

Pre-application submission for USDA NIFA and NSF I-CORPS program

1. Composition of the Team and roles:

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3. Relevant current/previous NIFA award(s) including award number, Title of the Project, and the NIFA program the award was found under:

Accession No: 1006741

Project No: OKLUTILAHUN2015

Title of the Project: Genome-Wide Association Analysis for the Identification of Alpine Goats With High Milk Production

The NIFA program the award was found under: Exploratory: Exploratory Research

4. Brief description of the potential commercial impact:

Goat milk is generally consumed at a much larger margin from cow milk when examining markets outside of the US. However, the niche market in which the US goat industry exists is slowly gaining increase in sales, by 10 to 15% or more annually in some parts of the country. Goats are ruminants that have the capacity to digest fibre and convert non-edible resources into high quality products utilized for nutrition. Eight main breeds of goats compose the area of ruminant dairy goat production. They are Alpine, LaMancha, Nigerian Dwarf, Nubian, Oberhasli, Saanen, Sable, and Toggenburg. Each of the breeds lend themselves credence to advantages and disadvantages in comparison with the others, depending on the biotic and abiotic conditions in which they are exposed.

There are many beneficial components of goat milk as can be seen by the comparison of goat, cow, and human milk (Bowen and Church, 1983; Pennington and Church, 1985; and Dronen, 1990). The GoatSNP50 chip has already been used to determine genetic diversity of Boar, Cashmere, and Rangeland goats (Kijas et al., 2012). High-density SNP data has been shown to be effective in identifying regions of the genome that are important for the prediction of genetic merit in production traits in many species (i.e. McCue et al., 2012; Sanchez et al., 2014).

The initial goals of this study were to identify regions of the genome that are important for predicting genetic merit in dairy goats as well as begin to develop genomic prediction equations for genetic evaluation of economically-important milk production traits, mainly regarding milk yield. The study has developed into a more comprehensive ability to identify other economically important traits (somatic cell count, fat yield, lactose content, fatty acid composition, and protein yield and percentage). These approaches are also the first step in identifying SNPs that could be used in the future to produce a low-density SNP assay that could be provided to goat producers at a reduced cost to facilitate both genetic selection and integration of genomic technologies into production systems. These tools would allow the selection of goats with superior genetic merit for milk production at an earlier age, thus facilitating appropriate use of resources and leading to genetic change in goat populations. Custom – designed genotyping tools

that are smaller and cheaper than the original have what are referred to as a pre-designed amount of “real estate.” The selection criteria involve but are not limited to small p-values (<0.001 or <0.0001), large estimated effect sizes (odds ratios) and previous reports of association, they also include biological relevant pathways, plausible function of the variation, or a combination of all these factors.

The potential commercial impact is very much significant do to the affordability of such a valuable amount of information that can be utilized throughout the world for commercial and sustainability reasons. A product formed from this data will indeed produce a great deal of revenue for its shareholders.

The plans for commercialization begin at meetings and symposiums where goat and livestock producers gather. There promotion of the product will be made. Additional promotions will be made in trade journals and shows where the impact of the technology will be described and shared with the public.

References

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