Cavy as Alternative Genetic Resource for Animal Protein Production in DR Congo

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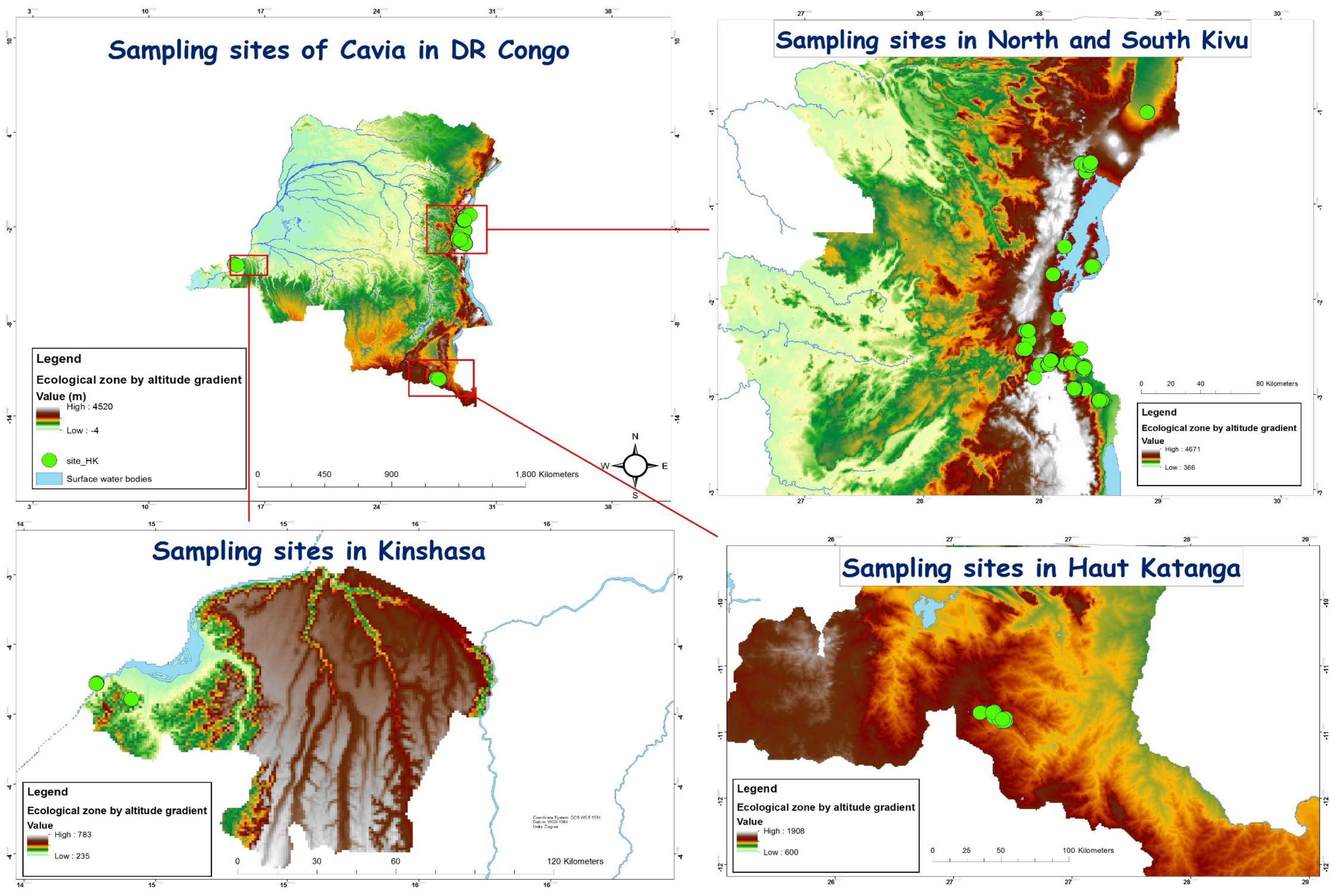
Introduction

Cavies (Guinea-pigs) are commonly used in sub-Saharan Africa for meat consumption, income generation and manure production in mixed crop-livestock systems (Niba *et al.* 2012; Maass *et al.* 2013; Yiva *et al.* 2014). It has been used for several millennia and continues to be used as an animal for slaughter by the natives of the Andean countries (Gade, et al., 1991). Introduced into Africa by missionaries during the colonial period. Cavy production system has evolved leading to enormous changes in their production and genetic diversity (Ngou Ngoupayou et al., 1994, Manjeli et al., 1998, Metre, 2005). Since its introduction to DRC, the adoption of the cavies by the locals became widespread covering the whole country. After 2004, cavies became one of the favorite vehicles for NGOs to combat poverty and malnutrition of poor and displaced people all over South and North Kivu (Raeymaekers, 2008; Maass *et al*., 2014). Largest cavy populations are known to exist in DR CONGO. Therefore, this study aimed in the evaluation of the genetic diversity of cavy in the different agro-ecological zones of DRC using microsatellites markers



Methodology

Blood samples were collected from 343 adults in four provinces of the DRC (South and North Kivu, Katanga and Kinshasa) based on their phenotypic variability and kept on FTA cards (Whatman® FTA® card technology, Sigma-Aldrich).

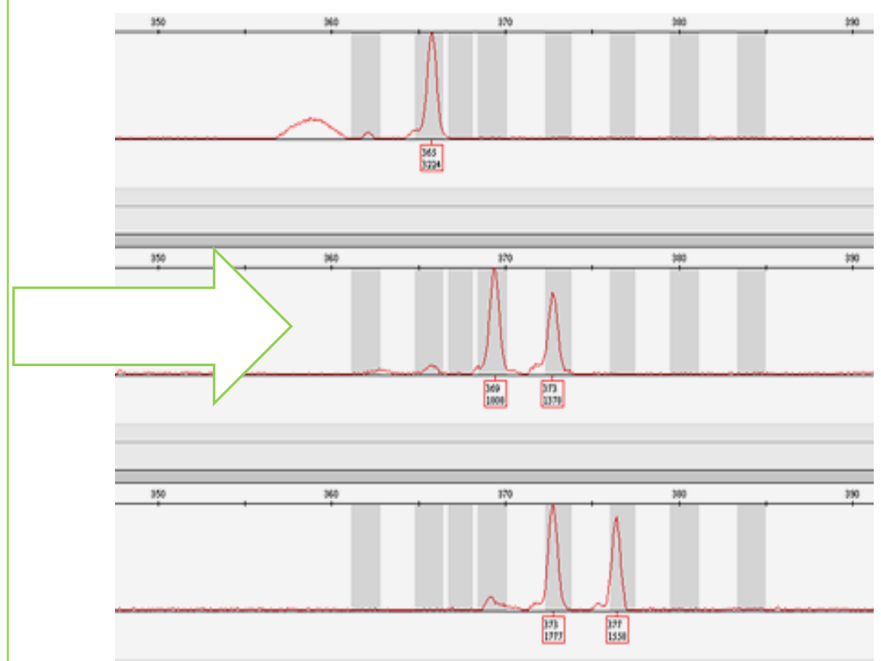
Blood collection

Total DNA extraction
Quality control check

SSR-PCR optimization & amplification (16 SSR)

Initial denaturation: 3 min at 95°C followed by 30 cycles of 30s denaturation at 94°C, 60s primer annealing at Δ°C and 1 min primer extension at 72 °C, and then a final extension step of 20 min at 72 °C

Capillary electrophoresis



Data Analysis

Alleles calling: GeneMapper

Genetic diversity : GenAIEx

Population structure: Structure

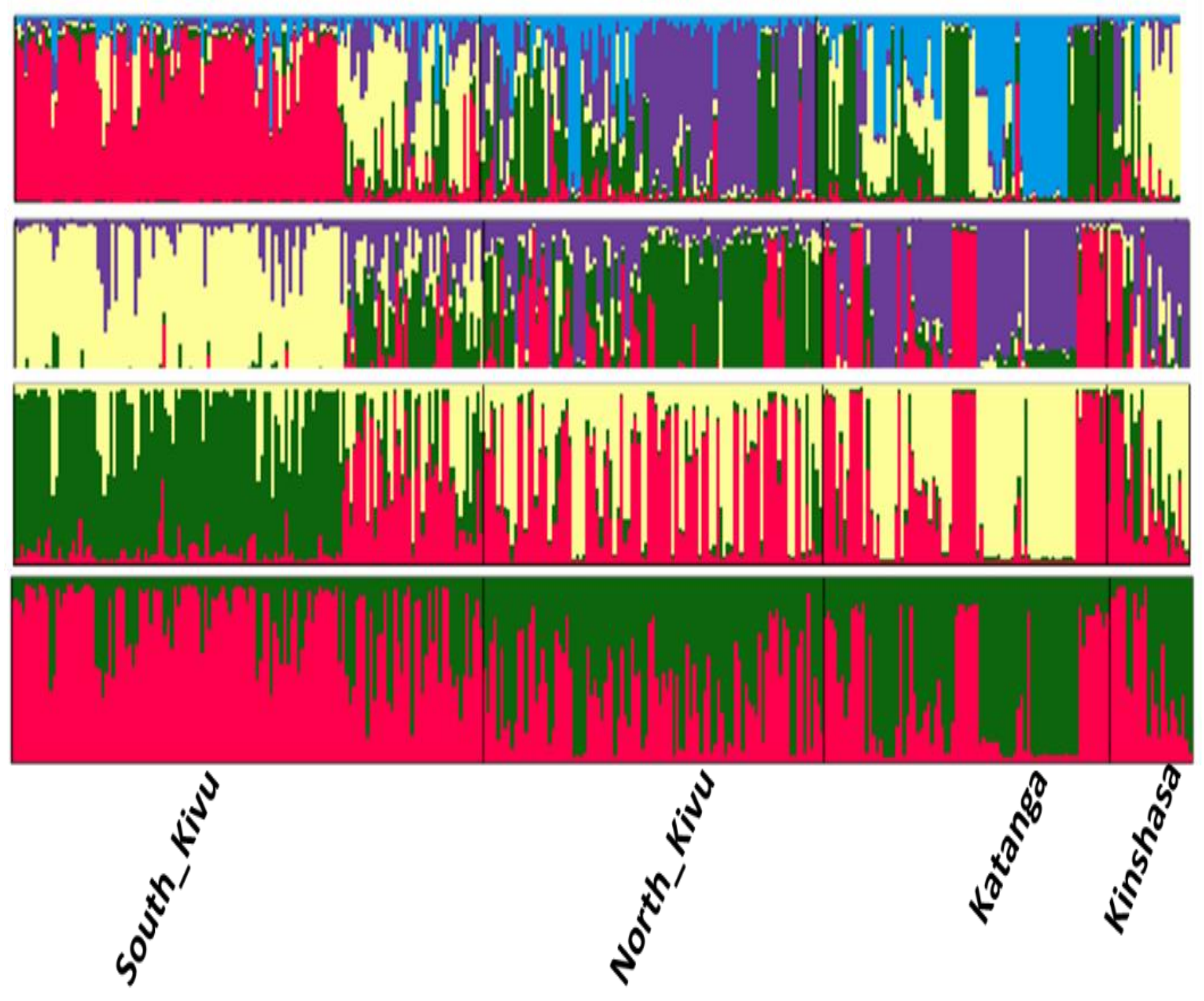
Phylogeny and core collection: Darwin

Results

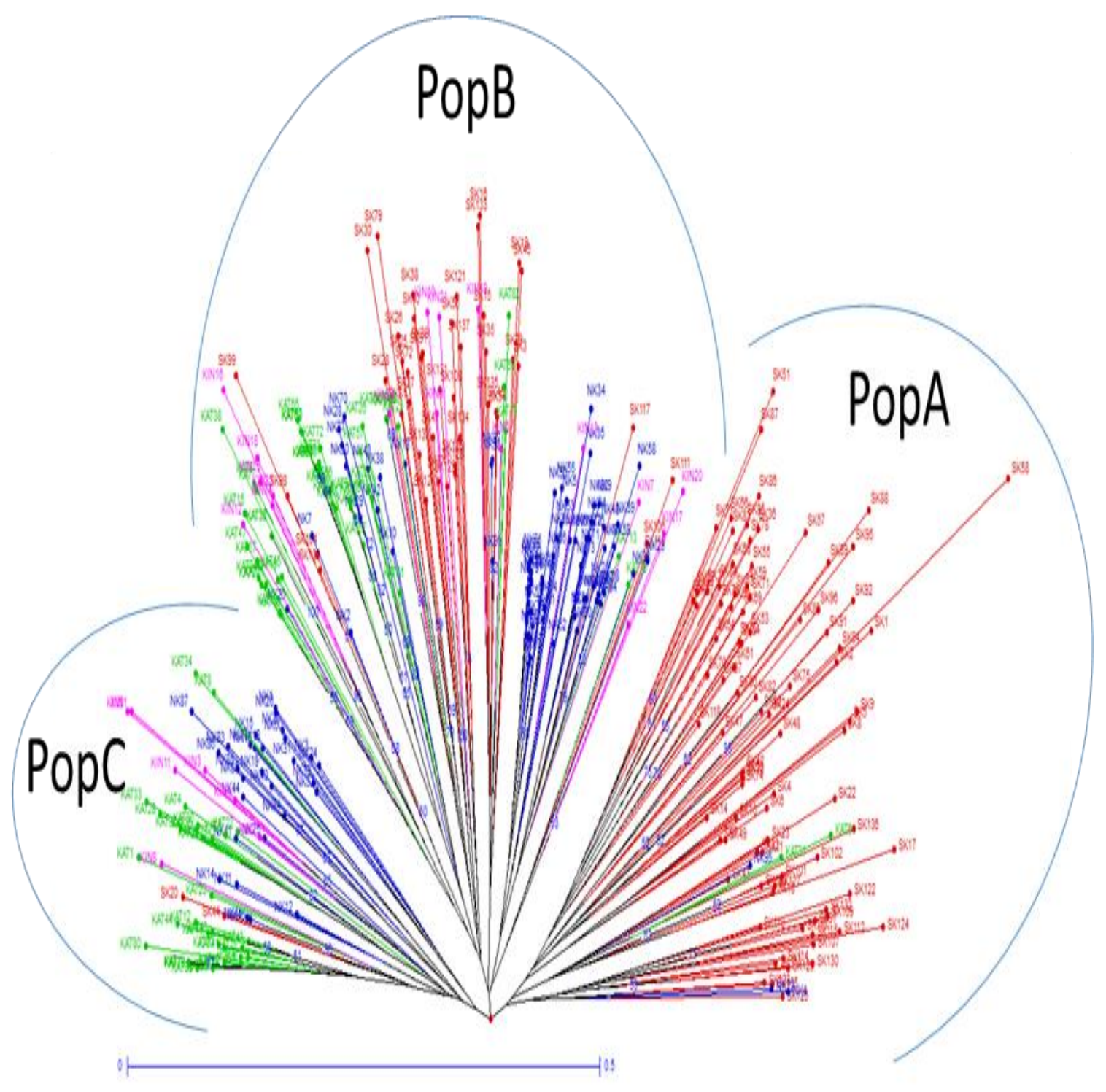
Genetic diversity measures for cavy populations from DR Congo

Population	Na	Ne	PaL	I	Ho	He	UHe	Fis
South_Kivu	7.23	3.07	22	1.33	0.42	0.65	0.65	0.35**
North_Kivu	5.54	2.15	6	0.96	0.30	0.49	0.50	0.37**
Katanga	5.62	2.66	7	1.10	0.23	0.56	0.56	0.57**
Kinshasa	4.69	3.18	2	1.22	0.39	0.63	0.65	0.38**
Mean	5.77	2.77	9.25	1.15	0.34	0.58	0.59	0.42**

A total of 113 alleles were detected across the 4 cavy populations. In total 37 privates alleles have been founded in the 4 studied populations and South Kivu and Kinshasa having the great number. Overall, the highest heterozygosity within population Ho was recorded in the South Kivu population, while the lowest value was recorded in Katanga. It was found that the inbreeding per population was significantly higher in Katanga population than in South Kivu population.



Bayesian clustering of 343 cavies under assumption of 3 clusters without a priori population information. The population names are given below the box plot, while the three gene pools compositions are represented by colors.



Dendrogram of individuals based on genetic distance among Cavy Population from DR Congo. Populations of origin are represented by colors (South-Kivu = red, North-Kivu = Blue, Katanga = Green and Kinshasa = Pink).

The 343 individuals were divided into three major groups, here denoted as population A, population B and population C. The population A composed with individuals from South Kivu doesn't have almost admixture while population B is admixed with the different populations of origin. The number of clusters K, was inferred to be three. The groups are then considered as three different gene pools from which DR Congo population are originated. However some individuals are sharing two or the three gene pools inferring that different parts of an individual's genome got inherited from different populations. The south Kivu population is mostly dominated by one gene pool (green colored) which is above reported to be one distinct cluster with no admixture.

Conclusions

DRCongo cavy population is composed with three gene pools considered as distinct groups. South Kivu population were more diverse compared to the rest. These results are useful for designing effective breeding programs. The molecular diversity provides useful information for breeding programs to aid selection of diverse parents for establishment of breeding populations that could be used for cavy improvement. To maintain the present genetic diversity, proper national breeding strategies should be implemented considering within and between population variations.

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