

BOOK OF PROCEEDINGS

**Fourth International Agronomic Symposium
“Agrosym 2013”**

AGROSYM 2013



Jahorina, October 3 - 6, 2013

BREEDING FOR CROP IMPROVEMENT

Desimir KNEZEVIC^{1*}, Danijela KONDIC², Sretenka MARKOVIC², Nikola MICIC², Gordana DJURIC²

¹Faculty of Agriculture, University of Pristina, Lešak, Kosovo and Metohia, Serbia,

²Faculty of Agriculture, University of Banja Luka, Republic of Srpska, Bosnia

*(Corresponding author: deskoa@ptt.rs)

Abstract

In a frame of plant breeding are developed different methodologies directed towards genotypes improvement. Thousand years ago, a man practiced selection through domestication, cultivation and production plants that have more desirable traits than wild plants. Cultivated crop species selected from wild populations is called a landrace. Creation of new cultivars has been done by using of simply plants selection techniques choosing desirable characteristics for propagation, to more complex molecular techniques. Conventional breeding is based on homologous recombination between chromosomes to generate genetic diversity. Also, breeders may use a number of *in vitro* techniques such as protoplast fusion, embryo rescue or mutagenesis to generate diversity and produce hybrid plants that does not exist in nature. Breeders have the task to incorporate into crop plants improved traits: quality and yield, tolerance to salinity, extreme temperatures, drought, resistance to viruses, fungi and bacteria, increased tolerance to insect pests and herbicides. The most cultivars are created by crossing two parents. Created cultivars have changes of architecture, ripening time, productivity. Soil moisture is the most limiting factor in dry land agriculture. It is lost as evaporation from the soil surface and as transpiration from the plant surfaces. Technology growing and soil fertilization related to productivity of plants. The evaporation losses can be reduced by mulches, antitranspirants, wind breaks, weed control. In the coming future with climatic changes are necessary protected wild relative species and other existing genetic resources in nature and gene bank for successful breeding.

Keywords: Breeding, crop, productivity, genetic resources, improving adaptability

Introduction

During the practice, the man is permanently treed to make changes in nature, structure of plants and their functional properties in the aim to provide for enough food. Since near the beginning of human civilization, by simple selection of plants, fruits and seeds man had the greatest benefit from cultivated plants. Man is learned from nature how to develop new and new approach for environmental protection, improvement and cultivation of crop species. That was base for developed efficient techniques and methods as well as developing of plant breeding. In the breeding practice man used heterosis in plants, induced mutations, and nowadays new techniques in biotechnology (Knezevic et al., 2012). From the beginning of manipulation with plants, man used from nature the superior cultivars according to yield and quality of fruit, seed, biomass of vegetative organs and resistance to environmental stress factors. These natural resources of plant species, man firstly use for: a) domestication and later for b) classical plant breeding, c) modern plant breeding as well as for d) genetic modification.

Within domestication of plant, which approximately started 10 thousand years ago, man selected and produced plants with more desirable plants. Numerous crops are cultivated today as a results of domestication of plants (wild relatives, landraces) in different period (neolith) in past in different region of Old Word (about 5 thousand years ago) and later in region of New World (about 3 thousand years ago). Generally we can say that plant crops for food originated from domesticated plant in ancient time. These crops characterize adopted morpho-physiological traits (resistant to lodging, resistance to pests and disease, tolerance to abiotic stress factors, pollination and ripening time) high productivity, quality and genetic diversity.

Plant breeding approaches

Classical plant breeding started by crossing of different individual plants in the aim of developing new crop or cultivar. On this way produced ofsprings possess mixed genetic material from both parents. For increasing yield in the practice obtained ofsprings crossed with the high yielding parent. Also, plants may be crossed with themselves to produce inbred cultivars for breeding. Produced ofsprings use for testing of productive, physiological traits and quality properties. Recombination of genes generates genetic diversity within created plant population. However, breeder can use *in vitro* techniques such as protoplast fusion, embryo rescue or mutagenesis to generate diversity and efficient creating cultivar or hybrids that would not exist in nature. Application of breeding methods contributed to improvement of agro economic traits of plant species. Developed cultivars and hybrids characterize increasing of yield in average 1% annually. Also, by classical breeding in the previous century improved quality of the crop, resistance to fungi, viruses and bacteria diseases, increased tolerance to insect pests, environmental stress factors (drought, frost, salinity) and tolerance to herbicides. Changes in characteristics of the plants in the cross breeding process have been carried out on the basis of reproductive compatibility (Kondic et al., 2012) and had a contribution to maintenance and increment of genetic variability and economic impact in terms of increasing the quantity and quality of food (Živan ev et al., 2012). Modern plant breeding use techniques of molecular biology that has converted classical plant breeding to molecular plant breeding. By using of molecular biology methods improved precise insertion and manipulation of genes controlling desirable traits. In modern plant breeding used marker assisted selection or marker aided selection (MAS) that is approach of a marker morphological, biochemical or one based on DNA/RNA variation. These markers are used for indirect selection of a genetic determinant of a desirable trait (productive components, quality properties, resistance to disease and tolerance to abiotic stress).

Natural resources used in breeding program of genetic improvement (uric 2009). Sufficient methods of molecular biology make possible modification of plants by adding or delete specific genes from evolutionary unrelated species. Plants produced on this way are named as transgenic plants. By this methods is possible create plant with the desired traits faster than by classical breeding because the majority of the plant's genome is not altered. The majority of commercially released transgenic plants, carried genes controlling resistance to insect pests and herbicides. For example Insect resistant plants created by transferring a gene from *Bacillus thuringiensis* (*Bt*) that encodes a protein that is toxic to some insects. Herbicides usually work by binding to certain plant enzymes (known as the herbicides *target site*) and inhibiting their action. In the case of herbicide resistance crops with achieved a version of target site protein that is not inhibited by the herbicide were produced glyphosate resistant crop plants. The new step in genetic modification is creation plants that can produce pharmaceuticals and industrial chemicals. This represents new

area of breeding which sometimes called pharmacrops. All produced transgenic plants and genetically modified organisms are in focus of discussion, question and dilemma of scientist, politicians, consumers, producers, salvers, public media wide and specific population (Knezevic *et al.*, 2012). In spite that GM plant have significantly increased production the negative effect of GM plants are reflected in the appearance of loss of genetic diversity of crops, change the nutritional quality of food, appearance of potential monopoly ownership of major food products and sometimes lead to non safe consumption.

Criteria and plant species in focus of breeding

As we told, cereal crops, domesticated from wild grasses thousands of years ago. Domestication of the cereals, maize (*Zea mays*), rice (*Oryza sativa*), and wheat (*Triticum spp.*), are conducted in different regions of the world 7,000 to 10,000 years ago. The main three food crops are selected with much higher annual production than others are. Also, the barley (*Hordeum vulgare*), is among the earliest domesticated cereals as the fourth important cereal crop used as human food, animal feed, and brewing grains. Considering the annually quantity of production the next important cereal is the Sorghum, oat (*Avena sativa*), rye (*Secale cereale*), and millets. The completion of rice genome sequencing has greatly accelerated knowledge about rice domestication and origin (Kovach *et al.*, 2007; Sweeney and McCouch, 2007; Vaughan *et al.*, 2008). Among the cereals, maize differs from barley, rice, and wheat by having a lot of different morphological modifications during domestication (Doebley *et al.*, 2006). The high progress in yield increase achieved in barley, rice, and wheat, through breeding improvement of phenotypic traits that allowed effective harvesting, such as reduction in shattering and improvement of threshing, enhanced quality.

Selection on phenotype is a powerful approach to realize directed desirable changes requires genetic variability of potential parent for crosses and long time of selection. For the successful breeding is important to know how many genes and mutations were enough for the crop improvement through domestication. The aim of breeders is to provide methods and materials for breeding for high productivity, resistance to stresses and specific demands on the quality of products, as well as for effective response to growing conditions. Utilization of genetic resources, as donors of important characters and creation of initial breeding materials also contribute to the improvement of biological potential of crops and broadening of their genetic diversity (Uric 2009). Breeders are used identified effect of mutations, example, a single mutation controls primarily no shattering in all rice cultivars, free threshing or naked seeds in barley, and naked grains of maize *tg1* (Wang *et al.*, 2005). Also, used genes with different mutations for the origin of white seeds of rice and six-rowed ears of barley. In maize, *tb1* was responsible for the reduction of lateral branches of the wild progenitor (Doebley *et al.*, 1997). For the efficient breeding is very important to know whether a single mutation or multiple mutations of independent origins were involved in this domestication transition (Clark *et al.*, 2006). The location of genes and other markers in DNA fragments is necessary determine to make physical maps of genes along a chromosome. Physical maps are important for gene cloning, the development of genetic markers for tagging genes during breeding.

Simultaneously, increased attention is paid to the conservation and utilization of genetic resources as irreplaceable sources of genes for further genetic improvement of crops. To meet all these demands intensive research on genetics, biotechnology, breeding techniques, genetic resources and seed technologies is needed.

Conventional breeding can manipulate multiple traits simultaneously and can manipulate genetically complex “quantitative traits” i.e. traits that are influenced by the environment and traits that are conditioned by multiple genes. Advances in wheat genetics and genomics are essential for the sustained development of wheat cultivars with increased yield potential, resistance to pests and diseases, and tolerance of adverse environmental conditions. Wheat is also polyploid; it originated by interspecific hybridization, and its nucleus contains three different genomes, designated A, B, and D, each originated from a different diploid species.

Scientists must have access to genetic diversity to help create new cultivars or hybrids that can resist pests, diseases, and environmental stresses and need to know molecular base of breeding (Karp *et al.*, 1997). The success of breeding depends from existing divergent crop germplasm, level of its preserving and evaluation, as well ability of distributing crop germplasm. The broad potential of recombinant DNA technology will provide the possibility of both molecular analyses of crop productivity and ways in which it may be possible to improve that productivity (Mifflin, 2000). The research may be approached in different ways: a) by generating complete sequences of the plant genome, b) by genetic analysis of phenotypes using genetic marker technology and c) by metabolic analysis.

The developments in molecular genetics in wheat have been relatively slow in comparison to other crops, such as maize, rice or tomato, due to wheat’s ploidy level and complexity of its genome, percentage of repetitive sequences and level of polymorphism. Much fewer maps exist in wheat and far fewer QTL studies have been reported when compared to other grass species.

However, due to the large number of disease and pest resistances controlled by major genes, the mapping of such genes has dominated the research activities in wheat molecular genetics. The hexaploid nature of wheat and its amenity to cytogenetic manipulation have offered unique tools for molecular geneticists of wheat. These include the use of various aneuploid stocks, such as nullitetrasonic and ditelosomic lines, to assign molecular markers to specific chromosome arms (Anderson *et al.*, 1992; Plaschke *et al.*, 1996), of chromosomal deletion stocks (Endo and Gill, 1996) for the physical mapping of markers (Röder *et al.*, 1998) and of single chromosome substitution lines to map genes of known chromosomal location (e.g. Galiba *et al.*, 1995; Peña *et al.*, 1997).

Breeding for adaptation to environment

Classical methodology of breeding also follows new trends in research an application of new techniques. This approach will contribute to the making progress of theoretical and methodological bases for applied research and breeding and to provide new developed materials for genetic improvement of agricultural crops. Such cultivars are also the most effective tool how to minimize negative impacts of agriculture on the environment. Among all inputs in agricultural systems, the genetic improvement of crops can be considered as the most effective way of increasing plant production and quality without significant increase in costs and negative effects on the environment. Specific combination of environment condition have influence to growth development and differed depends of crops (Micic, 1996). In addition, breeding for resistance to pests, diseases and abiotic stresses as well as for effective utilization of nutrients and effective response to growing conditions can lead to decreased demands on other inputs, especially inputs of agrochemicals. (Paunovic *et al.*, 2007).

A wider genetic diversity of crops and cultivars contributes to more stable production and its quality in balanced agro ecosystems. Nowadays, achieved progress in molecular and cell biology,

in vitro techniques as well as applied genetics and breeding methods speed up further progress in agriculture through new cultivars and technologies. The breeding of crops and other plant species directed to verify methods for selection of genotypes with high efficiency of water use in dry conditions concerning the effects on transpiration and photosynthetic assimilation of flag leaves. The tested winter wheat cultivars could be divided into four groups according to their water use efficiency in dry and wet conditions: 1) genotypes economized water in both dry and wet conditions, 2) economized water only during water stress, 3) wasted water no matter whether there was a water deficit or a water surplus, and 4) genotypes squandered water even when there was its deficit. The second group could be important for breeding.

Potato genotypes sensitive to water stress were found to differ significantly in the effectiveness of water utilization in both variants, in wet and dry conditions.

Drought-stressed leaves spring barley cultivars showed a significant drop in leaf conductance and a reduction of photosynthetic rate. The root system of winter wheat varieties is markedly more sensitive to water deficit in comparison with the root system in wet conditions (Dodig et al., 2007). For this study successfully can use methods based on gas analysis used to monitor the efficiency of water use in leaves showed high accuracy with high sensitivity to physiological changes of leaves during water stress. Anatomical and morphological studies can provide important data to complete the explanation of physiological responses of leaves and root systems to water deficit (Micic, 2009).

One of the criteria of breeding is to find the relationship between vernalization requirements and dynamics of frost tolerance in wheat cultivars and lines with substitutions of homoeologous group 5 chromosomes carrying vernalization genes (*vrn*). By crossing the substitutions of dominant genes *Vrn* from spring to winter cultivars resulted in spring lines lower cold tolerance. In the case of substitution genes between two winter cultivars Mironovskaya 808 and Bezostaya 1 resulted in lines with shorter vernalization requirements and high frost tolerance level and lines with a longer expression of both these traits. The very important to know that developmental genes for vernalization acted as a master switch regulating the duration of expression of low temperature genes i. e. in winter wheat these genes are expressed for a longer time and at a higher level than in spring wheat.

The breeding process in different locations in regard to latitude, altitude and rainfall has proven a most efficient way to introduce and select genes for photoperiod insensitivity. The photoperiod insensitive genes, *Ppd1* and *Ppd2*, mostly present in spring wheat, and along with the dwarfing genes, *Rht1* and *Rht2*, resulted in a new plant type, which was not only lodging tolerant but higher yielding with high biomass due to pleiotropic effects or close linkage (Hoogendoorn *et al.*, 1988).and provided adaptation to most irrigated wheat-growing areas. The *Rht1* and *Rht2* alone give a higher stem of wheat (over the 90 cm). The combination of both dwarfing genes would give a shorter stem (approximately 70 to 80 cm). There are additional height differences due to other minor gene effects. The *Ppd1* and *Ppd2* genes have individual effects on flowering. The presence of only one of these genes characterized intermediate flowering genotypes. Both genes effects of these genes are influence to early maturity.

The breeding under abiotic stress can directed to analyze changes in seed traits affected the root system in the successive generation. Combined stress of drought and high temperature had a substantial influence on the photosynthesis and respiration of winter and spring wheat. The basic changes can also, investigate by changes in the anatomic structure of the caryopsis. It was found that the pericarp and seed coat layers of stressed grains were thicker and the cuticle is more suberised. There were also great anatomic changes in the embryonic part of the caryopsis.

Cultivar differences in the analyzed traits were observed. Plants grown under stress conditions mainly showed decrease or increase ((N, P, Ca, K, Mg, Na, B, and Mn).

Both genetically improved cultivars for yield and better scientific farming cultural methods have contributed to the yield increases (Zecevic et al., 2010). The effect of each factor (genetic/agrotechnic) is difficult to quantify. Yield stability has increased substantially across environments largely due to the adoption of management-responsive, high-yielding, disease-resistant semi dwarf wheat cultivars throughout all over the world. Improved agronomic practices also played an important role in enhancing the stability of yields. The increasing production and yield influenced by water-supply, (irrigation) applied nitrogen fertilizer (Kovacevic et al., 2009, Knezevic et al., 2011). Nitrogen fertilizer use depending of soil fertility and economic power. In average between 20 and 40 kg ha⁻¹ in some region farmers apply about 60 kg ha⁻¹. That is not enough for numerous arable locations. On the other hand the high rates of nitrogen applications, as well as heavy manuring, may increase disease incidence. In vegetable crops, research suggests about a 50-50 split between genetic gain and gain attributed to management. “Green revolution” varieties have increased yields 2 to 3 fold (Miflin, 2000).

Efforts to control insect pests of cereal crops generally take a back seat to the more pressing problems of abiotic production constraints, such as heat, drought, low soil fertility, salinity, day-length and so on. Even when these constraints are met, insect pests are frequently considered secondary to other biotic stresses, such as disease. The symptoms of insect infestation may be masked by various abiotic and biotic factors, or the insect itself once discovered may be misidentified and incorrect treatments prescribed. In some cases, insect damage is mistaken for that caused by drought, heat, cold or disease.

Conclusion

Genetic diversity is the root of biodiversity and therefore important for agriculture, which are under the pressure factors such as climate change, loss of natural habitats, environmental degradation and population growth. Adopting methods to save plant diversity has the double benefit of protecting biodiversity and ensuring food security for farmers. Our interest is in how to make use of natural resources for the benefit of biodiversity to manage without risks and improve crop species by breeding.

Acknowledgements

The authors wish to thank to Ministry of Education and Science of Republic of Serbia, for financial support of the Project TR31092.

References

- Anderson, J.A., Ogihara, Y., Sorrells, M.E., Tanksley, S.D. (1992): Development of a chromosomal arm map for wheat based on RFLP markers. *Theor. Appl. Genet.*, 83: 1035-1043.
- Clark, R.M., Wagler, T.N., Quijada, P., Doebley, J.F. (2006): A distant upstream enhance at the maize domestication gene *tb1* has pleiotropic effects on plant and inflorescent architecture. *Nat Genet* 38: 594–597
- Dodig, D., Zoric, M., Knežević, D., Dimitrijević B., Šurlan-Momirović, G. (2007): Assessing wheat performance using environmental information. *Genetika*, 39, 3, 413-425

- Doebley, J.F., Stec, A., Hubbard, L. (1997): The evolution of apical dominance in maize. *Nature* 386: 485–488.
- Doebley, J.F., Gaut, B.S., Smith, B.D. (2006): The molecular genetics of crop domestication. *Cell* 127:1309–1321.
- uric, G., Tomic, L., Radun, M., PeCanac, D. (2009): O uvanje i održivo korišćenje biljnih genetičkih resursa u Republici Srpskoj. Zbor. rad. nau. no-stru. nog skupa sa me. u ešCem "Zaštita i zdravlje na radu i zaštita životne sredine", Banja Luka, 24-26. juni 2009. pp. 81-93.
- Endo, T.R., Gill, B.S. (1996): The deletion stocks of common wheat. *J. Hered.*, 87: 295-307.
- Galiba, G., Quarrie, S.A., Sutka, J., Morgounov, A., Snape, J.W. (1995): RFLP mapping of the vernalization (*Vrn1*) and frost resistance (*Fr1*) genes on chromosome 5A of wheat. *Theor. Appl. Genet.*, 90: 1174-1179.
- Hoogendoorn, J., Pfeiffer, W.H., Rajaram, S., Gale, M.D. (1988): Adaptive aspects of dwarfing genes in CIMMYT germplasm. In T.E. Miller & R.M.D. Koebner, eds. *Proceedings of the 7th International Wheat Genetics Symposium*, p. 1093-1100. Cambridge, UK.
- Karp, A., Edwards, K.J., Bruford, M., Funk, S., Vosman, B., Morgante M., Seberg, O., Kremer, A., Boursot, P., Arctander, P., Tautz, D., Hewitt, G.M. (1997): Molecular technologies for biodiversity evaluation: opportunities and challenges. *Nature Biotechnology*, 15, 625-628.
- Knezevic, D., Milosevic, M., Torbica, A., Brocic, Z., Ciric D. (2011): Variability of grain yield and quality of winter barley genotypes (*Hordeum vulgare* L), under the influence of nitrogen nutrition. *Növénytermelés*, suppl. 60, 25-28.
- Knezevic, D., Kondic, D., Markovic, S. (2012): Importance of genetically modified organisms. *Proceedings. Third International Scientific Symposium "Agrosym Jahorina 2012"*, Editorial in Chief: Dušan Kovačević, 15-17. novembar 2012. Jahorina, pp. 117-121.
- Kondic, D., Knežević, D., Paunovic, A. (2012): Grain weight of genotypes of triticale (*X Triticosecale* Wittmack) in agroecological conditions of Banja Luka. *Genetika*, 44, 2, 419-428.
- Kovach, M. J., Sweeney, M. T., McCouch, S. R. (2007): New insights into the history of rice domestication. *Trends Genet.*, 23: 578–587.
- Kovacevic, V., Stojic, B., Rastija, M., Brkic I., Drezner, G. (2009): Response of maize, wheat and barley to phosphorus and potassium fertilization. *Cereal Research Communications* Vol. 37 (supp.), 129-132.
- Micic N., uric Gordana, Jevtic S., Lučić P. (1996): The Basis for Defining a Model of Ecological Functions of the Organogenesis in Fruit Crops. *J. Sci. Agric. Res.* 57, 203, 89–99.
- Micic, N., uric Gordana, Cvetkovic, M., Lukic, D. (2009): Anatomical Histological and Chemical Properties of the Young Bearing Wood's Organs and Tissues in Apple. *Agroznanje*, 10, (4):5-20.
- Mifflin, B. (2000): Crop improvement in 21st century. *Journal of Experimental Botany*, 51, 1-8.
- Plaschke, J., Börner, A., Wendehake, K., Ganal, M.W. & Röder, M.S. (1996): The use of wheat aneuploids for the chromosomal assignment of microsatellite loci. *Euphytica*, 89: 33-40.
- Paunovic, A., Madic Milomirka, Knezevic, D., Bokan, N. (2007): Sowing density and nitrogen fertilization influences on yield components of barley. *Cereal Res. Commun.*, 35, 2, 901-904.
- Peña, R.C., Murray, T.D., Jones, S.S. (1997): Identification of an RFLP interval containing *Pch2* on chromosome 7AL in wheat. *Genome*, 40: 249-252.
- Röder, M.S., Korzun, V., Gill, B.S., Ganal, M.W. (1998): The physical mapping of microsatellite markers in wheat. *Genome*, 41: 278-283.

- Sweeney, M.T., McCouch, S.R. (2007): The complex history of the domestication of rice. *Ann Bot (Lond)* 100: 951–957
- Timothy, L., Frances, F., Shaptera, M., McDonald, S., Waters, L.E.D., Chivers, H.J., Drenth, A., Nevod, E., Henry, J.R. (2011): Genome diversity in wild grasses under environmental stress. *PNAS Early Edition*, 1-6.
- Vaughan, D.A., Lu, B.R., Tomooka, N. (2008): The evolving story of rice evolution. *Plant.Sci.*174:394-408.
- Zečević, V., Knežević, D., Bosković, J., Milenković, S. (2010): Effect of nitrogen and ecological factors on quality of winter triticale cultivars. *Genetika-Belgrade* 42 (3):465-474.
- Živanović, D., Torbica, A., Mastilović, J., Knežević, D., Čukić, N. (2012): Relation among different parameters of damaged starch content, falling number and mechanical damage level. *Ratar. Povrt.* 49:3 282-287
- Wang, H., Nussbaum-Wagler, T., Li, B.L., Zhao, Q., Vigouroux, Y., Faller, M., Bomblies, K., Lukens, L., Doebley, J.F. (2005): The origin of the naked grains of maize. *Nature*, 436: 714–719