Quick Summation of this morning's meeting with Dr. Huson (7/1 11:00AM)

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We introduced ourselves and the goals of iGEM as a whole. As the team gave the presentation, the process of how the team took samples from cattle, used RPA to amplify and detect the A2 allele, and used a flappase to cleave the sample into parts detectable by fluorescence.

The team introduced the new goals and theme of this year's project: SNPs (SNPFLAPs)

To answer her inquiry about the confusion between results of heterozygous and homozygous samples, we explained how the use of different colors for each allele would create a new, different, color for a heterozygous sample.

The team mentioned the points discussed with Dr. Dechow

-Scabies, ingrown horns, etc.

-Heather brought up that testing for a genetic disease may not be feasible.

Most genetic diseases are linked to multiple SNPs, which would be difficult to detect.

Dr. Huson showed the team how to read a colored SNP distribution chart to detect which traits are more dictated by fewer SNPs.

Some questions asked to Dr. Huson:

What do cattle breeders breed for?

There is usually one test that gives results for lots of different diseases. However, tests for some traits, like A2 and poldness, would still be beneficial for farmers.

How often do farmers do *whole genome* testing?

It often depends on the size of the farm and the value of the cattle.

Dr. Huson listed some proteins to look further into..

- Beta - Casein (A/B)
- Beta - Lactoglobulin
- Beta - Casein A2
- Alpha S1 Casein
- Kappa Casein I
- Kappa Casein II

Main Takeaways:

-An ideal audience for this team's type of genetic testing would be small-scale farmers with stock of <300 animals.

-Instead of genetic diseases with multitudes of SNPs, it may be more ideal to test for traits desirable by breeders and dictated by fewer SNPs (such as milk proteins or coat color).