Genetic improvements of Hawaiian beef cattle using genomic approaches

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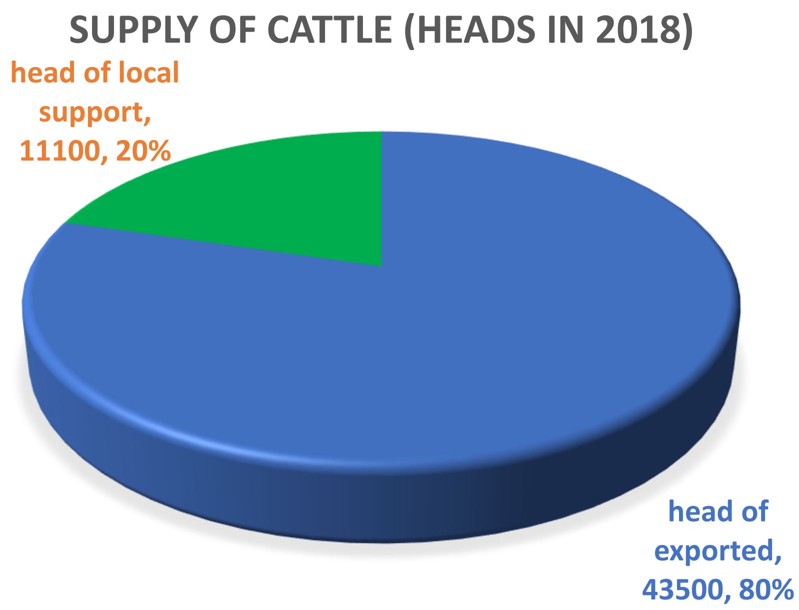
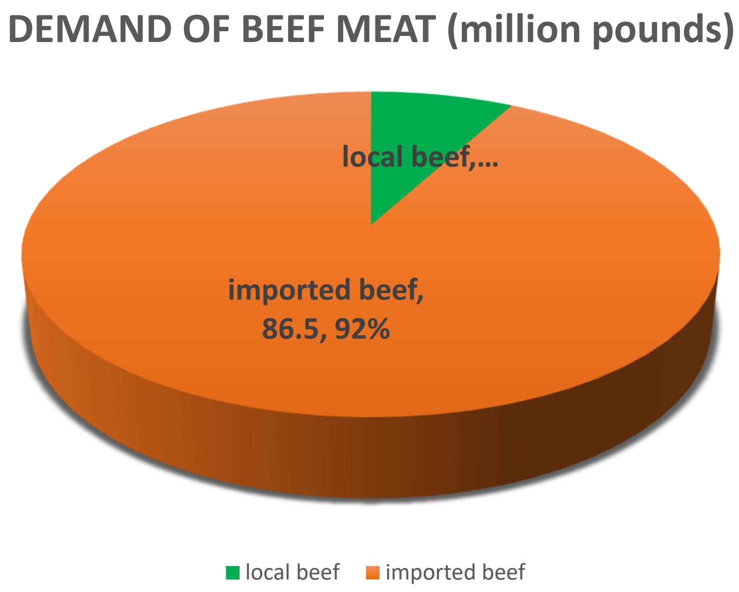
The current status of Hawaiian beef cattle





Data Source: UH CTAHR

Goals / Objectives

Potential opportunities to put efforts

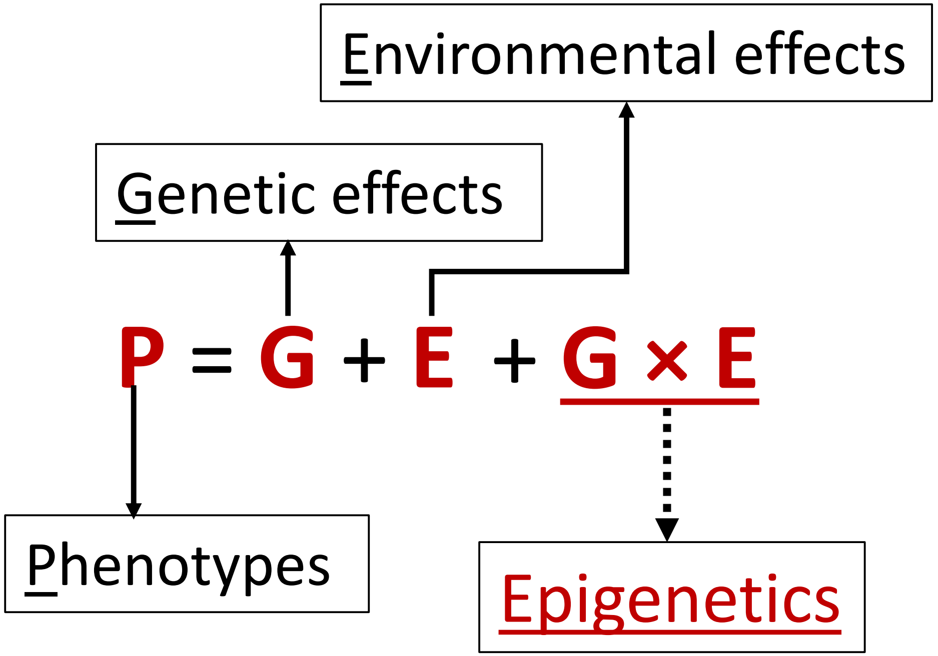
Tropical environment

Production and Reproduction

Meat quality

1) *Investigate the Geographic distribution of Hawaiian cattle*
2) *Investigate the genetic background of Hawaiian local beef cattle*
3) Screen the significant genetic and epigenetic marks associated with production and reproduction traits by using Genome-Wide Association Study (GWAS) and Next Generation Sequencing (NGS) approaches
4) Apply more accurate Genomic Selection (GS) in Hawaiian beef cattle populations to genetically improve their performance

The classical model in Genetics



Stage 1 $P = G + \boxed{E}$

Project 1:

Diverse Geographic Features of Hawaiian Ranches Affect Their Cattle Performance

Stage 2 $P = \boxed{G} + E$

Project 2:

An investigation of genetic background of Hawaii beef cattle

Stage 3 $\boxed{P = G} + E$

Project 3:

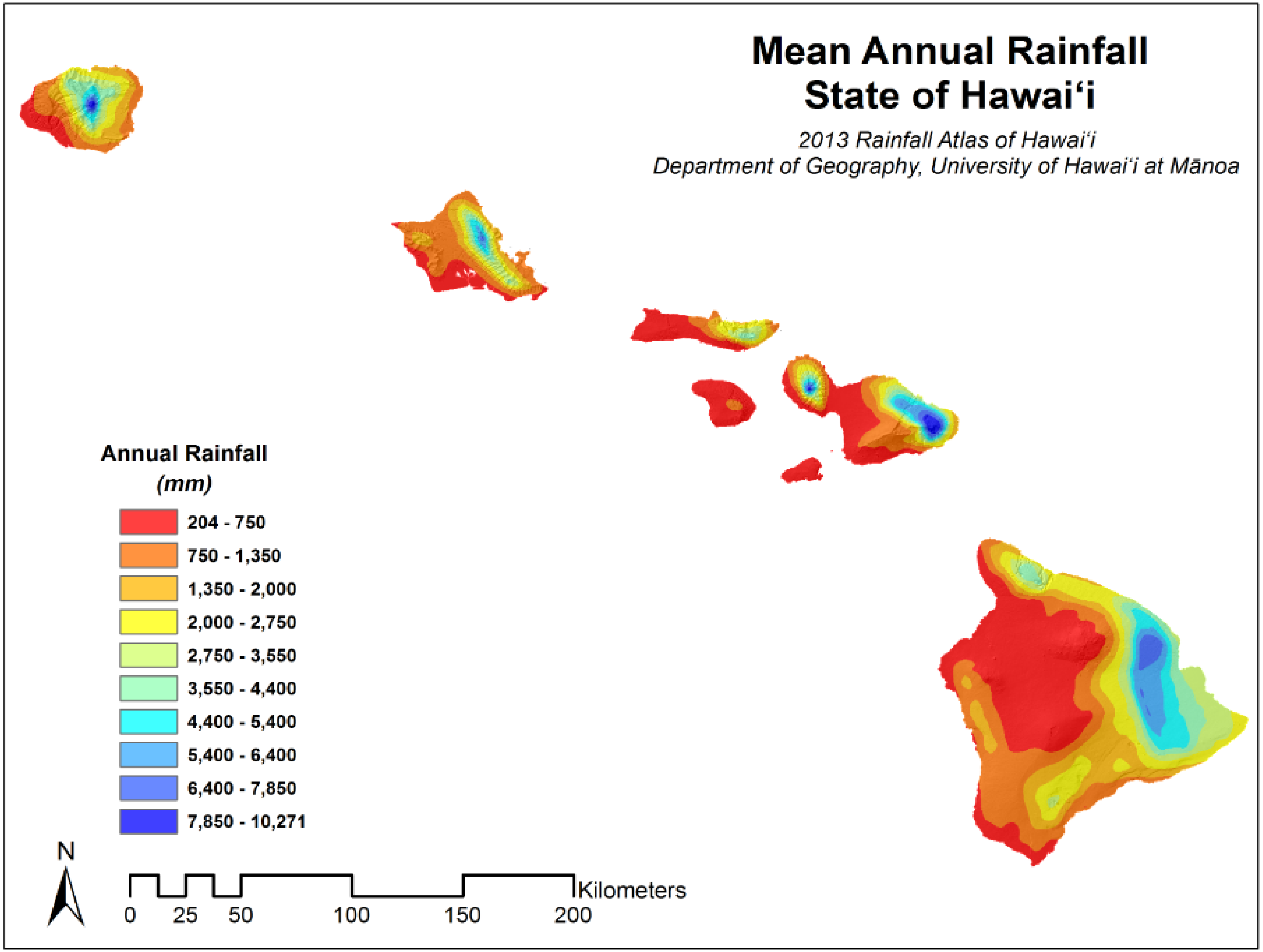
GWAS and GS in Hawaii beef population

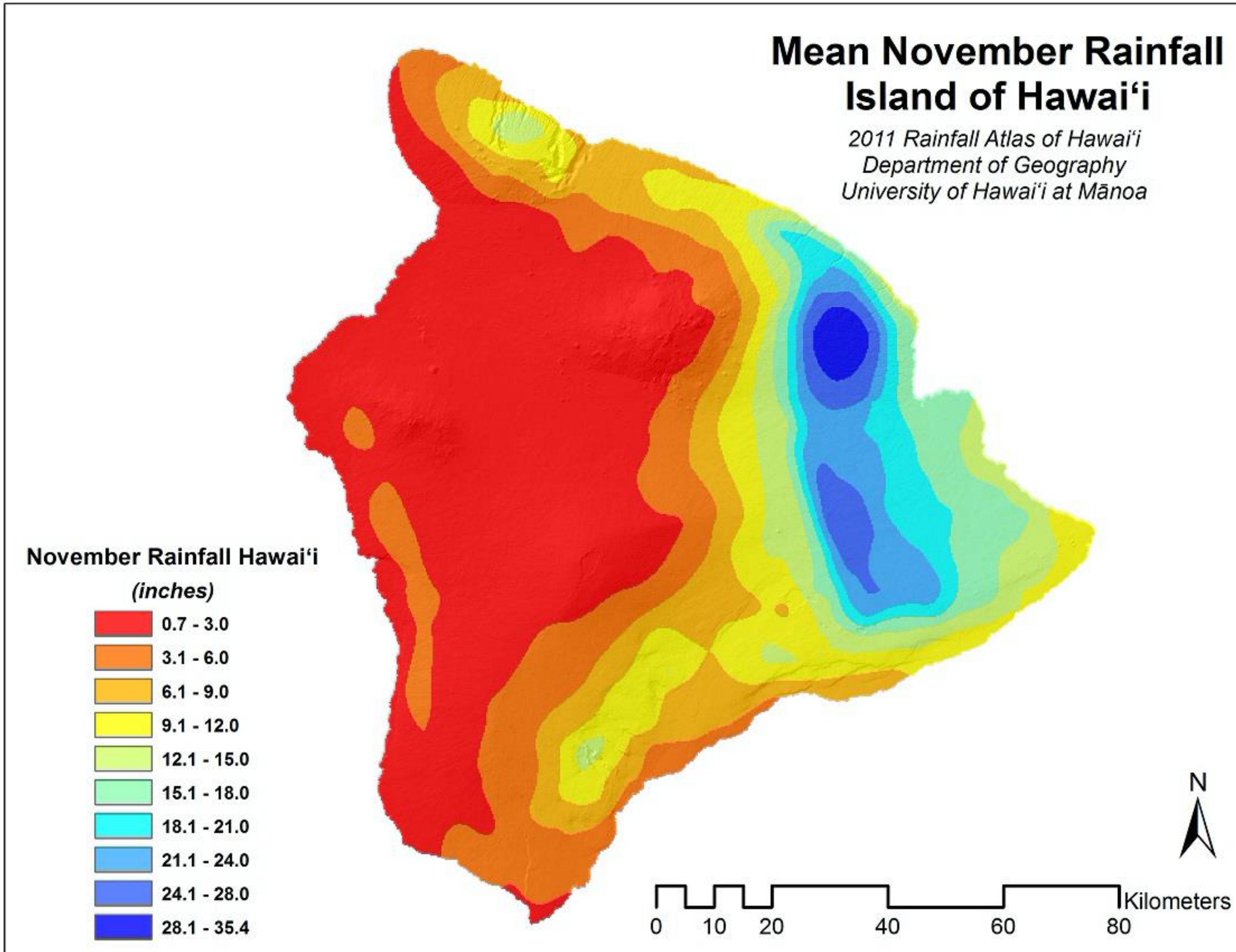
Stage 1

$$P = G + \boxed{E}$$

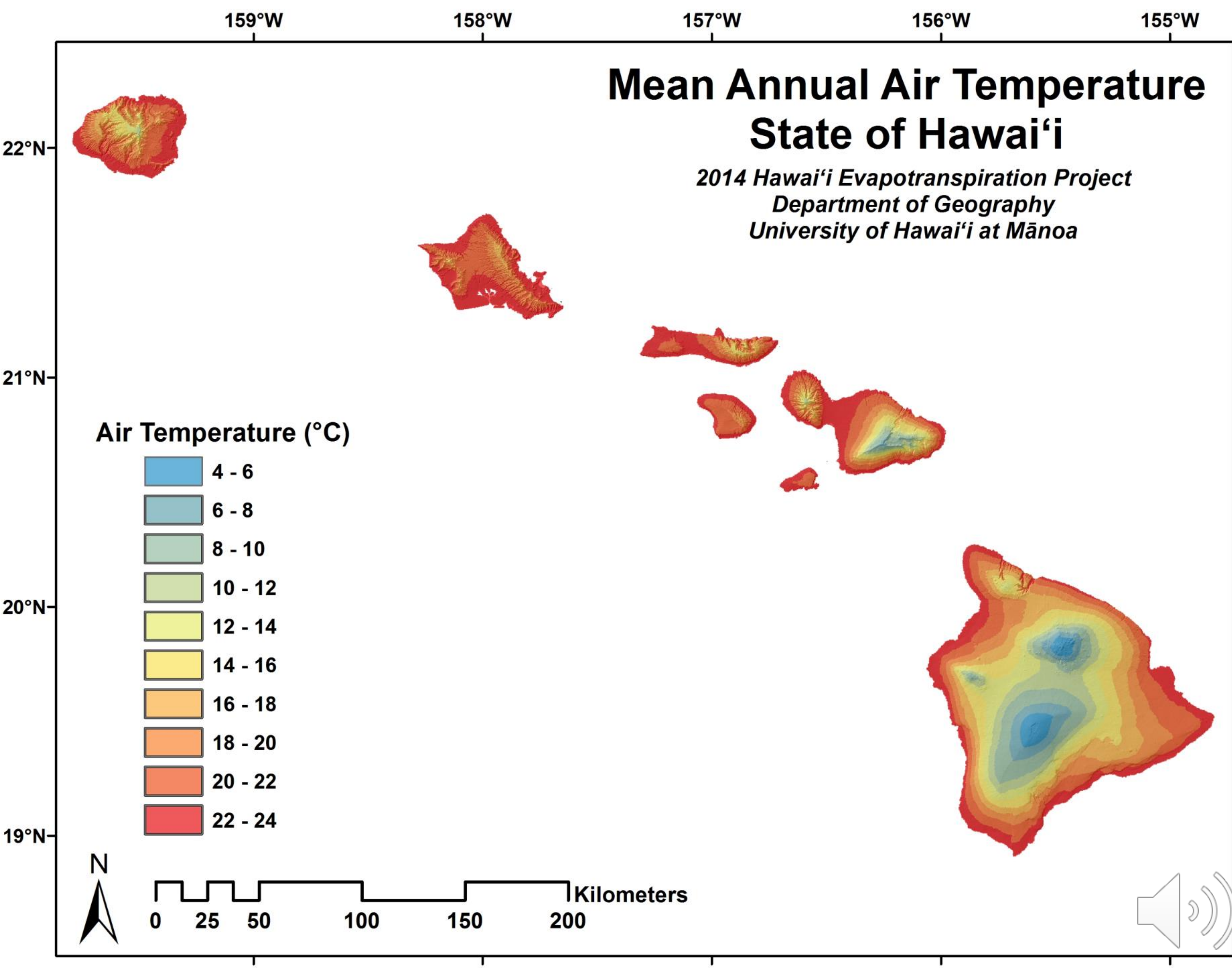
<u>Project 1:</u>
Diverse Geographic Features of Hawaiian Ranches Affect Their Cattle Performance

The Base Map of Hawai'i Rainfall

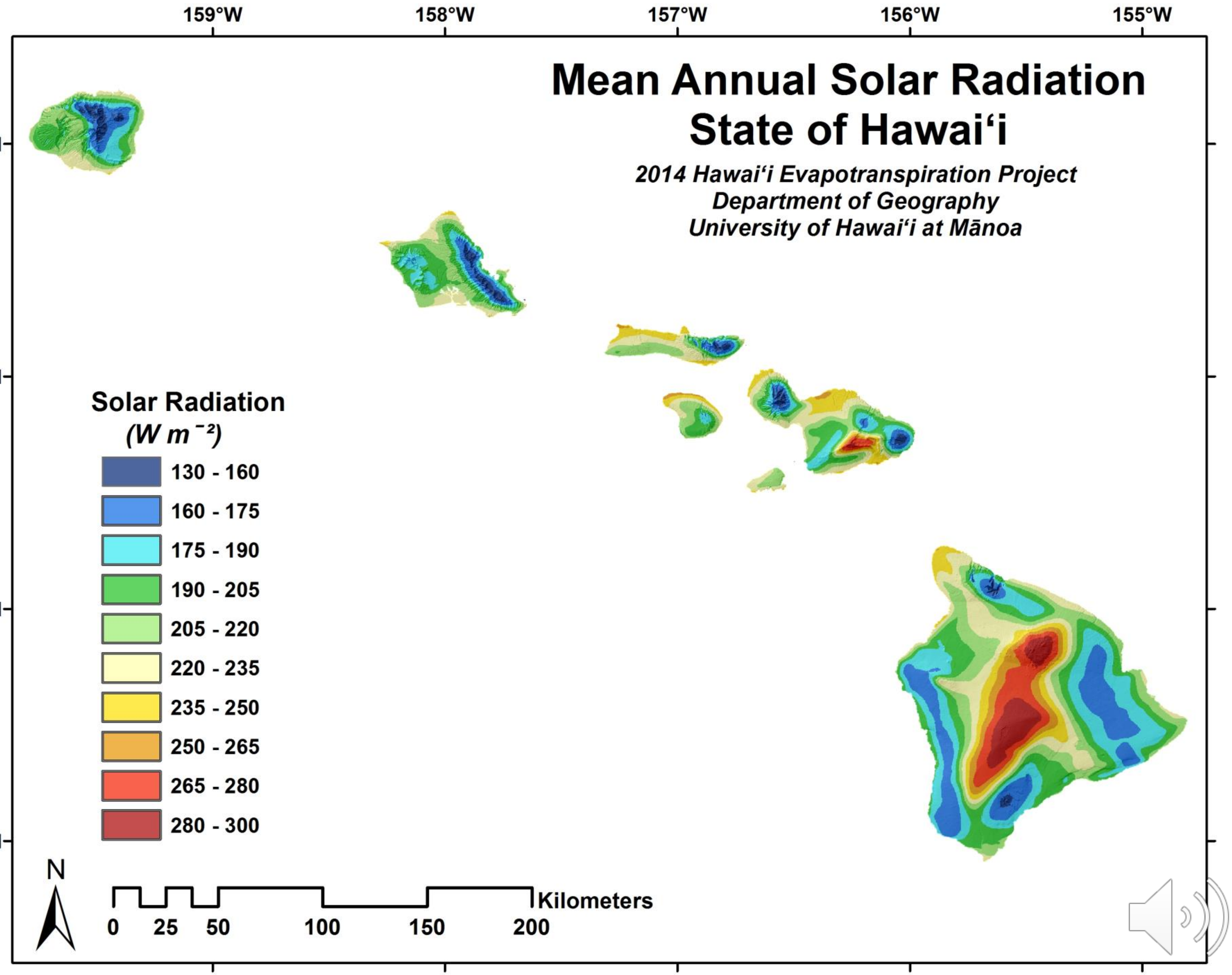




Mean November Rainfall
Island of Hawai‘i
2011 Rainfall Atlas of Hawai‘i
Department of Geography
University of Hawai‘i at Mānoa
November Rainfall Hawai‘i
(inches)
0.7 - 3.0
3.1 - 6.0
6.1 - 9.0
9.1 - 12.0
12.1 - 15.0
15.1 - 18.0
18.1 - 21.0
21.1 - 24.0
24.1 - 28.0
28.1 - 35.4
N
0
10
20
40
60
80
Kilometers

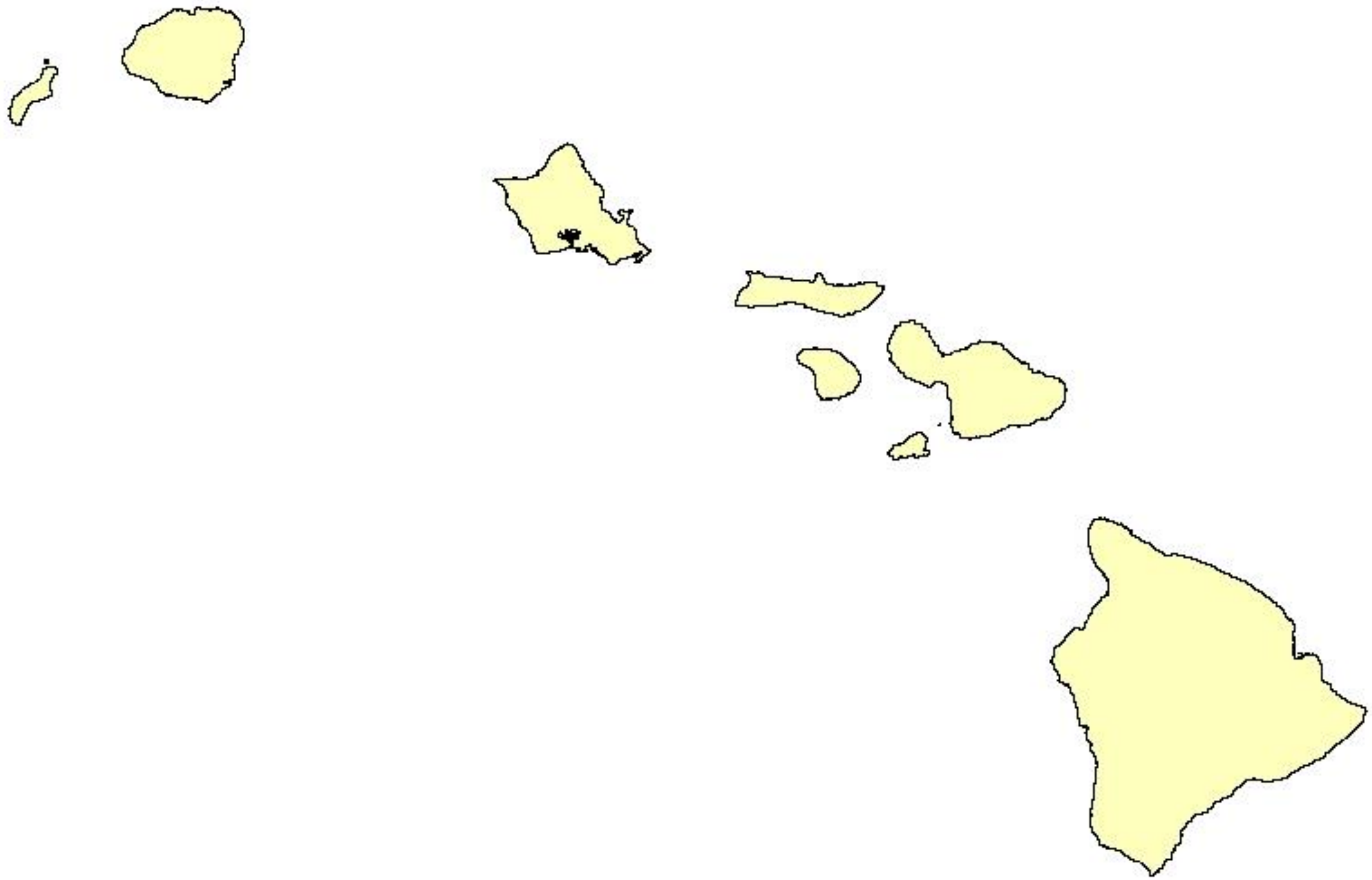


Mean Annual Air Temperature
State of Hawai‘i
2014 Hawai‘i Evapotranspiration Project
Department of Geography
University of Hawai‘i at Mānoa
159°W
158°W
157°W
156°W
155°W
22°N
21°N
20°N
19°N
Air Temperature (°C)
4 - 6
6 - 8
8 - 10
10 - 12
12 - 14
14 - 16
16 - 18
18 - 20
20 - 22
22 - 24
N
0
25
50
100
150
200
Kilometers



Mean Annual Solar Radiation
State of Hawai‘i
2014 Hawai‘i Evapotranspiration Project
Department of Geography
University of Hawai‘i at Mānoa
159°W
158°W
157°W
156°W
155°W
22°N
21°N
20°N
19°N
Solar Radiation
(W m⁻²)
130 - 160
160 - 175
175 - 190
190 - 205
205 - 220
220 - 235
235 - 250
250 - 265
265 - 280
280 - 300
N
0
25
50
100
150
200
Kilometers

Coastlines

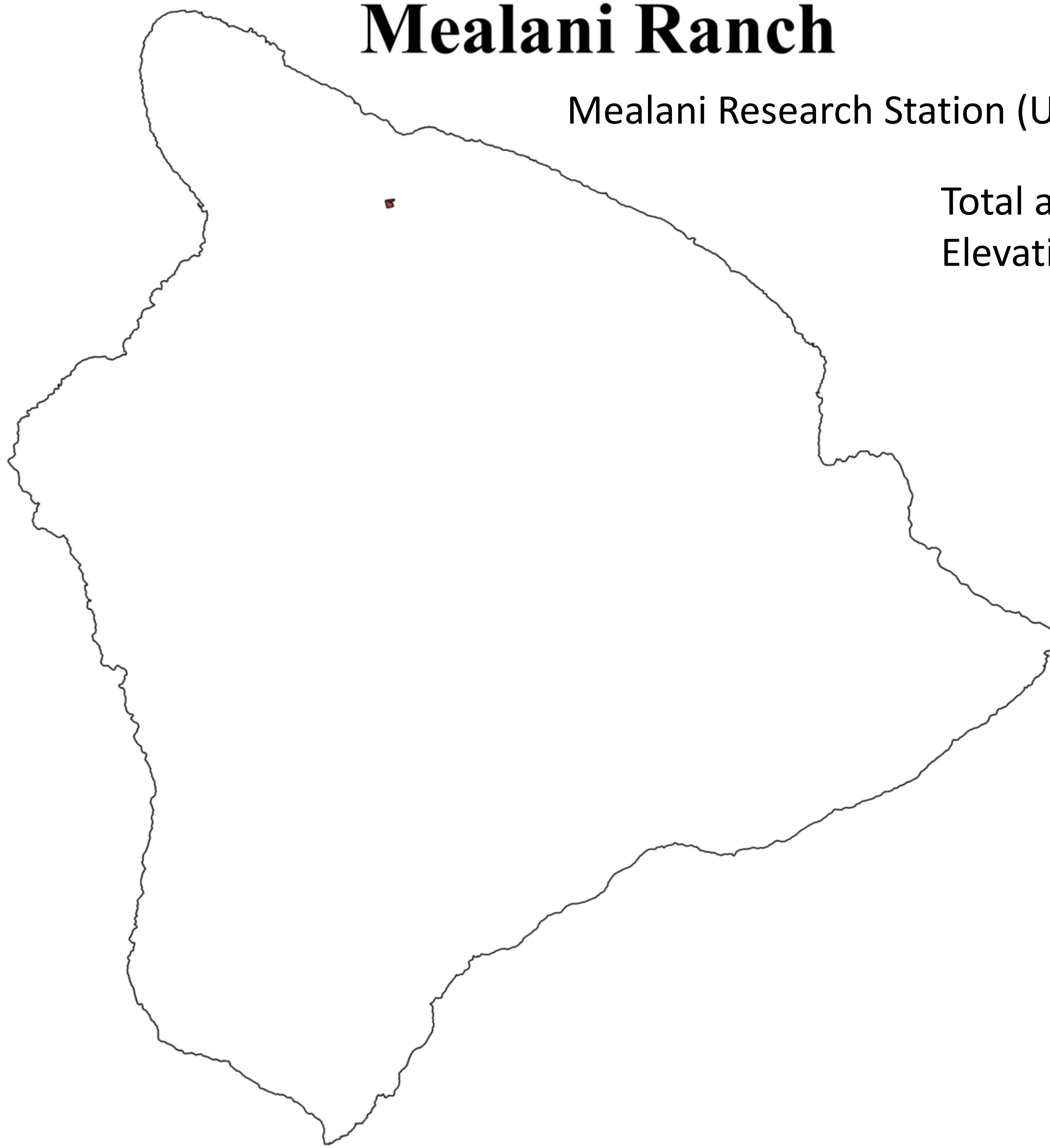


Main Hawaiian Islands

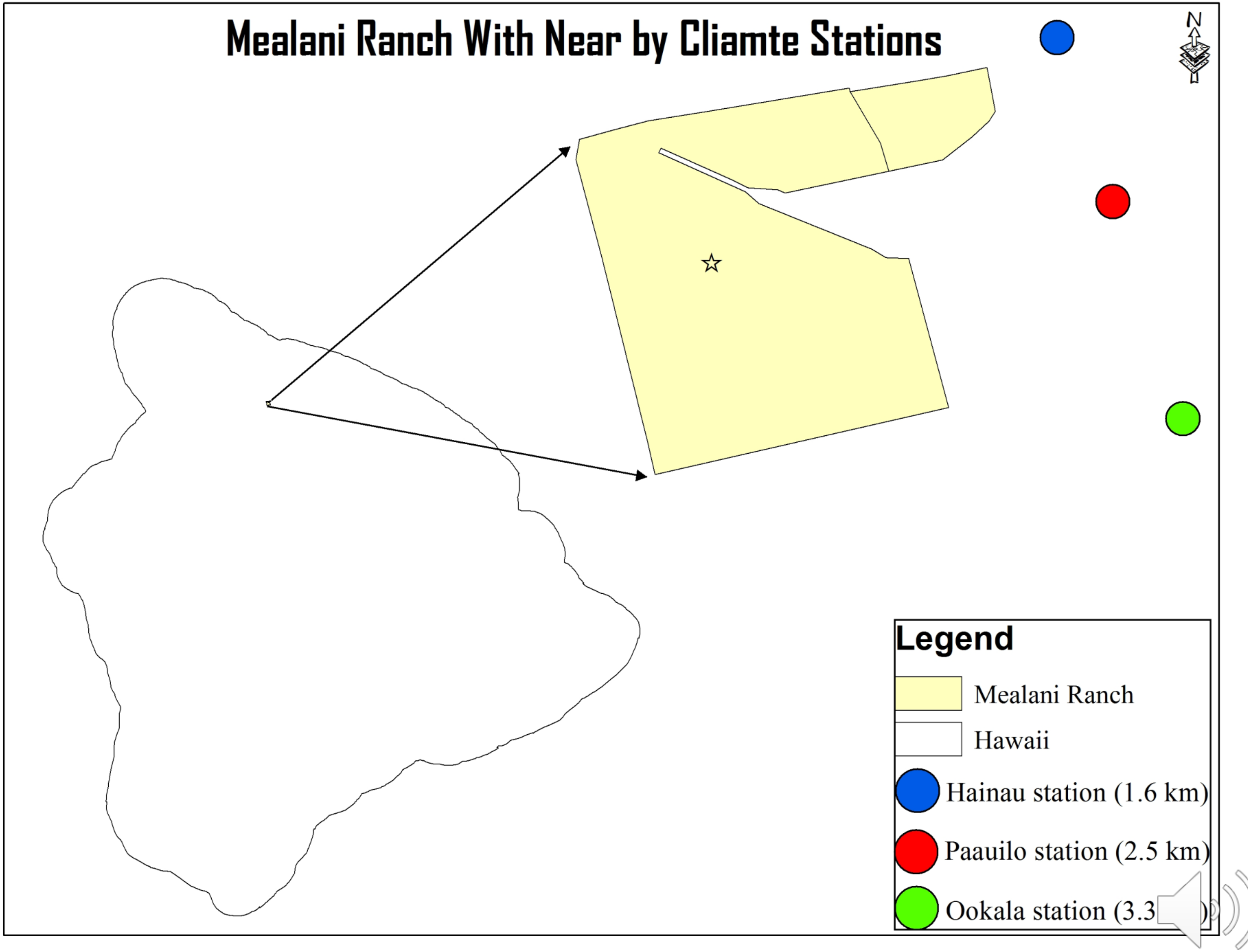
State of Hawaii, Office of Planning
November, 2000

Mealani Ranch

Mealani Research Station (UH), Hawaii County

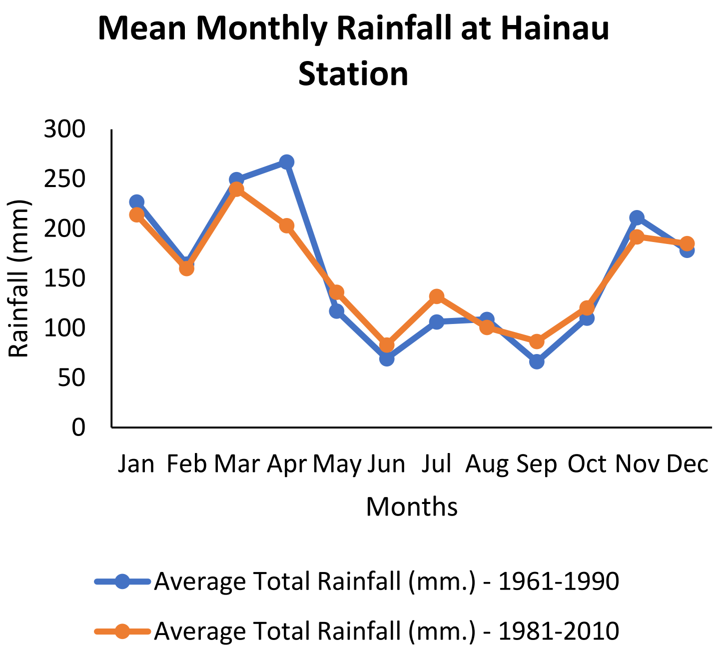


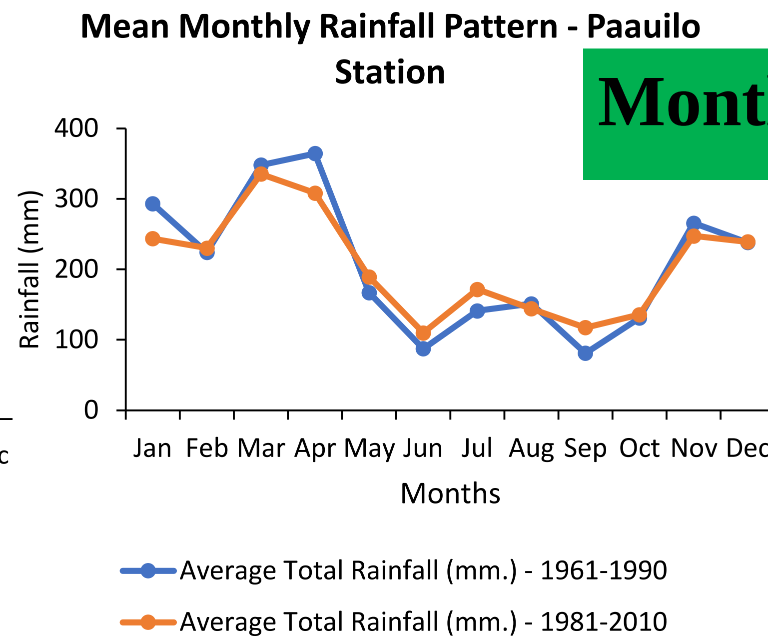
Total acres: 196
Elevation (ft): 2,800

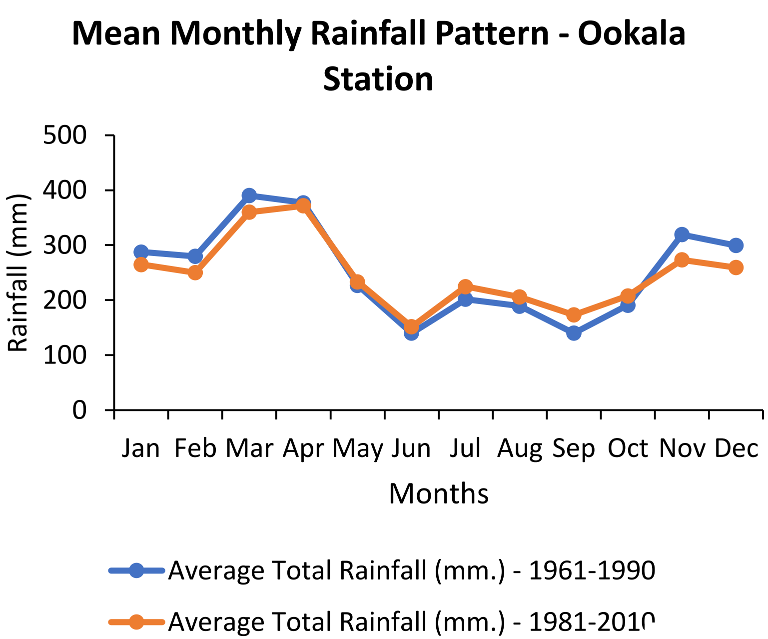


Data Source : Western Region Climate Center

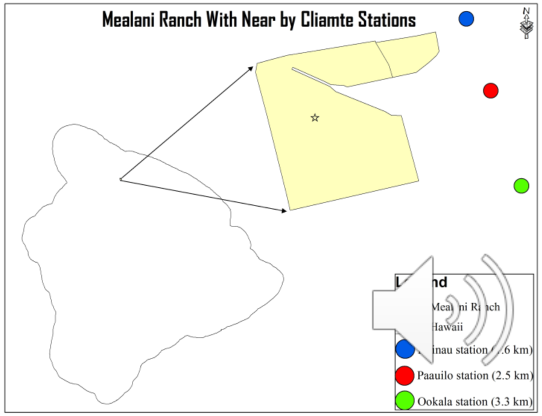
Monthly Rainfall





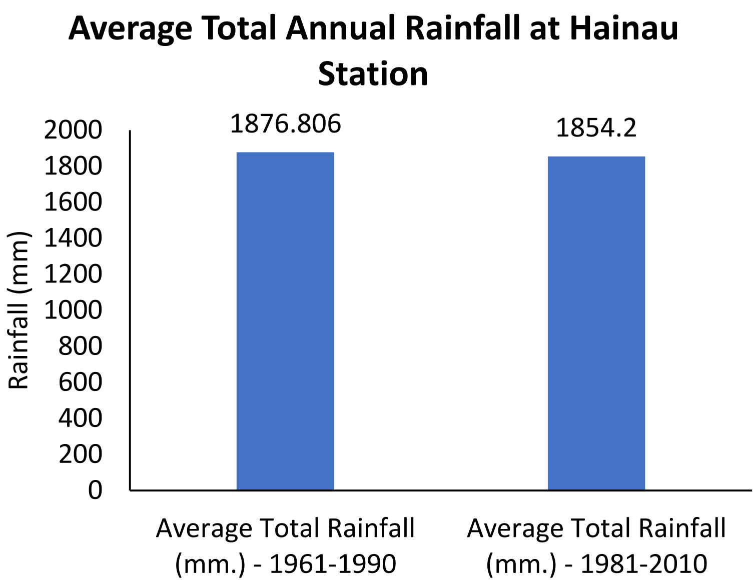


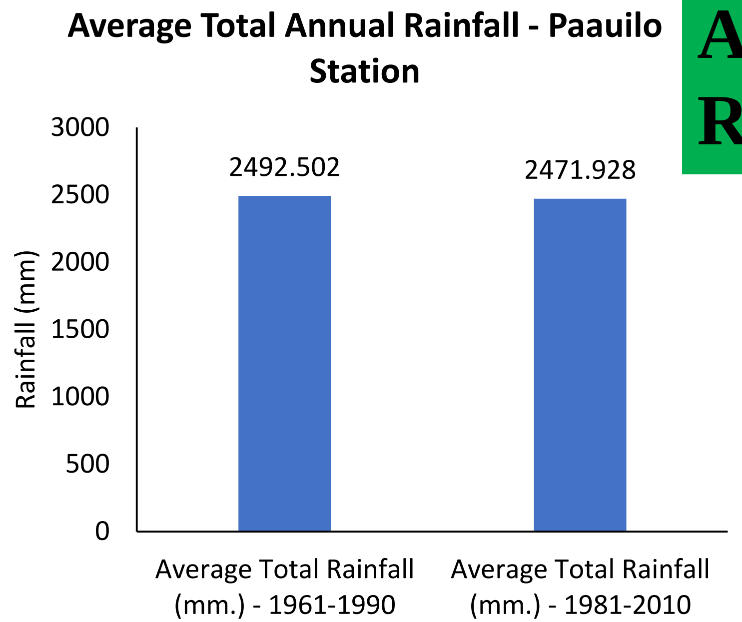
- June and September are driest months; Winter season from November until April is wet
- Ookala station received higher rainfall amount in general

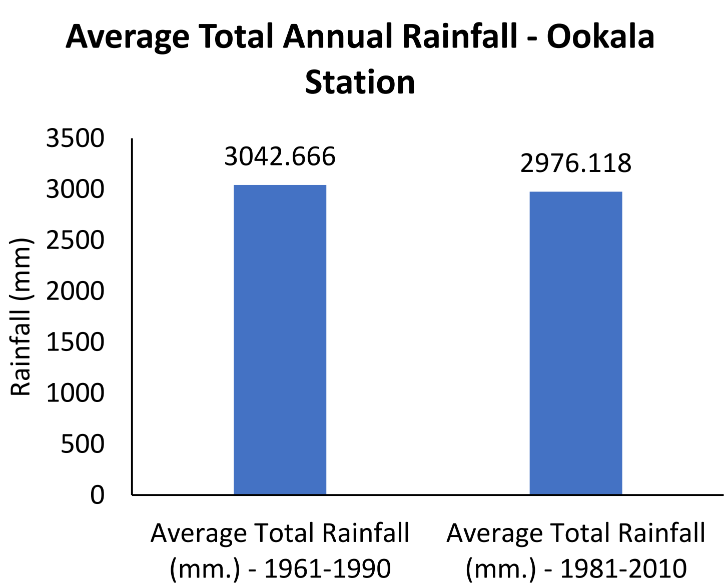


Data Source : Western Region Climate Center

Annual Rainfall

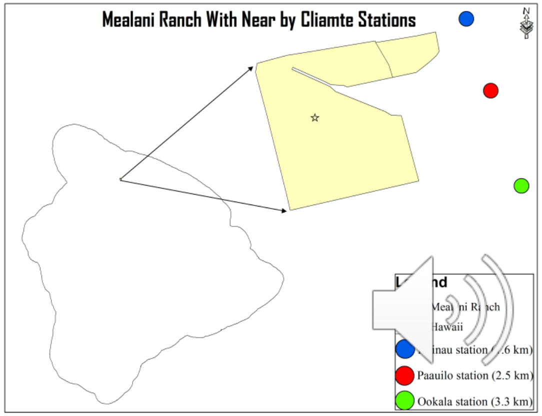




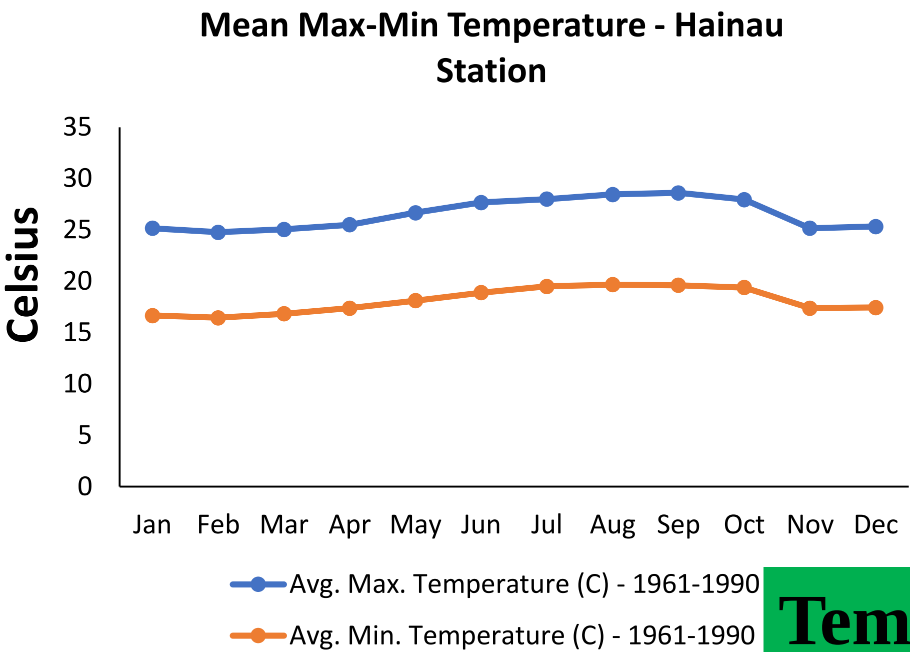


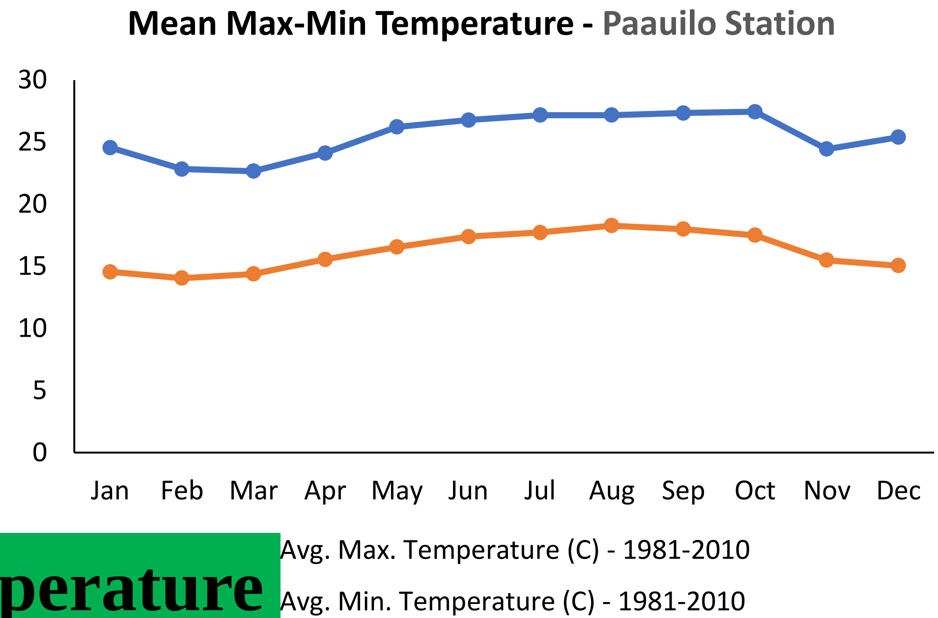
PAAUILO 221, HAWAII B5:N5

- There was no change for the rainfall at the same station in the past 50 years (1961-2010)
- Rainfall amount: Ookala > Paauilo > Hainau

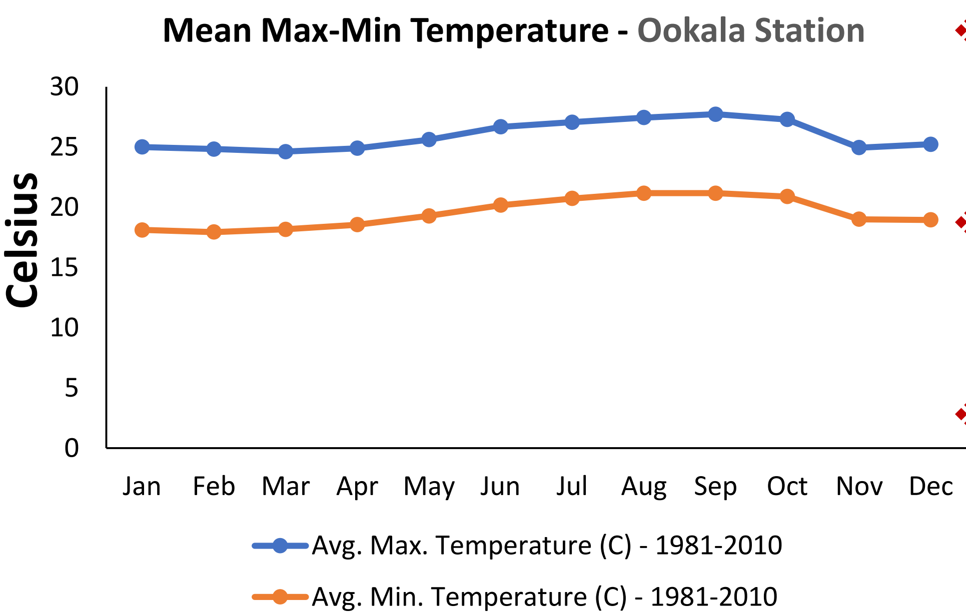


Data Source : Western Region Climate Center





Temperature



- August and September are hottest months (28-29C); February and March are coldest months (14-16C)
- There was no big change for the temperature at the same station in the past 50 years (1961-2010)
- Only available data at the Ookala Station shows that the minimum temperature was increased ~ 0.5C

Data Source : Western Region Climate Center

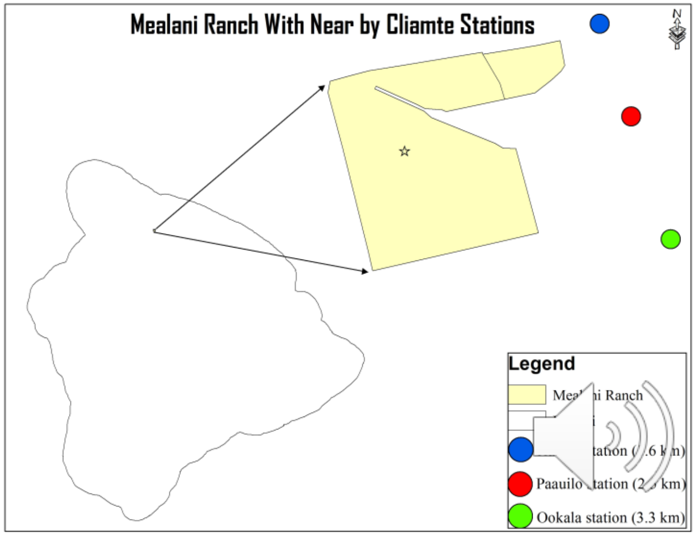
Summary – Mealani Ranch Rainfall and Temperature

Rainfall

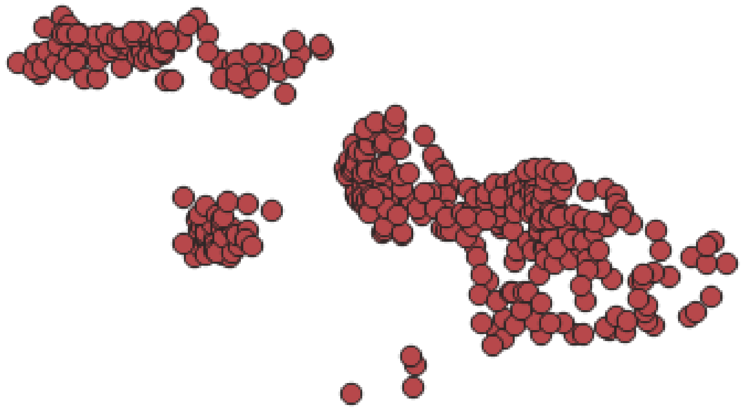
- June and September: driest months
- November-April: wettest months
- No change at the same station in the past 50 years (1961-2010)
- Rainfall amount: Ookala > Paauilo > Hainau

Air Temperature

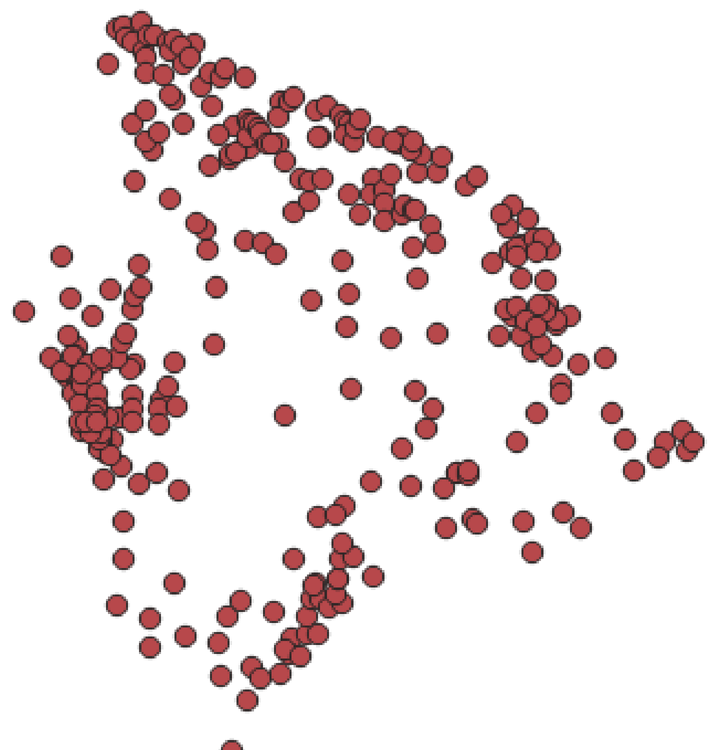
- August and September: hottest months (28-29C)
- February and March: coldest months (14-16C)
- No big change at the same station in the past 50 years (1961-2010) but the minimum temperature was slightly increased ~ 0.5C, indicating the impact of the global warming



Further Analysis - Clustered stations in Hawaii



- Future work will generate more precise picture of each climatic parameters.
- Collaboration and coordination with Department of Geography and climate.



● Geo stations

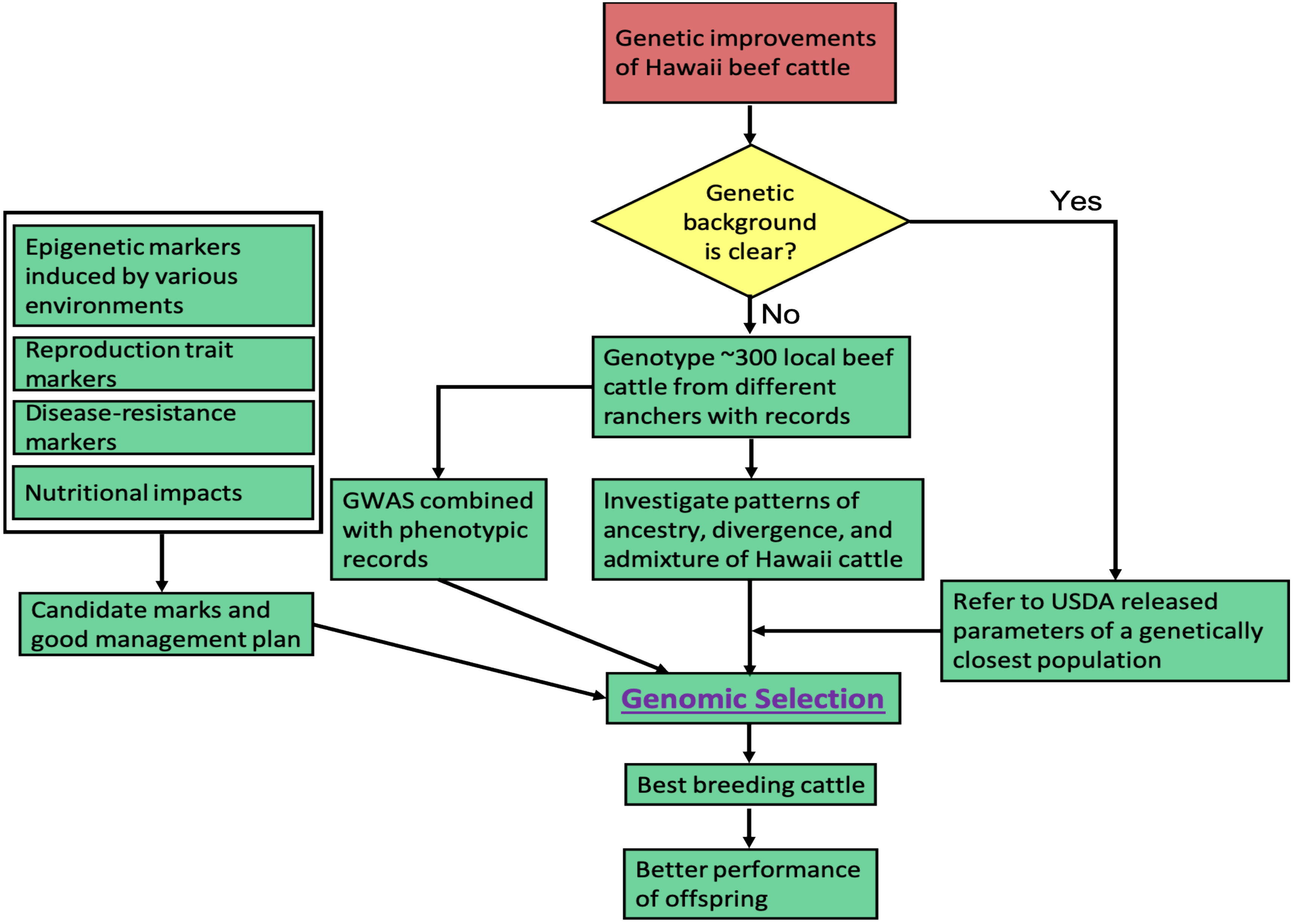
Collaborated with UH Geography Department

Stage 2

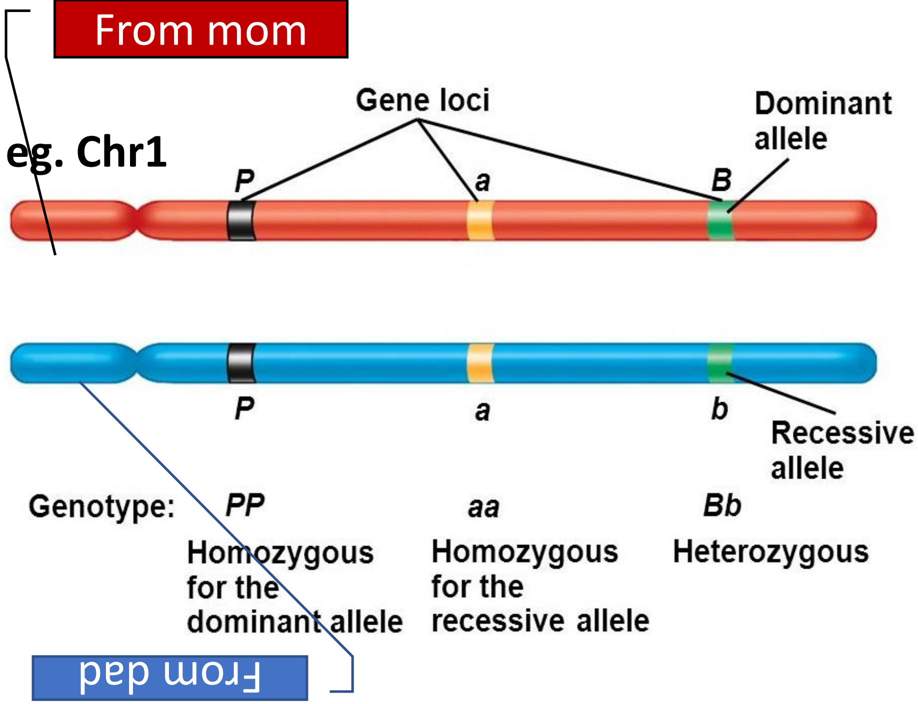
$$P = \boxed{G} + E$$

Project 2:

An investigation of genetic background of Hawaii beef cattle

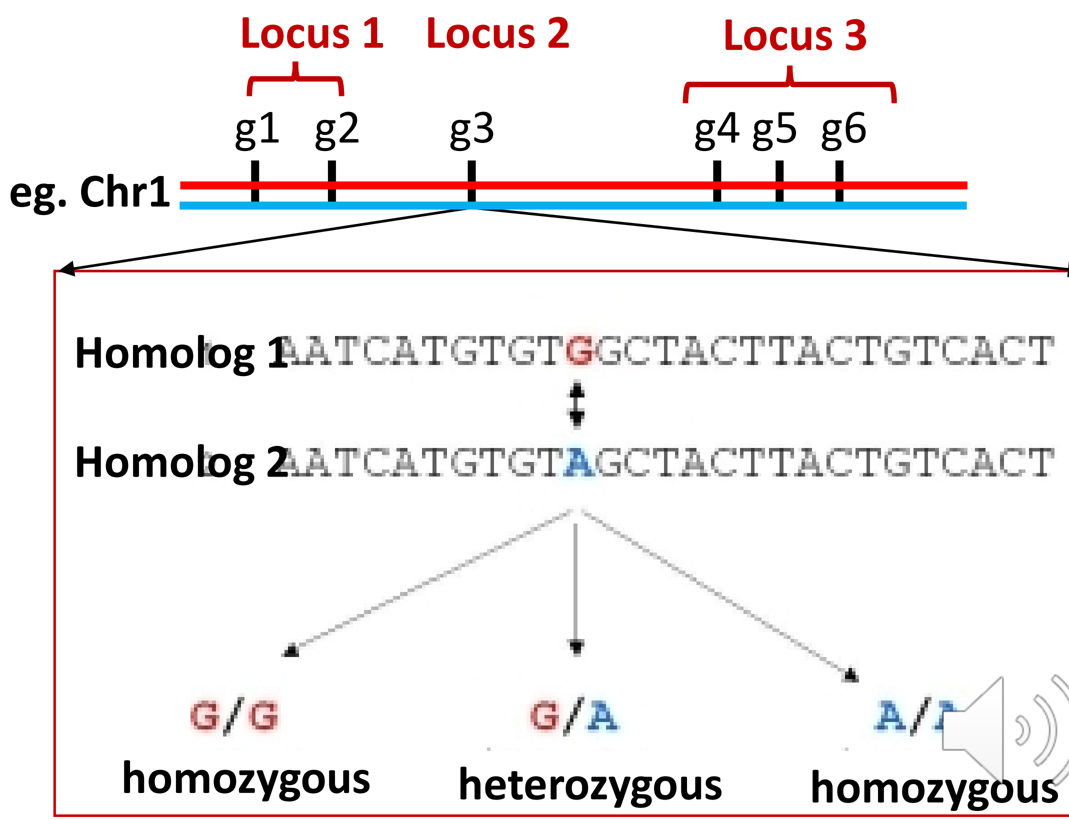


The strategy of genetic improvements of Hawaii beef cattle



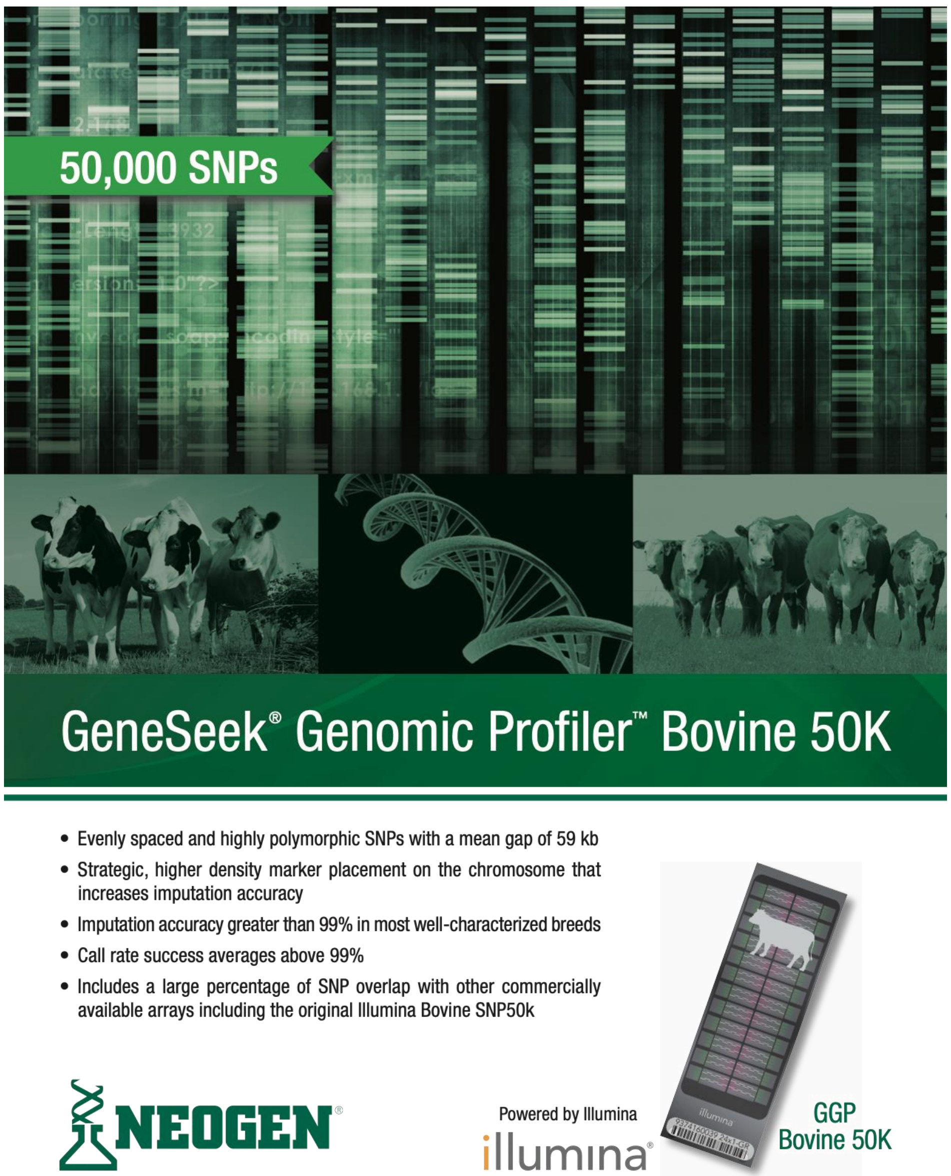
Definitions:

- **Homolog** – one of a pair of chromosomes having corresponding loci
- **Locus** – the specific location of a gene on a chromosome
- **Allele** – an alternative form of a gene
- **Gene** – the basic physical unit of heredity consisting of a DNA sequence at a specific location on a chromosome



SNP (Single nucleotide polymorphism)

DNA sequence variations that occur when a single nucleotide, A, T, C, or G, in the genome sequence is altered. For a variation to be considered a SNP, it must occur in every 1,000 nucleotides on average.



<u>Additional Key Features of the GGP Bovine 50K include:</u>

- **Comprehensive information**

Includes approximately 16,000 of the most informative SNPs from the original Illumina Bovine SNP50k. 39,000 SNP overlap with the GGP Bovine 150K and greater than 12,000 SNPs from the previous version of the GGP-LD array are included. More than 44,000 SNPs overlap with the Illumina Bovine HD array. Plus <u>comprehensive parentage, disease and trait relevant SNPs.</u>

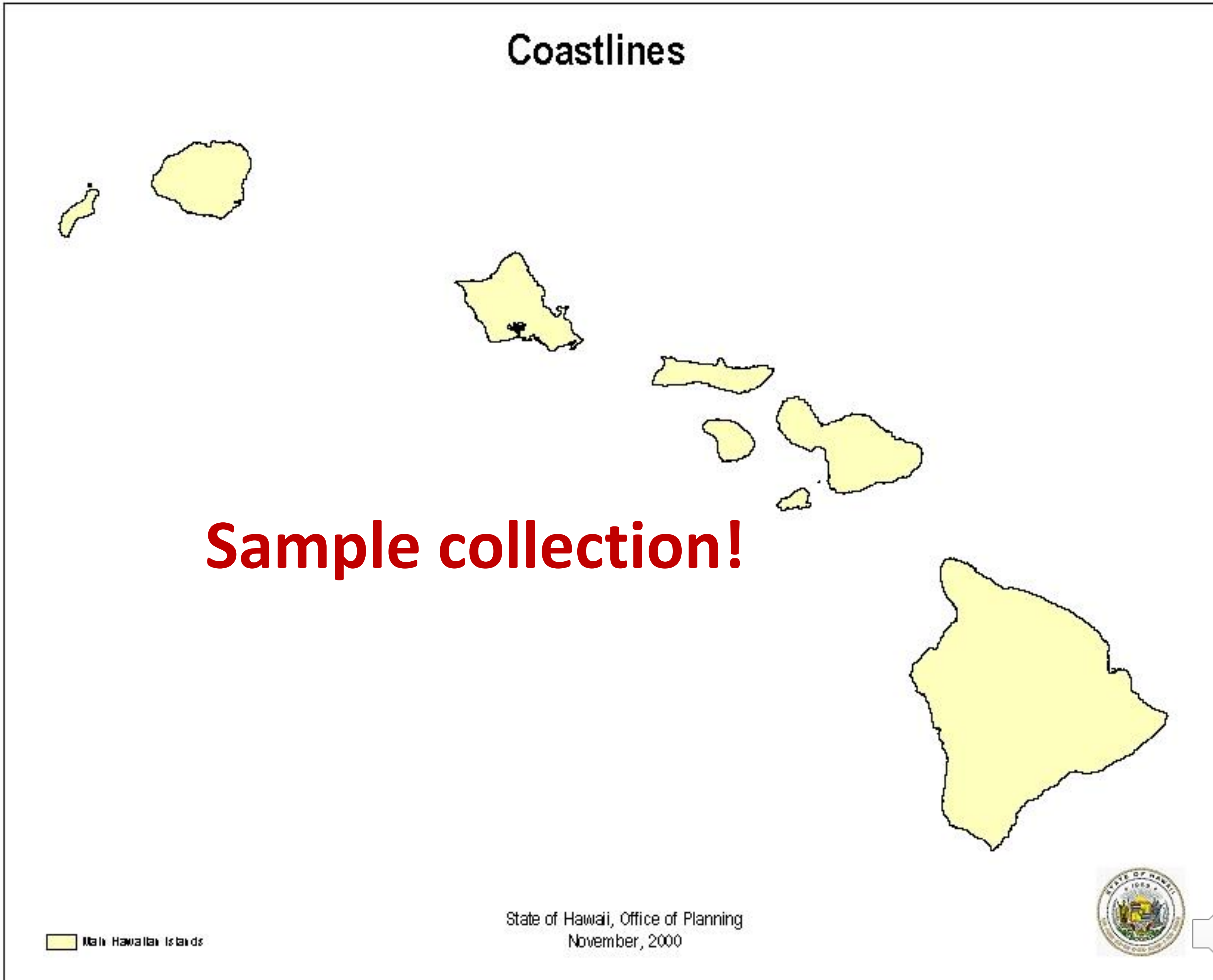
- **Verify parentage**

Includes all commonly utilized USDA and ISAG parentage SNPs. Hundreds of SNPs to enable conversion of ISAG microsatellite parentage data.

- **Breed identification**

Proper identification of Holstein, Jersey, and Brown Swiss cattle.

Sample collection!



Stage 3

$$\boxed{P = G} + E$$

Project 3:
GWAS and GS in Hawaiian beef population

GWAS: Genome-Wide Association Study
GS: Genomic Selection

Tropical environment

Production and Reproduction

Meat quality

$$P = G + E$$

Genomic Selection (GS)

GWAS:

Phenotypic data:

Growth traits:

- Birth weight
- Weaning weight
- Yearly weight
- Carcass weight
- Marbling score
- Tenderness

Reproduction traits:

- Conception rate
- Calving interval

→ Genetic marks

Liu *et al. Animal Microbiome* (2020) 2:33
https://doi.org/10.1186/s42523-020-00051-7

Animal Microbiome

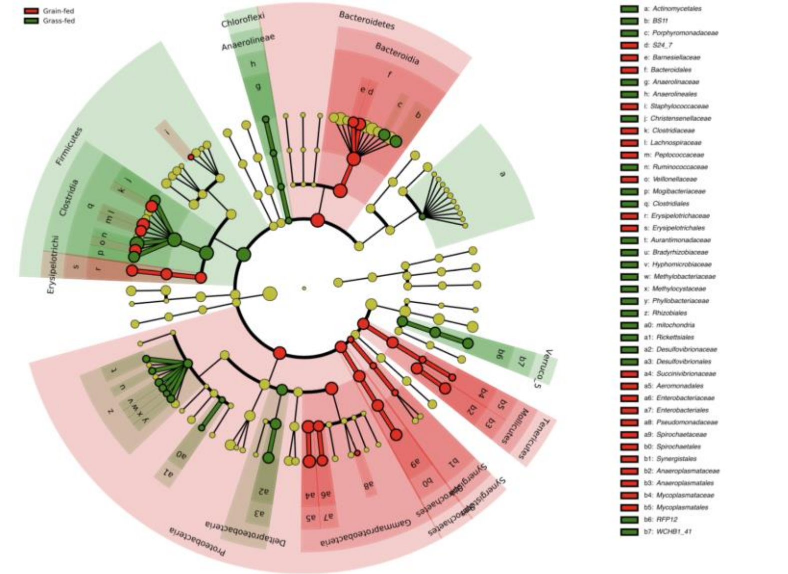
RESEARCH ARTICLE **Open Access**

2020

Check for updates

Diet-induced changes in bacterial communities in the jejunum and their associations with bile acids in Angus beef cattle

Jianan Liu[1,2], Fang Liu[3], Wentao Cai[1], Cunling Jia[1], Ying Bai[1], Yanghua He[4], Weiyun Zhu[5], Robert W. Li[2*] and Jiuzhou Song[1*]



Bai *et al. Journal of Animal Science and Biotechnology* (2020) 11:84
https://doi.org/10.1186/s40104-020-00482-x

Journal of Animal Science and Biotechnology

2020

RESEARCH **Open Access**

Check for updates

Diet induced the change of mtDNA copy number and metabolism in Angus cattle

Ying Bai[1,2], José A. Carrillo[2,3], Yaokun Li[2], Yanghua He[2,4] and Jiuzhou Song[2*]

2015

PLOS | ONE

RESEARCH ARTICLE

Ruminal Transcriptomic Analysis of Grass-Fed and Grain-Fed Angus Beef Cattle

Yaokun Li[1], José A. Carrillo[2], Yi Ding[2], YangHua He[2], Chunping Zhao[1], Linsen Zan[1]*, Jiuzhou Song[2]*

1 College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, P.R. China, 712100, 2 Department of Animal & Avian Sciences, University of Maryland, College Park, MD, 20742, United States of America

RESEARCH ARTICLE

Transcriptomic Profiling of Spleen in Grass-Fed and Grain-Fed Angus Cattle

Yaokun Li[1], José A. Carrillo[2], Yi Ding[2], Yanghua He[2], Chunping Zhao[1], Jianan Liu[2], George E. Liu[3], Linsen Zan[1]*, Jiuzhou Song[2]*

SCIENTIFIC REPORTS

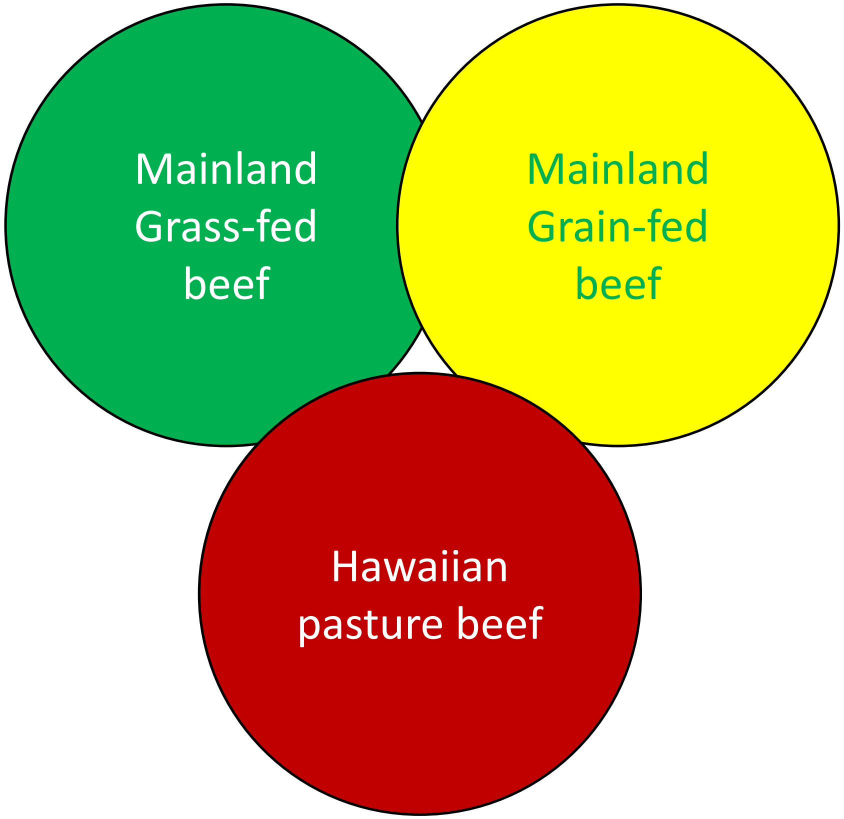
OPEN

Integrated metabolomic and transcriptome analyses reveal finishing forage affects metabolic pathways related to beef quality and animal welfare

2016

Received: 14 September 2015
Accepted: 18 April 2016
Published: 17 May 2016

José A. Carrillo[1], Yanghua He[1], Yaokun Li[2], Jianan Liu[1], Richard A. Erdman[1], Tad S. Sonstegard[3] & Jiuzhou Song[1]



Available data ⇒

- Phenotypic data
- Genotypic data (SNPs)
- Gene expression data (RNA-seq)
- Epigenetic data
- Metabolic data
- Metagenomic data (Microbiome)

Request data ⇒ **?**

Data collection!
Sample collection!

↓

Genetic marks

Controlling production and reproduction traits

Acknowledge

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- Water Resource Research Center

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- Dr. Matthew P. Lucas
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- Ms. Marla Fergerstrom
- Dr. Mark Thorne
- Dr. Michael DuPonte

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- Dr. Jonathan L. Deenik

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