# FROM GENETICS TO GENOMICS IN PLANTS AND ANIMALS

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The classical concepts in plant and livestock selection for economically important quantitative traits traditionally are based on phenotypic records, aiming at improvement of the traits by obtaining better genetic gain. The increase in genetic variation together with shortening of the generation interval is the major target of long term improvement of methods and tools for selection activities. The discoveries and implementations of biotechnology and molecular biology for selection purposes provide a stable background for generating of new knowledge and practical use in agricultural research and practice as well as to meet the growing demand for more and with better quality food and feed. The innovations in molecular knowledge related to practical selection aside with the quick quantification in breeding schemes allowed to reconsider the

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opportunities for sustainable development of selection methods for improvement of the traits of interest in agriculture, the quick invention and practical application of new high-throughput technologies for studying of the genomic variation, evolution, translation of proteins and metabolite determination altogether put in an open and communicative environment of information technologies provide a new holistic platform for better research and more knowledge for practical application of selection decisions.

*Key words:*agriculture, biotechnology, MAS

## INTRODUCTION

Since almost the beginning of human civilization, exploiting variation in the characteristics of the plant and animal genetic resources that are used for producing food and other agricultural products through breeding has been at the heart of efforts to increase and diversify agricultural production and productivity, enhance food security and incomes, and adapt farming to changing environmental conditions and social needs. Initially, this was achieved simply by selecting and reproducing preferred individuals or spontaneous variants, and indeed this practice remains important today as the basis for producing new generations of cultivated landraces and indigenous breeds. However, the crops, trees, livestock and fish that are farmed today have arisen largely from the introduction of knowledge based breeding approaches. (SPEIDEL *et al*., 2009)

The classical plant and livestock selection for economically important quantitative traits traditionally is based on phenotypic records. At the beginning of the twentieth century, with the inclusion of crosses into breeding schemes prior to artificial selection and application of Mendel's laws of inheritance to improve both simple and quantitative traits thus providing the foundation for modern genetics. (FALCONER and MACKAY, 1996; THE ROYAL SOCIETY, 2009, TESTER and LANGRIDGE, 2010, FEHR, 1987, LYNCH and WALSH, 1998).

On this classical knowledge background the rapid development and application of plant and animal biotechnology has gained new dimensions in the recent 50 years. The discoveries and break through developments in biotechnology and subsequently in genomics in last decade have brought a substantial change in the scientific knowledge, and has resulted in new and exciting advances in agricultural research and practice (MOOSE and MUMM, 2008, METZLAF, 2010, KONSTANTINOV and MLADENOVIC DRINIC, 2007).

The discoveries of molecular markers linked to specific regions in the genome of plants and animals have facilitated their introduction and monitoring via marker assisted selection (MAS). The use of MAS techniques increasingly reshaped breeding programs and facilitated the rapid gains from selection by accelerating the delivery of crop varieties and animals with improved traits (STUBER *et al.*, 1982, TANKSLEY *et al.,* 1989; KOEBNER, 2003, JOHNSON, 2004). The application of MAS in breeding has continued to increase in the public and private sectors but most

applications have been constrained to simple, monogenic traits (DEKKERS and HOSPITAL, 2002, XU and CROUCH, 2008). Currently, despite important strides in marker technologies, the use of traditional MAS has stagnated for the improvement of polygenic traits which are affected by many genes, each with small effect. Biparental mating designs for the detection of loci affecting these traits (quantitative trait loci, QTL) impede their application, and the statistical methods used are ill-suites to the traits polygenic nature (RUANE and SONNINO, 2007). The introduction of Genomic selection (GS), however, has shifted that paradigm. The GS predict the breeding values of lines in a population by analyzing their phenotypes and high-density marker scores. Selection based on GS predictions, potentially leads to more rapid and lower cost gains from breeding (MEUWISSEN *et al*., 2001, JANNINK *et al*., 2010).

The objectives of this article are to review essential aspects of the selection approaches as development and application in the context of recent advances of genetics from classical breeding to molecular breeding and genomic selection to meet the global challenges of the agriculture in the 21$^{st}$ century (OECD, 2009, ALSTON *et al*., 2009, BATTISTI *et al*., 2009, ATANASSOV, 2009).

## ACHIEVEMENTS IN SELECTION OF PLANTS AND LIVESTOCK SPECIES

### Genetics advances - state of art

The conventional plant and animal breeding strategies are based on crossing, selection and fixation of superior phenotypes to develop improved cultivars and breeds suited to specific conditions with the aim to fulfill the needs of farmers and consumers. During the past century selection plans for agricultural species has led to large improvements in yield and yield stability, especially by improving the abilities for resistance to plant pathogens or production traits in farm animals. For example the Green Revolution succeeded by using conventional breeding to develop F1 hybrid varieties of maize and semi-dwarf, disease-resistant varieties of wheat and rice. These varieties could be provided with more irrigation and fertilizer without the risk of major crop losses due to lodging (falling over) or severe rust epidemics. Artificial insemination and embryo transfer in livestock species have improved the most important productive and reproductive traits.

Such common breeding improvements led to narrowing of the genetic base of the germplasm. New sources of variation such as landraces and wild relatives were exploited to increase the crops and animals productivity and adaptive abilities (RUANE and SONINO, 2007)

These substantial changes in the agronomic- and management-based approaches developed new kind of knowledge related to the function of genes and traits of interest and the networks in which they are involved. Without this knowledge we will not be able to improve crops and livestock ability to maintain yields as well as the production quality under the changeable climatic conditions.

Agricultural practices were, for a long time, an empirical art that involved carrying out crosses to generate large segregating populations, which were grown and screened for individuals with favourable traits. Here it is pertinently to point the difference between 'qualitative' and 'quantitative' traits: showing either a simple segregation of distinct phenotypes or a wide spread of phenotypic variation, respectively. 'Quantitative' traits are often polygenic (i.e. determined by a large number of genes) and influenced by environment (HALLAUER, 2007).

Most of the traits considered in animal and plant genetic improvement programmes are quantitative, i.e. they are controlled by many genes together with environmental factors, and the underlying genes have small effects on the phenotype observed. Milk yield and growth rate in animals or yield and seed size in plants are typical examples of quantitative traits. In classical genetic improvement programmes, selection is carried out based on observable phenotypes of the candidates for selection and/or their relatives but without knowing which genes are actually being selected (WELLER, 1994).

Plant and animal scientists have made significant advances in understanding the agronomical, species-specific, breeding, biochemical and molecular processes that underlie important genetic, physiological, and developmental traits, or that affect the ability of plants and animals to cope with unfavourable environmental conditions for several decades (GEPTS, 2002). However, it was often difficult to exploit this information for plant and animal breeding practice, because the level of understanding was not deep enough, and because necessary techniques were not available. Recent developments in plant and animal molecular biology and genomics are greatly accelerating the speed with which knowledge gained in basic plant and animal science can be applied to species improvement (DEKKERS and HOSPITAL, 2002).

**Genetic engineering and agricultural biotechnology**

In addition to conventional breeding, the transgenic approaches ('genetic engineering') were also used to improve yield, reproduction traits, feed and food quality as well as to meet such major challenges as biotic and abiotic stress tolerance in plants. The technological breakthroughs made from 1983 onwards, when the first successful transfer of a foreign gene - Agrobacterium (BEVAN *et al*., 1983, FRALEY *et al.*, 1983, HERRERA-ESTRELLA *et al*., 1983) into a plant was reported came into widespread commercial use as it became possible to transform a large range of important crop plants (METZLAF, 2007, JAMES, 2009). It was possible to significantly reduce the breeding process and to introduce novel alleles and genes from diverse sources that are absent from plant genomes. The main limitation of this technology is the availability of preliminary knowledge about the role of a gene in determining a given trait and is, at present, only applicable for traits that are determined by one or a relatively small number of genes. To date, most applications that have reached the field involve the use of heterologous genes (i.e. genes from other organisms) to engineer various adaptive traits as herbicide and insecticide resistance (JAMES, 2009, MADSEN and STREIBIG, 2010).

In animal breeding sector - production of cloned animals with engineered innate immunity to diseases that reduce production efficiency has the potential to reduce substantial losses arising from mortality and subclinical infections. (RUANE and SONINO, 2007). Biotechnology could also produce plants for animal feed with modified composition that increase the efficiency of meat production and lower methane emissions.

Currently, the major commercialized transgenic crops involve relatively simple manipulations but next decade the development of combinations of desirable traits and the introduction of new, highly polygenic traits such as drought tolerance and nutritional quality will be expected based on application of genetic engineering approaches (BATTISTI and NAYLOR, 2009, FEDOROFF et al. 2010; THE ROYAL SOCIETY, 2009, JAMES, 2009):

Stress resistance. More and more research is addressing intensifying global concerns over water scarcity. Salt, heat, and drought resistant crops could play an important role in meeting emergency food needs in the developing world and stabilising crop yields in industrialised nations (THE ROYAL SOCIETY, 2009, JAUHAR, 2006).

Altered composition With the advent of genetic engineering, food enhancement and processing could take on a new dimension. Instead of adding new ingredients to foods in the factory, beneficial substances can now be put into the crops themselves. Both industry and consumers have much to gain from crops like "designer oilseeds" or starch crops custom tailored to specific applications (THE ROYAL SOCIETY, 2009, JAMES, 2009).

Improved animal feed. Phosphorous overabundance in poultry manure is a common environmental problem in areas of intensive livestock production. When added to animal feed, the enzyme phytase can alleviate this problem by reducing phosphorus discharge by up to a third. Scientists have genetically modified the forage crop alfalfa to contain high levels of phytase (THE ROYAL SOCIETY, 2009).

Novel products and 'quality traits'. Some of these new "quality traits" are already in use in the US, while others are well advanced in development. For the time being, no approval applications for GM plants for producing specialty substances have been submitted in the EU. However, the EU produces many important enzymes with the help of genetically modified microorganisms (THE ROYAL SOCIETY, 2009).

Transgenic plants can be used to produce an array of substances including pharmaceuticals, silk proteins, biodegradable plastics, or industrial enzymes. Such crops are only intended for industrial use and are not to be used as food (OECD, 2009, THE ROYAL SOCIETY, 2009).

Elimination of pollutants, environment protection, biofuels. Genetic engineering has given plants the ability to clean-up soils polluted with heavy metals or petroleum products. Such strategies can offer cheap and sustainable solutions to dangerous environmental problems (OECD, 2009, THE ROYAL SOCIETY, 2009).

Renewable energy. Production of bio-fuels has gained more territory in plant and animal breeding plans the use of animal waste as well the breeding of

plants for bio-fuel are major targets of genetic engineering. The future of world bio-economy has strong interest in enhancing the renewable energy sources and further biotech-based improvements are in the development pipeline (THE ROYAL SOCIETY, 2009, ATANASSOV, 2009).

Nevertheless these technologies permit the generation of novel variation beyond that which is available in naturally occurring populations and are still widely used, they will remain limited while regulatory demands impose high cost on realizing GM crops. Although it is likely that most of the important contributions to crop and livestock improvement in the coming decade will continue to be from non-GM approaches (OECD, 2009, JAUHAR, 2006)

**Molecular breeding accelerates favorable gene action**

The basic theoretical concept of quantitative genetics is the assessment of heritability which implies quantification of the proportion of phenotypic variation that is controlled by genotype. In reality, heritability is mostly greatly influenced by the genetic architecture of the trait of interest, which is defined by the number of genes, the measure of their effects, and the profile of the gene action associated with phenotypes. The advantages of better knowledge of genetic architecture and better evaluation of the favorable gene action (which is the purpose of selection) usually has the greatest impact on improving the selection response (MACKAY, 2001).

The recent very fast progress in molecular biology disciplines including genomics research produced a range of molecular markers applied to define the variation of the traits in the species: Random Amplification of Polymorphic DNAs (RAPDs), Sequence Tagged Sites (STS), Sequence Characterized Amplified Region (SCAR), Amplified Fragment Length Polymorphisms (AFLPs), Simple Sequence Repeats (SSRs) or microsatellites, Single Nucleotide Polymorphism (SNPs) and the Diversity Arrays Technology Markers (DArT) (AKHUNOV et al., 2009, CLOSE et al., 2009, CROSSA et al. 2007).

These marker systems were developed towards elaboration of high-density DNA marker maps (i.e. with information concerning the bigger number of markers with location, distributed over relatively short intervals throughout the genome). Such marker maps were constructed for a big number of agricultural species comprising a range of economically important traits, thus providing the framework needed for application of this information in selection programs.

The implementation of these genetic markers in livestock and plant selection was oriented towards their association both with traits with polygenic character and traits due to single genes economically important for the practical breeding systems. These developments provided a beneficial environment to increase the response to selection, in particular for traits that are difficult to be improved by conventional selection approaches - traits with low heritability or traits for which measurement of phenotype is difficult, expensive, only possible late in life, or not possible on selection candidates.

The elaboration of high density genetic maps, and appropriately structured mapping populations set up a firm background for defining of gene action and

estimation of genetic values of thousands of loci distributed across the entire genomes of many crop and livestock species. The outcomes from such mapping studies give significantly improved estimates for the number of loci, allelic effects, and gene action controlling traits of interest. Many, genomic segments can be identified showing statistically significant associations with traits of interest and quantitative trait loci (QTLs) . In addition to genetic mapping in families derived from biparental crosses, new advances in association genetics with candidate genes and approaches that combine linkage disequilibrium analysis in families and populations (HOLLAND, 2007, XU and CROUCH 2008) further enhance power for QTL discovery (KEARSEY and FARQUHAR, 1998).

Information about the QTLs can be exploited in several ways to increase genetic variation and the and favorable gene action. For the traits having low to moderate heritability, such as grain yield, QTLs, and their associated molecular markers often account for a greater proportion of the additive genetic effects than the phenotype alone. Aside with that genetic architecture can be exploited to add or delete specific alleles that contribute to the genetic value. When either genetic linkage or epistasis among loci with antagonistic effects on a trait limits the genetic gain, QTL information can be used to break these undesirable allelic relationships (VISSCHER *et al.*, 2008).

Success in using information about QTLs to increase genetic gain depends to a great extent on the magnitude of QTL effects, accurate assessment of QTL positions, stability of QTL effects across different environments, and whether QTLs are robust across relevant breeding germplasm. Prediction of QTL positions is improved additionally by further fine mapping, which facilitates testing QTL effects and genetic variation in populations. The genetic variation for a QTL can be determined better when the density of the observed recombinations is close to the resolution of single genes, (SALVI and TUBEROSA, 2005, YU and BUCKLER, 2006, BELO *et al.* 2008, HARJES *et al.* 2008). Molecular isolation of QTLs permits the development of suitable or functional molecular markers at the potential resolution and dramatically increases the accuracy by which genetic effects are estimated and manipulated in breeding programs.

One of the ways to study the effect of QTL and to enhance crop productivity is the use of desirable transgenic strategy. The use of transgenes can simplify the genetic architecture for desirable traits in ways that may be superior or not and possible to even when perfect markers are available for robust QTLs of large effect. The specific features of transgenes (carrying a single gene with dominant effect) can reduce complex quantitative improvement to a straightforward solution. An excellent example is the *Bt* corn maize with the resistance to *Bacillus thuringiensis*. Partial resistance in maize germplasm to this insect pest had been characterized by traits with low heritability (TOLLEFSON, 2007) but the *Bt* transgenic events offers a simply inherited trait that is effectively implemented in breeding programs. Transgenic events can also be designed to intervene at key regulatory steps for entire metabolic of developmental pathways, such that gene action

responsible for the corresponding traits are largely inherited as single dominant factors that are less sensitive to environmental effects.

**Marker assisted selection - a tool for efficient breeding**

Historically the practice of conventional phenotypic selection has been effective but for some traits such selection has made little progress due to challenges in measuring phenotypes or identifying superior individuals with highest genetic value. The influence of environment, it interaction with the genotype as well as some recording errors can also contribute to observed differences. Evaluation of genotypes in different environments with replicated designs accounts for more accurate estimation of breeding values but are time consuming and expensive. Molecular markers can be employed as a supplement to phenotypic observations in genetic evaluation (LANDE and TOMPSON, 1990).

The implementation of molecular markers closely associated with desirable traits is being used to increase the efficiency and effectiveness of conventional breeding by indirect selection of the desirable plants in segregating population. Such selection approaches, based on the use of markers and called in general MAS (marker assisted selection) has been used to increase the probability of identifying truly superior genotypes, by focusing on determination of genotypes with superior potential (i.e. early elimination of inferior genotypes), and by enabling simultaneous improvement for traits that are negatively correlated (KNAPP, 1998, DEKKERS and HOSPITAL, 2002, HOLLAND, 2004, VARSHNEY *et al.*, 2006, COLLARD and MACKILL, 2008, DEKKERS, 2004).

Marker-assisted selection is effective for the manipulation of large effect alleles with known association to a marker (ZHONG *et al.,* 2006) but it is showed to be not so effective when many alleles of small effect segregate and no substantial effects can be identified (Fig.1).
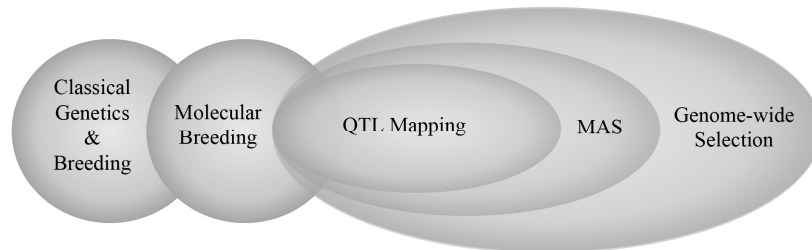
For example in plants, many key stresses associated with rapid environment changes, notably drought and salinity tolerance, are complex and highly variable. For these types of traits, it is necessary to dissect tolerance into component contributory traits and to identify genetic regions encoding the traits, rather than overall plant tolerance (MUMM and TESTER, 2008; SALEKDEH *et al.* 2009, REYNOLDS *et al.,* 2009). However, this genetic approach requires high-throughput phenotyping (phenomics) (FINKEL, 2009). Phenomics also allows screening of populations for particular traits and will facilitate the introgression of novel variation from wild germplasm. Phenomics will enable tighter definition of the properties of molecular markers, allowing introgression of appropriate combinations of tolerance traits into commercial varieties for particular target environments.

The combination of reliable phenotyping and MAS has been particularly important in transferring desirable alleles by simple backcrossing into elite germplasm. Although MAS has been used to track multiple independent loci (COLLARD and MACKILL, 2008), conventional breeding schemes become quite complex as the number of target loci expands.

Recent studies (BERNARDO, 2008, XU and CROUCH, 2008) have shown that MAS failed to significantly improve polygenic traits. The weaknesses of traditional MAS come from the way MAS splits the task into two components, first identifying QTL and then estimating their effects. QTL identification methods can make MAS poorly suited to crop improvement: (i) bi-parental populations may be used that are not representative and in any event do not have the same level of allelic diversity and phase as the breeding program as a whole (JANNINK *et al.*, 2001; SNELLER *et al.*, 2009); (ii) the necessity of generating such populations is costly such that the populations may be small and therefore underpowered; (iii) validation of discoveries is then warranted, requiring additional effort; (iv) the separation of QTL identification from estimation means that estimated effects will be biased (BEAVIS, 1994, MELCHINGER *et al.,* 1998; SCHON *et al.*, 2004), and small-effect QTL will be missed entirely (LANDE and TOMPSON, 1990) as a result of using stringent significance thresholds.

Association or linkage disequilibrium mapping applied directly to breeding populations has been proposed to mitigate the lack of relevance of bi-parental populations in QTL identification (RAFALSKI, 2002) and QTL have been mapped in this way (CROSSA *et al.*, 2007, KRAAKMAN *et al.*, 2004). This practice nevertheless retains the disadvantage of biased effect estimates and therefore poor prediction of line performance (LANDE and THOMPSON, 1990, MEUWISSEN *et al.*, 2001). In addition association mapping studies permit to identify false positive genetic markers scores in particular in studies with poorer recording. This accounts also for the population structure which is a major problem for accurate implementation of linkage disequilibrium mapping (HALL *et al.*, 2010). The implementation of newer high-throughput sequencing technologies and more detailed phenotyping will overcome the problem with the necessity of increasing number of genetic markers and the separation of true from false positives aside with a good validation of identified association.

Possible solutions to part of these problems concerning the precision of linkage disequilibrium mapping dealing with multiple loci, in particular, multiple loci of small genetic effect, can be given by two relatively new methods involving marker assisted selection: Marker-Assisted Recurrent Selection (MARS) and Genome-Wide or Genomic Selection (GS) (BERNARDO and CHARCOSSET, 2006, HEFFNER et al., 2009, MEUWISSEN et al., 2001).

MARS involves crossing selected individuals at each selection cycle so that desirable alleles at the target loci are introduced one at a time or through the merging of multiple crossing and selection streams. A problem with this approach is that it is most effective for genes or quantitative trait loci (QTLs) of major effect. This technique has been successfully applied to sunflower, soybean and maize to bring desirable alleles into single elite lines.
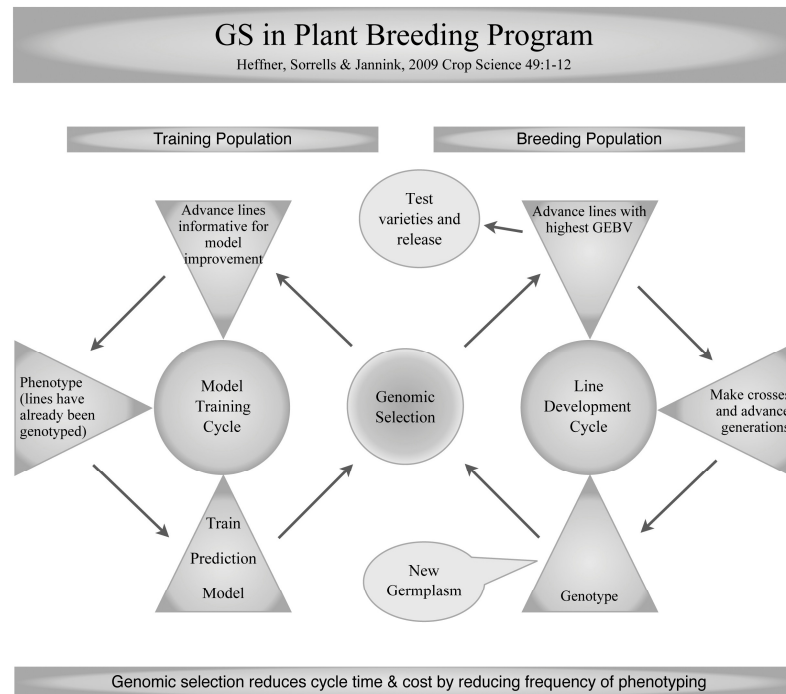
**Genomic Selection and the advance of high-throughput technologies**

By assumption - genomic selection (GS) is a form of marker-assisted selection in which genetic markers covering the whole genome are used so that all quantitative trait loci (QTL) are in linkage disequilibrium with at least one marker. This approach has become feasible thanks to the large number of single nucleotide polymorphisms (SNP) discovered by genome sequencing and new methods to efficiently genotype large number of SNP. A key to the success of GS is that it incorporates all marker information in the prediction model, thereby avoiding biased marker effect estimates and capturing more of the variation due to small-effect QTL.

In contrast to the MAS approaches, GS does not require prior information on marker trait associations and can be used to select for multiple loci of small genetic effect. GS uses a 'training population' of individuals that have been both genotyped and phenotyped to develop a model that takes genotypic data from a 'candidate population' of untested individuals and produces genomic estimated breeding values (GEBVs). Fig 2. These GEBVs do not explicitly explain the function of the underlying genes but they are the ideal selection criterion. In the plant breeding context, untested individuals would belong to a broader population defined as a crop market class or the breeding program as a whole. In simulation studies, GEBVs based solely on individuals' genotype have been remarkably accurate (MEUWISSEN et al., 2001, HABIER et al., 2007, ZHONG et al., 2009). These accuracies have held up in empirical studies in dairy cattle (HAYES et al, 2009, LUAN et al., 2009, VANRADEN et al., 2009), mice (LEE et al., 2008, LEGARRA et al., 2008) and in bi-parental populations of maize, barley and Arabidopsis (LORENZANA and BERNARDO, 2009). Given decreasing genotyping costs and stagnant or increasing phenotyping costs, and the ability to select individuals much earlier in the breeding cycle, GS is revolutionizing both animal (HAYES et al., 2009, SCHAEFFER, 2006) and plant breeding (EATHINGTON et al., 2007, HEFFNER et al., 2009).

Simulation results and limited experimental outcomes suggest that genetic merit can be predicted with high accuracy using genetic markers alone, reaching levels of 0.85 even for polygenic low heritability traits. These simulation studies also have shown that genomic selection can lead to high correlations between predicted

and true breeding value over several generations without repeated phenotyping (MEUWISSEN *et al*., 2001, HABIER *et al.,* 2007, JANNINK *et al*., 2010). This level of accuracy is sufficient to consider selecting for agronomic performance using marker information alone but more validation is required especially in samples of the population different from that in which the effect of the markers was estimated (GODDARD and HAYES, 2007, SCHAEFFER 2006, MISZTAL, 2006).

## GS in Plant Breeding Program
Heffner, Sorrells & Jannink, 2009 Crop Science 49:1-12

Training Population          Breeding Population

Advance lines informative for model improvement

Test varieties and release

Advance lines with highest GEBV

Phenotype (lines have already been genotyped)

Model Training Cycle

Genomic Selection

Line Development Cycle

Make crosses and advance generations

Train Prediction Model

New Germplasm

Genotype

Genomic selection reduces cycle time & cost by reducing frequency of phenotyping

The discussed above new breeding and selection strategies based on the use of molecular markers rely on the availability of cheap and reliable marker systems. A serious limitation in marker application for some species has been the paucity of useful markers. However, the new high throughput sequencing platforms have allowed large-scale discovery of single-nucleotide polymorphisms (SNPs) for species where few markers were previously available. The new marker systems combined with the new marker-based selection and screening strategies provide a base for a revolution in crop breeding and genetics.

Aside with that, the marker technologies on which GS methods depend are constantly changing. Next-generation sequencing technologies and improvement of genotyping platforms provide breeders with powerful tools for characterizing the genetic composition of their germplasm. As these technologies continue to evolve, they will provide quantitatively and qualitatively different information (e.g., copy number and epigenetic variation), (STRANGER et al., 2007, ZHANG et al., 2008), and statistical machinery will also need to evolve to use this information efficiently to increase prediction accuracy (JANNINK et al., 2010).

Next-generation sequencing technologies are able to re-sequence entire plant genomes getting more accurately providing quite larger information about discovering of new variations among individuals, strains and/or populations. The large amounts of nucleotide polymorphisms are effectively identified by mapping sequence fragments onto a particular reference genome data set, a capability that is of immense importance in all genetic research (VARSHNEY et al., 2009). The identification and determination of genetic variation is quite more efficient by tracking within large populations. Such achievements are expected to advance the expected response from genomic selection. And in addition whole-genome comparisons identifying chromosomal duplication and conserved synteny among related species provide evidence for hypotheses on comparative evolutionary histories with regard to the diversification of species in a related lineage.

With the advent of the newly emerged high-throughput technologies and its amalgamation with the new scientific domains: genomics, metabolomics, proteomics and bioinformatics it is observed not only a change of the methods but a shift of the paradigm of selection strategies. This breadth through development of new high-throughput technologies was successfully implemented for speeding up the gene discovery, functions and developmental processes and the evaluation of the selection strategies, physiological and metabolite profile and the molecular basis of biodiversity in order to protect it and to use the agricultural resources properly for the constantly growing demands of the humankind (MOCHIDA and SHINOZAKI, 2010). With the completion of the sequences of several plant and animal genomes as well as sequencing of the whole human genome a mighty knowledge based tool become available and gives significant improvement to the research in all disciplines of plant, animal and human biology.

## CONCLUSIONS

The achievements of the classical genetics applied to selection of plant and livestock species is rapidly improved by the use of both contemporary biotechnologies and new genomics tools. The use of molecular information for selection improvement purposes is undergoing further development and enhancement aiming at more precise and larger assessment of genetic variation. The advances of the newly selection approaches as genomic selection is expected to provide a significant increase of the effect of selection for numerous economically important traits using quite less efforts in genotyping and providing quite more accurate and predictive genetic evaluation for selection purposes. By entering in a

new era of direct application of high-throughput technologies in selection activities combined with the information of omics technologies is expected for significant change of the concepts concerning the selection objectives and criteria for practical implementations.

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# OD GENETIKE DO GENOMIKE BILJKA I ŽIVOTINJA

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I z v o d

Klasični koncept oplemenjivanja biljaka i životinja na ekonomski značajne kvantativne osobine se tradicionalno bazira na fenotipskim osobinama sa ciljem dobijanja bolje genetičke dobiti. Povećanje genetičke varijabilnosti uz skraćivanje intervala generacija je glavni cilj dugoročnih programa unapređenja metoda u selekiji i oplemenjivanju. Otkrića u biotehnologiji i molekularnoj biologiji i njihova implementacija u programe selekcije su obezbedila stabilnu osnovu za nova znanja i praktičnu primenu u istraživanjima u poljoprivredi i njihovu primenu u zadovoljavanju sve većih potreba za kvalitetniju hranu za ljude i životinje.

Inovacije u oblasti molekularne biologije vezana za praktičnu selekciju i oplemenjivanje koje omogućuju brzu kvantifikaciju u šemama oplemenjivanja dozvoljavaju preispitivanja mogućnosti održivog razvoja metoda selekcije i oplemenjivanja na osobine od interesa u poljoprivredi, brza otkrića i praktičnu primenu novih sofisticiranih tehnologija u ispitivanju variranja genoma, evolucije, sinteze proteina i determinaciju metabolita. Stavljanjem svega navedenog u okvire informacionih tehnologija stvara se nova platforma za istraživanja i sticanje novih znanja za praktičnu primenu u donošenju odluka u procesima selekcije i oplemenjivanja.