have been used to cover these necessities. In time, toxic accumulation of these chemicals in nature reduced their routine usage. Later, basic agricultural approaches have left their seats to modern techniques which were supported as next generation systems and bioinformatics tools. In the opposite of traditional agricultural practices, modern agriculture has displayed the ability for

feeding the human population in several countries. But, nobody could be able to guess the capacity of cultivated crops will reach the saturation phase at genome level. Because, it is clearly understood that extensive use and artificial practices caused shrinkage of some important agronomical traits. Genetic uniformity and producing monoculture crops threatened the species survival and caused an agrobiodiversity loss. In addition, rapid food consumption and unplanned agricultural efforts merged with the environmental stresses started to alarm for sustainable agriculture. To overcome these conflicts, global funding sources still continue to support development of high yielded and stress

tolerant crop breeding projects with an increasing speed. There is also need to extend our understanding on agricultural policies and their outputs in the area of state based approach under the legal action plans (Tilman et al., 2002). In this term, damages originated from biotic and abiotic stresses will also help to identify the continent based crop production and future planning will be done according to food and feed requirements, territorial pressure and climate change.

As indexes indicate that there is an urgent need to feed the increasing human population. Synchronously, some precautions should also be taken into account to conserve the genetic heritage of cereals. Plant breeders and farmers still in the propensity of obtaining high yielded and more resistant crop materials and continue to purify the desired traits by filtering other useful traits as artifact. The problem arise from the point of these wrong crop breeding practices and the solution will be possible by saving and serially barcoding the genetic pools of crop populations according to origin, trait and genome structure. Moreover, in situ and ex situ conservation are likely to be fundamental techniques and help to survival of endangered species. Research on genome based interactions between cultivated and wild crops have been started with physiology level and furtherly issued by molecular tools to gain clues about trait based genome regions. Before embarking on breeding populations, phenome and genome- based outcomes can be collected to extract the unnecessary individuals. In the long-term, physical mapping and experiences on genotype annotations will have to be concentrated on different wild crops. Also, decreasing sequencing costs will enable to capture unexplored genome regions from important crops and their wild relatives. The integration of next generation sequencing, metabolomic and phenomic technologies into plant breeding will actively help to unravel the functional traits related to stress tolerance. Thus, the capacity of wild crop relatives will be more considered in the field of plant development. Briefly, crop wild relatives are important sources and their struggle to survive till today may strongly help understanding of the modified traits with functional roles during crop cultivation under fluctuated environmental conditions.

Acknowledgement

I would like to express my special thanks to the anonymous reviewers due to their valuable suggestions during improvement of this review, and Ceren Dimarco and Ali Sarikas for their critical

reading. I would like to also sent my sincerest thanks for the figure permissions to the Plant Health Progress journal, and Turkish Seed Gene Bank Manager Dr. Kursad Ozbek who is working for Ministry of Food Agriculture and Livestock in Turkey, General Directorate of Agricultural Research and Policy Central Research Institute for Field Crops, Department of Biodiversity and Genetic Resources.

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