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Development of a database on genetic characterization of animal genetic resources

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ABSTRACT

Conservation of breeds of domestic animal species is essential to preserve genetic diversity and maintaining future breeding options. Phenotypic and genetic characterisation of breeds has been taken up all over the globe as a prerequisite for conservation. Detailed genetic data on within and between-breed diversity are essential for effective management of Farm Animal Genetic Resources. Only few databases are available on this aspect. This paper reports development of a database on genetic characterisation using microsatellite markers. The database contains genetic diversity parameters of breeds as reported in published studies. It has uses as a source of composite information at one site and for comparing genetic diversity of breeds for making decision on their prioritisation for conservation.

Key words: Genetic characterization, animal genetic resources, breed, microsatellite, database

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INTRODUCTION

Domestic animal species have been a dominant source of food, draft power and fibre since advent of human civilization. More than 7000 breeds and strains of about forty animal species constitute the global animal genetic resources (AnGRs) (FAO 2007). Over centuries, natural evolutionary forces together with human interventions through selective breeding of farm animals has resulted in the development of a large number of breeds of domestic animal species such as cattle, buffalo, sheep, goat, pig, poultry, horse, camel, etc. However, the process of genetic improvement has accelerated during last five decades as a result of the adoption of modern biotechnological tools like artificial insemination and embryo transfer with focus on propagating high producing breeds. As a result, highly productive breeds have replaced local ones across the World. Consequently low producing local breeds have become uneconomical and thus lost attention and have become threatened. Approximately 10% of the breeds became extinct during the past century. Currently about 20% of the roughly 7600 breeds reported worldwide, belonging to 18 mammalian species and 16 avian species, are at risk (FAO 2007).

Management and conservation of farm animal genetic resources have become essential for saving existing breeds from possible extinction and for sustainable agricultural systems as well as for long-term food security. Comprehensive knowledge of breed characteristics is essential for their effective management. It includes information on breed characteristics and performance, farming systems, geographical distribution, socio-economic significance and population size, and structure and within and between breed diversity. Modern biology aims to understand the genetic basis of phenotypic diversity within and among species (Anderson and Georges 2004). It is commonly acknowledged that comprehensive molecular data on within and between breed diversity is essential for effective management of animal genetic resources (Toro et al. 2009; Groeneveld 2010). Molecular genetic information can be used as an alternative to prevalent pedigree information for prioritization for conservation of AnGRs (Boettcher et al. 2010).

Genetic characterization of AnGR involves sampling of breeds followed by genotyping at a given set of loci. It detects variation among individuals in a population through use of molecular markers. Food & Agriculture Organization (FAO) has suggested species-specific microsatellite markers for uniformity of genetic characterization of AnGR in various regions of the world. Following the

guidelines of Maintenance of Domestic Animal Genetic Diversity (MoDAD) project of FAO (FAO, 1998), microsatellite-based genetic diversity parameters have been generated and published for a large number of breeds across species throughout the globe (Canon et al. 2001; Rosenberg et al. 2001; Behl et al. 2003; Chenyambuga et al. 2004; Martin-Burriel et al. 2007). FAO, (2011) emphasizes on generation of genetic diversity values for all the breeds in various countries.

Farm animal diversity database is a desired tool for comparison of diversity parameters of breeds within and across countries and decision making on conservation. National websites have been put in place by each country with a complete coverage of breed descriptors of all the breeds considered to be part of their national heritage. In comparison to this, only few genetic databases on primary information emanating from various laboratories are available. A multitude of smaller publicly accessible microsatellite genotype databases, often with more specific purposes, are available. For individual livestock records, a few databases are available: AVIANDIV for chickens (http://aviandiv.tzv.fal.de/), CaDBase for cattle (http://www.projects.roslin.ac.uk/cdiv/) and PigDBase for pigs (http://www.projects.roslin.ac.uk/pigbiodiver/) (Russell et al. 2003) to store data generated by the EC-funded Pig Diversity Project.

Various studies on genetic characterisation used different methods to generate primary microsatellite data on alleles in breeds and analyse it to obtain genetic diversity parameters such as observed number of alleles, effective number of allele, observed heterozygosity, expected heterozygosity, F_{st}, genetic distances, etc. The genetic diversity parameters need comparison for decision making on conservation of animal genetic resources. Therefore, a database on genetic diversity parameters of animal genetic resources is required in different regions and

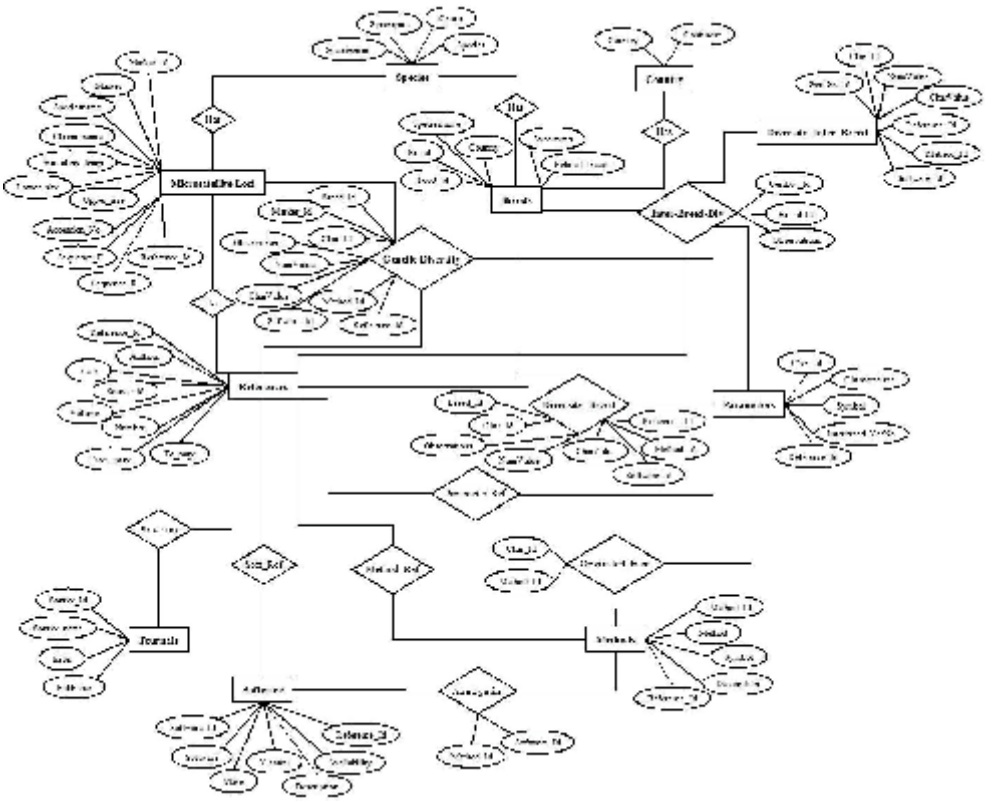

Figure 1: Entity-Relationship Diagram of the Database on Animal Genetic Resources

countries, similar to the National phenotypic breed description databases. This paper presents such an attempt toward the development of a database on genetic characterization of AnGRs derived from published sources.

Database Development

The database on genetic characterisation of animal genetic resources has been designed using entity-relationship approach (Chen, 1976). The approach considers real-world objects as entities having certain attributes along with relationships between two or more entities, which may be defined by a set of attributes. Conceptual data modelling consists of identifying entities and relationships in the database theme and allocating attributes (data elements) to identified entities and relationships.

Figure.1 details entity-relationship diagram for the database. The database stores information on countries, animal species, breeds, microsatellite markers, diversity parameters, published references, methods and software used for analysis, and genetic diversity parameters reported in the published literature. Diversity parameters have been treated as separate entity with a separate table in the database (Ayalew et al. 2003). This arrangement doesn't restrict number of traits / parameters in the database. The database has provision of storing microsatellite-locus-wise, breed-wise and inter-breed genetic diversity parameter values.

The database schema has been created using Microsoft Access 2003 database management system running on MS-Windows platform. User-interface has been developed using ASP.NET and VB Script in Visual Studio 2008 environment.

Currently the database has entries exclusively from Indian work incorporating 107 references from studies on 154 Indian breeds of cattle, buffalo, goat, sheep, camel, horses, and poultry species. Table 1 shows the number of breeds and microsatellite markers for various animal species available in the database. It stores genetic diversity information on 30 breeds and 76 microsatellite markers for cattle. Diversity information on four populations of mithun is stored with microsatellites of other bovines.

User-Interface

The database has internet-enabled user-interface. It has facilities for data entry as well as data view, which have been designed with biological focus (Birney and Clamp 2003). Figure 2 displays flowchart of user-interface of the database as sequence of steps for entering and viewing data on various entities. For example, microsatellite markers are entered after entry of animal species and relevant reference for the marker.

The database has been so designed that any user can add fresh data on entities to the database. Facilities exist for data entry for species, breeds, microsatellite markers, diversity parameters, references, and methods and software for analysis.

Table 1. Contents of the Database on Genetic Characterisation of Animal Genetic Resources

Species	Breeds	Microsatellite Loci
Buffalo	11	18
Cattle	30	76
Goat	28	39
Sheep	46	19
Camel	6	23
Horse	6	26
Mithun	4	-
Pig	5	23
Poultry	18	26

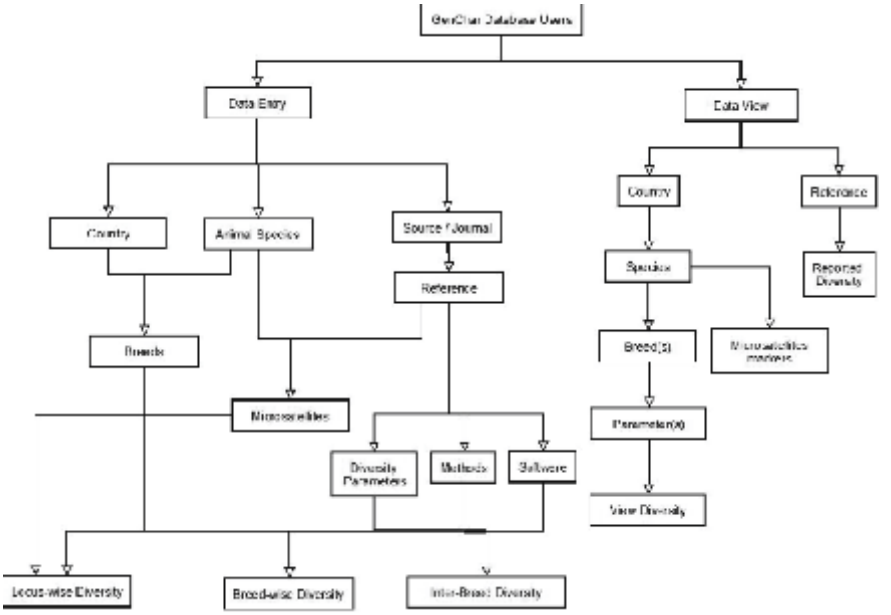

Figure 2. Flowchart of user-interface for the database on genetic characterization of animal genetic resources

It accepts locus-wise, within-breed and inter-breed genetic diversity values from secondary sources entered as references into the database. Locus-wise diversity values can be entered after entry of data on breeds, microsatellites, diversity parameters, methods and software.

Diversity can be viewed species wise. User selects a species from drop-down list and it displays breeds and microsatellite loci for the species. A breed can be selected from the list and its genetic diversity can be viewed as values of genetic diversity parameters along with references. Features of microsatellite loci of a species such as annealing temperature, sequence, reference, etc. are also available in the database. The option to view genetic diversity has facilities for selection of one or more breeds of an animal species from a country and one or more diversity parameters. User can view locus-wise diversity, breed-wise diversity and inter-breed relations and differentiation. Locus-wise diversity displays values of parameters on each microsatellite locus for a breed. Breed-wise diversity displays average values of parameters for all the loci studied for a breed as reported in the published literature. Inter-breed diversity displays values of inter-breed diversity parameters such as breed differentiation (F_{st} values) and genetic distances. References as well as methods and software used for analysis of data are also displayed.

There is provision for searching references on genetic diversity on title keywords, author and year of publication. Locus-wise, breed-wise and inter-breed genetic diversity as sourced from a listed reference is displayed on clicking a reference.

There are links on the menu to view list of softwares and methods for genetic diversity analysis used in the study. It provides description of the available methods and software for analysis of genetic diversity. Diversity parameters values on various breeds of a species from different studies can be viewed and compared, provided same set of markers have been utilised.

The database is available through web-browser at the Institute LAN. Registered users are provided facility of data view after login to the system. Data entry is permitted after verifying credentials of a user through his publication history in the relevant field as well as through a referee.

CONCLUSION

Large amount of data is available on genetic characterisation aspects in the published literature. The database makes available information on genetic diversity to various categories of users such as students, researchers, conservationists, etc. at one site. It provides an opportunity to use genetic

diversity values on breeds for comparison and prioritisation for conservation of animal genetic resources.

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