Marker Assisted Selection-Applications and Evaluation for Commercial Poultry Breeding

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Abstract Poultry industry is abounding day by day as it engrosses less cost of investment per bird as compared to large animals. Poultry have the most copious genomic tool box amongst domestic animals for the detection of quantitative trait loci (QTL) and marker assisted selection (MAS). Use of multiple markers and least square techniques for mapping of QTL affecting quality and production traits in poultry is in vogue. Examples of genetic tests that are available to or used in industry programs are documented and classified into causative mutations (direct markers), linked markers in population-wide linkage disequilibrium (LD) with the QTL (LD markers), and linked markers in population wide equilibrium with the QTL (LE markers). Development of genome-wide SNP assays, role of 42 K, 60 K (Illumina) and 600 K (Affymetrix® Axim®) SNP chip with next generation sequencing for identification of single nucleotide polymorphism (SNP) has been documented. Hybridization based, PCR based, DNA chip and sequencing based are the major segments of DNA markers which help in conducting of MAS in poultry. Economic index-marker assisted selection (EI-MAS) provides platform for simultaneous selection for production traits while giving due weightage to their marginal economic values by calculating predicted breeding value, using information on DNA markers which are normally associated with relevant QTL. Understanding of linkage equilibrium, linkage dis-equilibrium, relation between the markers and gene of interest are quite important for success of MAS. This kind of selection is the most useful tool in enhancing disease resistance by identifying candidate genes to improve the immune response. The application of marker assisted selection in selection procedures would help in improvement of economic traits in poultry.

(Key words : chicken genomics, chicken breeding, molecular markers, marker assisted selection, traits)

INTRODUCTION

Poultry production has been the fastest growing livestock industry over the last decades (FAO, 2013) especially in middle and low income countries (Taha, 2003). In 2011, world poultry production of meat crossed the bar of 100 million metric tons for the first time in history, out of which 36.5 million metric tons and 4 million metric ton production was recorded in Asia and Africa respectively. During the last decade, egg production in the whole world touched the mark of 68893 thousand tonnes (FAO, 2013; Fig. 1). Since 2000, 43% and 25% increase has been recorded in poultry meat and egg production, respectively in the whole world (Best, 2011). Out of the accumulative production of poultry sector, 85% meat and 96% egg production is contributed by chicken only (Bilgili,

2001; Arthur and Albers, 2003; Taha, 2003). Moreover, during the last decade from 2000~2010, 2.9% growth in poultry population has been observed as compared to 0.8% growth in cattle heads (FAO, 2013). At the same time 3.6% increase in the poultry meat products has been observed as compare to 1.0% increase in cattle meat (FAO, 2013; Table 1). Less cost of investment per bird and increased consumer demand makes poultry breeding an important segment of research. The comprehensive genomic tool box of poultry provides opportunities for the application of different types of selection procedures.

Assembly of an individual animal's entire genome sequence or specific region of interest is important for genetic comparison (Bai et al., 2012). In the livestock breeding programs for quantitative traits most of the genetic progress has been made through phenotypic selection or on the basis of esti-
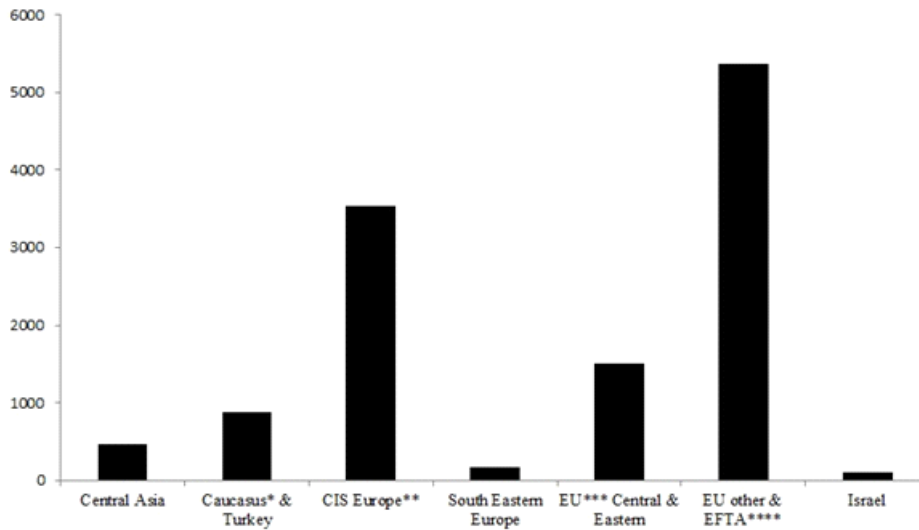
Fig. 1. Total egg production (1,000 tones represented on Y-axis) of the different continents. Source : FAO Statistical Yearbook 2012, Food and Agriculture Organization of United Nations, Rome. * Caucasus : Region at the border of Europe and Asia situated between Black and the Caspian seas, ** CIS Europe : Commonwealth of Independent States Europe, *** EU : Europe, **** EFTA : European Free Trade Association.

Table 1. Per cent per annum growth in the livestock population and meat products in the world during 2000~2010

	Cattle	Pig	Sheep	Poultry
Population	0.8	0.7	0.2	2.9
Meat product	1.0	2.0	0.9	3.6

Source : FAO Statistical Yearbook 2012, Food and Agriculture Organization of United Nations, Rome.

mated breeding value; obtained from the phenotype of an individual. This kind of selection is mainly without the knowledge of the number of genes affecting the trait or the effects of each gene. To overcome the flaws of this pattern of selection, molecular genetics provides tools to improve the selection procedures. Advances in molecular genetics for genotyping helps in the incorporation of molecular data in the programs of genetic improvement (Dekkers, 2005). Many traits are under the influence of several genetic loci contributing to the variation in the traits and are known as quantitative trait loci (QTL). Advances in molecular genetics have led to the identification of multiple genes or genetic markers associated with genes that affect traits of interest (Bahmanimehr, 2012), including genes for single-gene traits and QTL or genomic regions that affect quantitative traits. Genetic markers for QTL those are linked to the gene under study can be used in the selection of animals for selecting breeding programs (Williams, 2005). Similarly, it has been observed that in genome-wide marker assisted selection, an optimal genomic

evaluation has been a multi trait and involves all traits and records on which selection is based (Chen et al., 2011).

Detonation of information on genomics and functional genomics has discovered new possibilities for the creation of molecular markers (Bakhtiarizadeh et al., 2012). In general, although molecular genetic information has been used in industrial programs for several decades and is growing, the extent of use has not lived up to initial expectations. Most of the applications till date have been integrated in existing programs on temporary basis. Objectives of current paper are to review strategies for the use of genes or markers and application of recent molecular selection techniques assisted by markers for the production of high potential and economic poultry strains along with their future possibilities in poultry industry. The current attitude towards MAS is one of the cautious optimism.

CHICKEN GENOME

Poultry is the species which has the most comprehensive genomic tool box amongst domestic animals (Kerje, 2003). Three separate populations of poultry have been used to develop linkage maps (Bumstead and Palyga, 1992; Critten-den et al., 1993; Groenen et al., 1998). It was confirmed that linkage maps of poultry were later on merged to provide a unison map with 1889 markers (Groenen et al., 2000). The genome sequence efforts were accompanied by partial se-quencing of three distinct poultry breeds (a broiler, a layer and a Chinese Silky) to identify single nucleotide polymorphisms (SNPs) between and among these breeds (Groenen et al., 2000) and the Red Jungle Fowl sequence was used as refe-rence (De Koning and Hocking, 2007). A review of Burt (2005) has been described in details on chicken genome. A unique characteristic of avian genomes is the large variability in chromosome size. In addition to a pair of sex chromosomes, chickens have 38 pairs of autosomes: 5 macro-, 5 intermediate and 28 microchromosomes.

Hillier et al. (2004) assembled a draft of the chicken ge-nome using a whole-genome sequencing strategy, including fosmid, BAC, and plasmid paired-end reads (WASHU). Such approach produced a high-quality assembly, in part because of the relatively small size of the chicken genome, one third that of a typical mammal. On comparisons with known func-tional sequences suggested that 75% of coding regions and 30~40% of regulatory elements are conserved. Only 2.5% of the chicken sequence could be aligned with that of the human (44% coding, 25% intronic, and 31% intergenic) and, given that 5% of the mammalian genome is under selection, almost all of this is likely to be of functional significance. This fraction of genome provides scope for the efficient applica-tion of strategies for selection.

MOLECULAR MARKERS（MMs）

Fixed landmarks in the genome of an individual, present at specific locations and identifiable sequences of DNA are known as "molecular markers". Copy number variation in intron 1 of *SOX5* causing pea comb phenotype in chicken is a fine example of molecular markers (Wright et al., 2009). MMs are passed from one generation to the next generation by following Mendel's Laws of Inheritance (Johan and Andrea,

2007) but are not to be considered as normal genes. In comparison to the markers based on visible traits and proteins produced by genes, MMs bank upon DNA assays (Ruane and Sonnino, 2007). DNA markers are used to characterize the genetic makeup and estimate the performance of an animal (Beuzen et al., 2000). On comparison with accustomed back-crossing system, it is observed that the use of DNA markers is beneficial in faster recovery of the recurrent genome and is more efficient in selecting genomes that have recombination events close to the target gene (Ribaut and Hoisington, 1998). For the appraisal of the genetic basis of the perceived pheno-typic variability, genetic polymorphisms eventualizing at DNA level are used as markers (Gholizadeh et al., 2008). DNA based markers changed the whole concept of gene mapping and it had huge impact in the field of animal genetics. These markers help to exploit diversity present in DNA sequence. DNA markers can be used to access sequenced DNA fragments and assays for genetic polymorphisms which are clubbed into the category of fingerprinting markers (Dodgson et al., 1997).

Classification of Molecular Markers

Depending upon their type and according to their utility in different aspects of molecular genetics, markers have been classified in different ways by researchers. Markers have been classified as Direct Markers, Linkage Disequilibrium Markers (LD) and Linkage Equilibrium Markers (Dekkers, 2005) (Fig. 2). Molecular markers have also been categorized on the basis of (a) technical requirements (i.e. whether MMs can be auto-mated or require the use of radioactivity), (b) involvement of time, money and labour needed in the use of MMs, (c) on the basis of their accountability in the genome (e.g. the number of genetic markers that can be detected throughout the ge-nome) and (d) the amount of genetic variation found in each marker in a given population (Ruane and Sonnino, 2007).

MMs have also been classified for their ability to appraise polymorphism in DNA (Teneva, 2009). These are differen-tiated in to the following three groups:-

1）Hybridization-based DNA Markers
Hybridization-based DNA markers like Restriction Fragment Length Polymorphism (RFLP). Detection of RFLPs involves
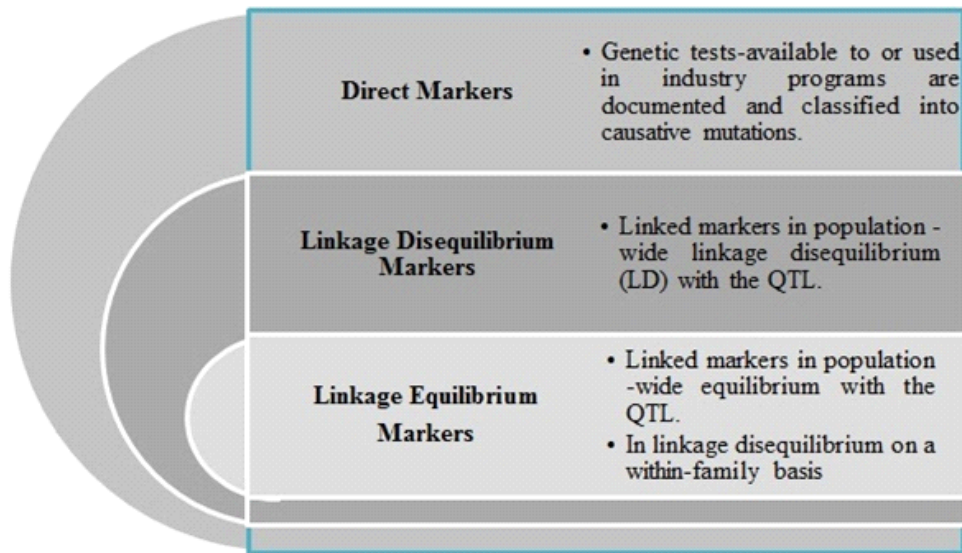
Fig. 2. Classification of markers on the basis of relationship between the markers and the genes of interest.

the fragmentation of genomic DNA by restriction enzymes that recognize specific DNA sequences/motifs (generally frequent cutters 4~10 bp in length).

2) PCR-based DNA Markers

In vitro amplify specific DNA sequences with the help of intentionally chosen oligonucleotide sequences (primers) and a DNA polymerase enzyme which are stable to heat. The best examples of this class are, random amplified length polymorphic DNAs (RAPDs), simple sequence repeats (SSRs) or microsatellites, amplified length polymorphism (AFLPs). Although currently RAPDs is no longer used in poultry industry, but it had been applied to detect similarities between the strains selected for egg and meat production (Ali et al., 2003). These days restriction fragment length polymorphisms (RFLPs) are solely PCR based.

3) DNA Chip and Sequencing-based DNA Markers

e.g. Single nucleotide polymorphism (SNPs) - A SNP array is a type of DNA microarray which is used to detect polymorphisms within a population. SNP is a variation at a single site in DNA, is the most frequent type of variation in the genome. Development of genome-wide SNP assays is hand-carried by the SNP map, ranging from 5,000~20,000 SNPs per assay (De Koning et al., 2004). Since 2008, SNP

chips are in use and 60K SNP chip (Illumina Inc., San-Diego, CA) are proprietary in this field. More success rate of the SNPs on the Illumina chicken 60K beadchip emphasized the power of next generation sequencing for the identification of SNP (Groenen et al., 2011). Due to its non-availability for academic use, 42 K SNP chip (Illumina Inc., SanDiego, CA) was developed (Fulton, 2012). To test genome-wide MAS in commercial chickens an Illumina islet array has been selected. To fill in the vacuum of a lack of commercially available genotyping array for chicken, recently a high density Affymetrix Axiom array has been developed under an umbrella of BBSRC/DEFRA LINK grant project with collaboration of various institutes/companies (Kranis et al., 2013).

Authors have expected widespread usage of 600 K SNP both in research and commercial application such as in genomic selection, genome-wide association studies, selection signature analyses, fine mapping of QTLs and detection of copy number variants. The loci and candidate genes for body composition and meat quality traits in Beijing-You chickens have been identified through genome wide association (Liu et al., 2013). Another type of DNA variant, copy number variation (CNV) is emerging as a significant contributor to phenotypic variation in many species. CNVs potentially affect the gene expression (Baily et al., 2008). A recent study of Crooijmans et al. (2013) have been identified 3,154 CNVs, grouped into 1,556 CNV regions (CNVRs) with the average size of 46.3 kb.

MARKER ASSISTED SELECTION (MAS)

High density DNA marker maps constructed by the molecular marker systems for the species are economically crucial in the area of agriculture. Mapped MMs provide a framework required for its consequential use in the application of MAS. Genetic diversification in breeding population is utilized with the help of mapping and can be used to adjust the whole range of desirable traits (Beuzen et al., 2000).

There are different types of traits for which MAS has created avenues for enhancing response to selection. Poultry genome was the first to be mapped in 1992 among the livestock species followed by cattle, pigs and sheep (Dekkers, 2004). Chicken genomic toolbox is the most extensive for detection of quantitative trait loci (QTL) and MAS. An idea about the linkage equilibrium and disequilibrium is considered before the role of relationship between the markers and the genes of interest is discussed for the success of MAS. Linkage equilibrium (LE) exists when genotype present at one locus is in equanimity with the genotype at a second locus and alternatively, when genotypes at the two loci are not in equanimity with one another, then there is linkage disequilibrium (LD) or the random association of alleles at different loci is known as linkage disequilibrium (Slatkin, 2008).

MMs are preferred in the order as Direct Markers > Linkage Disequilibrium > Linkage Equilibrium for their effective implementation in MAS. On the basis of the ease of application and potential for extra genetic gain the same order of ability is followed for these markers as far as their use is concerned (Dekkers, 2004). High-density genotyping of SNPs enables detection of QTL by LD mapping (Andreescu et al., 2007). Description of LD between markers and QTL can consequentially be used for MAS. The success of LD mapping and MAS depends on the extent of LD and the use of associations those require LD between loci to be consistent across populations (Andreescu et al., 2007). For classification of genetic markers and their promising use in MAS for chicken, the genome sequence and high density SNP maps are available these days (Abasht et al., 2009). It has been ascertained that markers maintaining high LD with linked QTL are very close to each other across the two generations and will be effective for MAS (Abasht et al., 2009).

Recently in plant and animal breeding, the concept of QTL affecting the variance of quantitative traits (vQTL) has gained importance because of the increasing importance of uniformity (Wolc et al., 2012). The first of published studies on vQTL was on recombinant inbred lines of maize for economically important traits (Ordas et al., 2008), whereas in animals, researchers failed to detect significant vQTL while working on back fat thickness in pigs (Yang et al., 2011). Later, few studies have reported vQTL for egg weight, which could be due to the large data sets that are needed because of low power to detect vQTL (Visscher and Posthuma, 2010).

1. Route to Adoption of MAS in Chicken Breeding Programmes

Numbers of egg laid in layers and body weight at 6 weeks of age in broilers are the quantitative traits of economic importance which are controlled by many genes along with environmental factors (Sewalem et al., 2002; Liu et al., 2011). These traits are necessary for the genetic improvement programmes in poultry. In the traditional genetic improvement programmes with the selection on the basis of phenotype, there is lacuna regarding the knowledge of the kind of gene being selected. Transitional shift in the selection procedures based on genotype, also do not have much authenticity due to lack of appropriate markers. Concept of DNA based markers is in vogue to identify markers spread all over in the genetic material of the species of interest. Genes and genetic markers can be used to potentiate the genetic improvement of breeding stock through marker-assisted selection (Dekkers and Hospital, 2002).

The first use of a complete RFLP linkage map to resolve quantitative traits into discrete Mendelian factors, in an interspecific back-cross of tomato (species of interest) revolutionized the field of academic research (Paterson et al., 1988). Same modus operandi is targeted towards the quantitative inheritance of physiological, morphological and behavioural traits based on separate genetic approaches in any higher plant or animal. In plant and animal populations, molecular genetic analysis of traits has destined for better understanding of quantitative trait genetics. It has been reported that in the base population, during selection when marker and QTL are in linkage equilibrium then polygenic variance approaches

equilibrium, QTL variance decreases continuously over time and the transmission of marker alleles is traceable in an outbred poultry breeding nucleus (Vander and van Arendonk, 1996).

MAS uses DNA markers for the selection of animals which give superior genetic merit for phenotypic traits which are normally too expensive or too difficult to measure practically. QTL affecting quality and production traits in layers are being mapped via multiple markers and least square techniques (Tuiskula et al., 2002). Quality of egg shell has always been a very important trait. QTL for egg shell strength and white thinning of egg shell have been found on the chromosomes "Z" and "2" respectively (Tuiskula et al., 2002). Advances in the characterization and identification of genes, coding for eggshell matrix proteins has made it possible to consider these genes as candidate genes for the improvement of quality of eggshell by MAS (Bain, 2004). Still in the developing countries, due to lesser investments in the field of molecular markers, MAS is not being used to its full potential.

Concept of EI-MAS has provided platform for simultaneous selection for production traits while giving due weightage to their marginal economic values. EI-MAS uses information on DNA markers which are associated with relevant QTL to calculate predicted breeding value (Lahav et al., 2006). It has been observed that EI-MAS is advantageous for the traits which have low heritability. Study on the chicken has confirmed that the response to EI-MAS is more when the map distance between the marker and the quantitative trait gene is small and vice- versa. Also the selection of the traits in the poultry breeding programs using cluster analysis is quite helpful in establishment of a selection index, by combining all economical traits in one equation to increase the efficiency of selection process   (Rosario et al., 2008).

2. Applications and evaluation of marker assisted selection in poultry

It is necessary to have knowledge about the extent of relationship between marker and the trait under consideration for the implementation of the MAS. The extent of relationship between molecular marker and the trait under consideration can be judged by the studies based on the quantitative trait loci, gene of interest and the studies for the underlying genetic mechanisms.

Through fine mapping analysis, the responsible gene mutation had only been described for some disease resistance QTL (Liu et al., 2001a; Liu et al., 2001b; Liu et al., 2003). For Marek's disease (costing about $1 billion per annum to poultry industry (Vallejo et al., 1997; Yonash et al., 1999), two inbred lines *"63"* (MD resistant) and *"72"* (MD susceptible) were mated to identify the QTL affecting MD susceptibility. It was reported for the first time on the mapping of non-major histocompatibility complex QTL affecting MD susceptibility (Vallejo et al., 1997). Use of MAS to boost the genetic resistance to MD, is an alluring alternative to augment control with vaccines (Liu et al., 2001a). Equal attention is given to the production traits and improvement of egg quality, in layers. Feed efficiency and meat quality are the traits of consideration by the breeders for improvement in broilers with the help of marker, as these are not easy to measure in an accustomed manner.

MAS is useful in enhancing disease resistance by identifying candidate genes to improve the immune response (Malek and Lamont, 2003). To investigate the genetic control of response to *Salmonella enteritidis* (SE) in chicken, several candidate genes e.g. *inducible nitric oxide synthase* (*INOS*), *tumour necrosis factor related apoptosis inducing ligand* (*TRAIL*), *transforming growth factor-β2* (*TGF-β2*), *transforming growth factor-β3* (*TGF-β3*) and *immunoglobulin G light chain* (*IgL*), had been selected. These candidate genes were selected on the basis of their role in the host's response to intracellular bacteria (Malek and Lamont, 2003). A QTL comprising of 198 microsatellite markers which covers two-third of the chicken genome has provided platform for high-resolution mapping and positional cloning of the resistant genes (Heifetz et al., 2007). Single strand conformational polymorphism (SSCP) analysis and DNA sequencing have been used to detect SNPs of *FATP1* gene in chicken and to extricate the suggested association between *FATP1*- SNPs and chicken carcass traits (Wang et al., 2010). *FATP1* gene polymorphisms are associated with chicken carcass traits or are linked with the major gene. The SNPs in this gene can be utilized as poten- tial markers for MAS during chicken breeding programme. A fast improvement in QTL studies has been

observed in chicken, which led to the enhancement of a QTL database especially for chicken (NAGRP, http://www.animalge-nome.org/QTLdb/chicken.html). Planning for selection procedures, based on QTL is becoming more feasible for the rest of the poultry species by deploying dense genetic linkage maps (Saszanov et al., 2010). It is difficult to quantify the effect of MAS under the conditions laid down for experiment especially when response is not large or MAS is part of multi trait breeding goal. Response to MAS can be evaluated at: changes in gene frequencies for the locus of the marker under study and targeted; secondly to estimate the effect of targeted loci on the traits in the population under target and thirdly for improvement of the selected individuals in overall genetic level for trait of interest (Dekkers, 2004).

3. Scope for Markers Assisted Selection in Poultry

Chickens are considered eminent for signifying new approaches where QTL studies are complemented by gene expression studies (Liu et al., 2001a). It has been reported that QTL has become fully distributed within "genetical genomics" (De Koning et al., 2003, 2007; De Koning and Haley, 2005). Now, the major question in front of breeders, before they accept MAS is whether the breeders are ready to adjourn their breeding programmes with MAS?

It has been observed that, MAS could increase the intensity of selection in poultry breeding programme for the traits which are (1) measured later in life, (2) costly to measure, (3) traits having low heritability (reproductive traits i.e. fertility and hatchability (Savegnago et al., 2011), (4) traits for which measurement of phenotype is difficult, expensive or is not possible on selected candidates (5) traits for which selection is within full-sib families for sex-limited traits (Muir, 2003; Dekkers, 2004).

Major drawback of MAS is its usance in traits like reproductive traits and its considerations related to its efficacy (Muir, 2003). Identification of multiple genes or genetic markers which are associated with the genes, affecting the traits under consideration in livestock species has become possible due to advancement in molecular genetics (Dekkers, 2004). Subsequently, the location of QTL for body weight (BW) and abdominal fat traits on chicken chromosome 1 has been

confirmed and redefined (Liu et al., 2008). By the use of the linkage analyses, the confidence interval for body weight and abdominal fat percentage has narrow down sharply. It had been confirmed that effective decrease in the confidence interval of QTL could be due to the use of more markers and individuals (Liu et al., 2008).

Use of SNP in selection has been proven to be an added effect. Aid of next generation sequence (NGS) in the classification and induction of SNPs has increased the rate of success for SNPs in chicken (Groenen et al., 2011). Genetic mapping based on SNP helps in conducting population studies and linkage disequilibrium analysis (Emara and Kim, 2003). It has been observed that SNPs can be fully descriptive in chicken populations that are derived from inbred line crosses (Lindblad et al., 2000). Inbred lines diverging widely in their phenotypic traits can be compared by SNPs. Tag SNP helps to find chromosome regions that have different haplotype distribution in two groups of individuals i.e. with response and without response. It has been observed that tagging SNPs is efficient for genome-wide selection (Halldorsson et al., 2004). Tag SNPs can be asserted across chromosomal regions with high and low level linkage disequilibrium. Tagging of SNPs can contribute in a two to three time savings compared to selecting random SNPs (Halldorsson et al., 2004). Many SNPs show correlated genotypes or linkage disequilibrium (LD), which proposes that only a subset of all SNPs which are known as tag SNPs, can be genotyped for disease association studies (Howie et al., 2006). Evaluation of economic returns after implementation of MAS from increased profit at the production levels is proportional to the genetic gain (Hayes and Goddard, 2003). It has also been observed that the most of the commercial breeding programs derive profit from increased market share of breeding stock (Dekkers, 2004).

Since, known gene mutations provide a comfortable path for implementation along with underlying biology, breeders prefer to work with these kinds of mutations. Keeping in mind the goals, these molecular techniques can be implemented successfully by following well defined, crisp and integrated strategy. With this view point in mind, the application of MAS in selection procedures would help in improvement. There is dire need of the time that poultry breeder should now decide

that at which molecular stage they want to exploit information and especially for which trait?

4. Scope for MAS in Poultry in Developing Countries

In the developing countries, appropriate facilities and resources are available in poultry breeding industry. Poultry industry is expanding day by day as it involves less cost of investment per bird as compared to large animals. Poultry farming today is a big occupation that is spread over into various accomplishments including hatcheries, pullet farms (for meat production) and farms for egg production (Hamra, 2010). High rate of proliferation and short generation interval in poultry make them more acceptable (Lwelamira et al., 2008). Except few intensive breeding units, developing countries often have low input systems. There is lack of phenotypic and pedigree information in these systems which makes it more difficult to understand the accent of selection assisted by markers. Moreover, these conditions pose more difficulties and expenses in confirming the linkage by using linked markers. Because of lesser investment in the field of molecular markers, the full potential of MAS is not being capitalized in developing countries. A practical complication analysed for MAS is the loss of relationship between distinct marker allele and favourable trait, when marker is not in proximity of the region to be selected (Fulton, 2012).

In developing countries, where resources are very limited and there is lack of record keeping, it becomes very difficult to apply new techniques like MAS. It is also necessary that poultry breeders should be ready to change their breeding strategies and willing to adopt new molecular techniques. Once, breeders develop inclination towards these techniques and have proper record keeping, it would become very easy to adopt MAS in developing countries. While comparing marker assisted introgression and selection within breeds, genotypic information is used in a much better way by marker assisted introgression as compared to the later selection procedure in developing countries (Visscher et al., 1996; Visscher and Haley, 1999). It holds potential for improvement in developing countries and should thus be targeted. Since there is more number of small poultry holdings in developing countries which help the farmers to sustain their livelihood, therefore much empha-

sis is given on the development of dual - purpose birds which can be kept for both egg and meat.

CONCLUSION

Uptake of MAS will depend strongly on whether the industry wishes to supplement its current selection programme with a known gene variant, or if it is prepared to restructure breeding programmes around Marker Assisted Selection. To implement MAS successfully, one must tackle the following issues like problems of identifying the traits for selection and their economic significance, the lack of current knowledge of the genes or markers associated with these traits, and their association with other economic selection criteria. The current "toolbox" provides the means to answer some of these questions but there are obvious concerns about human and capital resources. There is a need for Governments and organizations to inform the public about the benefits of MAS and its potential role in the management of genetic resources. While building national development and global strategies, it is very crucial to address the questions of public awareness, education and information. Although, grouped with some limitations or barriers, MAS must be the very evident successful tool for current breeding programmes in achieving many desirable commercial goals.

ACKNOWLEDGEMENTS

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