Genetic and Phenotypic Characterization of African Goat Populations to Prioritize Conservation and Production Efforts for Small-holder Farmers in Sub-Saharan Africa

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ABSTRACT: Food production systems in Africa depend heavily on the use of locally adapted animals. Goats are critical to small-holder farmers being easier to acquire, maintain, and act as scavengers in sparse pasture. Indigenous goats have undergone generations of adaptation and genetic isolation that have led to great phenotypic variation. These indigenous goats serve as a genetic reservoir for the identification of genes important to environmental adaptation, disease resistance, and improved productivity under local conditions.

The immediate goal is to characterize African goat populations to prioritize conservation and production efforts and to develop genomic tools for use in selective breeding programs. We have established a standardized phenotypic scoring system to characterize goats including geographical information data, body measurements, photo characterization, and DNA. To date, 2,443 goats from 12 countries, representing 46 breeds have been sampled. Using the 50K goat beadchip, we report parameters of population structure of 620 African goats.

Keywords: goat; genetics; Africa; population structure

Introduction

In 2012, Africa held approximately 35% of the world's goat population, being the most abundant production livestock species on the continent (FAO 2014). In addition to providing nutritional value as sources of milk and meat, goats are part of African culture and provide financial stability to the small-holder farmer. Thousands of years of adaptation, human initiated migration, and geographic isolation has led to a high degree of phenotypic variation of the indigenous goat populations. In contrast, there has been minimal artificial selection for production parameters including growth, milk yield, or reproductive traits with the exception of the Boer breed (2 % of African goat population) in South Africa. Cross-breeding of high-producing milk goats with indigenous goats has shown minimal success as exotic breeds do not possess the hardiness for survival in the African ecotypes. The result of these factors has created indigenous goat populations uniquely adapted for resiliency and sustainability in diverse African ecosystems with untapped potential for production improvement. The African Goat Improvement Network (AGIN) was launched as a collaborative endeavor of the USAID Feed the Future initiative combining local African expertise of goat populations, culture, and ecosystems with genomics researchers from the USDA-Agricultural Research Services and multiple international universities (Woodward-Greene 2013). The aim of this project is to lay the foundation for future selection programs by characterizing goat populations across Africa and generating data to develop genomic tools to assist in selection decisions.

Materials and Methods

Standardized Phenotyping. The four basic components of the AGIN sampling protocol include geographical information system (GIS) data, physical body measurements, photo characterization, and DNA sample collection.

GIS data including latitude, longitude, and elevation were collected for each sampling site. These measurements provide accurate details on where sampling was done as well as coordinates to direct climatology data collection in the future.

Six physical body measurements including chest girth, height at the withers, body length, shoulder width, pin-bone width, and body weight were collected on all individual goats sampled. Measurements of size and body structure allows for physical characterization of breeds or populations. The degree of physical variation is also a factor investigated for correlation in genetic variation. All measurements were with goats standing with their legs perpendicular to the ground (Figure 1). Chest girth was measured as the body circumference at the heart, just behind the elbows

and up to the withers (Figure 1.A-CG). Height was measured from the ground at the front hoof to the point of the withers (Figure 1.A-HW). Body length was measured from the point of the shoulder to the pin bone (Figure 1.A-BL). Width of pin bones was measured between the rear bones at either side of the anus (Figure 1.B). Shoulder width was measure from the points of the shoulders on the front chest (Figure 1.C). Body weight was measured with a hanging small livestock scale and sling.
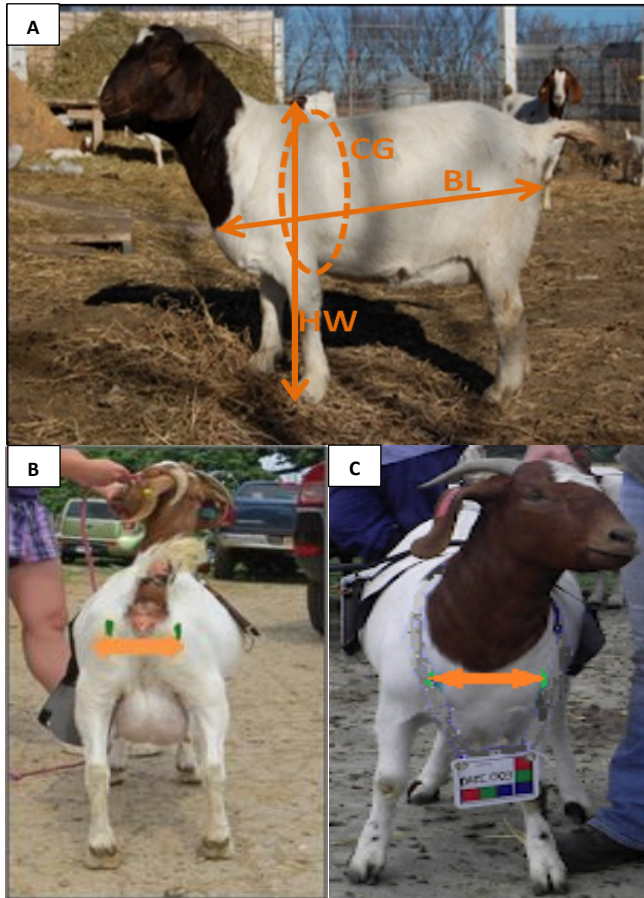
Figure 1. Physical body measurements

Photo characterization included a set of six photos with a standard blue background, data sign of specific size and color panel for photo analysis, and photographer and animal positioning. Photo characterization allowed for quick data collection on coat color characteristics and is being developed as an alternative system for body measurement calculations. Livestock crayons were used to mark physical points on the body including shoulder and pin bones. A custom made harness held the data sign. Photos included a rear, profile, front, teeth, FAMACHA card/eye, and "naked" (profile with no data sign obscuring coat color pattern) photo. The teeth photo was for age assessment and the FAMACHA card photo was for anemia assessment.

Lastly, two biological samples were obtained from all study individuals for DNA extraction and genotyping. Tissue samples were most commonly obtained through ALLFLEX tissue applicator system where a small (~1.5mm diameter) ear punch biopsy was extracted and automatically deposited in a collection unit for preservation. Whole blood (6-8ml) was obtained through jugular venipuncture and collected in ACD or EDTA vacutainer vials.

Goat Breeds and Sampling Sites. Eleven African countries plus a population of New Zealand Boer goats directly descended from the early South African importation were sampled. Ten of the African countries used the established protocol with sampling sites chosen for unique climatic zones and distinct goat populations. Approximately 30-50 individual goats were sampled per site or breed.

DNA Extraction and Genotyping. DNA extraction was performed with the Qiagen PurGene tissue or whole blood procedure. Whole-genome genotyping was performed using the Illumina 50K Goat beadchip standard protocol (Illumina 2012). A total of 620 individual goats were genotyped from five African countries (Ethiopia, Nigeria, Kenya, Egypt, South Africa), New Zealand, Italy, and the United States. Standard quality control measures were used to filter the single-nucleotide polymorphism (SNP) genotypes producing an informative genome-wide panel of 51,267 SNPs on 577 individuals.

Genetic Analysis. Principle Component Analysis (PCA) was performed on the African breeds and in combination with reference breeds from the US and Italy.

Results and Discussion

The African Goat Improvement Network has succeeded in developing a standardized sampling protocol for characterizing African goat populations. Two project development workshops have been held to establish short and long-term goals, implementation plans, and sharing of expertise. Training for collaborators and local scientists was held during the second workshop to demonstrate implementation of the sampling protocol. The protocol has been successfully completed in ten African countries through AGIN efforts and has four new FAO partnership projects starting in the coming year. In addition, individual researchers in Africa, Europe, and Brazil have joined AGIN efforts by sharing their genotypic data for population comparison.

Principle component analysis has established that the Illumina 50K goat beadchip can effectively distinguish goat populations, specifically indigenous African goat populations in which the chip was not previously used for. In a comparison of the 14 African goat breeds, New Zealand Boer, 3 Italian Alpine, and six US breeds, PC1 generates a continental separation of Italy, US, and Africa with PC2 distinguishing the Boer breed (Figure 2). PC1 could potentially be a manifestation of artificial selection with the Italian Alpine breeds undergoing the greatest production selective pressure and the African populations, with the exception of the Boer,

having little to no selection to date. Analysis of just the African goat populations allows for finer separation of the populations within Africa to their breed designation and country of origin (Figure 3). The Kenyan breeds of Galla and Small East African cluster together with very little genetic variation. In contrast, the South African breeds show a higher degree of variation with the exception of the Tankwa breed. Surprisingly, not all of the Boer goats from South Africa cluster together or with the New Zealand lineage of South African Boer. Continued breed genotyping will add to the genetic analysis of population structure and lend insight into the degree of genetic variation among breeds. Links between climatology, production uses such as dairy versus meat, and ancestral diversion from a single domestication event will be explored. These insights into the genetic structure of African goat populations as well as the fostering of relationships with African communities will allow for future implementation of community based breeding programs utilizing genomic selection techniques towards production improvement.
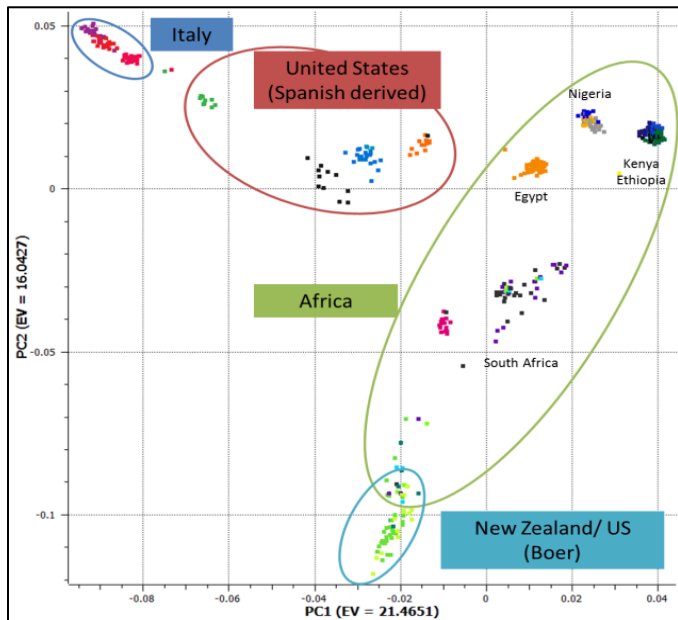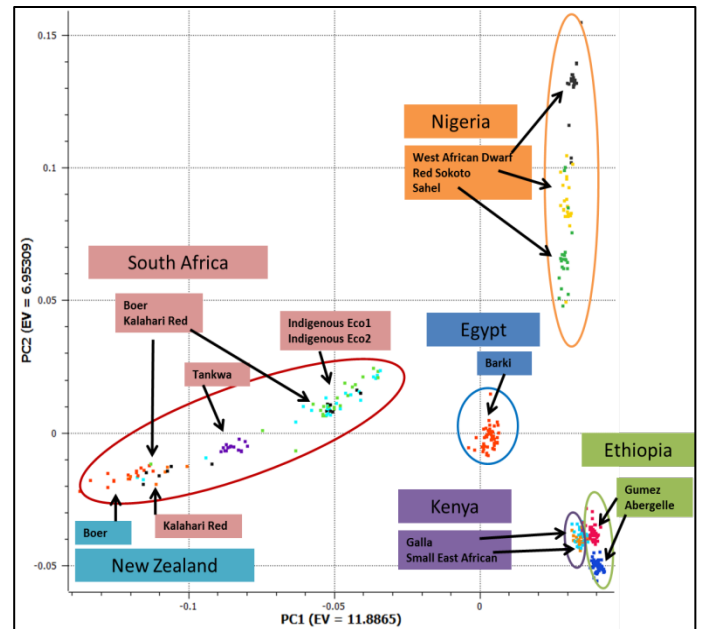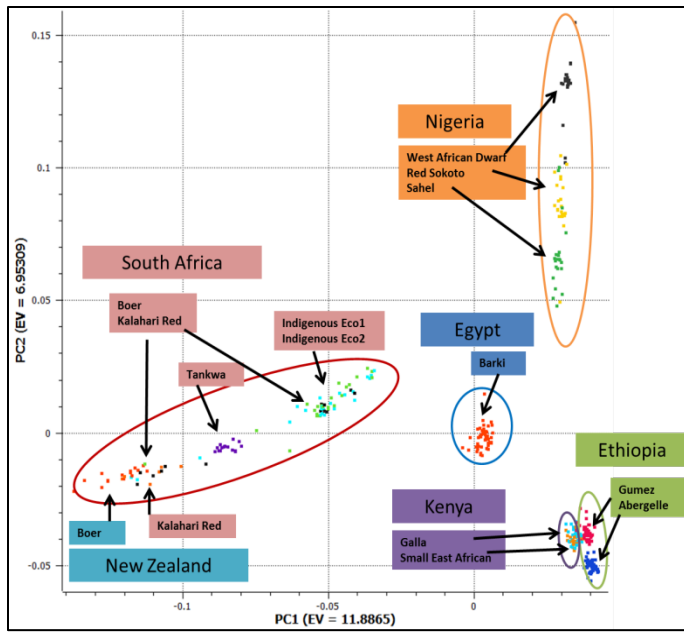

Figure 3. Principle Component Analysis, PC 1 and 2 of African goat breeds.

Figure 2. Principle Component Analysis, PC1 & PC2.

Conclusion

The central aim of this project is to encourage cooperative efforts to develop and apply genomic tools for the identification and preservation of locally adapted goat populations, and to leverage these collaborations to enhance African expertise in genomics. The long-term goal is to develop genetically superior adapted goats to help meet the demands of local food security through self-sustaining community breeding programs.

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