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Using of DNA Fingerprinting in Poultry Research

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Abstract: Genetic fingerprinting, DNA testing or DNA profiling is a technique to distinguish between individuals of the same species using only samples of their DNA. In modern animal breeding and production, with welfare and optimum nutrition, the major health problems arise mainly from genetic background. Obviously the selection does not affect the genome, but rather changes gene frequencies in the population and modifies the range of genetic variation of selected and correlated traits. These effects can be detected at the DNA level with the use of appropriate tools. DNA fingerprinting is a powerful tool in poultry for investigating genetic diversity within stocks and establishing relationships among stocks, characterizing individuals or populations genotypically, studying the relative contribution of evolutionary forces to genetic differences between populations, for marker assisted selection, to assist in gene introgression, to predict hybrid vigor and provide useful information for the pre-selection of populations to be used in crossbreeding. This review summarizes the use of genetic fingerprinting in poultry research, especially in some genetic resources of economically important species such as chickens, quails, ducks, goose, turkey and other poultry.

Key words: DNA fingerprinting, poultry, DNA testing or DNA profiling

INTRODUCTION

Genetic fingerprinting, DNA testing or DNA profiling is a technique to distinguish between individuals of the same species using only samples of their DNA (Sharma *et al*., 2001). DNA fingerprints depend on the genetic differences between individuals, we have called such genetic differences DNA markers; they are also called DNA polymorphisms (The term polymorphism literally means "multiple forms"), the term DNA polymorphism refers to a wide range of variations in nucleotide base composition, length of nucleotide repeats, or single nucleotide variants. DNA polymorphisms are important as genetic markers to identify and distinguish alleles at a gene locus and to determine their parental origin, there are three types of genetic polymorphism: A) Single Nucleotide Polymorphism (SNP), these allelic variants differ in a single nucleotide at a specific position. At least one in a thousand DNA bases differs among individuals. The detection of SNPs does not require gel electrophoresis, this facilitates large-scale detection. A SNP can be visualized in a Southern blot as a Restriction Fragment Length Polymorphism (RFLP) if the difference in the two alleles corresponds to a difference in the recognition site of a restriction enzyme. Single Nucleotide Polymorphism (SNP) in genes and non-coding parts of the genome is considered as a worthwhile tool for the biodiversity assessment (Weigend *et al*., 2004). B) Simple Sequence Length Polymorphism (SSLP), these allelic variants differ in the number of tandemly repeated short nucleotide sequences in noncoding DNA. C) Genetic variation in the cervid mitochondrial genome has been utilized largely in population genetic analysis or phylogenetic studies. Mitochondrial DNA (mtDNA) sequence variation is highly appropriate for phylogenetic analysis amongst closely related species, as compared to nuclear DNA markers. This is because mtDNA shows more rapid evolution (especially the hypervariable D-loop region), maternal inheritance and the absence of recombination, although there is some evidence that recombination may occur in the mtDNA of ruminants.

Nevertheless, DNA fingerprinting has been shown to be a cost-effective method to detect hypervariable loci for investigating genetic relationship within and between populations (Kuhnlein *et al*., 1989, 1990; Gilbert *et al*., 1990, 1991; Siegel *et al*., 1992; Dunnington *et al*., 1994; Grunder *et al*., 1994; Jin and Chakraborty, 1994). DNA fingerprinting is a powerful molecular-genetic technique that uses human probes for hypervariable minisatellite DNA to identify individuals and to determine parentage with a high degree of accuracy (Jeffreys *et al*., 1985). In poultry, DNA fingerprints have been used (1) to characterize individuals or populations genotypically, (2) to study the relative contribution of evolutionary forces to

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genetic differences between populations, (3) for marker assisted selection, (4) to assist in gene introgression, and (5) to predict hybrid vigor (Hillel *et al*., 1992). Genetic variation, both within and between breeds, is essential for the genetic improvement of domestic animals. Loss of variation will restrict the selection for desirable economic characteristics within current commercial lines. Therefore poultry breeders have an interest in maintaining or increasing genetic variation within and between commercial lines or exotic populations. Polymorphism at the DNA level is greater than that at the level of gene products and it is detectable independently of environment, age, sex and tissue (Ponsuksili *et al*., 1998).

In present-day genetics, DNA markers are widely used for genomic mapping, identification of genes controlling commercial traits and analysis of consequences of long term selection and inbreeding (Geldermann and Ellendorff, 1990; Darvasi, 1998; Heyen *et al*., 1999; Kumar, 1999; Riquet *et al*., 1999; Buitkamp *et al*., 2005). Mitochondrial DNA (Dong *et al*., 2002), Random Amplified Polymorphic DNA (RAPD) (Smith *et al*., 1996; Singh and Sharma, 2002; Dehghanzadeh *et al*., 2009) DNA fingerprinting (Siegel *et al*., 1992; Ye *et al*., 1998a) and microsatellites (Takahashi *et al*., 1998; Kaiser *et al*., 2000) were widely used to study genetic variability among populations. DNA Fingerprints (DFP) with multi-locus probes detecting several types of repeats, provide a tool to assess the genome as a whole. Such probes could be divided into three general types: (1) micro-satellite probes, detecting DNA repeats, usually consisting of 2-8 bp, (2) mini-satellite probes detecting DNA repeats 9-65 bp in length (variable number tandem repeats, VNTRs) and (3) middle-repetitive DNA probes that detect DNA elements several kbp in length (Gavora, *et al*., 1993). DNA fingerprinting patterns obtained with multilocus minisatellite probes proved to be the most adequate to characterize the consequences of long-term selection at the genomic level. To determine specific changes in the genome of a particular line (line specific bands) (Plotsky *et al*., 1993; Ponsuksili *et al*., 1998).

The DFP analysis of relative band intensity is an effective method of estimating the relative proportion of genome contributed by parental populations (Haberfeld *et al*., 1992). The Random Amplified Polymorphic DNA (RAPD) method was used to identify the species of forensic biological samples (Lee and Chang, 1994). The analysis of Restriction Fragment Length Polymorphisms (RFLPs) is one of the most efficient means of monitoring genetic diversity in domestic animals (Atzmon *et al*., 2007). Rastogi *et al*. (2007) suggested that mitochondrial markers are more efficient than nuclear markers for the purpose of species identification and authentication. Among PCR fingerprinting approaches, RAPD was proved to be more discriminatory, accurate and efficient than action fingerprinting. As the avian genome is characterized by a low frequency of microsatellite repeats, minisatellite markers are exceptionally valuable sequences in the search for major genes of poultry production traits (Haley, 1991). Simultaneous screening of many polymorphic loci in the genome provides an effective tool for identifying markers associated with loci determining selected traits (Dunnington *et al*., 1990; Plotsky *et al*., 1993). By detecting genetic variation, genetic markers may provide useful information at different levels: population structure, levels of gene flow, phylogenetic relationships, patterns of historical biogeography and the analysis of parentage and relatedness (Sharma *et al*., 1998a; Feral, 2002).

The aim of this publication is to summarize the use of genetic fingerprinting in poultry research, especially in some genetic resources of economically important species such as chickens, quails, ducks, goose, turkey and other poultry.

Different techniques of DNA profiling: Over past 3 decades, the fundamental DNA technology developments-restriction enzymes coupled with Southern-blot hybridization, sequencing and PCR have contributed to a burst of applications in multiple research areas, including genetic variation and diversity in chickens (Weigend *et al*., 2004).

Restricted fragment length polymorphism (RFLP): Originally, RFLP referred to analysis of band patterns derived from DNA cleavage using restriction endonuclease enzymes based on SNP. RFLP and related techniques are usually modifications of the Southern blot method when the whole genomic DNA or its fraction is cut with restriction enzymes, transferred to a membrane and hybridized with radiolabeled or fluorescent probes. The latter can be cloned fragments of endogenous avian viruses, particular nuclear genes, MHC genes, EST, or mitochondrial DNA (mtDNA) genes. Individual or pooled RFLP patterns can easily be compared with identify variation within and among populations studied. The technique is time consuming but might still be useful in species for which no or little sequence information is available (Soller *et al*., 2006).

PCR-Based techniques: According to Soller *et al*. (2006) Amplification of noncoding or coding regions of a genome using PCR has revolutionized molecular genetics research and provided an impressive variety of new markers to tackle diversity problems:

Random amplified polymorphic DNA (RAPD): The random amplified polymorphic DNA technique employs single short primers of random sequence, usually 10-mers, which produce multiband patterns similar to DNA fingerprints. No sequencing information is needed

before genotyping. Use of RAPD markers to study poultry genetic diversity was thought to be promising and they were heavily exploited in the 1990s. However, because of poor PCR reproducibility and dominance mode of inheritance, they are no longer markers of choice.

Amplified fragment length polymorphism (AFLP): AFLP molecular markers have been an important tool to enrich existing genetic maps in plants, bacteria and less widely in animal genomes. As developed by Keygene (Keygene N.V., Wageningen, The Netherlands), the amplified fragment length polymorphism technique involves the restriction of genomic DNA, followed by ligation of adaptors complimentary to the restriction sites and selective PCR amplification of a subset of the adapted restriction fragments. Although this type of markers is popular, especially among plant researchers, there are just a few examples of its application to examine genetic variation in chickens. Like RAPD markers, AFLP markers are characterized by a dominant nature, which is a main disadvantage of this technique. Microsatellites, these types of single-locus markers are also known as short (or simple) tandem repeats, simple sequence repeats, or simple sequence-length polymorphisms and belong to a variable number of tandem repeat loci, the most extensively used class of highly polymorphic molecular markers. Unlike all the above techniques, prior sequence information of flanking regions is necessary to develop these markers. Major advantages of microsatellites are that they are detectable by PCR representing unique sequences in the genome that can be mapped and easily be exploited for many genetic applications. Also, they show extensive allelic differences in length, mainly based on variation in the number of repeats and partly on polymorphism of flanking regions.

Sequencing approach: Direct sequencing became possible for wide application with the invention of PCR amplification. More recently, it has become popular in discovering Single Nucleotide Polymorphism (SNP) markers. There are several other molecular techniques used for investigating inter- and intra-population genetic variation in chickens, for instance, PCR-RFLP. This is a combination of 2 major approaches when DNA regions of interest are amplified by PCR and sequence polymorphisms of these fragments are subsequently detected by RFLP assays (Soller *et al*., 2006).

Single nucleotide polymorphism (SNP) as molecular markers: A SNP is a minimal DNA variation that occurs as a replacement of a single nucleotide with 1 of the 3 other possible nucleotides. SNPs are the most common class of genetic polymorphism, often outside of coding regions, and they make up a new generation of biallelic markers that become promising for use in biodiversity studies due to their abundance and applicability for high throughput analyses (Schmid *et al*., 2005), they also reported that, for SNP-based genotyping, the major techniques are oligonucleotide chips, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry and pyrosequencing. Because a circumstantial SNP map of the whole genome was created, we can screen genomes of various breeds and populations to determine the following: 1) SNP profile of a given breed, population, or both and SNP allele frequencies across populations, 2) the uniqueness of the breed, population, or both in terms of harboring rare SNP or haplotypes, or 3) the value of the breed, population, or both concerning economically important SNP.

TaqMan real-time PCR: TaqMan real-time PCR is one of the two types of quantitative PCR methods. Unlike the other type of real-time PCR, the CYBR Green method, which uses a florescent dye that can bind to any double-stranded DNA, TaqMan uses a fluorogenic probe which is a single stranded oligonucleotide of 20-26 nucleotides and is designed to bind only the DNA sequence between the two PCR primers. Therefore only specific PCR product can generate fluorescent signal in TaqMan PCR. To do TaqMan PCR, besides reagents required for regular PCR, additional things required are a real-time PCR machine, two PCR primers with a preferred product size of 50-150 bp, a probe with a fluorescent reporter or fluorophore such as 6-carboxyfluorescein (FAM) and Tetrachlorofluorescin (TET) and quencher such as Tetramethylrhodamine (TAMRA) covalently attached to its 5' and 3' ends, respectively.

Applications of DNA fingerprinting in different poultry species

Chickens: DNA fingerprints have been shown to be a useful tool for assessment of genetic distances between genetic groups of poultry, genetic distances between the original population and the selected chicken lines, reflected the history of breeding (Kuhnlein *et al*., 1989; Dunnington *et al*., 1990; Haberfeld *et al*., 1992; Siegel *et al*., 1992; Haberfeld *et al*., 1996; Tixier-Boichard *et al*., 1996; Sharma *et al*., 2000; Dmitriev *et al*., 2001) and revealed specific hybridization bands that could serve as DNA markers (Zhang *et al*., 1995; Dmitriev *et al*., 2001; Schmidt *et al*., 2003; Sacharczuk *et al*., 2005). A DNA fingerprinting technique was used to assess the extent of genetic variation within and between lines of chickens of different origin and to construction of the phylogenetic trees (Ponsuksili *et al*., 1998; Wimmers *et al*., 1999; Wimmers *et al*., 2000), to determine the degree of inbreeding (Kuhnlein *et al*., 1990; Dunnington *et al*., 1991), to estimate the average allelic frequency at a hypervariable locus and the

average mutation frequency per locus and generation (Kuhnlein *et al*., 1990), to determine the effects of selection on the genetic variation within and between lines of chickens (Ponsuksili *et al*., 1999; Sacharczuk *et al*., 2005). DFP may be useful in predicting heterosis (Haberfeld *et al*., 1996; Gavora *et al*., 1993; Liu *et al*., 2009). Multi-locus DNA fingerprint markers used to identify marker-associated Quantitative Trait Loci (QTLs) affecting various juvenile traits of chickens (Mishra *et al*., 2002). A potential limitation of the use of a dominant molecular marker system such as DNA Fingerprinting (DFP) is the inability to distinguish homozygous from heterozygous allele state in an individual and a resulting inaccuracy in estimating effects of the marker alleles (Kaiser *et al*., 2003).

Genetic variability within and between the reference populations was reflected well by the DNA fingerprint pattern. Different methods to analyze the DNA fingerprint data were evaluated and the degree of band sharing was found to be the best measure of genetic similarity (Tropical and Subtropical Agriculture, Third STD Programme, 1992-1995). Genetic diversity within and among nine pure lines of Beijing White Leghorn chickens was determined by DNA fingerprinting, to demonstrate relationships between the variability of DNA fingerprints of parental lines and the performance in some production traits of their hybrids (Meng *et al*., 1996).

Dunnington *et al*. (1993) suggested that associations between DFP bands and quantitative traits may not be consistent in different genetic backgrounds. DNA fingerprints probed with the repetitive sequence revealed a characteristic pattern in each chicken and in line; DFP was useful for parentage analysis and for eluddaing of the genetic structure of a chicken strain (Kimura *et al*., 1993).

Methods of multilocus genome fingerprinting (DNA fingerprinting) and the PCR with random primers were used to detect genome variability of eleven chicken breeds. The diagnostic value of the markers used for differentiating breeds and detection of origin of several breeds of Russian selection was demonstrated (Semenova *et al*., 1996). If total DNA is used, RAPD yields abundant information about the analyzed genome in a rapid and inexpensive way (Xena de Enrech, 2000). Naoyuki and Tomita (1993) were attempting to detect the DNA fragment of the irradiated donor sperm DNA in transgenic chicken embryos by using a DNA fingerprint method.

Recent information in literature have revealed that microsatellite markers are more accurate and efficient method for estimating genetic variation in chicken populations than other methods that have been used previously (Chen *et al*., 2004; Takezaki and Nei, 1996). However, only a limited number of investigations have used microsatellites across Chinese indigenous chicken populations in Southern China (Zhang *et al*., 2002). According to Yu Ya-Bo *et al*. (2006) microsatellite DFP used to determine the genetic relatedness among different Chinese indigenous chicken populations and evaluating of genetic variations and genetic distance between populations and to construct the topology of phylogenetic trees. The genetic variability of various local chicken populations derived from Bolivia, India, Nigeria and Tanzania was evaluated with 22 microsatellites, a dendrogram was constructed based on CHORD distance by upgMa analysis (Wimmers *et al*., 2000). Yu-Shi *et al*. (2005) reported that, microsatellite fingerprint was feasible to analysis genetic relationships among Chinese native chicken breeds. Using allele ladders for each microsatellite, scoring can be standardized between gels and even between laboratories. It has also been shown that microsatellite typing can be applied to pooled DNA samples for population studies (Khatib *et al*., 1994; Crooijmans *et al*., 1996; Hillel *et al*., 2003). The genetic diversity of the Turkish native chicken breeds (Denizli and Gerze) was evaluated with 10 microsatellite markers (Kaya and Yildiz, 2008), they reported that, information about Denizli and Gerze breeds estimated by microsatellite analysis may also be useful as an initial guide in defining objectives for designing future investigations of genetic variation and developing conservation strategies.

In chickens DFP loci, detectable by minisatellite probes, are extremely polymorphic. Individuals have unique patterns of DFP and thus can be selected for maximal genomic similarity to the recipient line and minimal similarity to the donor line, using their DFP patterns as the criterion for similarity. It's a tool to reduce the required number of backcross generations in introgression breeding programs (Hillel *et al*., 1990).

RAPD analyses have been used for genome mapping (Levin *et al*., 1993, 1994; Cheng *et al*., 1995), parentage analysis, genetic analysis of relatedness and diversity in chickens (Smith *et al*., 1996), genetic characterization of chicken lines (Plotsky *et al*., 1995), identification of marker for QTL (Tercic *et al*., 1998) and estimation of genetic variation in different breeds of chickens (Welsh and McClelland 1990; Sharma *et al*., 1998b; Hillel *et al*., 1992; Mohamed *et al*., 2001; Ivgin and Bigen, 2002), applied to detect genetic similarity between five local chicken strains in Egypt (Ali *et al*., 2003). RAPD was effective tool used to detect polymorphism among five breeds of chicken (Sharma *et al*., 2001), construct dendogram to show phylogenetic relationship among breeds of chickens (Mohamed *et al*., 2001; Sharma *et al*., 2001). More importantly, the level of polymorphism detected by using RAPDs will provide chicken breeders with environment independent DNA markers, which should be regarded as essential tools for selection (Mohamed *et al*., 2001).

Salem *et al.* (2005) indicated that, RAPD analysis should lead to the saturation of the genome without the requirement of previous genetic information and using few expensive oligonucleiotides. The genomes of three local strains of chickens were screened by randomly amplified polymorphic DNA bands, using RAPD-PCR analysis. RAPD-DFPs used to assessment of genetic diversity and relationships between the breeds of chickens and to construct the phylogenic tree (El-Gendy *et al.*, 2006). We have also presented some preliminary data showing molecular differences between Egyptian chicken strains (Ali and Ahmed, 2001) and indicating the potential use of RAPD markers for a wide range of applications in poultry breeding.

RFLPs, were used to construct a physical map of the chicken genome, provides a powerful platform for many areas of chicken genomics, including targeted marker development, fine mapping of genes and QTL alleles, positional cloning, analysis of avian genome organization and evolution, chicken-mammalian comparative genomics and large-scale genome sequencing (Chengwei Ren *et al.*, 2003).

Recently, molecular AFLP technique has been used to search DNA markers for discriminating slow- and fast-growing chicken strains and to authenticate certified products (Fumiere *et al.*, 2003). The AFLP is a powerful tool for investigating the genetic diversity of animals (Ajmone-Marsan *et al.*, 1997; Ajmone-Marsan *et al.*, 2001; Martino *et al.*, 2005) as well as the genetic markers for discriminating between purebred and crossbred of the slow- and fast-growing chicken strains (Fumiere *et al.*, 2003; Mekchay *et al.*, 2005). AFLP also used to phylogenic tree analysis in chickens (Mekchay, *et al.*, 2005). Based on AFLP DNA fingerprinting, genetic diversity, genetic relationship and identification of chicken breeds can be analyzed (Yu-Shi *et al.*, 2006).

Single Nucleotide Polymorphism (SNPs) were analyzed in 20 distinct chicken breeds, phylogenetic trees were constructed. Nevertheless, SNPs have obvious advantages and are an efficient and cost-effective genetic tool, providing broader genome coverage and reliable estimates of genetic relatedness (Twito *et al.*, 2007).

Commercially: Hy-Line International was the first poultry primary breeding company to establish an on-site molecular genetics laboratory. Over the last several years, Hy-Line molecular scientists and geneticists have been working closely to apply the technology to the Hy-Line breeding program through marker-assisted selection. While marker assisted selection is rapidly being integrated into the Hy-Line breeding program, we can also use DNA markers to protect brand integrity and identify counterfeit products at the DNA level (O'Sullivan and Greaves, 2007).

In quail breeding: DFPs were used to study genetic variations, correlations and for mapping of the quail genome. Hanotte *et al.* (1992) emphasized the desirability of determining, in each new species, the optimal experimental conditions as a preliminary to any behavioral or population genetic studies that use the multi-locus DNA fingerprinting methodology. However, fingerprint patterns will often be adequate for use in paternity analyses, such as in behavioral studies, despite the occurrence of haplotypic sets of bands. DNA fingerprinting of individual quail showed characteristic pattern and individuals could be distinguishable from each other even within a line, no commonly shared DNA fingerprints band was observed among 18 quails examined, each line had peculiar DNA fingerprint pattern, from which we could construct a dendrogram, inbreeding coefficients estimated from band sharing (Hideyuki *et al.*, 1993). In the other hand, Ye *et al.* (1998b) found that, in Japanese quail, the DNA fingerprinting technique produced distinct banding patterns, selection has increased genetic homogeneity within the selected lines using DFP, the band sharing of DNA fingerprints within lines was not closely related to accumulated inbreeding, some known relationships among lines were not predicted by the DNA fingerprinting.

The first genetic map for quail was produced exclusively with AFLP markers (Roussot *et al.*, 2003). Hence, it would be beneficial in the future to integrate the microsatellite and the AFLP maps in order to provide a powerful tool for the ongoing search for quantitative trait loci controlling egg production and fear-related behavioral traits in quail. A linkage map of the Japanese quail (*Coturnix japonica*) genome was constructed based upon segregation analysis of 72 microsatellite loci in 433 F2 progeny of 10 half-sib families. This map, which is the first in quail based solely on microsatellites, is a major step towards the development of a quality molecular genetic map for this valuable species. It will provide an important framework for further genetic mapping and the identification of quantitative trait loci controlling egg production and fear-related behavioral traits in quail (Kayang *et al.*, 2004). Genetic coadaptability of wiled Japanese quail, wiled common quail and domestic quail populations in China was studied using 7 microsatellite DNA markers (Guobin *et al.*, 2006). Microsatellite have been reported in the literature for Japanese quails (Pang *et al.*, 1999; Kayang *et al.*, 2002).

We found that, a few papers had investigated DNA fingerprinting in other poultry species such as turkey, duck, goose and ostrich.

In Turkey: RAPD analyses have been used for parentage analysis, genetic analysis of relatedness and diversity in turkeys (Smith *et al.*, 1996). Genetic

relatedness among five turkey strains was investigated using three molecular marker systems: Randomly Amplified Polymorphic DNA (RAPD), microsatellite and SNPs derived from a sequence tagged site and a cloned RAPD fragment. These data provide, for the first time, molecular evidence of the potential relationships among noncommercial domesticated turkey strains (Smith *et al*., 2005).

In ducks: DNA-fingerprinting used to study genetic similarity (Triggs *et al*., 1992). The technique of (RAPD-PCR) was applied to elucidate the genetic variation within and between duck populations and estimating the phylogenetic relationships among them by El-Gendy *et al*. (2005) and to estimate genetic similarity between four breeds by Gholizadeh *et al*. (2007), microsatellite have been reported in the literature for ducks (Maak *et al*., 2003). A genetic linkage map for the duck (*Anas platyrhynchos*) was developed within a cross between two extreme Peking duck lines by linkage analysis of 155 polymorphic microsatellite markers, including 84 novel markers reported in a study by Huang *et al*. (2006), this genetic and cytogenetic map will be helpful for the mapping QTL in duck for breeding applications and for conducting genomic comparisons between chicken and duck. The first AFLP linkage map in duck (*Anas platyrhynchos*) constructed by (Huang *et al*., 2009), this map provides important information for establishing a duck chromosome map, for mapping quantitative trait loci (QTL mapping) and for breeding applications.

In goose: We find only one publication by Maciuszonek *et al*. (2005), they reported that, several specific DNA fragments described may facilitate identification of genotypes and as follows, may be used in germplasm conservation in goose breeds.

In ostrich: Hinckley *et al*. (2005) indicated that, W-linked markers amplified from ostrich genome may be species specific markers. These results demonstrate that RAPD analysis using bulked DNA samples provides an efficient means for the detection of W-chromosome markers in avian species. The SCARS developed can be used for identifying sex in immature ostriches. The objective of their study was to develop reliable PCR-based DNA markers that can be used for sex identification in the ostrich with lower costs. On the other hand, the suitability of 29 chicken microsatellite markers was evaluated as potential genetic linkage markers in the ostrich. No sequence homology was stated (0.00% similarity) between any of the 29 chicken microsatellites and the genome of the ostrich. This leads to the conclusion that the former are not suitable for genome mapping of the latter. In light of this, more work should especially be done to widen our knowledge of ostrich specific markers (Horbañczuk *et al*., 2007). Analyses of the representative DNA fingerprinting band patterns failed to distinguish bands specific for the high and low performance groups of ostrich layers (Kawka *et al*., 2010). Further investigations are required, in which another combination of probe/enzyme and especially the application of highly polymorphic microsatellites should be applied, since the microsatellite analysis provides more detailed information and is widely used in linkage mapping of farm animals.

Other uses of DFP: in fish breeding, Multi-locus DNA fingerprinting, RAPD and simple sequence repeat-anchored PCR (SSRa-PCR) techniques were able to show that clone founders as well as gynogenetic offspring were genetically homozygous. Multi-locus DNA fingerprinting and RAPD were used to demonstrate that carryover of male chromosomal DNA by the use of UV-irradiated sperm for induction of gynogenesis did not occur and that the clonal lines could be accurately distinguished from each other. In contrast to these methods, the used primers in SSRa-PCR did not have the power to determine the absence of paternal genomic transmission due to a lack of visible informative paternal bands (Jenneckens *et al*., 1999). In the field of quality control of meat products: Calvo *et al*. (2001) reported that, the RAPD-PCR pattern was useful to identify species composition of pork, duck, duck-pork, goose, and poultry pates. This study demonstrates the usefulness of RAPD fingerprinting to distinguish between species in pates. RAPD-PCR fingerprintings allowed the discrimination amongst pork, beef, lamb, chicken and turkey in all cases. AP-PCR also allowed identification of the five tested species in every sample although more complex patterns were generated, including some low intensity bands. RAPD- and AP PCR are molecular techniques which are easier, faster and cheaper than other DNA-based techniques. Overall, the assayed techniques could be robust and simple methods to be considered as additional quality control tools in meat species identification (Saez *et al*., 2004). The development of species-specific real-time PCR assays for the detection of pheasant and quail in commercial food products are reported (Chisholm *et al*., 2008). The assays successfully detected pheasant and quail in complex food matrices of raw, oven-cooked and autoclaved meat, demonstrating their suitability for use in enforcement and food control laboratories.

Conclusion: As reviewed in this paper, DNA fingerprinting techniques are currently available to provide detailed assessment of the molecular genetic variation in the structure of the different poultry species genome. It is important to mention the fact that data results from DNA-fingerprintings assays can be

extended to enhance populations by management decisions based on a more accurate understanding of their biodiversity and can make directed improvement in poultry populations by incorporating genomic marker information into breeding programs. There is also the opportunity and need to study sequences of specific polymorphic bands, to determine the genes detected by fingerprinting experiments. There are various well-developed strains of poultry that are used commercially. However, information about the genetic characterization of these strains and the amount of genetic diversity among them is minimal, especially for most important traits. Hence more studies are needed to characterize these strains genetically and to estimate the genetic variability between them in order to enhance selection and breeding.

REFERENCES

Ajmone-Marsan, P., G. Vecchiotti-Antaldi, G. Bertoni, A. Valentini, M. Cassando and M. Kuiper, 1997. AFLP™ markers for DNA fingerprinting in cattle. Anim. Genet., 28: 418-426.

Ajmone-Marsan, P., R. Negrini, P. Crepaldi, E. Milanesi, C. Gorni, A. Valentini and M. Cicogna, 2001. Assessing genetic diversity in Italian goat populations using AFLP markers. Anim. Genet., 32: 281-288.

Ali, B.A. and M.M.M. Ahmed, 2001. Random amplified polymorphic DNA in some chicken strains. First conference of Role of Biochemistry in Environment and Agriculture, 6-8 February, pp: 23-31, part 1. Cairo University, Egypt.

Ali, B.A., M.M.M. Ahmed and O.M. Aly, 2003. Relationship between genetic similarity and some productive traits in local chicken strains. Afr. J. Biotechnol., 2: 46-47.

Atzmon, G., S. Blum, M. Feldman, U. Lavi and J. Hillel, 2007. Detection of agriculturally important QTLs in chickens and analysis of the factors affecting genotyping strategy. Cytogenetic Genome Res., 117: 327-337.

Buitkamp, J., H. Ammer and H. Geldermann, 2005. DNA fingerprinting in domestic animals. Electrophoresis, 12: 169-174.

Calvo, J.H., P. Zaragoza and R. Osta, 2001. Random amplified polymorphic DNA fingerprints for identification of species in poultry pate. Poult. Sci., 80: 522-524.

Chen, G.H., X.S. Wu, D.Q. Wang, J. Qin, S.L. Wu, Q.L. Zhou, F. Xie, R. Cheng, Q. Xu, B. Liu, X.Y. Zhang and O. Olowofeso, 2004. Cluster analysis of 12 Chinese native chicken populations using microsatellite markers. Asian-Aust. J. Anim. Sci., 8: 1047-1052.

Cheng, H.H., I. Levin, R.L. Vallejo, H. Khatib, J.B. Dodgson, L.B. Crittenden and J. Hillel, 1995. Development of a genetic map of the chicken with markers of high utility. Poult. Sci., 74: 1855-1874.

Chengwei Ren, Mi-Kyung Lee, Bo Yan, Kejiao Ding, Bettye Cox, Michael N. Romanov, Jennifer A. Price, Jerry B. Dodgson and Hong-Bin Zhang, 2003. A BAC-based physical map of the chicken genome. Genome Res., 13: 2754-2758.

Chisholm, J., A. Sánchez, J. Brown and H. Hird, 2008. The development of species-specific Real-time PCR assays for the detection of pheasant and quail in food. Food Anal. Methods, 1: 190-194.

Crooijmans, R.P.M.A., A.F. Groen, A.J.A. Van Kampen, S. Van Der Beek, J.J. Van Der Poel and M.A.M. Groenen, 1996. Microsatellite polymorphism in commercial broiler and layer lines estimated using pooled blood samples. Poult. Sci., 75: 904-909.

Darvasi, A., 1998. Experimental strategies for the genetic dissection of complex traits in animal models. Nature Genet., 18: 19-24.

Dehghanzadeh, H., S.Z. Mirhoseini, M.N. Romanov and A. Ghorbani, 2009. Evaluation of genetic variability and distances among five iranian native chicken populations using RAPD markers. Pak. J. Biol. Sci., 12: 866-871.

Dmitriev, V.B., I.V. Churkina, A.F. Smirnov and E.K. Nikolaeva, 2001. Destabilizing effect of chicken selection for the functional adrenal reserves. Russian J. Genet., 37: 412-417. Translated from Genetika, 37: 517-523.

Dong, N., Y. Fu, L. Jing, R. Hui, X.P. Yu, C. Gong and Y.P. Zhang, 2002. The origin and genetic diversity of Chinese native chicken breeds. Biochem. Genet., 40: 163-174.

Dunnington, E.A., L.C. Stallard, J. Hillel and P.B. Siegel, 1994. Genetic diversity among commercial chicken populations estimated from DNA fingerprints. Poult. Sci., 73: 1218-1225.

Dunnington, E.A., L.C. Stallard, P.B. Siegel and J. Hillel, 1993. Evaluating linkage between DNA fingerprint bands and quantitative traits in chickens: interactions. Poult. Sci., 72: 1000-1004.

Dunnington, E.A., O. Gal, P.B. Siegel, A. Haberfeld, A. Cahaner, U. Lavi, Y. Plotsky and J. Hillel, 1991. Deoxyribonucleic acid fingerprint comparisons between selected populations of chickens. Poult. Sci., 70: 463-467.

Dunnington, E.A., O. Gal, Y. Plotsky, A. Haberfeld, T. Kirk, A. Goldberg, U. Lavi, A. Cahaner, P.B. Siegel and J. Hillel, 1990. DNA fingerprints of chickens selected for high and low body weight for 31 generations. Anim. Genet., 21: 247-57.

El-Gendy, E.A., M.A. Helal, N.H. Goher and A. Mostageer, 2005. Molecular characterization of genetic biodiversity in ducks, using RAPD-PCR analysis. Arab J. Biotechnol., 8: 253-264.

El-Gendy, E.A., M.K. Nassar, M.S. Salama and A. Mostageer, 2006. Genotype-environment interaction in relation to heat tolerance in chickens. 1. RAPD-PCR analysis for breeds local to warm regions. Arab J. Biotechnol., 9: 1-16.

Tropical and Subtropical Agriculture, third STD programme, 1992-1995. Evaluation of local poultry resources for creating genetic stock with improved adaptability, productivity and disease resistance in tropical environments. Summary reports of European Commission supported STD-3 projects (1992-1995), published by CTA 1999.

Feral, J.P., 2002. How useful are the genetic markers in attempts to understand and manage marine biodiversity?. J. Exp. Mar. Biol. Ecol., 268: 121-145.

Fumiere, O., M. Dubois, D. Gregoire, A. Thewis and G. Berben, 2003. Identification on commercialized products of AFLP markers able to discriminate slow- from fast-growing chicken strains. J. Agric. Food Chem., 51: 1115-1119.

Gavora, J.S., R.W. Fairfull, B. Benkel, W.J. Cantwell and J.R. Chambers, 1993. DNA fingerprints as predictors of heterosis. Centre for Food and Animal Research, Ottawa, Ontario Canada K1A 0C6.

Geldermann, H. and F. Ellendorff, 1990. Genomic analysis in domestic animals, Eds., Weinhem, Germany.

Gholizadeh Mohsen, Ghodrat Rahimi Mianji, Abbas Ghobadi, Hadi Sayyah Zadeh and Shahab Montazami, 2007. Measurement of within and between genetic variability in duck breeds by RAPD markers. Pak. J. Biol. Sci., 10: 982-985.

Gilbert, D.A., C. Packer, A.E. Pusey, J.C. Stephens and S.J. O'brien, 1991. Analytical DNA fingerprinting in lions: parentage, genetic diversity and kinship. J. Heredity, 82: 378–386.

Gilbert, D.A., N. Lehman, S.J. O'brien and R.K. Wayne, 1990. Genetic fingerprinting reflects population differentiation in the California Channel Island fox. Nature, 344: 764-767.

Grunder, A.A., M.P. Sabour and J.S. Gavora, 1994. Estimates of relatedness and inbreeding in goose strains from DNA fingerprints. Anim. Genet., 25 (suppl 1): 81-88.

Guobin, C., C. Hong, L. Xiangping, Y. Zhangping, C. Gouhong, Z. Wenming, J. Dejun, X. Yan, H. Feng and H. Hussein, 2006. Study on genetic coadaptability of wild quail populations in China. Science in China: Series C Life Sciences, 49: 172-181.

Haberfeld, A., E.A. Dunnington and P.B. Siegel, 1992. Genetic distances estimated from DNA fingerprints in crosses of white Plymouth Rock chickens. Anim. Genet., 23: 167-173.

Haberfeld, A., E.A. Dunnington, P.B. Siegel and J. Hillel, 1996. Heterosis and DNA fingerprinting in chickens. Poult. Sci., 75: 951-953.

Haley, C.S., 1991. Use of DNA fingerprints for the detection of major genes for quantitative traits in domestic species. Anim. Genet., 22: 259-277.

Hanotte, O., M.W. Bruford and T. Burke, 1992. Multilocus DNA fingerprints in gallinaceous birds: General approach and problems. Heredity, 68: 481-494.

Heyen, D.W., J.I. Weller, M. Ron, M. Band, J.E. Beever, E. Feldmesser, Y. Da, G.R. Wiggans, P.M. VanRaden and H.A. Lewin, 1999. A genome Scan for QTL influencing milk production and health traits in dairy cattle. Physiol. Genomics, 1: 165-175.

Hideyuki Mannen, Soichi Tsuji, Satoru Okamoto, Yoshizane Maeda, Hideji Yamashita, Fumio Mukai and Nobou Goto, 1993. DNA fingerprints of Japanese quail lines selected for high and low body weight. Japanese Poult. Sci., 30: 66-71.

Hillel, J., E.A. Dunnington and P.B. Siegel, 1992. DNA markers in poultry breeding and genetic analyses. Poult. Sci. Rev., 4: 169-186.

Hillel, J., E.A. Dunnington, A. Haberfeld, U. Lavi, A. Cahaner, O. Gal, Y. Plotsky and P.B. Siegel, 1992. Multilocus DNA markers: applications in poultry breeding and genetic analyses. In: Manipulation of the avian genome (Gibbins A and Etches R, Eds). Boca Raton, Florida: CRC Press, pp: 243-256.

Hillel, J., M.A.M. Groenen, M. Tixier-Boichard, A.B. Korol, L. David, V.M. Kirzhner, T. Burke, A. Barre-Dirie, R.P.M.A. Crooijmans, K. Elo, M.W. Feldman, P.J. Freidlin, A. Mäki-Tanila, M. Ortwijn, P. Thomson, A. Vignal, K. Wimmers and S. Weigend, 2003. Biodiversity of 52 chicken populations assessed by microsatellite typing of DNA pools. Genet. Selection Evol., 35: 533-557.

Hillel, J., T. Schaap, A. Haberfeld, A.J. Jeffreys, Y. Plotzky, A. Cahaner and U. Lav, 1990. DNA Fingerprints Applied to Gene Introgression in Breeding Program. Genetics, 124: 783-789.

Hinckley, J.D., R.L. Park, S. Xiong, W.R. Andersen and D.L. Kooyman, 2005. Identification and Development of Sex Specific DNA Markers in the Ostrich Using Polymerase Chain Reaction. Int. J. Poult. Sci., 4: 663-669.

Horbañczuk, J.O., M. Kawka, M. Sacharczuk, R.G. Cooper, K. Boruszewska, R. Parada and K. Jaszczak, 2007. A search for sequence similarity between chicken (*Gallus domesticus*) and ostrich (*Struthio camelus*) microsatellite markers. Anim. Sci. Papers Rep., 25: 283-288. Institute of Genetics and Animal Breeding, Jastrzêbiec, Poland.

Huang, C.W., Y.S. Cheng, R. Rouvier, K.T. Yang, C.P. Wu, H.L. Huang and M.C. Huang, 2009. Duck (*Anas platyrhynchos*) linkage mapping by AFLP fingerprinting. Genet. Selection Evol., 41: 28-35.

Huang, Y., Y. Zhao, C.S. Haley, S. Hu, J. Hao, C. Wu and N. Li, 2006. A genetic and cytogenetic map for the duck (*Anas platyrhynchos*) Genetics, 173: 287-296.

Ivgin, R. and G. Bigen, 2002. Estimation of genetic distance in meat and layer pure lines using randomly amplified polymorphic DNA. Turk. J. Vet. Anim. Sci., 26: 1117-1120.

Jeffreys, A.J., V. Wilson and S.L. Thein, 1985. Hypervariable 'minisatellite' regions in human DNA. Nature, 314: 67-73.

Jenneckens, I., A. Muller-Belecke, G. Horstgen-Schwark and J.N. Meyer, 1999. Proof of the successful development of Nile tilapia (*Oreochromis niloticus*) clones by DNA fingerprinting. Aquaculture, 173: 377-388.

Jin, L. and R. Chakraborty, 1994. Estimation of genetic distance and coefficient of gene diversity from singleprobe multilocus DNA fingerprinting data. Mol. Biol. Evol., 11: 120-127.

Kaiser, M.G., N. Lakshmanan, J.A. Arthur, N.P. O'Sullivan and S.J. Lamont, 2003. Experimental population design for estimation of dominant molecular marker effect on egg-production traits. Anim. Genet., 34: 334-338.

Kaiser, M.G., N. Yonash, A. Cahaner and S.J. Lamont, 2000. Microsatellite polymorphism between and within broiler populations. Poult. Sci., 79: 626-628.

Kawka, M., M. Sacharczuk and R.G. Cooper, 2010. Identification of genetic markers associated with laying production in ostriches (*Struthio camelus*) - a preliminary study. Anim. Sci. Papers Rep., 28: 95-100.

Kaya, M. and M.A. Yildiz, 2008. Genetic diversity among Turkish native chickens, denizli and gerze, estimated by microsatellite markers. Biochem. Genet., 46: 480-491.

Kayang, B.B., A. Vignal, M. Inoue-Murayama, M. Miwa, J.L. Monvoisin, S. Ito and F. Minvielle, 2004. A first-generation microsatellite linkage map of the Japanese quail. Anim. Genet., 35: 195-200.

Kayang, B.B., M. Inoue-Murayama, T. Hoshi, K. Matsuo, H. Takahashi, M. Minezawa, M. Mizutani and S. Ito, 2002. Microsatellite loci in Japanese quail and cross-species amplification in chicken and guinea fowl. Genet. Selection Evol., 34: 233-253.

Khatib, H., A. Darvasi, Y. Plotsky and M. Soller, 1994. Determining relative microsatellite allele frequencies in pooled DNA samples. PCR Methods Appl., 4: 13-18.

Kimura Tomoki, Hideyuki Mannen, Soichi Tsuji, Fumio Mukai, Nobuo Goto, Noboru Kano, Tugito Yamamoto and Tadaaki Sato, 1993. Chicken DNA fingerprints using six different probes. Japanese Poult. Sci., 30: 287-297.

Kuhnlein, U., D. Zagworny, Y. Dawe, R.W. Fairfull and J.S. Gavora, 1990. Assessment of inbreeding by DNA fingerprinting: Development of a calibration curve using defined strains of chicken. Genetics, 125: 161-166.

Kuhnlein, U., Y. Dawe, D. Zadworny and J.S. Gavora, 1989. DNA fingerprinting: A tool for determining genetic distances between strains of poultry. Theor. Applied Genet., 77: 669-672.

Kumar, L.L., 1999. DNA markers in plant improvement: an overview. Biotechnol. Adv., 17: 143-182.

Lee, J.C. and J.G. Chang, 1994. Random amplified polymorphic DNA polymerase chain reaction (RAPD PCR) fingerprints in forensic species identification. Forensic Sci. Int., 67: 103-107.

Levin, I., L.B. Crittenden and J.B. Dodgson, 1993. Genetic map of the Z chromosome using random amplified polymorphic DNA (RAPD) markers. Genomics, 16: 224-230.

Levin, I., L.B. Crittenden and J.B. Dodgson, 1994. Mapping DNA polymorphism using PCR primers derived from the sequence of an avian CR1 element. J. Hered., 85: 73-78.

Liu, X.P., K.W. Chen, K.H. Wang, J.Y. Wang, G.J. Dai, X.Y. Zhang and G.B. Chang, 2009. Study on relations between heterosis and band J in DNA fingerprints of xiaoshan and SR92 chickens in China. J. Anim. Vet. Adv., 8: 1765-1767.

Maak, S., K. Wimmers, S. Weigend and K. Neumann, 2003. Isolation and characterization of 18 microsatellites in the Peking duck (*Anas platyrhynchos*) and their application in other waterfowl species. Mol. Ecol. Notes, 3: 224-227.

Maciuszonek, A., B. Grajewski and M. Bednarczyk, 2005. RAPD-PCR analysis of various goose populations. Folia Biologica (Kraków), 53: 83-85.

Martino, C., C. Targhetta, M. De Marchi, C. Dalvit, G. Barcaccia and G. Bittante, 2005. DNA fingerprinting characterization of 4 Italian poultry species. Plant and Animal Genomes XIII Conference, January 15-19, Town and Country Convention Center, San Diego, CA.

Mekchay Supamit, Amnuay Leotaragul, Anchali Wongsa and Patcharin Krutmuang, 2005. Molecular marker-based genetic diversity assessment of Thai native chicken and broiler chicken. Conference on International Agricultural Research for Development, Tropentag, Stuttgart, Hohenheim, October 11-13.

Meng, A., G. Gong, D. Chen, H. Zhang, S. Qi, H. Tang and Z. Gao, 1996. DNA fingerprint variability within and among parental lines and its correlation with performance of F1 laying hens. Theor. Applied Genet., 92: 769-776.

Mishra, S.K., V. Thiagarajan, A.M. Nainar and P. Ramadass, 2002. Genetic variation in juvenile growth traits of chickens as influenced by DNA fingerprint markers. Proceedings of the 7th World Congress on Genetics Applied to Livestock Production, Montpellier, France, August, 2002. Session 11.

Mohamed, N.A., E.N. El-sayed, N.T. Hamdoon and K.A. Amein, 2001. Chicken strains identification using SDS-PAGE protein and RAPD-PCR markers. Assiut J. Agric. Sci., 32: 101-113.

Naoyuki, Y. and T. Tomita, 1993. Detection of γ-Ray irradiated donor sperm DNA in the transgenic chicken embryo by DNA fingerprint analysis. Japanese Poult. Sci., 30: 114-122.

O'Sullivan, N. and J.A. Greaves, 2007. Protecting brand identity through DNA fingerprinting. New Horizons, A publication of Hy-Line International, Volume 1, Issue 1.

Pang, S.W., C. Ritland, J.E. Carlson and K.M. Cheng, 1999. Japanese quail microsatellite loci amplified with chicken-specific primers. Anim. Genet., 30: 195-199.

Plotsky, Y., A. Cahaner, A. Haberfeld, U. Lavi, S.J. Lamont and J. Hillel, 1993. DNA fingerprinting bands applied to linkage analysis with quantitative trait loci in chickens. Anim. Genet., 24: 105-110.

Plotsky, Y., M.G. Kaiser and S.J. Lamont, 1995. Genetic characterization of highly inbred chicken lines by two DNA methods: DNA fingerprinting and polymerase chain reaction using arbitrary primers. Anim. Genet., 26: 163-170.

Ponsuksili, S., K. Wimmers and P. Horst, 1998. Evaluation of genetic variation within and between different chicken lines by DNA fingerprinting. J. Heredity, 89: 17-23.

Ponsuksili, S., K. Wimmers, F. Schmoll, P. Horst and K. Schellander, 1999. Comparison of multilocus DNA fingerprints and microsatellites in an estimate of genetic distance in chicken. J. Heredity, 90: 656-659.

Rastogi, G., S.D. Mahesh, S. Walujkar, A. Kumar, M.S. Patole and Y.S. Shouche, 2007. Species identification and authentication of tissues of animal origin mitochondrial and nuclear markers. Meat Sci., 76: 666-674.

Riquet, J., W. Coppieters and N. Cambisano, 1999. Fine mapping of quantitative trait loci by identity by descent in outbred populations: application to milk production in dairy cattle. Proc. Natl. Acad. Sci. USA, 96: 9252-9257.

Roussot, O., K. Feve, F. Plisson-Petit, F. Pitel, J.M. Faure, C. Beaumont and A. Vignal, 2003. AFLP linkage map of the Japanese quail (*Coturnix japonica)*. Genet. Selection Evol., 35: 559-72.

Sacharczuk, M., R. Parada and K. Jaszczak, 2005. DNA fingerprinting of chicken lines divergently selected for high or low incidence of skeletal malformations. Animal Science Papers and Reports vol. 23 no. 2, 119-127 Institute of Genetics and Animal Breeding, Jastrzebiec, Poland.

Saez, R., Y. Sanz and F. Toldra, 2004. PCR-based fingerprinting techniques for rapid detection of animal species in meat products. Meat Sci., 66: 659-665.

Salem, H.H., B.A. Ali, T.H. Huang and D.N. Qin, 2005. Use of randomly amplified polymorphic DNA (RAPD) markers in poultry research. Int. J. Poult. Sci., 4: 804-811.

Schmid, M., I. Nanda, H. Hoehn, M. Schartl, T. Haaf, J.M. Buerstedde, H. Arakawa, R.B. Caldwell, S. Weigend, D.W. Burt, J. Smith, D.K. Griffin, J.S. Masabanda, M.A. Groenen, R.P. Crooijmans, A. Vignal, V. Fillon, M. Morisson, F. Pitel, M. Vignoles, A. Garrigues, J. Gellin, A.V. Rodionov, S.A. Galkina, N.A. Lukina, G. Ben-Ari, S. Blum, J. Hillel, T. Twito, U. Lavi, L. David, M.W. Feldman, M. E. Delany, C.A. Conley, V.M. Fowler, S.B. Hedges, R. Godbout, S. Katyal, C. Smith, Q. Hudson, A. Sinclair and S. Mizuno, 2005. Second report on chicken genes and chromosomes. Cytogenet. Genome Res., 109: 415-479.

Schmidt, G.S., F.P. Hellmeister and E.L. Zanella, 2003. Characterization of selection effects on broiler lines using DNA fingerprinting. (Revista Brasileira de Ciencia Avicola) Rev. Bras. Cienc. Avic. vol. 5 no. 2 Campinas May-Aug.

Semenova, S.K., A.L. Filenko, V.A. Vasil'ev, M.I. Prosniak, A.A. Sevast'ianova and A.P. Ryskov, 1996. Use of polymorphic DNA markers for differentiation of chicken breeds of varying origin. Genetika, 32: 795-803.

Sharma, A.K., J.D. Joshi, R.K. Singh, S. Kumar and D. Sharma, 2000. DNA Fingerprinting using synthetic oligonucleotide probe in native and exotic chicken breeds. Int. J. Poult. Sci., 3.

Sharma, D., K.B. Appa Rao, R.V. Singh and S.M. Totey, 2001. Genetic diversity among chicken breeds estimated through randomly amplified polymorphic DNA. Anim. Biotechnol., 12: 111-120.

Sharma, D., K.B.C. Appa Rao and S.M. Totey, 1998a. Estimation of genetic diversity among various breeds of poultry using randomly amplified polymorphic DNA. 10th European Poultry Conference, Israel, "The Poultry Industry Towards the 21st Century", pp: 259-262.

Sharma, D., K.B.C. Appa Rao, H.P. Singh and S.M. Totey, 1998b. Randomly Amplified Polymorphic DNA (RAPD) for evaluating genetic relationships among varieties of guinea fowl. Genetical Analysis: Bimolecular Eng., 14: 125-128.

Siegel, P.B., A. Haberfeld, T.K. Mukherjee, L.C. Stallard, H.L. Marks, N.B. Anthony and E.A. Dunnington, 1992. Jungle fowl-domestic fowl relationships: a use of DNA fingerprinting. World's Poult. Sci. J., 48: 147-155.

Singh, R.V. and D. Sharma, 2002. Within and between strain genetic variability in White Leghorn population detected through RAPD markers. Br. Poult. Sci., 43: 33-37.

Smith, E.J., C.P. Jones, J. Bartlett and K.E. Nestor, 1996. Use of randomly amplified polymorphic DNA markers for the genetic analysis of relatedness and diversity in chickens and turkeys. Poult. Sci., 75: 579-584.

Smith, E.J., T. Geng, E. Long, F.W. Pierson, D.P. Sponenberg, C. Larson and R. Gogal, 2005. Molecular analysis of the relatedness of five domesticated turkey strains. Biochem. Genet., 43: 35-47.

Soller, M., S. Weigend, M.N. Romanov, J.C.M. Dekkers and S.J. Lamont, 2006. Strategies to assess structural variation in the chicken genome and its associations with biodiversity and biological performance. Poult. Sci., 85: 2061-2078.

Takahashi, H., K. Nirasawa, Y. Nagamine, M. Tsudzuki, and Y. Yamamoto, 1998. Genetic relationships among Japanese native breeds of chicken based on microsatellite DNA polymorphisms. J. Heredity, 89: 543-546.

Takezaki, N. and M. Nei, 1996. Genetic distance and reconstruction of phylogenetic trees from microsatellite DNA. Genetics, 144: 389-399.

Tercic, D., A. Holcman and P. Dovc, 1998. Segregation analysis of RAPD markers associated with body weight in chickens. 10th European Poultry Conference, Israel, "The Poultry Industry Towards the 21st Century". Abstr. 61.

Tixier-Boichard, M., N. Kritchmann, M. Morisson, A. Bordas and J. Hillel, 1996. Assessment of genomic variability through DNA fingerprinting within and between chicken lines divergently selected for residual food consumption. Anim. Genet., 27: 163-169.

Triggs, S.J., M.J. Williams, S.J. Marshall and G.K. Chambers, 1992. Genetic structure of blue duck (*hymenolaimus malacorhynchos*) populations revealed by DNA fingerprinting. The auk, 109: 80-89.

Twito, T., S. Weigend, S. Blum, Z. Granevitze, M.W. Feldman, R. Perl-Treves, U. Lavi and J. Hillel, 2007. Biodiversity of 20 chicken breeds assessed by SNPs located in gene regions. Cytogenetic Genome Res., 117: 319-326.

Weigend, S., M.N. Romanov and D. Rath, 2004. Methodologies to identify, evaluate and conserve poultry genetic resources. World's Poult. Congr. Exhib., Istanbul, Turkey.

Welsh, J. and M. McClelland, 1990. Fingerprinting genomes using PCR with arbitrary primers. Nucl. Acid. Res., 18: 7213-7218.

Wimmers, K., S. Ponsuksili, T. Hardge, A. Valle-Zarate, P.K. Mathur and P. Horst, 2000. Genetic distinctness of African, Asian and South American local chickens. Anim. Genet., 31: 159-165.

Wimmers, K., S. Ponsuksili, T. Hardge, A. Valle-Zarate and P. Horst, 1999. Genetic distance estimation between chicken populations of tropical and subtropical countries based on microsatellites. Deutscher Tropentag in Berlin. Session: Biodiversity and development of animal genetic resources.

Xena De Enrech, N., 2000. A decade of the RAPD method: possibilities and limitations for plant genetics relationship studies. Acta. Cient. Venez., 51: 197-206.

Ye, X., J. Zhu, S.G. Velleman and K.E. Nestor, 1998a. Genetic diversity of commercial turkey primary breeding lines as estimated by DNA fingerprinting. Poult. Sci., 77: 802-807.

Ye, X., J. Zhu, S.G. Velleman, W.L. Bacon and K.E. Nestor, 1998b. Measurement of Genetic Variation Within and Between Japanese Quail Lines Using DNA Fingerprinting. Poult. Sci., 77: 1755-1758.

Yu Ya-Bo, Wang Jin-Yu, D.M. Mekki, Tang Qing-Ping, Li Hui-Fang, Gu Rong, Ge Qing-Lian, Zhi Wen-Qi and Chen Kuan-Wei, 2006. Evaluation of genetic diversity and genetic distance between twelve Chinese indigenous chicken breeds based on microsatellite markers. Int. J. Poult. Sci., 5: 550-556.

Yu-Shi Gao, Li Hui-Fang, Chen Guo-Hong, Tu Yun-Jie, Wang Ke-Hua and Chen Kuan-Wei, 2005. Construction of Microsatellite DNA Fingerprinting and Analysis of Genetic Diversity of Native Chicken Breeds. J. Yunnan Agric. Univ., 20: 313-318.

Yu-Shi Gao, Tu Yun-Jie, Tong Hai-Bing, Wang Ke-Hua and Chen Kuan-Wei, 2006. AFLP fingerprinting analysis of genetic polymorphism of 12 indigenous chicken breeds. J. Agric. Biotechnol., 14: 498-502.

Zhang, X., C.R. Mcdaniel and J.R. Giamborne, 1995. Random amplified polymorphic DNA comparisons among broiler lines selected for incidence of tibia dyschondroplasia. Poult. Sci., 74: 1253-1258.

Zhang, X., F.G. Leung, D.K.O. Chan, G. Yang and G. Wu, 2002. Genetic diversity of Chinese native chicken breeds based on protein polymorphism, randomly amplified polymorphic DNA, and microsatellite polymorphism. Poult. Sci., 81: 1463-1472.