

One of the Least Studied Ruminants Finally Gets Its Time in the Genomics Spotlight

The USDA is employing Illumina sequencing to uncover the genetic differences between the world's goat breeds, identifying mutations that enable goats to thrive in harsh environments.



Recognizing that its technology could play a critical role in alleviating global hunger, malnutrition, and poverty, Illumina created the Agricultural Greater Good initiative. Each year, Illumina awards Greater Good grants to agricultural research organizations that are focused

on identifying and breeding plants and animals that will increase the sustainability, productivity, and nutritional density of crop and livestock species. Under the grants, Illumina sequencing and genotyping reagents are provided free of charge.



U.S. Department of Agriculture 2012 Illumina Greater Good Initiative Award Winner

Introduction

In 2007, the U.S. Department of Agriculture (USDA) substantially expanded its mandate beyond providing safe, healthy food for Americans to supporting global food security initiatives. Ensuring food security for nations with emerging economies is now one of the five pillars of research for scientists in the USDA. "Our team was charged with finding an area where we could make a contribution," said Tad Sonstegard, Ph.D., Research Scientist at the Agricultural Research Service (ARS)¹, the research arm of the USDA. "We chose goats because when you look at the United Nation's Food and Agriculture



Tad Sonstegard, Ph.D., is a Research Scientist at the Agricultural Research Service (ARS), the research arm of the USDA.

Organization (FAO) statistics on livestock numbers², you see that goats are important in Africa and Asia. Scientists predict that Africa will face a shortage of food because the population is growing so quickly. Countries on the African continent are already on the threshold of not producing enough food for their inhabitants³, with many people suffering from malnutrition."

Through their meat and milk, goats provide protein essential for early childhood development. Many African households have at least one goat, with women responsible for tending to their care. From a protein output, these goats can't compare to their European cousins. "Dairy production of African goats is about half per annum of those found in Europe," said Dr. Sonstegard. "If you could close that milk production yield gap by half, imagine how much additional animal protein would be available for children's diets, for selling to generate income, etc. The same is true for meat yield, with meat production critical for the large commercial ventures that raise goats for sale to Middle East buyers."

The lower protein yield is in part influenced by years of negative selection. "Unfortunately, the biggest and best producing goats are killed for family celebrations, such as weddings," Dr. Sonstegard said. "What remains is a gene pool lacking contribution from some of the superior goats."

Tapping Into the Goat Genome

Genomic analysis is enabling researchers to determine the differences between the goats found in Africa and elsewhere in the world. "It began with mitochondrial DNA research that indicated goats were domesticated somewhere in Northern Iran," Dr. Sonstegard said.



Native to San Clemente island off the coast of California, the inbred San Clemente goat provided an ideal genome for sequencing with Illumina HiSeq and MiSeq systems.

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"They were derived from the Bezoar goat, which can still be found in the Middle East. From there, goats radiated out everywhere across the globe."

When the USDA originally drafted the project in 2010, there had been little research into the goat genome. In 2012, the International Goat Genome Consortium sequenced the first goat genome and worked with Illumina to develop a goat SNP array, the Caprine53K BeadChip.

"We need to understand genetic differences among the world's goat populations, the differences that make them unique and which differences are adaptive," Dr. Sonstegard said. "We initiated our project by collecting samples from 96 goats, representing different U.S. breeds and used the Caprine 53K BeadChip to identify which animal was the most inbred," said Dr. Sonstegard. "The most inbred animal would be the best animal to sequence, because it's easier to assemble. We found that the San Clemente goat was the most inbred, and have generated sequence from this animal on a number of next generation platforms including short paired-end reads and fosmid ends using both the MiSeq[®] and HiSeq[®]."

The data from these runs will enable Dr. Sonstegard's team to build a genome assembly as a resource for future BeadChip development. "We'll use them to continue characterizing goat populations across the globe," Dr. Sonstegard said. "We're already performing a genetic survey of unique populations of goats in Africa that possess special traits, looking for genomic regions where there's complete homozygosity that could reflect positive selection and the location of genes that contribute to survivability."

Taking a World View with Big Data

While it's important to conduct this survey in African goat populations, it's equally important to look at populations in other parts of the world where goats are in similar environments and undergoing drought or parasite stress. "If we're going to suggest goats for families and ranchers to breed, we want to be sure the progeny can survive and thrive in harsh environments and against endemic disease," Dr. Sonstegard said.

As Dr. Sonstegard and his team identify SNPs that are segregating in African goats, they'll be added to the Caprine BeadChip to support continued research and breeding of goats worldwide. "Bringing in scientists from all over the world to work on this project builds a stronger community where people can share ideas," Dr. Sonstegard added. "It also allows everybody to access each other's resources. Funds are limited for goat research—they're probably the least studied domesticated ruminant to date as far as genomics goes." Researchers worldwide are jumping on the goat sequencing band wagon. "People want to participate in this project," Dr. Sonstegard said. "To name a few, we have the Brazilians from Embrapa and the University of Sao Paulo State wanting to collaborate. The FAO has goats in Chile that they would like to be included. We're trying to contact people in St. Croix where goats are reported to be resistant to parasites found in the Caribbean. We also have a partner in Australia who has been looking at feral goats. They all want to apply genomic technologies in goat breeding."

The ADAPTMap⁴ project is an international effort initiated by Dr. Alessandra Stella of Parco Tecnologico Padano (Lodi, Italy) designed to coordinate the disparate goat breed genotyping and resequencing efforts of organizations worldwide. "We're putting our data into the pool so we can make more comparisons, Dr. Sonstegard said. "3SR, a small ruminant EU project, as well as INRA, the French National Institute for Agricultural Research, are also a part of the ADAPTMap project. It's all about big data being shared, people looking at results, and identifying new breeding paradigms."

Greater Good Award Expands Goat Research

"The Greater Good award enabled us to double the size of our sampling budget," Dr. Sonstegard stated. "In the future, we'll be obtaining samples from goat populations along the eastern side of Africa, from Kenya to South Africa. The larger sample size means we'll have a much larger impact and a better chance of finding survivability genes that will positively impact goat breeding. In turn, the expanded sampling has attracted other groups to the project and leverages additional researchers and resources. If it hadn't been for receiving Illumina's Greater Good award, this would have been a relatively small project."

Dr. Sonstegard believes that global food security is going to be a big focus area in agriculture research, especially in animals. "It's an area that scientists have been ignoring, because most have been focused on national interests. It's become a smaller world and everyone is starting to look outside of their own country."

References

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