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The genetic diversity of local african chickens: A potential for selection of chickens resistant to viral infections

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Primary Audience: Researchers, Breeders, Extension services, Animal Genetic Resources

SUMMARY

Viral infections impose a great threat to backyard chicken production among poor rural households in developing countries. These infections limit the contribution of chicken production in improving the livelihoods of poor communities, particularly in Africa. Chicken viral infections lack treatment options; control and prevention depend primarily on adoption of vaccines and good farm management practice such as the institution of biosecurity measures. In backyard production systems, these control options are less practical and less feasible to implement. Research has demonstrated the role of genetic diversity of farmed animals and birds in explaining variation in resistance to infectious diseases and suggests that heterogeneous populations are less susceptible to disease than homogeneous populations. Local African chicken ecotypes have high genetic diversity and have demonstrated the ability to survive persistent exposure to pathogens and harsh environmental conditions. This suggests that local African chickens have the genetic potential to enhance breeding strategies for resistance to viral infections. Despite the ongoing threat of infectious disease and dynamic of diseases epidemiology attributed by climate change, little has been done to harness the genetic potential of local African chicken ecotypes to breed for resistant traits. To lay the foundation for future research, this review paper presents a summary of challenges facing current chicken viral infections control and prevention options in local African chickens, and gives an overview of documented information on the genetic diversity and population structure of local African chicken ecotypes.

Key words: backyard production systems, disease resistance, indigenous chickens, backyard poultry, genetic diversity, local African chicken, animal genetic resource, climate change

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INTRODUCTION

Chickens are the most common species of poultry raised globally with the world population of chickens estimated at 18 billion [1].

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About 80% of chickens that are raised in Africa are local African chickens [1]. The majority (60%) of African households raise local African chickens under backyard systems [2, 3]. Local African chickens are well adapted to harsh and stressful environmental conditions and are good scavengers [1, 4]. Local African chickens serve as a chief source of high-quality meat protein and a source of income [3, 5, 6], and play significant role in sociocultural activities such as traditional ceremonies and rituals [1, 3].

The production of local African chickens is constrained by high mortality rates due to infectious diseases [7, 8]. Viral diseases such as Newcastle disease (ND), Marek's disease (MD), and infectious bursal disease (IBD, Gumboro) cause enormous losses in chicken productivity under backyard production [9–11]. More importantly, chicken viral infections do not have well-known treatment options; control and prevention depend on proper vaccine administration and appropriate implementation of biosecurity measures to halt spread and transmission of infections between chicken flocks [1, 12–14]. In backyard systems, the implementation of vaccination and biosecurity measures is a challenge due to farmers' lack of resources to buy vaccines and because local chickens are free ranging [1, 12, 13].

Selection for chickens resistant to viral infections is a promising approach for control and prevention of chicken viral infections [15]. Phenotypic and genotypic individual variations within and between chicken breeds or ecotypes have been documented [15–17]. For example, chicken lines, which are less susceptible to MD, have been under development for years [15]. This individual variation in resistance and susceptibility to infectious disease is attributed to genetic diversity within and among populations [18, 19].

Genetic diversity can buffer populations against infectious diseases, and populations with high genetic diversity are more resistant to infections than homogeneous populations [20–22]. Local African chicken populations are highly genetically diverse and are heterogeneous [24–26]. Most of the local African chickens have not been subjected to purposive artificial selection, but have instead subjected to natural selection through exposure to harsh and stressful environmental conditions and endemic infectious disease agents [27]. Local African chickens may harbor genes responsible for disease resistance, and may be appropriate in the changing environmental conditions caused by climate change [23–25]. However, despite the well-known genetic diversity of local African chickens, little has been done to investigate their genetic potential for disease resistance through artificial selection.

Most studies investigating genetic diversity and population structure of local African chicken ecotypes use microsatellite markers and mitochondrial DNA D-loop region, which yields limited information relative to variations in resistance and susceptibility to viral infections [24, 25, 28, 29]. There is a paucity of studies involving molecular tools with high genomic coverage which would perform genome-wide scan of genomic variations such as microsatellite markers, single nucleotide polymorphism (SNP), and genomic structural variations (such as copy number variants [CNV]), and decipher how these genomic variations may be associated with the variability in resistance and susceptibility of African local chickens to viral infections. The dearth of information may lead to underestimates of the genetic potential of local Africa chickens for selection of chickens resistant to viral infections. The present review paper is aimed at: (i) presenting a summary of information on challenges of control and prevention of chicken viral infections in African local chickens under backyard production systems and (ii) presenting a summary of documented information on the genetic diversity and population structure of locally adapted African chicken ecotypes and its implication for selection of chickens resistant to viral infections in the changing environment due to climate change.

LOCAL AFRICAN CHICKENS AND KUROILERS

Local African chickens are chickens that are reared under backyard production systems [1, 10]. Various names are used depending on the country of origin to refer to local African chicken (Table 1). In this paper, the name 'local African chicken' will refer to African indigenous chicken

Table 1. Summary of Production Dynamic Studies for Local African Chickens.

Study	Country	Name*	Production system	Average flock size	Reason of keeping chickens	Constraints
[28]	Sudan	Native chicken	Extensive /backyard	25	Meat provision and cash generating	Infectious diseases and predation
[7]	Tanzania	Rural chicken	Extensive /backyard	5	Food and sale (source of income)	Poor nutrition, infectious diseases, and predation
[8]	Kenya	Indigenous chicken	Small-scale free range	22	Food and cash income	Infectious diseases and poor nutrition
[29]	Ethiopia	Indigenous chicken	Extensive	16	Food and source of income	Infectious diseases and predation
[23]	Malawi	Scavenging chicken	Scavenging	13	Food and sociocultural functions	

*Various names, which are synonymously, used referring to local African chickens.

genotypes adapted to harsh tropical environmental conditions.

The main characteristic of local African chickens under backyard production settings is unlimited movement of birds, which allow birds to search for nutrition needs [3, 26, 27]. Rearing local African chickens require little or no feed supplementation, as they are scavengers. This makes production of local African chickens under backyard systems cost effective, and, therefore, appropriate for resource-poor households in rural communities of African. Further information on production systems of local African chickens is reviewed in detail elsewhere [2, 27].

A new hybrid chicken called the Kuroiler was introduced to Africa from India [30–32]. The Kuroiler is dual-purpose scavenger chicken raised for egg and meat production [33]. Like local African chickens, Kuroilers can thrive under harsh tropical environmental conditions, and they can scavenge for nutrition needs just like local African chickens [33–35]. The breed outperforms local chickens in terms of meat and egg production [32, 34, 35]. In a pilot study conducted in Uganda, Kuroilers and local Ugandan chickens were kept under the same scavenging settings, and the Kuroilers had higher production performance compared to local Ugandan chickens [30]. At 25 wk of age, the average body weight of the male Kuroiler chickens was 2.6 kg, compared to 1.6 kg for the male local Ugandan chicken [30]. Additionally, at 6-wk of age, Kuroilers had a higher average body weight than Sasso, a chicken originated from France, and Fulani, an indigenous chicken from Nigeria [32]. Furthermore, the Kuroiler chicken reported to lay 4–5 times more eggs compared to Desi, a local Indian chicken breed [35]. Although not supported by empirical studies, Kuroilers are said to be resistant to infectious diseases [30, 31]. Thus, increased production of Kuroiler chicken may have a significant impact on improving the quality of livelihood for resource-poor rural households.

THE GENETIC DIVERSITY OF LOCAL AFRICAN CHICKENS

Genetic diversity is derived from genes, segments of DNA that contain essential information for life on earth [21]. The concept of genetic variation derives from the possibility that individuals in a given population may carry polymorphic (different) DNA sequences of a given genomic region [21]. Therefore, genetic diversity can be defined as varieties of genes within a species [21]. The genetic diversity is at three levels: species, population, and individual [36]. Within a population of a given species, individuals may have unique genetic composition resulting in genetic variability among members of the same species leading to population substructuring [37]. Individual genomic differences in population are determinant of genetic diversity of a given population [21, 37, 38].

Local African chickens have high genetic diversity based on qualitative and quantitative traits [3, 16, 16, 39, 39]. The phenotypic diversity in terms of physical and morphological parameters such as plumage color and type, body shape

and size, and productivity performance is evident among local African chicken ecotypes [4, 16, 40, 41]. Variability in phenotypic parameters within and among local African chickens has been reported in most African countries, including Sudan [42], Ethiopia [43], Botswana [40], Nigeria [44], and Algeria [45].

The pattern of variations in phenotypic parameters is geographic and ecotype specific. Using morphological measurements, Lyimo et al. [41] were able to differentiate individuals of 5 Tanzania chicken ecotypes into 3 clusters, and ecotypes from the same geographical area tend to cluster together [16, 41, 46]. These findings are consistent with another report that involved 2 Benin chicken ecotypes from the Forest and Savanna ecological areas where the 2 ecotypes were different in terms of phenotypic parameters [47]. These observations are in agreement with Mahammi et al.'s [48], who postulated that the genetic diversity of Algerian chicken ecotypes are under 2 opposite evolutionary forces: the geographical location and climatic conditions, which induce differentiation and the high level of distribution and gene flow which homogenizes the population genetically [48]. The abundance of phenotypic variability within and between local African chickens may be an indication of their high genotypic variations. The phenotypic diversity of African chickens has been reviewed in detail elsewhere [49–51].

Genotypic diversity analysis of microsatellite markers has been extensively used to evaluate the genetic diversity and population structure in chickens [39, 52, 53]. Based on the mean number of alleles and heterozygosity values, reports indicate that local chickens from different parts of the world are highly genetically diverse as compared to pure commercial breeds (Table 2). When compared to local chickens from other parts of the world, local African chickens have demonstrated higher genetic diversity (Table 2).

Based on population structure indices, reports indicate that local chicken populations are genetically closely related [39, 53, 54]. The genetic variation of local African chickens is largely accounted for by the within ecotype variations. For example, 96.8% of the total variation among Zimbabwean chickens attributed to within ecotype variations [20]. Similar findings were observed among local chicken ecotypes of Tanzania [41], Kenya [39], Egypt [55], Sudan [56], Ethiopia [57], South Africa [53], and Algeria [48]. The available information suggests little differentiation among African local chicken populations.

CHICKEN VIRAL INFECTIONS IN BACKYARD PRODUCTION SYSTEMS

Infectious diseases are the major constraint of local African chicken production in backyard systems (Table 1). Diseases caused by viruses are most important in backyard chicken production as they lack treatment options [64, 65]. Viral infection that rank as most important to smallholder farmers in Africa is ND [23, 26, 66], followed by IBD and MD [13]. Here, we summarize some of the most important viral diseases affecting chickens in backyard systems.

Newcastle disease is highly contagious, devastating, and endemic in many developing countries where backyard chickens are common [11]. The disease is caused by Newcastle disease virus (NDV), an avian paramyxovirus serotype 1 [11, 64]. The majority (80%) of losses in local African chicken production and about half of the early chick mortalities (chicks from hatch to 6 wk of age) were caused by ND [10].

Novel virulent NDV strains have been reported in chicken flocks in African continent [67, 68]. The evolution and emergence of new virulent NDV genotypes may explain the reported cases of vaccine failures [67–69]. Along with the effort to develop antigenic-matched ND vaccines to improve the efficacy of the current ND vaccines, selection of chicken resistant to the circulating virulent NDV strains is a promising alternative strategy.

Infectious bursal disease is a contagious viral disease that affects young chickens [70]. The disease compromises the immune system of infected birds and predisposes infected birds to opportunistic viral and bacterial infections [71]. High morbidities and mortalities due to IBD have been reported all over the world, and the disease is of economic importance as it affects the productivity and well-being of birds [71, 72]. The worldwide prevalence and distribution of IBD have been reviewed in detail [73, 74].

Table 2. Genetic Diversity and Population Structure Statistics Estimated in Local and Commercial Chickens.

Country	Chicken type	MNA[1]	Ho[2]	Fst[3]	Reference
Ethiopia	Local chicken	11	0.5	0.12	[58]
Tanzania	Local chicken	5.7	0.62	0.05	[41]
South Africa	Local chicken	6.6	0.6-	0.01	[53]
	Conserved local chicken*	4.7	0.5	0.16	
Algeria	Local chicken	7.1	0.5	–	[48]
	Commercial	3.9	0.2	–	
Sudan	Local chicken	5.3	0.5	0.03	[59]
	Commercial	3.2	0.4	0.32	
Ghana	Local chicken	6.6	0.6	0.01	[60]
	Commercial	6.0	0.5	0.29	
Egypt	Local chicken	6.9	0.6	0.08	[61]
Britain	British chicken	3.6	0.4	0.25	[62]
Sweden	Swedish chicken	4.7	0.3	0.44	[63]

[1]Mean number of alleles per locus.

[2]Average observed heterozygosity.

[3]Population differentiation index.

*The local chicken under conservation program characterized by limited movement leading to inbreeding.

In an outbreak of IBD among broiler and layer chickens of Ethiopia, mortality was estimated to be 50% [71]. Mazengia et al. [75] reported morbidity of 38% and case mortality of 99% among Ethiopian locally adapted chickens. In a serosurvey conducted among local Tanzanian chickens, 59% of the chickens were seropositive, and more importantly, 83% of flocks were seropositive [76]. This information indicates that IBD is widespread amongst exotic and local chickens in the African continent.

Another important chicken viral infection is MD, a lymphotropic and highly contagious disease, that affect mostly immature birds [77]. The disease is caused by the herpes virus, Marek's disease virus (MDV) [77]. The disease spreads easily through contact with infected birds, bird droppings, and fomites, and can spread through aerosol and dandruff [78, 79]. The morbidity of MD is about 50%, and mortality can reach up to 100% if occurs in susceptible flocks [79].

CHICKEN VIRAL INFECTION CONTROL STRATEGIES IN BACKYARD PRODUCTION SYSTEMS

Under backyard production settings, the prevention and control of chicken viral infections are a challenge. The control and prevention of chicken viral infections solely depend on vaccination and institution of appropriate biosecurity measures [64, 65]. Like other viral infections in animals, chicken viral infection lacks treatment options.

Vaccination adoption significantly decreases chicken mortalities from viral infections [65, 80]. For example, in a community-based ND vaccination program conducted in Tanzania, ND vaccination effectiveness was almost 70% [81]. Under experimental settings, ND vaccination can result in 100% of flock protection to the disease [82]. However, control of chicken viral infections by vaccination remains a challenge, particularly under backyard systems due to lack of vaccination programs and improper vaccination attributed to limited veterinary extension services in rural areas [83]. Limited financial resources among poor rural households to purchase vaccines and lack of storage facilities, like unavailability of the cold chain for ND vaccines, are significant constraints facing vaccination adoption in backyard production systems [64, 84]. Furthermore, chicken viral infection control by vaccination has limited ability to prevent the spread and transmission of viruses to uninfected chickens [84]. The vaccination aims to prevent clinical disease [84], and vaccinated birds can shed viruses in their secretions such as in feces, tears, and mucosal, thereby spreading infections in the surrounding area [85].

Another strategy is biosecurity, which is designed to prevent the spread of infectious

agents within and between flocks. Biosecurity has three main components: isolation, traffic control, and sanitation [1]. The main characteristic of isolation is the confinement of birds within a controlled environment [1, 86]. Traffic control is designed to limit movement within and between flocks. Sanitation deals with disinfection of materials, people, and equipment entering and leaving the farm, and cleanliness of farm caretakers [86]. Biosecurity is an essential means of preventing infections; however, not much information is available to support its feasibility in backyard production systems [87]. A systematic literature review by Conan et al. [1] found that most of the biosecurity measures devised under intensive production systems are not feasible or effective under backyard chicken production systems. Given the challenges of implementing vaccination and biosecurity measures in backyard systems, genetic selection of chickens resistant to viral infections could be a more robust and cost-effective solution to preventing and controlling infectious diseases.

CLIMATE CHANGE AND CHICKEN INFECTIOUS DISEASES

Climate change is an average change in weather pattern: temperatures, humidity, wind, and rainfall [88]. The change in weather patterns caused by climate change is linked with the dynamic of diseases epidemiology [89, 90]. The change in average temperatures, rainfall, and climate extremes impacts the distribution of pathogens and host–pathogen interaction due to disruption of ecosystem structure [90]. Environmental stressors like weather extremes, infectious agents, and dwindling of feeds influence chicken production [89–91]. More importantly, these environmental stressors are increased by direct and indirect impact of global climate change.

Extreme temperatures and relative humidity compromise the ability of birds to resist infections [92]. The extreme weather like high ambient temperatures is associated with chicken's oxidative stress due to lipid peroxidation and disruption of energy balance, which may lead to immunosuppression [24]. On the other hand, in cold conditions, some pathogens like NDV survive for longer time increasing the chance of diseases occurrence [25]. The change in the pattern of pathogens distribution and host–pathogen interaction poses an unprecedented risk of new disease occurrence in susceptible chicken populations.

Environment is a main driver of selection pressure of a given population to adapt for survival and reproduction [92, 93]. For example, difference in chicken genomic regions is demonstrated to be linked with the environmental conditions of chicken population [91]. It is likely that chicken populations adapted to harsh environmental conditions like local African chickens may have selection signatures for adaptation to extreme environmental conditions attributed to climate change. The understanding of genetic mechanisms responsible for chicken adaptation to harsh environmental conditions is critically important for breeding chickens resistant to infectious diseases [92]. Likewise, along with the effort to mitigate effect of climate change, it is prudent to breed and conserve chicken genetic resources adapted to survive extreme weather conditions caused by global climate change.

GENETIC DIVERSITY AND DISEASE RESISTANCE VARIABILITY

Genetic diversity contributes to population fitness in response to a changing environment [20, 22, 94]. Population genetic variations allow individual adaptation to the changing environment like adaptations to endemic infectious diseases and climate change [95, 96]. The correlation between genetic diversity and population fitness is demonstrated using molecular quantitative genetics data [20]. Springbett et al. [97] demonstrated that a heterogeneous population is less likely to suffer from catastrophic disease epidemics as compared to homogeneous population using stochastic models [97]. In contrast, the loss of genetic diversity has been associated with species extinction [20, 22, 94].

Disease resistance is defined as the ability of the host to resist infections [36]. For the host to resist infection, the infectious agent should be cleared before getting into the host cell. The resistant host should prevent pathogen attachment and entry into the host cell [36]. Alternatively,

genetic resistance to disease refers to the ability of the host to suffer minimal adverse effects following infection, also, is known as tolerance [36, 98].

At the molecular level, mechanisms of disease resistance are complex and not fully understood. Genetic resistance to infectious agents is polygenic and influenced by the interaction of biological and environmental factors [71, 99]. The mechanisms of disease resistance are mainly controlled by immune responses, which are comprised of both innate and adaptive immunity [100, 101]. The innate immune response is the first line of defense, which clears pathogens in the very early stages of infection and initiates adaptive immune responses [101, 102]. Most of the studies on the mechanisms of disease resistance investigate the role of innate immune responses with the assumption that the innate immune responses determine an individual resistance or susceptible to infectious agents [100–102].

The major histocompatibility complex (MHC) haplotypes are associated with variation in disease susceptibility and resistance [101, 103–105]. The MHC molecules play a significant role in antigen processing and presentation [106]. The MHC can process and present all possible antigens due to the presence of multiple variants of each gene within the population [106]. The MHC genotype restricts the antigen recognition by T-cells. The defect in the MHC molecule may prevent the antigen recognition by specific T-cells. Therefore, the antigen specificity of T-cell is controlled by the MHC molecules [106].

Reports indicate that chicken variations in susceptibility to infectious diseases are linked with the MHC haplotypes [107, 108]. For instance, antibody responses to NDV are significantly associated with 2 MHC LEI0258 microsatellite alleles, 205 and 307 bp, in Tanzanian chicken ecotypes [109]. The allelic variant 205 bp was positively associated with the elevated level of antibody responses to NDV vaccine, whereas allelic variant 307 bp was negatively associated with the same trait [109]. Also, chicken with the same genetic composition may respond differently when exposed to different infectious agents. Chicken populations with similar MHC haplotype (B1B1) vary on antibody responses to *Salmonella pullorum* and susceptibility to MDV infection [110]. Interestingly, chickens with high antibody responses to *S. pullorum* antigen had high mortality rate to MDV challenge, whereas chickens with low antibody responses to *S. pullorum* antigen had low mortality rates in response to MDV challenge [110]. The association of the MHC variants with chicken variations in susceptibility to disease was reviewed elsewhere [111].

The toll-like receptor (TLR) genes signaling and interferon (IFN) signaling feature explain a significant role played by non-MHC genes for chicken's variation in susceptibility to diseases [112, 113]. Toll-like receptors constitute a group of pathogen-associated molecular patterns that play a crucial role in infectious agent's recognition and induction of innate immune response [114]. Although the role of TLR in chicken variations in susceptibility to diseases is not fully understood, reports indicate that TLR allelic variants are associated with variability in chicken resistance to diseases (Table 3). Specifically, 2 non-conservative mutations within the leucine-rich region domain (Tyr383His and Gln611Arg) of TLR4 are associated with susceptibility to *Salmonella* infection in two lines of chickens (line C and 72, Table 3).

The Mx protein, an IFN-induced dynamin-like GTPase, is among non-MHC genes that play significant antiviral activities [115]. The Mx allelic variants have been associated with chicken variability in susceptibility to viral infections [115, 116]. The Mx gene genotypes (genotype AA and GG) among Indonesian chicken, Tolaki, had significant differences in antiviral activities. Genotype AA had a higher antiviral activity of 50% compared to genotype GG, which had the antiviral activity of 10% [117].

Taken together, the literature in the present review suggests that local African chickens may have higher resistance to infectious disease compared to exotic breeds and commercial. Local African chicken are genetically diverse and have not been subjected to purposive artificial selection, and subjected to natural selection due to persistent exposure to harsh tropical environmental conditions and endemic infectious diseases. Additional evidence is provided by Jovanović et al. [36], who argued that local breeds adapted to endemic infectious diseases have an evolutionary advantage over exotic breeds. Considerable studies have been conducted among African chicken ecotypes to support this

Table 3. Genes/Variants Associated with Disease Resistance/Susceptibility in Chickens.

Disease	Gene/variant	Role	Reference
Salmonellosis	TLR4	Two non-conservative changes in leucine-rich region domain associated to chicken susceptibility to salmonellosis	[104]
	NRPMP1	Single SNP A101991G associated with chicken resistance to salmonellosis	[118]
Marek's disease (MD)	GH1	Conferred chicken resistance to MD	[119]
	CHTF18	Indel mutation with an additional of 7 nucleotides associated with chicken resistance to MD	[120]
Lymphoid leukosis	LDLR	Cysteine-to-tryptophan change in low density lipoprotein receptor (LDLR) for Avian leukosis viruses reduces binding affinity of the virus	[121]
Influenza	Mx gene	Amino acid substitution of Mx protein at position 631 (Ser to Asn) enhance antiviral activities in chicken	[122]
Coccidiosis	LEI 0071	The LEI 0071 is associated with reduction of parasite growth (*Eimeria maxima*) in chicken.	[123]

assumption [16, 109, 124]; however, few studies have been conducted to associate the observed variation in disease phenotypic parameters among individuals in the chicken populations with genomic structural variation such as SNP and CNV using a whole genome scan approach.

CONCLUSIONS AND APPLICATIONS

1. Chicken is the dominant poultry species raised by the majority of poor rural households in Africa as a chief source of high-quality meat and egg protein and for income generation. However, local African chicken productivity is primarily compromised by diseases, particularly diseases due to chicken viral infections. Chicken viral infections control and prevention by vaccination and institution of biosecurity measures are less effective and plausible in backyard production systems.
2. The genetic selection of resistant chicken to viral infections is a promising strategy. African local chickens have demonstrated to be highly genetically diverse and adapted to harsh tropical environmental conditions. Therefore, local African chicken is a potential candidate chicken population for selection of resistant chicken to viral infections in changing environment attributed by climate changes. However, there is a paucity of information on the possible linkage between the genetic diversity of local African chickens and their variability in resistance and susceptibility to chicken viral infections. Here, we call on concerted effort to identify and breed chickens that are resistant to viral infections and adapted to extreme environmental conditions. The endeavor should consider the untapped potential of the genetic diversity of local African chickens by performing genetic association studies to identify allelic variants associated with chicken variation in resistance and susceptibility to chicken viral infections.
3. The conservation of genetic diversity potential of local African chickens is highly recommended considering unprecedented effect of climate change on global chicken production. We call on the establishment of institutions within respective ministries in African countries responsible for coordination of animal genetic resource conservation activities and mobilization of resources for the same.

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