

Chapter 1 : Animal Genetic Resources | IUCN

Over the past twenty years substantial progress have been made in conserving animal genetic resources for food and agriculture (AnGR). 1 Globally, national programs, non-government organizations (NGOs), and producer-based activities are executing in vivo and in vitro (gene banking) conservation (FAO, , FAO,).

This reserve remains one of the most popular tourist destinations in Madagascar due to the guaranteed opportunity to view quite closely the Indiri, the largest remaining lemur. However, due to habitat destruction, the four forests are now relatively isolated yet remain home to vast biodiversity, including many endemic rare and endangered species. The endangered Diademed sifaka and the critically endangered black and white ruffed lemur were once among the fauna found in Analamazaotra Special Reserve. In , hunting pressures led to the regional extinction of the Diademed sifaka. Three years later, the black and white ruffed lemur followed. Although forest management regimes have improved protection efforts of the forests, not all of the voices of the forest have returned. These translocated lemurs created new groups and have produced numerous offspring in the following years. The project has succeeded by re-established the wild lemur populations, collecting data, preserving fecal samples for hormone analysis, increasing protection within the reserve and habituating the re-introduced groups to human presence. These introduced lemurs, taken from threatened populations or small, unsustainable forest tracts, are doing so well that visitors have been lucky enough to see three generations of babies born at the park. This project has also helped the Malagasy community through the training of Malagasy doctorate and graduate students and local field guides and educating the local communities about the biodiversity of their local eco-region. The program incorporates multiple lemur monitoring initiatives, a regional community-based reforestation effort, as well as the introduction of alternative technologies that reduce the pressures on the natural habitat while improving the quality of life for participating residents. The program is based out of the Kianjavato Ahmanson Field Station, which serves as a community center, teaching hub and site for the introduction of new technologies and procedures. This nocturnal lemur with unusual traits, including an elongated, thin, highly flexible middle finger leads a solitary life. Aye-Ayes have the largest species range of any existing lemur. Due to the demand of the forests they call home, aye-ayes may especially be vulnerable to extinction due to deforestation. Four local guides, hired and trained by the Madagascar Biodiversity Partnership, follow the elusive primates through the forest and collect data regarding demography, habitat use and food resources. Our monitoring program has been utilizing radio collars to monitor these elusive lemurs since Radio collars allow for the collection of GPS data, which allows for the estimation of home range sizes. We currently follow three adult males and one female, named Bozy, who gave birth to her second baby in June Greater Bamboo Lemur Monitoring The greater bamboo lemur *Prolemur simus* in the humid forests of eastern Madagascar is critically endangered. In fact, it ranks among the top 25 most endangered primates in the world and, at one point, was even thought to be extinct. Its rediscovery in in Ranomafana was one of the leading factors in designating the area as a national park. It was simultaneously rediscovered in the Kianjavato coffee plantation, an area that currently harbors the greatest concentration of the species. Once widely distributed across vast areas of the country, massive deforestation and hunting have resulted in dwindling numbers of greater bamboo lemurs. An estimated individuals now remain. A team of international volunteers and local field guides track individuals of this endemic and endangered lemur species daily, collecting a variety of data. The program is conducting a comprehensive study on the population genetics of the greater bamboo lemur, which is keystone information in developing effective in-situ conservation plans. For this project, non-invasive techniques are used, relying on fecal samples instead of tissue as the source of DNA. This means less stress on the lemurs, less expense and the ability to make a research team of Malagasy residents and provide modest amounts of training. Varecia Monitoring Black and white ruffed lemur populations are found in the forest fragments surrounding the commune of Kianjavato. This lemur species is listed among the 25 most endangered primates in the world due to habitat loss and hunting. As with the greater bamboo lemur study, the Varecia study is comprehensive, looking at the population genetics of the black and white ruffed lemur, a vital component for developing

effective in-situ conservation plans. The collection of fecal samples from this important seed-dispersing species is particularly vital to our reforestation program. Under the EPRP, Madagascar Biodiversity Partnership personnel, volunteers and graduate students track the lemurs through the forest, collecting fecal samples and plant the seeds in nurseries. Some tree species serve to restore habitat and enable movement of future lemur populations while other species have a commercial value and benefit residents as an additional source of income. As we have seen throughout the program, community awareness and support has increased due to the regular participation of many local community members to monitor lemurs, maintenance and preparation of seedlings in the local nurseries, as well as the transplantation of trees. The EPRP had modest beginnings focused on seven-kilometer stretch in which 60, trees were planted. However, with the help of local participants, we have planted more than , trees in the region in the past two years, making the future brighter and hopefully greener for these communities and the lemurs. We believe that our innovative forest corridor program can be one facet in a larger, overarching vision to reduce poverty while promoting a sustainable future for the residents of Kianjavato. These items included fuel-efficient rocket stoves, biofuel briquettes, commercially valuable trees, Water Hippo rollers and Tough Stuff solar panels and accessories. The distribution of incentive items as part of the conservation credit program is strengthening community ties to forest and habitat preservation. Participants will soon receive electronic identification cards to track their involvement and reward earnings. This technology will provide us with other valuable data collection like number and species of trees planted and the location for each planting. Encouraging communities to sustain themselves by conserving their resources through the use of alternative technologies will be a long-term process, but is the most effective way of steering Madagascar onto a healthier, more prosperous course. Yet, rapid extinction of the northern sportive lemur is a very real possibility due to habitat loss associated with the extensive production of charcoal throughout its restricted range. Rocket Stove Project Charcoal production is resulting in large swaths of trees being cut for fuel with little to no opposition from government or park officials. The land is then left exposed in a hot and dry environment risking desertification. Eventually, local villages will not be able to supply themselves with supplies elsewhere. Residents of nearby Andavakoera participate in this illegal activity as they previously had not been introduced to affordable alternatives. Overall, the community has been receptive to new ideas and eager for change that will improve the standard of distributing fuel-efficient cooking stoves coupled with an intensive education program to participants in the forestation program in Antsiranana. The income-generating potential of these technologies increase the likelihood of long-term acceptance. Simultaneously, a reforestation program incorporating native trees and a sustainable agriculture component will restore ecosystem services. Aquaponics Pilot Program Recent research indicates that small-scale fisheries in Madagascar have a significant and positive impact on local economies due to their contribution to food security and poverty reduction, both critical factors in development of sustainable societies. This is a sustainable food production method that combines aquaculture techniques of raising fish for food with hydroponics methods of growing plants in a liquid medium. When the system is properly balanced, both the vegetation and fish can be regularly harvested, providing much needed food security to the community. We are partnering with Whispering Roots, an Omaha-based non-profit that specializes in aquaponics to design a system using locally available materials that are robust enough to withstand the climate and incorporate local vegetation and dish preferences to ensure acceptance by the community. As of September , we have constructed and are currently testing a pilot program in which we will mirror the concepts that we hope to build in Madagascar. This test system is allowing us to learn the process hands-on as well as evaluate vegetation and fish productivity in the system for deployment in Madagascar. We hope to transfer this knowledge to our field team in Madagascar in Lavavolo Radiated Tortoise Project The spiny forests near the village of Lavavolo in southwestern Madagascar is one of the last strongholds of the critically endangered radiated and spider tortoises, known to the Malagasy as sokake. The poor economic conditions of southern Madagascar leave many desperate to provide for their families. Poaching of these tortoise species for bushmeat and the illegal pet trade is rapidly driving them toward extinction. Illegal sokake hunting camps operate year-round businesses in Madagascar and Asia. These camps harvest hundreds of radiated tortoise individuals to sell on the black market. Confiscations from the camps are reported every year.

This is compounded by the slashing and burning of the endemic spiny forest for agriculture and charcoal for cooking fuel. With the current rate of harvesting and habitat loss, wildlife experts predict that the tortoises will become extinct in the wild in the next 20 years. This project follows our philosophy of combining community development to ease human pressure on the ecosystem along with field research and tortoise monitoring. The Radiated Tortoise Project is long-term conservation that utilizes extensive fieldwork and molecular genetic data collection. However, this fady has not been respected by outsiders that have immigrated into southern Madagascar to set up tortoise harvesting operations. In , the Madagascar Biodiversity Partnership began an intensive monitoring program of radiated tortoise nest sites at Lavavolo. During the first phase of this study, Malagasy graduate students were taught how to locate the tortoises, collect genetic samples and morphological data, while local field assistants were trained to monitor nest sites throughout the incubation period. The second phase of the project is ongoing and consists of daily nest observation and subsequent sampling of new tortoises. Like the black and white ruffed lemurs, the equally threatened ring-tailed lemur is a prominent seed dispersing species in this arid region, eating fruit whole and passing the seeds intact. Thus, the ring-tailed lemur is a perfect candidate for a monitoring program and fecal collection efforts for a reforestation initiative in the region. To facilitate this, 10 ring-tailed lemurs from a number of populations throughout the area have been radio-collared, enabling local field assistants and students to study and monitor the lemurs and collect fecal samples. As with the Kianjavato Education Promoting Reforestation Program EPRP , the Lavavolo Education Promoting Reforestation Program will result in the production of seedlings that will be transplanted as part of a community-supported reforestation program that will utilize native trees to restore habitat and enable movement of lemur and tortoise populations. Once mature, endemic trees planted will entice lemurs to forage and continue the process of forest regenerations themselves, thus requiring less future human intervention. Additionally, employing local community awareness and support. This work is coupled with intense community education and outreach efforts that integrate alternative agricultural practices, habitat restoration and species protection, resource conservation, sustainable energy technologies and entrepreneurial opportunities. Additionally, Conservation Fusion is working to build a school in this commune that historically has had little access to education. This training and employment of local people directly involves them in conservation and encourages them to be advocates of their natural environment. The Madagascar Biodiversity Partnership also supports more than 75 full-time Malagasy employees as field assistants, project supervisors, office employees, drivers and supporting field personnel. In addition, at least 10 international graduate students have partnered with the program and have since successfully completed their graduate or veterinary degrees. More than two dozen international volunteers have worked with the program, gaining valuable field experience and inspiring many to pursue a graduate degree focused on conservation. In , for example, more than 15, conservation-based activity books were distributed to primary school children throughout Madagascar. Students that resided in areas of high biodiversity that was under threat from habitat destruction and hunting were specifically targeted. Following the distribution of these books, we detected a noticeable decline in the evidence of hunting. This indicates the critical role of conservation-based education and community-wide participation in preservation activities are vital for sustained preservation of natural resources and wildlife. Our Supporters The Madagascar Biodiversity Partnership would like to thank the following zoos, schools and organizations for their support: Publications Runhua Lei, Adam T. Nash, Richard Randriamampionona, Colin P. Mittermeier and Edward E. Primate Conservation, issue 29, Defining Species in an Advanced Technological Landscape. Evolutionary Anthropology 23, Issue 1: Testudines - Turtles, Astrochelys Radiated Tortoise. Herpetological Review 45, Issue 1: Journal of Threatened Taxa www.

Chapter 2 : Plant and Animal Genetic Resources Preservation : USDA ARS

Cryoconservation of animal genetic resources is a strategy wherein samples of animal genetic materials are preserved cryogenically.. Animal genetic resources, as defined by the Food and Agriculture Organization of the United Nations, are "those animal species that are used, or may be used, for the production of food and agriculture, and the populations within each of them.

The use, distribution or reproduction in other forums is permitted, provided the original author s or licensor are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms. This article has been cited by other articles in PMC. Abstract Livestock conservation practice is changing rapidly in light of policy developments, climate change and diversifying market demands. The last decade has seen a step change in technology and analytical approaches available to define, manage and conserve Farm Animal Genomic Resources FAnGR. However, these rapid changes pose challenges for FAnGR conservation in terms of technological continuity, analytical capacity and integrative methodologies needed to fully exploit new, multidimensional data. The final conference of the ESF Genomic Resources program aimed to address these interdisciplinary problems in an attempt to contribute to the agenda for research and policy development directions during the coming decade. Therefore, this challenging target demands better coverage, understanding and utilization of genomic and environmental data, the development of optimized ways to integrate these data with social and other sciences and policy analysis to enable more flexible, evidence-based models to underpin FAnGR conservation. At the conference, we attempted to identify the most important problems for effective livestock genomic resource conservation during the next decade. Twenty priority questions were identified that could be broadly categorized into challenges related to methodology, analytical approaches, data management and conservation. It should be acknowledged here that while the focus of our meeting was predominantly around genetics, genomics and animal science, many of the practical challenges facing conservation of genomic resources are societal in origin and are predicated on the value e. The overall conclusion is that despite the fact that the livestock sector has been relatively well-organized in the application of genetic methodologies to date, there is still a large gap between the current state-of-the-art in the use of tools to characterize genomic resources and its application to many non-commercial and local breeds, hampering the consistent utilization of genetic and genomic data as indicators of genetic erosion and diversity. The livestock genomic sector therefore needs to make a concerted effort in the coming decade to enable to the democratization of the powerful tools that are now at its disposal, and to ensure that they are applied in the context of breed conservation as well as development. In this context, the concept of horizon scanning has been developed and applied annually in the field of biodiversity conservation since Sutherland and Woodroof, , using a variety of systematic and semi-systematic methods to mine trending issues from web engines and social media and by analyzing focused questionnaires. Similar approaches have also been taken to identify emerging issues in agriculture Pretty et al. Such exercises have identified a number of issues of relevance to the conservation of FAnGR, such as genetic control of invasive species Sutherland et al. In , Pretty et al. Since Cardellino and Boyazoglu no attempt has been published to identify research priorities for FAnGR conservation, despite genetic erosion sensu Aichi Target 13 continuing apace e. While not following the standard systematic approaches adopted by conventional Horizon Scanning exercises, all 43 attendees of this focused meeting took part in the exercise, including scientists and policy-makers from South and East Asia, North America, Europe and Africa involved in a range of disciplines from genomics to animal breeding, genetic resource management, economic and social sciences and global agricultural policy development. Methods and results During the course of the conference, attendees were asked to contribute up to five questions of highest priority for research, infrastructure and policy development during the coming decade. Eighty-six suggestions were received. Table 1 Summary of the Top 20 questions in farm animal genomics research identified by the participants of the Cardiff symposium. Next generation phenotyping The mismatch between molecular and phenotypic data has increased dramatically. Which key phenotypic traits should be

used as common measures for diversity studies to define breed characteristics in the face of climate change? Which strategy shall be used to enable SNP arrays to be developed in a rapid, cost effective and widely applicable manner? Reference genomes Which common reference genomes and test panels of individuals should be used for array development and diversity studies? Environment WAS How to characterize environmental parameters in extensive production systems? Male-mediated genetic diversity Which methodological approach can be applied to promote reliable assembly of the Y-chromosome, still lacking for many livestock species, as well as to develop polymorphic Y-chromosome markers? Ancient DNA and paleoenvironmental analyses Which strategies should be followed to collect zooarchaeological specimens from critical geographic sites and promote the analysis of ancient genomes? Conservation of genomic diversity How to design a management program that evaluates genomic regions for conservation? Polygenic adaptive and economic traits Haplotypes vs. GW diversity statistics Which combination of parameters will be required to adequately summarize genome diversity? Data management How can links between major FAnGR databases be promoted to be able to federate resources and act as an educational central point? Data availability Which format should be used to make NGS, phenotyping and GIS data publicly available, and how can industry contribute toward population and maintenance of such database? Participatory projects How can participatory projects, including citizen science, for example, the use of smart-phone technologies be encouraged to enable data collection on FAnGR at a large scale? Prioritization for conservation Why are prioritization methods not being applied by policy makers and managers and is there a lack of dissemination or penetrance? Genomic prioritization How to implement genomic approaches systematically in conservation prioritization to include genes important in functionally valuable traits? Utilization in practice How to reconcile the cost of genomic analysis vs. What is the demand and willingness to pay within the sector? Systematic collection How to ensure that genetic and genomic data are collected sufficiently systematically to be applied to new indicators? Defining goals Which indicators can be applied to most efficiently monitor genetic trends in domestic populations? Frequencies are not included for each question and the questions are not listed in rank order. Methodological challenges Next generation phenotyping The need for high-resolution phenotypic data to be collected for in-depth characterization of FAnGR was identified, especially in light of the rapid advances that have been made in molecular breed characterization. Developing methods for phenotypic characterization was also identified by Cardellino and Boyazoglu following from FAO recommendations FAO, a and has clearly remained an under-explored research area. However, with the richness of molecular data increasing dramatically since , the mismatch between molecular and phenotypic data is widening for all except highly commercial transboundary breeds and lines with genomic breeding values. Inherent in high-resolution breed characterization is a need to define key phenotypic traits and characteristics particularly those potentially involved in local adaptation based on guidelines that can be used as common measures for such studies with stringent field protocols for their collection. In this way more comparable data can be generated, and breed characterization can have a more functional basis, especially with the urgent need to understand breed characteristics in the face of climate change Hoffmann, Also an improved description of the specific production environment and epidemiological history in which populations of a breed are kept would allow better comparison of phenotypes and performances e. The establishment of a working group to define guidelines, protocols and tools for collecting such data under the auspices of the FAO, International Society for Animal Genetics or the International Committee for Animal Recording www. Omics data and association studies The dramatic acceleration in genome sequencing means that all domesticated species and their few remaining wild relatives will become genome-enabled in the coming decade e. To enable SNP arrays to be developed in a rapid, cost effective and widely applicable manner, the identification of common reference genomes and test panels of individuals for array development and diversity studies is key. However, it is important to note that with the rapidly falling cost of whole genome resequencing e. De Donato et al. Indeed these methods are sufficiently cost-effective now, that they can be in principle used as standard assaying approaches, with a cost in the low tens of dollars for GBS now feasible for analysis of tens of thousands of SNPs. A major issue identified for genome-wide association studies GWAS is experimental design including, but not confined to, sample size considerations Kadarmideen, and the

availability of different SNP genotyping arrays for some species and their compatibility or lack thereof Nicolazzi et al. Characterization of environmental parameters in extensive production systems is another key challenge for GWAS but may be assisted by the application of E environment WAS methodologies as applied in humans e. Additionally, understanding the role of the epigenome and its role in environment-dependent phenotypic diversity and plasticity is becoming an increasing focus in livestock genetics e. Ultimately, the integration of genomic, epigenomic, transcriptomic, and environmental data will be required if meaningful large-scale studies are to be successful in identifying selection and conservation targets in heterogeneous environments Jones et al. Non-autosomal inheritance Non-autosomal inheritance Y-chromosomal, X-chromosomal, and mitochondrial is a comparatively neglected area of research in livestock conservation. While studies of non-autosomal genetic markers have been extensively used in studies of evolutionary history, both singly and combined e. This oversight is surprising given the well-documented links between mitochondrial sequence variation and fitness in human populations e. Technical challenges have long been acknowledged with finding polymorphic markers on the Y-chromosome in mammals and W-chromosome in birds, however such markers, although elusive, have been shown to provide novel insights into livestock diversity when available e. Ancient DNA studies Although firmly established as a major route into a deeper understanding of livestock evolution and diversity e. These include limited access to samples from geographic areas where local domestication may have taken place e. Nonetheless, recently developed methodological and bioinformatics tools allowed for increased accuracy in the analysis of high-throughput ancient DNA data and even the characterization of complete genomes of Pleistocene horses Orlando et al. Also, alternative sources of material such as parchment are, however, providing promising outcomes Teasdale et al. Exciting opportunities have recently been opened up by the discovery of livestock DNA in lake sediment samples in Lake Anterne, Switzerland Giguet-Covex et al. Analytical challenges Conservation of genomic diversity The concept of genome conservation has been discussed extensively in the literature but advances in genome data and technologies only now allow the development of breed management programs able to achieve this aim. For example, Herrero-Medrano et al. However, to design a management program that evaluates genomic regions for conservation, not only do polymorphisms need to be identified, the functional architecture of those genomic regions and the genes they contain needs to be assessed and the interaction among those genes needs to be considered. Recently, a study of chicken breeds examined functional variation in copy number variants CNV at over genes overlapping quantitative trait loci, including some putatively involved in traits such as skin color and skeletal characteristics Han et al. For example, many of such traits are polygenic and distributed around the genome, making whole-genome resequencing, and medium and high-density SNP arrays a powerful approach to locating them and elucidating their variation e. However, for certain linked traits, haplotypes may provide a more efficient unit of assessing diversity in QTL regions than individual SNPs e. Consequently, at the initial stages of studies aiming to identify the genetic basis of phenotypic variation, general genome-wide SNP analyses may be more suitable. It is worth noting, however, that phasing haplotypes in divergent populations lacking complementary pedigree data presents a non-trivial challenge. Haplotype analysis can provide an especially powerful tool to investigate the hybrid origin of domesticated populations. For instance, modern Western commercial pig genomes are a mosaic of Eastern and Western Eurasian biogeographic origin. In addition, this strategy has been shown to be powerful to infer selection on specific haplotypes post-hybridization Bosse et al. This therefore raises the immediate problem of how to integrate data from the two marker types and how to manage the transition from microsatellite-based FAnGR characterization much of which has been carried out using markers recommended by ISAG, FAO, to SNP-based characterization. One option is to re-genotype many of the breeds that already have microsatellite genotypes with SNPs Ajmone-Marsan et al. Pragmatically, it seems that microsatellite data are perfectly adequate for estimating genetic diversity and describing demographic relationships e. However, for cost reasons the full set of microsatellite markers was frequently not applied, especially in developing countries. Also, microsatellite data will not be as efficient for enabling the identification and targeted conservation of genomic regions under selection since data are usually produced with a few tens of quasi-neutral markers e. Nevertheless, it is becoming clear that data produced using SNP arrays are more repeatable and do not suffer

from scoring differences that have made the combination of microsatellite datasets sometimes problematic and requiring statistical evaluation Lenstra et al. Genome-wide diversity statistics The emergence of whole genome sequencing and medium-high density SNP arrays means that summarizing genetic diversity can now be a more nuanced and genomic region-specific exercise. It is well known that ascertainment bias of SNP arrays can strongly underestimate the diversity of the usually autochthonous and less commercial breeds not used to design the arrays Porto Neto and Barendse, This phenomenon does not impact on whole-genome resequencing as all polymorphisms are captured provided sufficient sequence depth is achieved. A combination of parameters will be required to adequately summarize genome diversity e. Effective population size N_e estimates can be obtained with as little as a single genome using methods such as the Pairwise Sequential Markovian Coalescent, although these analyses can prove inconclusive if genome coverage is insufficient or if admixture pertains Li and Durbin, ; Orozco-terWengel and Bruford, ; Schiffels and Durbin, ; Frantz et al. For recently evolved populations, such as many domestic species, linkage disequilibrium-based LD estimates may be more accurate and methods are now emerging to carry out these analysis e. Runs of homozygosity ROH; e. ROH are already used as a genomic proxy for inbreeding e. This approach promises to be an efficient way to avoid the production of offspring homozygous for deleterious alleles at specific genomic regions that are associated with inbreeding depression Pryce et al. Data management Data accessibility As also identified by Cardellino and Boyazoglu there remains a major need to provide much better links between the major FAnGR databases, which have largely been set up independently and are breed-focused Groeneveld et al. The livestock genomics community needs either to build on an existing platform such as the ARKDB, <http://www.arkdb.org/>: Such resources are already being developed, including the Adaptmap project for goats <http://www.adaptmap.org/>: Information on livestock related data should be made available and useful recommendations are required to inform stakeholders on how to record data, and where to store what type of information. In particular, it is important to promote within the community of users that raw and meta-data are key components and that they should be made available in public datasets together with elaborated datasets. When there are existing public resources for a given datatype such as those listed above, they should be used for their ability to set standards and centralize data access.

Chapter 3 : THE STATE OF THE WORLD'S ANIMAL GENETIC RESOURCES FOR FOOD AND AGRICULTURE

The genetic diversity comprised in farm animal species and breeds is an important resource in livestock systems. For several reasons, within the different species used for food production, only a few breeds are developed towards high-output breeds fitting in high-input systems.

By effectively managing these ecosystems, we can help preserve threatened and endangered species. Information gained from studying these organisms informs decisions that will ensure their survival into the future. The science of Genetics looks at inherited characteristics and the genes that underlie them. Put the two together and you get the science of Conservation Genetics. What is Conservation Genetics? Conservation genetics uses a combination of ecology, molecular biology, population genetics, mathematical modeling, and evolutionary taxonomy to study family relationships. It is both a basic and an applied science. Then wildlife managers use techniques to preserve biological diversity in these species. The organisms that conservation geneticists study usually belong to endangered or threatened populations. To develop ways to help these populations, scientists ask two questions: What has brought these populations to the brink of extinction, and what steps can we take to reverse this trend? Information about the genetic diversity of the organisms under study helps scientists and managers form strategies to Past conservation efforts have addressed populations from a mathematical, evolutionary, or taxonomic point of view. Modern efforts include genetic studies, giving conservation scientists and ecological managers much more information about the diversity among the individuals in a population. Genetic Diversity To measure the genetic diversity of a particular gene, scientists look at how many different versions of it called alleles are present in a population. For example, one gene may determine the flower color of a plant. Different alleles may exist for that gene. In each case, the same gene determines flower color—but the exact order of DNA letters that make up the gene are different for each allele. When all or nearly all members of a population have the same allele, that population is said to have low genetic diversity at that gene. But when many different versions of the gene exist in a population, the population has high genetic diversity at that gene. Why is genetic diversity important? Populations or species with low genetic diversity at many genes are at risk. When diversity is very low, all the individuals are nearly identical. If a new environmental pressure, such as a disease, comes along, all of the individuals within the population may get the disease and die. But in a population with high genetic diversity, chances are better that some individuals will have a genetic makeup that allows them to survive. These individuals will reproduce, and the population will survive. The genetic diversity of a species is always changing. No matter how many variants of a gene are present in a population today, only the variants that survive in the next generation can contribute to species diversity in the future. Once gene variants are lost, they cannot be recovered. When is Conservation Genetics Used? Habitat Destruction When habitat destruction or other factors put a population at risk, scientists and conservation managers may target that population for investigation. For example, they may study a population of plants whose habitat will be destroyed by the building of a new shopping mall. Or they may study duck and geese populations when new hunting regulations have been put in place. Human interference is not the only danger to plants and animals. Natural factors, such as storms and diseases, can also cause populations to dwindle. Change in Population Size Surveillance of small populations is critical, because they are particularly sensitive to change. Random or unpredictable events such as natural catastrophes, environmental changes, or genetic mutations can cause a sudden decrease in population size. When the population of a species is small to begin with, further reduction of their remaining numbers can sharply reduce genetic diversity. Small populations are also more sensitive to genetic drift, as well as the problems that come with geographic isolation and establishing a new population from only a few individuals founder effect. Each of these factors affects which individuals will give rise to the next generation, and therefore which alleles will be passed on. Genetic Drift With each generation, some individuals survive to reproduce and pass on their genes, while others are eliminated. Over time, individual alleles can become more or less common in a population. When inherited characteristics determine who will survive and who will not, the process is called natural selection. When random factors determine who will

survive, the process is called genetic drift. Through genetic drift, some alleles can entirely disappear from a population. A small population is more susceptible to genetic drift than a large population. When just a few individuals carry a particular allele, it becomes more likely that just by chance those individuals will not reproduce, and the allele will be lost.

Geographical Isolation Sometimes even a large population can lose genetic diversity. One way loss can happen is through geographical isolation. Geographical isolation can happen if a new barrier is imposed through a habitat. For example, if a river changes course or a new housing subdivision is built, a population of plants or animals may be divided into two groups. Just by chance, the pool of gene variants in the two separated populations may differ from one another. As an example, imagine a flower species with two forms that share a habitat. A new subdivision, including new houses and roads, divides the habitat, isolating the two forms to different areas. The first form, a tall, sturdy plant with few flowers, is isolated to the north end of the subdivision, while the second form, a more delicate plant with prettier flowers, is isolated to the south end. Even though the new homeowners may preserve both populations, the two are sufficiently isolated from each other that they can no longer exchange genes. In this situation, each type is exposed to environmental pressures without the ability to crossbreed with the other type to form plants with new, perhaps more advantageous, combinations of genes. The new pressures created by building the development may affect the two types of plants differently. For example, the more-delicate variety might die from a lack of shade caused when trees were cut down for the subdivision. When they are gone, so is the allele responsible for the attractive flower and the overall population size decreases.

How is Conservation Genetics Done? Conservation geneticists use DNA data from an organism to inform management choices. As in any scientific field, conservation scientists use a defined approach to their work: Identification, Inventory, and Analysis

Define populations and areas of interest. Because there are so many species of organisms, endangered or threatened species usually take priority. What are the known forms of the species? What are known or suspected relatives of the species? What are the physical characteristics used to classify the different forms and species? Use mathematical models to analyze the data. Determine how much diversity exists in separate populations of the species, as well as the rate at which genes are exchanged among populations gene flow.

Interpretation and Management Scientists and managers work together to identify endangered organisms. Determine the degree to which the organism is adaptable to various temperatures, soils, and water conditions. Examine factors that influence genetic diversity, such as the identity and characteristics of plant pollinators. The health and welfare of pollinating species may be critical to the survival of an endangered plant species. Once all of the aspects of the population and its environment are understood, scientists and managers can develop an intelligent preservation plan.

Chapter 4 : Prospects and challenges for the conservation of farm animal genomic resources,

The need to reduce the degradation of farm animal genetic resources and establish programmes for their conservation and sustainable use is well recognized. It is embodied in the objectives of the Convention on Biological Diversity and in the development of the Global Strategy for the Management of Farm Animal Genetic Resources, led by the Food.

The lengthy generation times make conservation of tree populations in their natural environment essential for any sort of experimental use. A survey of 18 crops grown in the United States from to , revealed that from 1 percent sweet clover to 90 percent sunflower and tomato of the available cultivars had been improved in part using wild germplasm. Use of wild relatives in crop breeding has obvious economic significance and is growing C. Colorado potato beetles take only a bite or two of this insect-resistant potato plant before they are repelled. The plant has been genetically engineered to contain a gene from wild potatoes that produces a substance distasteful to these insects. Department of Agriculture, Agricultural Research Service. Page Share Cite Suggested Citation: In Situ Conservation of Genetic Resources. Managing Global Genetic Resources: Agricultural Crop Issues and Policies. The National Academies Press. Breeders in search of a particular character may explore quite thoroughly the variability of the crop itself. However, they seldom explore much of the variability contained within its wild relatives. Wild gene pools are an important biological resource for developing new crops, particularly for the timber industry, the livestock industry forage and fodder crops , and rural development fuelwood. Like the breeders of established crops, domesticators of new crops differ in the extent to which they explore the genetic variability of the species concerned. In general, the economically most successful new domesticated crops are those that have tapped a diversity of germplasm sources C. Genetic Conservation Areas Wild genetic resources may be conserved in situ in a protected area. This is an area of land or water allocated to some form of conservation management. It may be established expressly to maintain the genetic resource, or it may have other objectives as well. Both types of genetic conservation areas are included in the term genetic reserves Jain, a. The principal objective of a genetic reserve is to maintain the individual and population-level variation of one or more species in their natural range or habitats. Genetic reserves have the following characteristics: An explicit objective to maintain population variation. An established protocol for providing information on and access to the protected resources by ex situ collections, breeders, researchers, and other germplasm users, including a procedure for the sustainable collection of reproductive material by authorized agencies and individuals. A procedure for monitoring the status of the populations conserved as part of a national genetic resources information system. The primary role of the genetic reserves is to secure the long-term Page Share Cite Suggested Citation: Consideration of the extent to which intraspecific variation is encompassed in an area is required to preserve the genetic structure of the target species. Multiple sites may be required to capture a reasonable amount of the allelic variation of a species Food and Agriculture Organization, a. For example, the committee has examined the challenges of preserving the genetic structure of forest trees National Research Council, b , the in situ conservation of which is particularly important because of their lengthy generation times Ford-Lloyd and Jackson, As discussed in greater detail in Chapter 4 , the targets of germplasm sampling strategies are common alleles population frequency, equal to or greater than 5 percent that are widespread found in many populations or local found in one or a few populations Brown and Moran, ; Marshall and Brown, These common alleles define representative and unique gene pools that could be candidates for in situ conservation. However, the characterization of gene pools is not necessarily a simple task. The variation among alleles can be inferred individually through studies of intraspecific variation in biochemical characters for example, enzymes, other proteins, or terpenes , morphology, phenology, growth rate, environmental adaptations, and many other characters. Direct measures of DNA variation are also possible using restriction fragment length polymorphisms or randomly amplified polymorphic DNA markers see Chapter 7. Genetic variation in characters strongly influenced by environment phenology, growth rate, morphology of vegetative parts must be measured through tests that compare responses with different environments. There are, however, few studies of the degree to which biochemical variability reflects morphologic or other phenotypic variation

National Research Council, b. However, real efforts at in situ conservation have been slow to emerge International Board for Plant Genetic Resources, a; Noy-Meir et al. Department of Agriculture, a research geneticist examines hybrids made by crossing native American wild ryegrasses with a wild species from the former Soviet Union. These new, taller ryegrasses stay green later, reducing fire hazards, and may enable animals to graze 2 months longer than usual each year. Their leaves cure well and protrude above the snow so cattle and sheep can graze them well into the winter. Germany is using its system of nature reserves as the basis of in situ conservation of the wild progenitors of apples and pears and other wild genetic resources Schlosser, The Commonwealth of Independent States is reported to have established reserves for the protection of wild relatives of crops Korovina, A few reserves have been designated for the protection of particular Page Share Cite Suggested Citation: Few reserves have been established or are managed as genetic resources conservation areas. A European survey of wild crop relatives of apples, plums, cherries, peaches, almonds, and Allium species found that although reserves existed within the range of these wild species, lists of the plant species they contained were available for few of those areas. No information on genetic diversity was available Hoyt, The goals of genetic conservation can be combined with those of natural or biosphere reserves. Teosinte is generally found in the untilled soil bordering maize fields and, to a lesser degree, throughout some maize fields. There are eight geographically isolated population clusters of annual teosinte. Six of these are found in Mexico and two are found in Guatemala. There are also two perennial populations in Mexico. Teosinte populations range in size from 1 to 1, square kilometers. Three of the annual populations are considered rare, occurring at single locations. Most of the populations are considered vulnerable and are declining at a rate such that they could become endangered. As land use is intensified, teosinte is squeezed out of the margins bordering maize fields. The replacement of maize with cash crops, such as short-stature sorghum, leaves teosinte as a visible weed, making it easier to remove. Finally, because of outcrossing to maize, small and isolated stands of teosinte can lose their ability to disperse. This allows monitoring of teosinte without incurring the costs of establishing and maintaining an in situ preserve. There are other examples of genetic conservation goals being combined with those of natural or biosphere reserves. A small portion of this reserve about 10 ha contains the only known stands of the primitive wild relative of maize. The area contains wild species related to walnuts, apples, pears, Prunus species, and other temperate fruit and nut crops Hoyt, Obstacles to In Situ Conservation of Wild Genetic Resources Two main obstacles to in situ conservation of wild genetic resources are sectoralism and lack of knowledge R. Prescott-Allen, resource policy analyst, personal communication, June The conservation focus of protected areas is typically on the level of ecosystems and species, not on the maintenance of crop genetic resources. To the extent that agencies responsible for protected areas are aware of the need for conserving genetic resources, they tend to regard it as an additional responsibility for which additional resources are generally not forthcoming. Ministries of agriculture or their equivalents have a direct interest in conserving wild relatives of crops, but they may be ambivalent about the importance of in situ conservation. In part, this may be because they often lack authority over the appropriate lands. Thus, difficulties in establishing a protected area may quickly outweigh the benefits of doing so, especially if the goal is protection for only one or two wild relatives of a single crop. Lack of knowledge of the degree and distribution of interpopulation genetic variation in the wild relatives of crops is another obstacle International Board for Plant Genetic Resources, a; Noy-Meir et al. This information is needed for answering questions such as where in situ conservation areas should be established, how large should they be, and what ways should they be managed. Ecogeographical surveys International Board for Plant Genetic Resources, a that assess the genetic variation of a species across its entire geographical and ecological range are needed Hoyt, It can take years to obtain a complete ecogeographical survey.

Chapter 5 : Conservation of animal genetic resources.

An assessment is made of the present Canadian situation regarding livestock and poultry genetic resources and of the need to take conservation measures as insurance against future needs. Loss of resources in poultry has been extreme, and loss is occurring rapidly now in dairy cattle. A complete.

What should be preserved: February 23, ; Paris pp. Food and Agriculture Organization of the United Nations, The Livestock Conservancy, n. Merck Animal Health, June A Systematic Review and Meta-analysis. National Center for Biotechnology Information. National Geographic Society, March 15, Wageningen Academic Publisher, Livestock Systems in Integrated Rural Development, n. American Society of Animal Science. Colorado State University, January 27, Techniques for Training Boars for Semen Collection. Virginia Cooperative Extension, Jan. Colorado State University, August 11, Queensland Government, July 2, Indigenous Chicken Improvement Programme. Embryo Transfer in Cattle. Oklahoma State University Extension Service. University of Wisconsin-Madison, n. Babol University of Medical Sciences. An Introduction For Non-Scientists. University of Washington, April 6, University of Missouri-Columbia, July American Association of Swine Veterinarians. Basic Knowledge And Biophysical Effects. A Traditional European Breed. Asian Wild Cattle Specialist Group. Asian Wild Cattle Specialist Group, The Embryo Project Encyclopedia, July 26,

Chapter 6 : Conservation Genetics

The global plan of action for animal genetic resources and the conservation of poultry genetic resources. World's Poultry Science Journal, Vol. 65, Issue. 02, p.

Dung used as fertilizer Draught Power Diversity also allows the flexibility to change breeding goals if needed and emphasize alternative traits in response to changes in markets or other conditions. For example the Holstein Friesian Cow which is widely used for its whole milk production. Changes in cereal feed availability or demand for low-solid content milk may decrease the advantage of breeding Holstein cows. Different breeds produce specific wool, hairs and leather for clothing, carpets and furniture and are often the basis for traditional garments. Local breeds that were developed by a given community often have a huge cultural significance for that community. Livestock are often a source of wealth and are critical for its maintenance. They appear frequently in art and often play key roles in traditional customs, such as religious ceremonies, sporting events and weddings. Cultural ecosystem services also create significant economic opportunities in fields such as tourism including, in the context of food and agriculture, farm holidays and visits to areas with historical or scenic farming or forest landscapes and recreational hunting. Breeds that have been developed primarily through natural selection have effectively evolved with their environments and usually provide ecosystem services, such as landscape management, vegetation control, and promotion of biodiversity, that are critical for maintaining those landscapes. Having access to a range of diverse livestock traits may allow for greater ability to cope with harsh climates and emerging diseases. Animals with unique adaptive abilities, such as resistance or tolerance to diseases and pests, or ability to thrive on poor feed and cope with dry or hot climates can help humans be more resilient to changes in climate. Within breeds, greater genetic diversity allows for continued selection for improving a given trait, such as disease resistance. Values of animal genetic resources [edit] "From a formal economic perspective, AnGR can have various different types of value for conservation. These values can be categorized as follows Direct use value " results from benefits obtained from the utilization of animal genetic resources, such as the production of milk or meat. Indirect use value " results from the provision of support or protection to other activities that produce benefits, such as through the provision of regulating and supporting ecosystem services e. Option value " results from the potential benefits of having a given resource available for the future; for example, having genetic variability available that can be used to respond to market and environmental changes. Bequest value " results from benefits that might be obtained from the knowledge that others may derive benefits from the animal genetic resource in the future. Existence value " results only from the satisfaction of knowing that a given animal genetic resource exists, even if no other type of value can be derived from it. Increasing the direct use value will contribute to the economic sustainability of a breed and therefore to the potential for successful conservation activities. Changes in climate will affect livestock and food production in many ways. For example, parts of Madagascar and Mozambique are predicted to have a drier than average rainy season, while just north in parts of central Africa, a wetter December-January season is expected. Although many diverse species and breeds of animals are currently available for food and agricultural production, there is more work to be done on classifying their risk of extinction: Nearly livestock breeds have gone extinct between and Unlike plants, which can be easily conserved in seed banks, a large portion of livestock genetic diversity relies on live populations and their interactions with the environment. Progress is being made in the characterization and management of animal genetic resources for food and agriculture. Recent advances in molecular genetics have provided data on the history and current status of animal genetic resources. Genetic markers and molecular studies are being used to characterize livestock diversity and to reconstruct the events that have shaped the present diversity patterns, including ancestry, prehistoric and historical migrations, admixture, and genetic isolation. In, six years after the completion of the human genome project, cattle became one of the first livestock species to have a fully mapped genome. Additionally, breeds with well-defined and appreciated traits tend to be inbred and have low genetic diversity, while non-descript local populations tend to have high molecular genetic diversity. Advances in molecular genetics have provided us with tools to better understand

livestock origin and diversity. There are many technologies capable of determining genetic profiles, including whole genome sequencing , shotgun sequencing , RNA sequencing and DNA microarray analysis. These techniques allow us to map genomes and then analyze their implications through bioinformatics and statistical analysis. Molecular genetic studies, especially genome-wide association studies and whole-genome sequencing allow adaptive traits to be linked to genomic regions, genes, or even mutations. For example, horn size, meat quality, gait, and prenatal growth in cattle all have single genes found to be responsible for these phenotypic traits. However, DNA polymorphisms that are not linked to specific traits are now more commonly used as markers for genetic diversity studies. Different levels of genetic diversity information can be obtained from different kinds of genetic markers. For example, autosomal polymorphisms are used for population diversity estimates, estimation of genetic relationships and population genetic admixture , whereas mitochondrial DNA polymorphisms are used to detect geographic regions of domestication, [27] reconstructing migration routes and the number of female founders. Systems range from completely human-controlled to wild. They differ in terms of animal management, animal treatment, environmental impact, and market infrastructure. Intensive Chicken Farming Industrial livestock production Industrial livestock production or intensive animal farming employs large-scale, principally landless systems. The animals are separated from the land where their feed is produced, and their environment is highly controlled by management interventions. Since a vast majority of consumers demand low-cost products, industrial livestock production has become common. However, there are several issues with industrial livestock production systems including disease, antibiotic use and ethical animal treatment. Living in densely packed cages or small spaces makes animals more prone to disease transmission from one animal to another. Small-scale livestock production Small-scale livestock production entails less intensive production cycles, access to outdoors or pasture, typically judicious use of antibiotics, and a connection to local niche markets. This type of livestock production can be maintained in peri-urban and rural settings. There are advantages and disadvantages to each. While it is more difficult and costly to find land for livestock in peri-urban settings, incorporating livestock to small-scale farms can greatly increase the local food supply, reduce garden waste, and provide manure. Peri-urban environments can also provide excellent foraging for bees , with less exposure to the pests , diseases , and even pesticides that can be devastating to a colony. However, access to formal markets, both to acquire inputs and to sell outputs, is critical for economic sustainability. Close rural-urban linkages are important to overcome constraints of feed scarcity and to better utilize the advantages of each system. Mixed farming Mixed farming systems involves livestock keeping integrated with other agricultural activities. These systems are similar to small-scale systems, but tend to be in a more rural setting, given the need for larger tracts of land for crop production. As with small-scale livestock production, access to formal markets is critical. Ranching or grass-based production These systems revolve around access to privately owned or rented grasslands, which the ruminant livestock feed on. In general, the livestock keeper has a fixed home and animals move around the property as needed to obtain freshly grown grass. Pastoralism Pastoralism Pastoralism plays an important role in livestock management and food security, since pastoralists can produce food where no crops can grow. This system usually relies entirely on publicly-owned grasslands. Pastoralists move their livestock herds based on the season, which is also known as transhumance. Nomadic pastoralists follow an irregular pattern of movement. Current issues that pastoralists face include conflict over land rights, access to water, limited food resources, integration into global markets, and animal diseases. Climate change has been believed to harm pastoralists, but evidence suggests that the root causes of land disputes are historical and political, rather than climate-related. Conservation of animal genetic resources[edit] For some breeds, opportunities for sustainable use are limited. For such breeds, to ensure that their critical genetic diversity is not lost, conservation programs are required. Several approaches for conservation can be applied, including in situ conservation with live animal populations, and ex situ conservation or cryoconservation involving the freezing of genetic materials. In many instances, both of these approached are used in a complementary manner. In order to establish and strengthen these programs, more research on methods and technologies must be undertaken, especially for less common livestock species, and greater financial investment is required. Many countries are currently operating conservation programs for their animal genetic resources, at least for

some species and breeds. In situ conservation programs are the most commonly used approach. With this knowledge it can make recommendations and advise the Commission on these matters, and consider progress resulting from proposed interventions. In , the GPA was adopted by countries as the first agreed international framework for the management of livestock biodiversity. The funding for this program arrives from a wide range of actors, under the guidelines of the Funding Strategy for the Implementation of the Global Plan of Action for Animal Genetic Resources. The Nagoya Protocol entered into force on 12 October and aims to provide a legal framework for the fair and equitable distribution of benefits arising from the utilization of all genetic resources, including animal genetic resources for food and agriculture. Number of plant and animal genetic resources for food and agriculture secured in either medium or long term conservation facilities. Proportion of local breeds, classified as being at risk, not at risk or unknown level of risk of extinction. Lack of adequate policies can lead to the insufficient capacity to manage AnGRs, further a loss of genetic diversity and marginalization of relevant stakeholders, such as pastoralists , who are valuable players in maintaining livestock diversity. To help regulate the ownership of genetic resources and control their utilization is one example where policies are necessary. Patenting of genetic resources is one approach that has been applied. Patenting of animal genetic resources reached its apex in the late s, focusing on expressed sequence tags ESTs and single nucleotide polymorphisms SNPs with associations in economically important traits. SNPs are important in marker-assisted breeding for the identification of traits such as meat or milk quality. At the same time, patenting activity involving transgenic livestock also increased. However, work on patents and characterization of AnGR declined sharply from , caused by a combination of factors including an increasingly restrictive approach to the patentability of DNA sequences by patent offices and a lack of markets for food products from transgenic animals. Increasingly complex issues are emerging that require balancing the interests of many stakeholders. In a time of rapid and unregulated change, livestock and their products should be used sustainably, developed and ultimately conserved. National planning should integrate "consumer affairs, human health matters, and the management of new biotechnologies, as well as physical and spatial planning of animal production in the context of urban expansion and protected areas.

Chapter 7 : Animal genetic resources for food and agriculture - Wikipedia

Conservation Genetics Resources promotes the conservation of genetic diversity and advances the study of conservation genetics through the rapid publication of technical papers and reviews on methodological innovations and improvements, computer programs and genomic resources.

Introducing high-yielding exotic breeds to the highlands and drylands is the sort of thing scientists talk about, because they are unfamiliar with the realities of pastoral environments or with the extreme risks that are implicit in replacing tried-and-tested breeds with animals that have been tried and failed. For decades, the breeds developed by pastoralists were scorned by animal scientists as unproductive. An increasing genetic homogeneity of livestock with millions of stock descending from a very small pool of hybrid animals can be observed as a result of well-intentioned, but often technically misguided breeding programmes. It has been realized that there is a danger that certain breeds, especially indigenous livestock breeds become extinct and people are beginning to become concerned about the loss of the diversity of breeds, or the watering down of their genes. The recognition of the value of indigenous livestock breeds The value of indigenous livestock breeds has always been beyond doubt for pastoralists and they have developed refined techniques and institutions for breeding activities. Having developed in harsh environments, pastoralist breeds represent reservoirs of genetic diversity and retain many genetic traits, such as fertility, vitality, and resistance to diseases and drought, that no longer exist in animals kept in industrial systems. This value is increasingly being recognized also by the commercial livestock production industry. Interest in the traditional breeds of pastoral people has risen after it has been realized that bacteria and internal parasites have started to become resistant to antibiotics and other medicines. This creates the need to breed animals that are both highly productive and disease resistant. Scientists are systematically screening livestock breeds for genetic traits that may have commercial potential. Multinational companies, well aware of the future potential that lies in these breeds, are eager to appropriate the genetic material of pastoral livestock and patent the breeds for their own commercial gain. The recognition of the immense work of pastoralists as creators of breeds Since the value of these genes has been discovered by scientists the question is discussed who is having the intellectual property right over these genes. Having invested considerable resource in their research for such genes scientists wish to patent the gene they discover and license it right to use so that they can recover these costs. This neglects the immense work the livestock breeder and his community have undertaken over years to come out with such a breed. Furthermore, the protection of a large reservoir of Animal Genetic Resources is best pursued by in situ conservation and protection and preservation of specialized livestock production systems and their livelihoods. Despite this fact livestock keepers are in danger of losing the right to breed their own animals in the long term. For pastoralists to continue to survive in the drylands, and for them to continue to sustainably manage these environments, they need to maintain viable breeding stock of animals that are adapted to their environment. They also need the skills and resources to enable them to identify genuine opportunities for enhancing their breeds and to share their genetic resources with pastoralists in similar environments. However, this is where the similarity stops, and the concept has been further developed to take into account the specificity of dealing with living species. Because the concept so far has only been backed by Civil Society, the term is not even included in the draft State of the World Report on Animal Genetic Resources although the individual cornerstones are. However, efforts are gradually being made to change this. Such support includes removing policy disincentives, satisfying rights to social services and to good governance, protecting resource rights and land tenure, providing infrastructure and encouraging investment.

Chapter 8 : Cryoconservation of animal genetic resources - Wikipedia

Conservation of animal genetic resources is the third Strategic Priority Area of the Global Plan of Action. Conservation involves both in vivo maintenance and management of genetic.