Development of Genomic Tools for the Bison Industry

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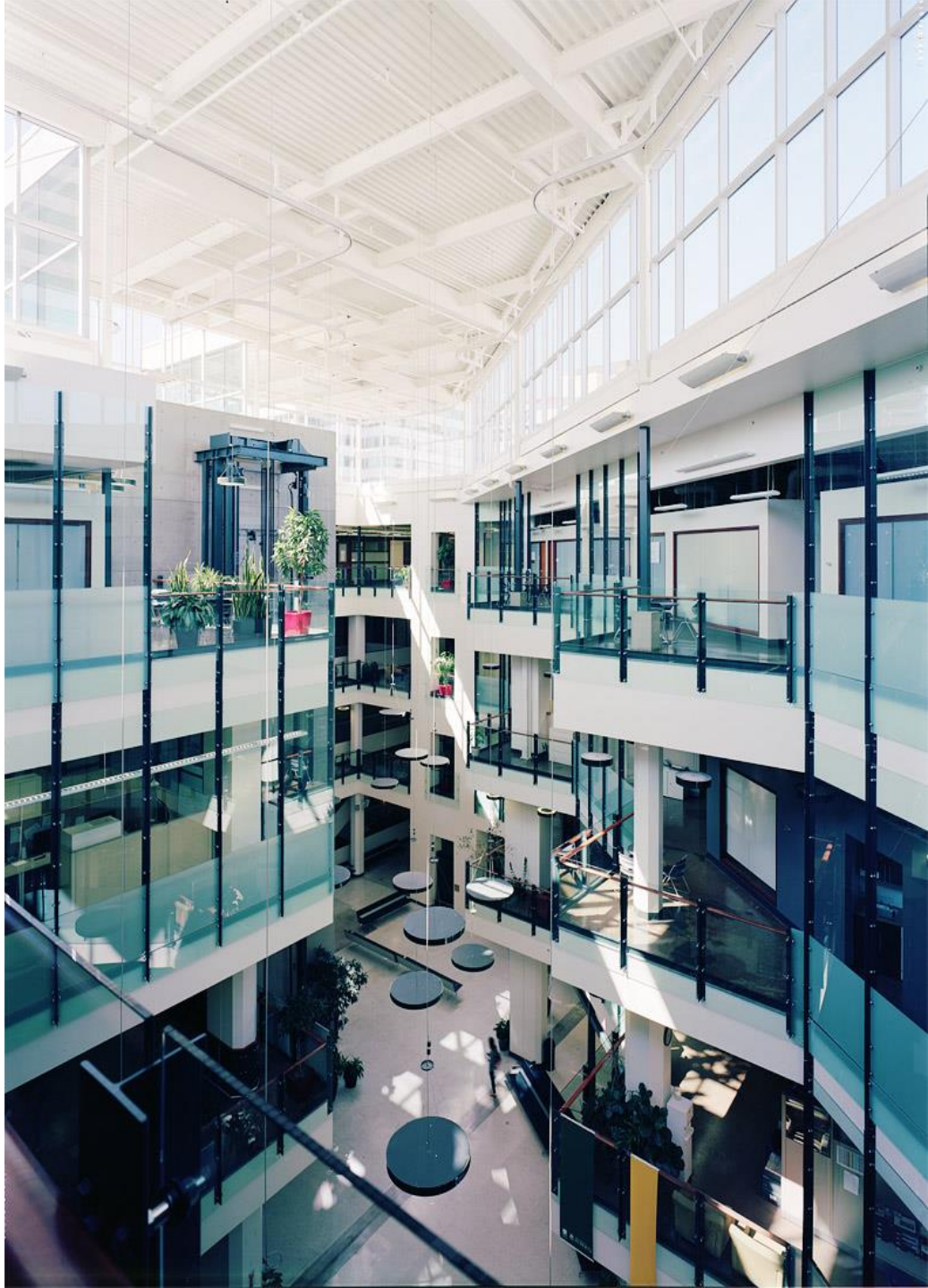
Chief Executive Officer

CBA Annual Convention 2018
November 18, 2018



Delta Genomics

- Incorporated in 2012 as a Not-for-Profit Organization
- Spun-out of the University of Alberta on April 1, 2014
- 9 Current Employees
- Processes approx. 50,000 samples per year (primarily beef cattle)

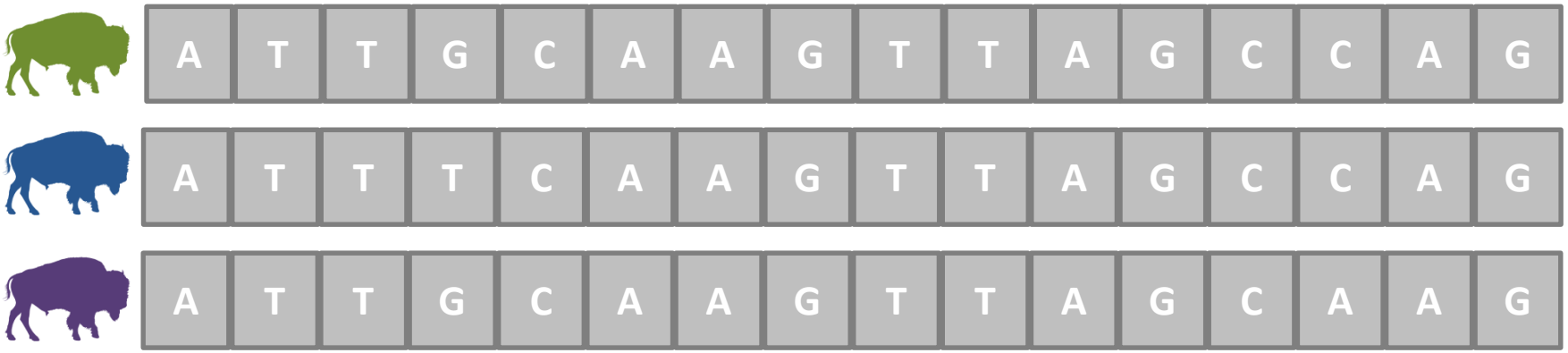
The Goal of Delta Genomics

To increase the **profitability**, **competitiveness**, and **sustainability** of the Canadian Livestock Industry

Introduction to DNA

- Made up of units called Base Pairs
- Four types of Base Pairs
  - A, T, G, C
- Mammals have around 3 billion Base Pairs

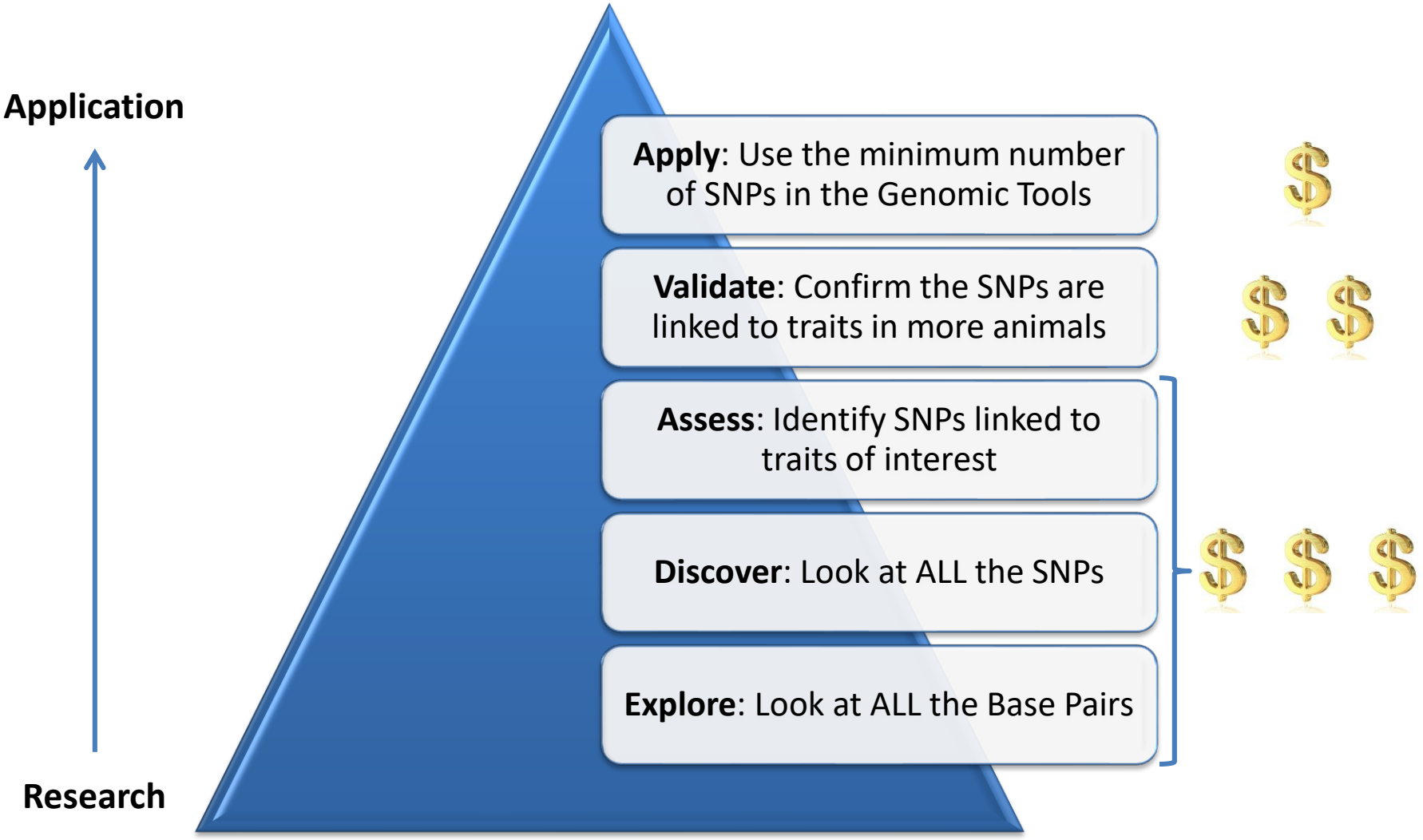
SNPs = Small Nucleotide Polymorphisms
(small changes in the DNA)



SNPs show us the differences in the DNA

Through research we can link SNPs to traits and features we want

The Process: Research to Application



The CBA's Genomics Project

- ✓ Whole Genome Sequencing of 27 bison
- ✓ Share Whole Genome Sequence Data with Dr. James Derr's group at Texas A&M
- 3 Discovery of SNPs for Parentage Verification, Wood-Plains Sub-species composition, and Cattle Introgression
- 4 Validation Genotyping of 480 bison where we already know the answer
- 5 Final edits and launch of the Genomic Tools

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The CBA's Genomics Project

This project is not possible without funding from:

Alberta Agriculture and Forestry

CGEn
Canada's Genomics Enterprise

Agriculture and Agri-Food Canada

Mitacs Accelerate

1. Whole Genome Sequencing

- Look at ALL approximately 3 billion base pairs in 27 bison

- Bison that were Sequenced:
  - 5 Wood bison from before 1925
  - 3 Wood bison from 2018
  - 8 Plains bison from before 1925
  - 10 Plains bison from five geographical regions (and some with known cattle introgression)

1. Whole Genome Sequencing – a tangent

- CanSeq150 is an initiative to sequence 150 of Canada's most iconic species
- Wood Bison male from Elk Island National Park has been included

Why we're sequencing the genomes of Canada's iconic species

By sequencing the genomes of other species, we can better understand our place in natural history.

theconversation.com

CGEn
Canada's Genomics Enterprise

2. Sharing Whole Genome Sequence Data

- We shared the raw data from the 27 animals we sequenced with Dr. Derr's group at Texas A&M

- In return, we received:
  1. 14 Whole Genome Sequences from Plains bison

     (from Elk Island National Park, Caprock Canyons State Park, and Yellowstone National Park)
  2. 87 SNP genotypes (50,000 SNPs each) from Plains bison

3. SNP Discovery & Link to Traits

- Using the sequence data from 41 bison we will identify all the SNPs (ie: the differences between these animals)
- From all those SNPs, we will select the SNPs that work best for:

1. Parentage Verification
2. Woods vs Plains sub-species composition
3. Cattle Introgression

4. Validation Genotyping

- We will create a SNP genotyping assay based on the SNP lists from Activity #3 and test 480 bison where we already know the answer
  - Answer may come from pedigree information or from previous testing
- **Purpose: to make sure the test works the way it's supposed to work**
- CBA member engagement: do you have animals that were previously tested?

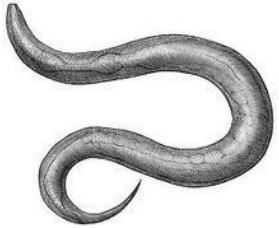
5. The Genomic Tools

Currently envisioning two genomic tools:

1. Parentage Verification Tool
   - Aiming for the $25 ballpark by end of 2019

2. Parentage, Sub-Species Composition, & Cattle Introgression Tool
   - Aiming for less than $100 (?) by Q2 2020

Genomics and Livestock



An Example: Genomics and Beef

Genomic testing started with **Parentage or Not?**

An Example: Genomics and Beef

Genomic testing progressed to simple questions: **Red or Black?**

An Example: Genomics and Beef

Horned or Polled?

An Example: Genomics and Beef

Genomics is now able to answer complex questions:

How do I select the best replacements?

Genomics and Beef: Two Roads

Genetic Predictions

- Predict the genetic merit of an animal for specific traits like marbling, calving ease, and feed intake
- Examples:
  - Genetic evaluations through IGS, AAA, ABRI, etc.
  - Igenity Profiles, GeneMax
  - Leachman Indexes

Genetic Measurements

- Measure and quantify the differences between animals relative to the trait you're interested in
- Examples:
  - Parentage
  - Genetic conditions
  - EnVigour HX™

Genomic Evaluations in Livestock

EPDs + Genomics = Genomically-Enhanced EPDs (gEPDs)

- Genomics increases the accuracy of EPDs earlier in the animal's life so better breeding decisions that align with your goals can be made sooner

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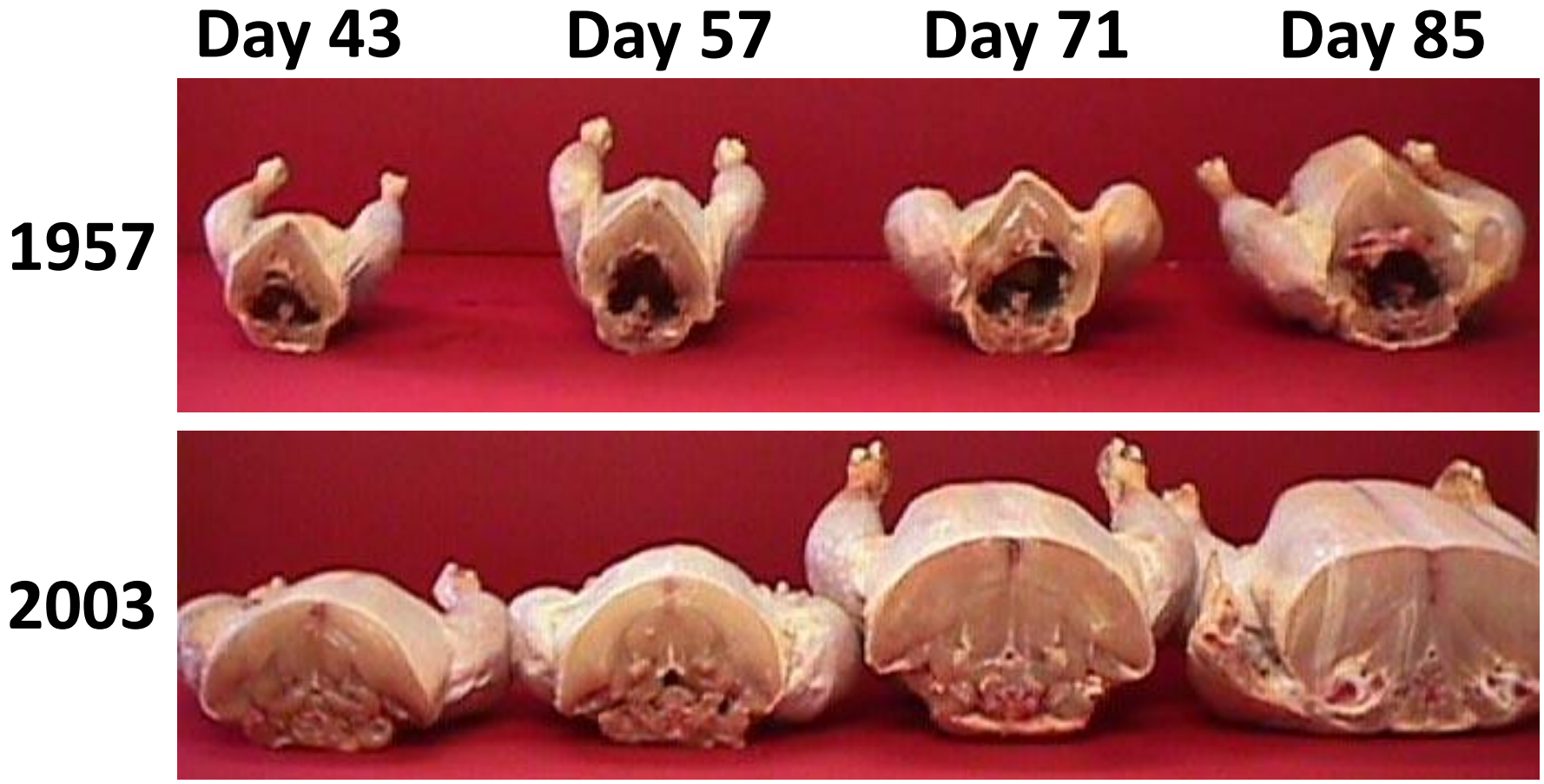
EnVigour HX™

A Made in Canada Genomic Tool for Crossbred Cattle

Does Genomics Work?



(Havenstein *et al.*, 2003)

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Does Genomics Work?

Past Success in feed efficiency (Plastow 2012)

1972

836 pounds

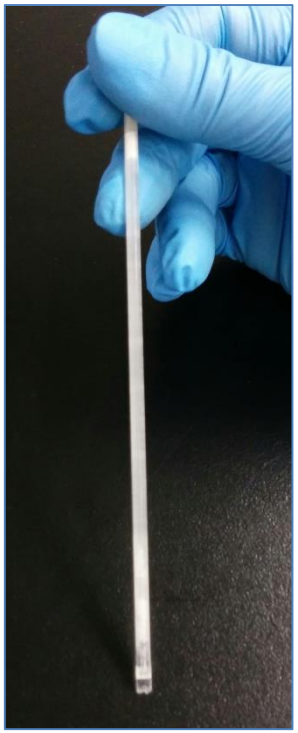
220 pounds

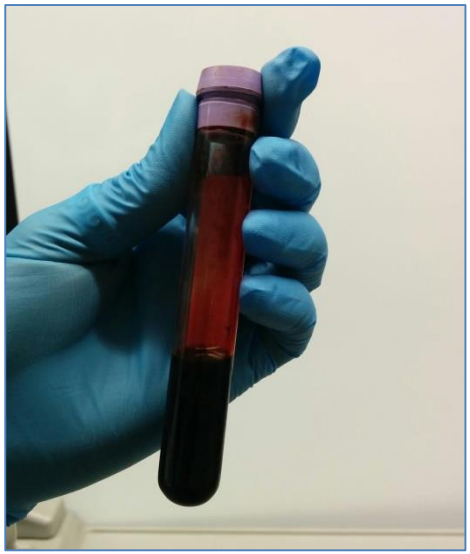
Interested in Genomics?

- What kind of samples can I send to the lab?
- How do I collect a good sample for the lab?
- What happens at a DNA testing lab?

Sample Types

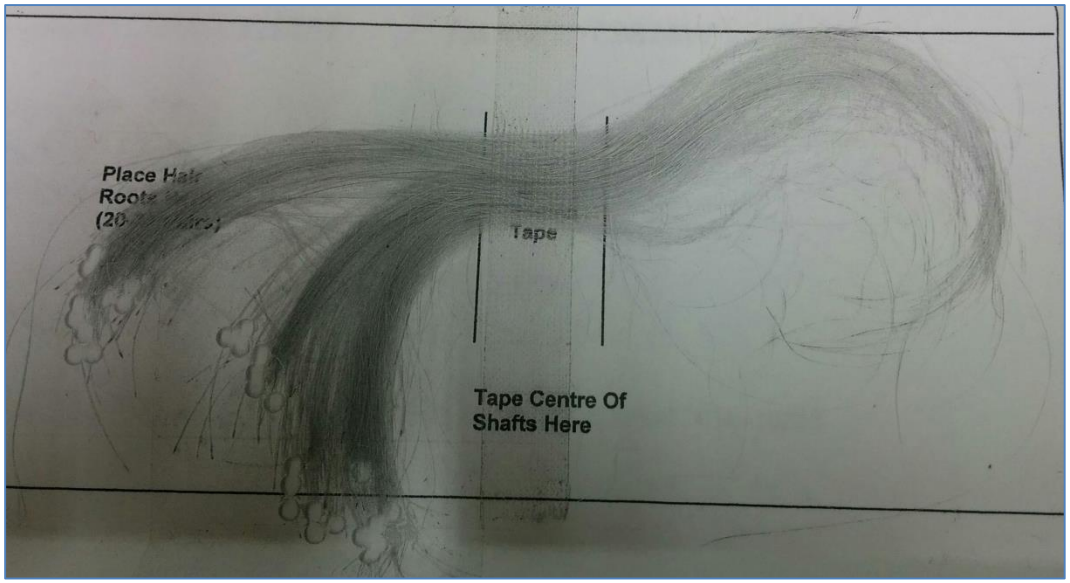
The Good





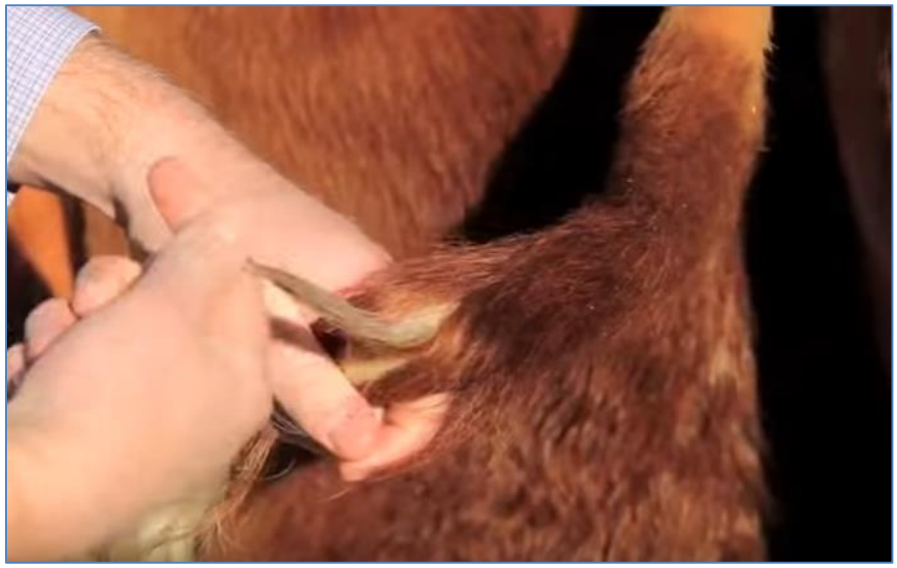
Sample Types

The Bad



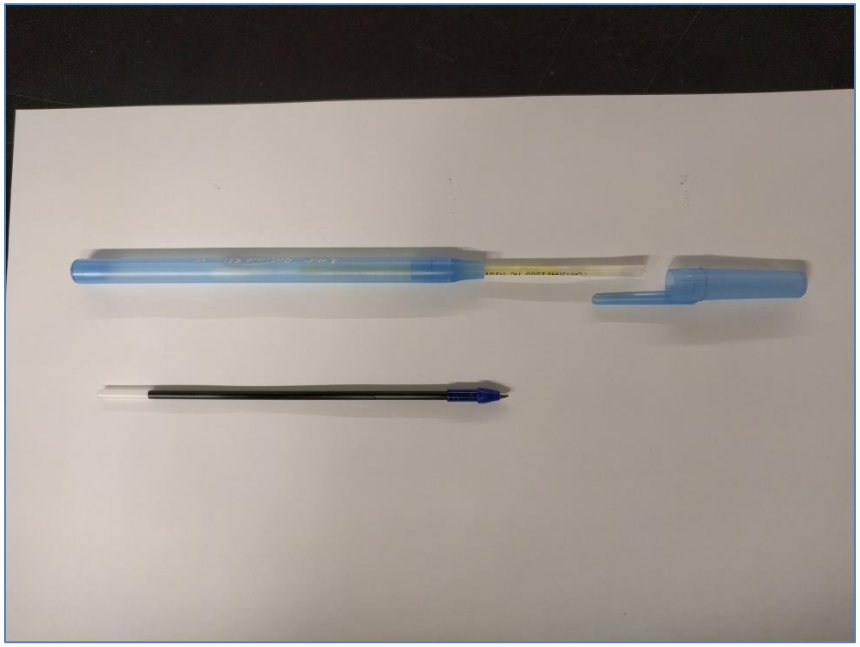
How to Take a Hair Sample

- From the ***Tail Switch***
- Wrap some hair around your finger
- Pull up towards to top of the tail
- 30-40 follicles



Plenty of really good YouTube videos

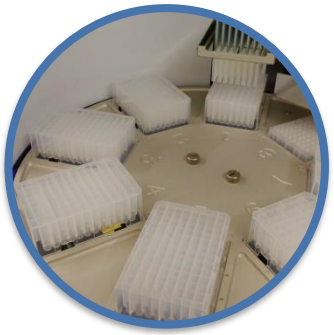
Getting Samples to the Lab



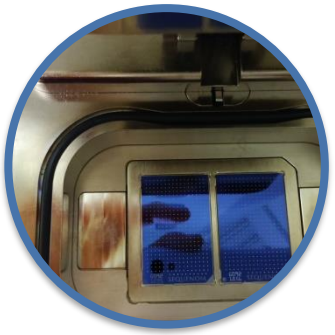
- Regular mail or courier if you're in a hurry
- Blood vials and raw tissue needs to be kept cold and shipped fast
- Semen straws need to be kept intact

The Laboratory Process

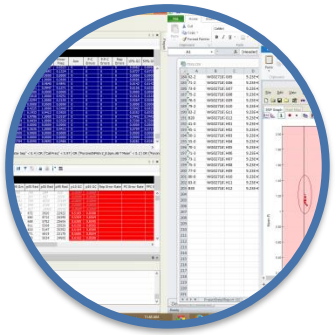
Sample Inventory



DNA Extraction



Testing



Data Analysis

10 days to 25 days

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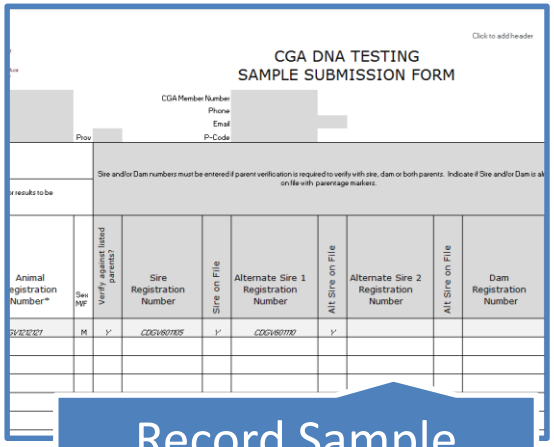
1. Sample Inventory

1-2 Days



CGA DNA TESTING
SAMPLE SUBMISSION FORM

CGA Member Number
Phone
Email
P-Code

Sire and/or Dam numbers must be entered if parent verification is required to verify with sire, dam or both parents. Indicate if Sire and/or Dam is al on file with parentage markers.

Animal Registration Number*	Sex M/F	Verify against listed parents?	Sire Registration Number	Sire on File	Alternate Sire 1 Registration Number	Alt Sire on File	Alternate Sire 2 Registration Number	Alt Sire on File	Dam Registration Number
GV1212121	M	Y	CDGV807805	Y	CDGV807770	Y			

Record Sample Information

Store Original Samples

Store Extracted DNA

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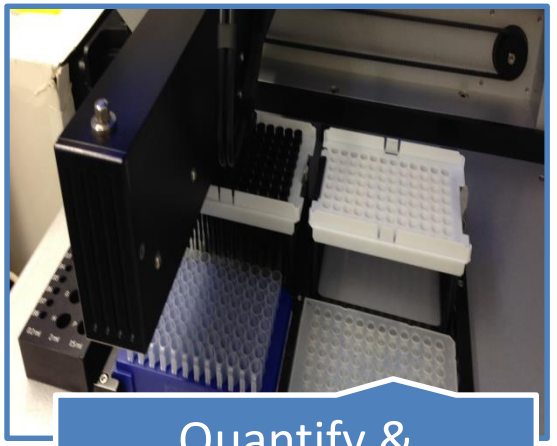
2. DNA Extraction

2-3 Days

Cut & Clean

Digest & Extract

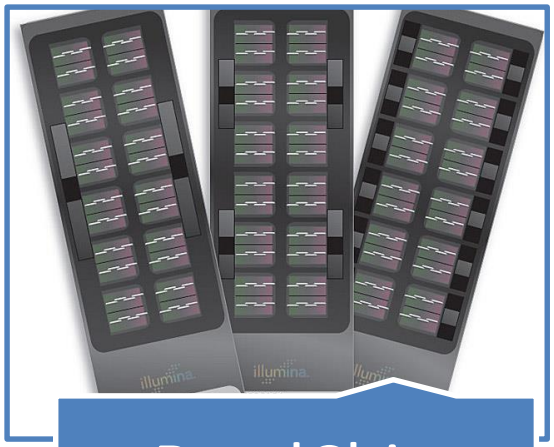


Quantify & Normalize

3. SNP Genotyping

3 Days

96 Animals



BeadChip

Chip Scanning

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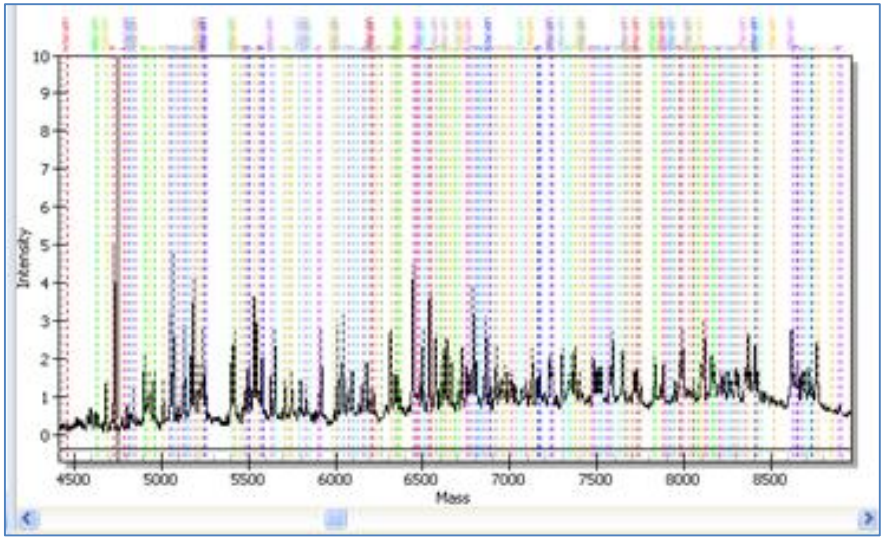
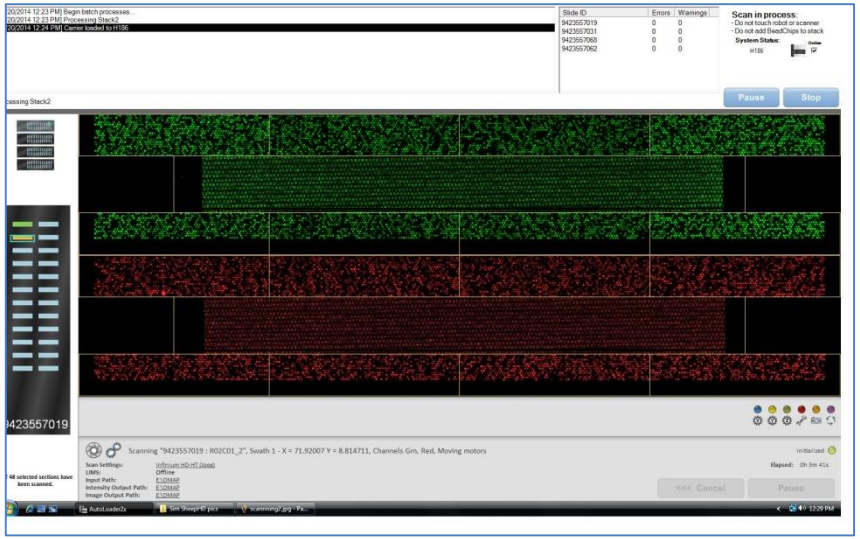
4. Data Analysis: Part 1

1-2 Days





SNPs

A	T	T	G	C	A	A	G	T	T	A	G	C	C	A	G

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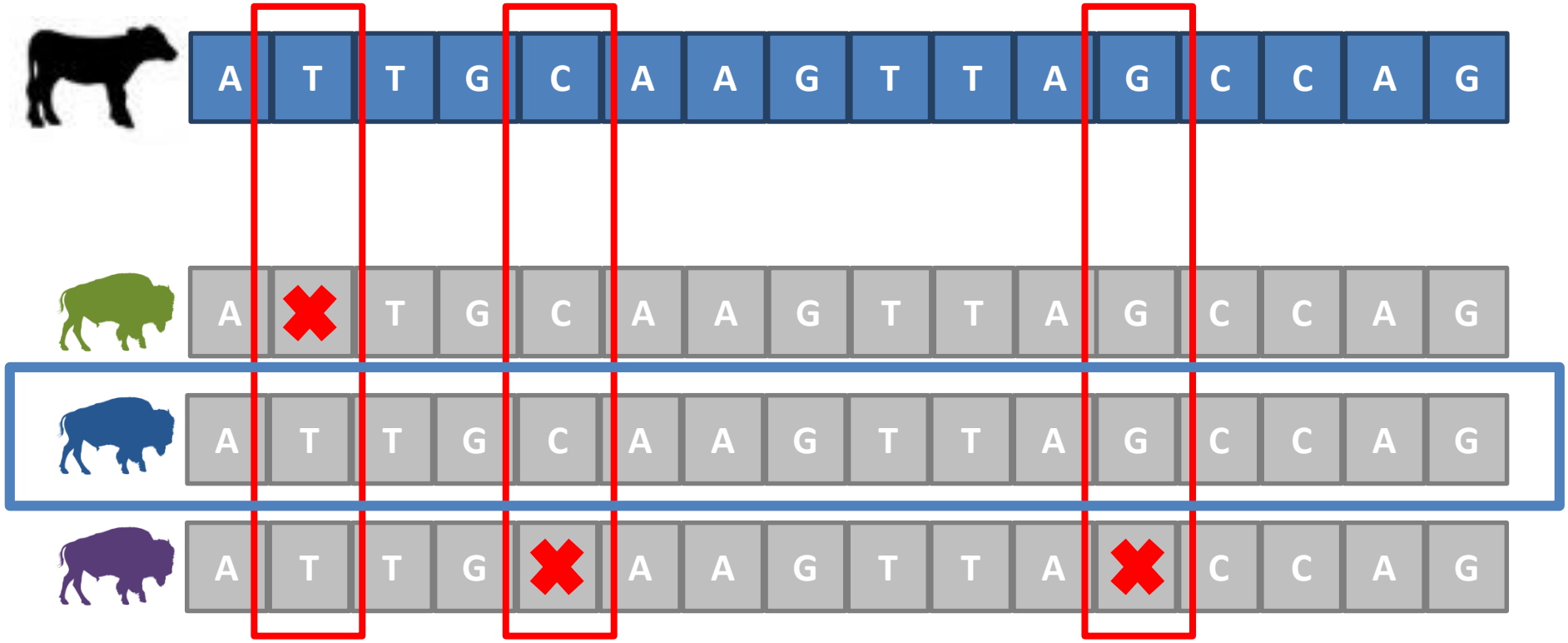
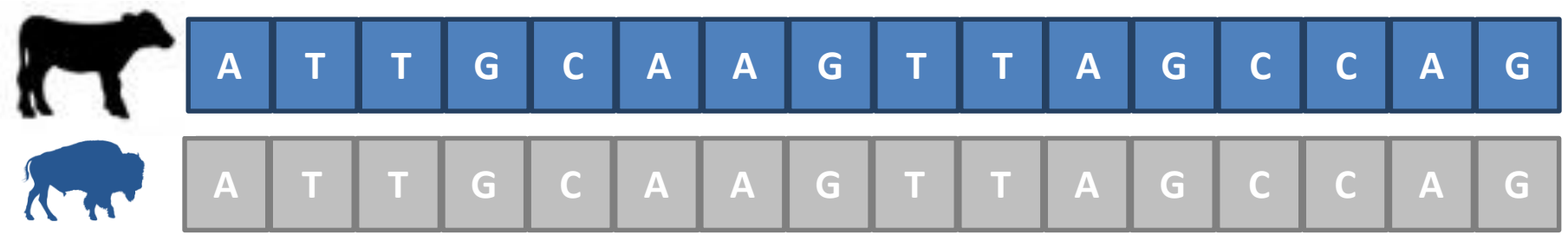
4. Data Analysis: Part 2

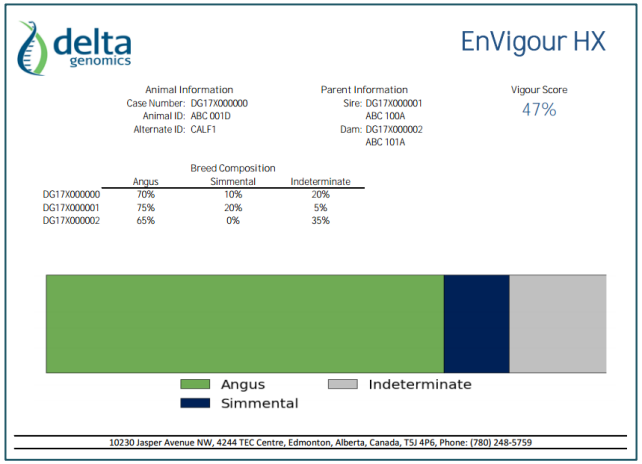
1-2 Days



4a. Results Reporting

1-2 Days





Research Team

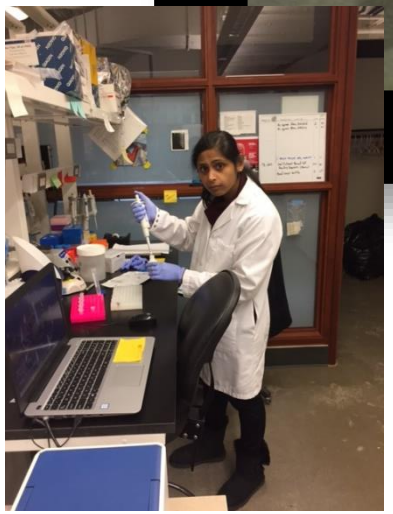
Dr. John Crowley

Dr. Paul Stothard

Dr. James Derr

Dr. Tianfu Yang*

Thank-you!



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~~Micro~~Satellites

Microsatellites

Microsatellites tell us how large these repeated regions are: Measure of **SIZE**