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PROCEEDINGS
INTERNATIONAL CONFERENCE

TRANSFORMATION TO SUSTAINABLE LIVESTOCK PRODUCTION

2025

October 17th, 2025
Vietnam National University of Agriculture

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PREFACE

This is the International Conference to be organized within the framework of the KOICA Project on "Higher Education Program for Vietnam National University of Agriculture to Enhance Human Resources Specialized in Animal Husbandry of Vietnam". The conference took place at Vietnam National University of Agriculture, Hanoi, Vietnam on October 17, 2025. It is a great privilege for us to present the Proceedings of this conference to the authors and delegates of the event. We hope that you will feel useful and inspiring.

Our higher education project is a project which funded by the Korean Government through KOICA (Korea International Cooperation Agency) from 2021 to 2030 with the project budget is $12,700,000. The project covers many activities which focus on enhancing human resources in Animal Science of Vietnam, including organizing an international conference every year in which the topic is diverse. This year, the topic would be Animal nutrition and Feed technology.

The purpose of this conference was to contribute to the understanding of the technologies and innovations in livestock production.

The conference has about 150 participants from 4 countries including South Korea, Australia, Indonesia and Vietnam; and more than 30 papers have been submitted from universities and research institutes of different countries in order to be considered for presentation at the conference.

We would like to take this opportunity to thank KOICA and Ministry of Agriculture and Rural Development for their support; the invited speakers for their acceptance to give keynote presentations on their respective fields of expertise; the participants, especially those of you coming from abroad, for joining us and sharing your valuable experience and opinions. We bless you all a fulfilling experience and very pleasant stay in our country.

The Organizing Committee

2025 INTERNATIONAL CONFERENCE ON TRANSFORMATION TO SUSTAINABLE LIVESTOCK PRODUCTION

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CONFERENCE PROGRAM OF INTERNATIONAL SYMPOSIUM ON ANIMAL NUTRITION AND FEED TECHNOLOGY

Hanoi, October 17th, 2025

Time	Contents
8:30-9:00	**Registration**
9:00-9:10	**Opening speech**
	Morning session
	Chairman: Prof. Vu Dinh Ton & Prof. Lee Jun-Heon
9:10-9:40	**State management of livestock breeding** *Dr. Pham Thi Kim Dung* *Department of Animal Breeding, MAE*
9:40-10:10	**Recent research progress for the Korean native chicken** *Prof. Lee Jun-Heon* *President of KSAST, Korea*
10:10-10:40	**Overview of H'Mong cattle - a valuable livestock genetic resource** *Prof. Nguyen Xuan Trach* *Vietnam National University of Agriculture*
10:40-10:50	**Tea-break**
10:50-11:10	**Building climate-smart buffalo enterprises through precision farming, artificial intelligence, and genomic selection** *Dr. Mehar Khatkar* *Davies Livestock Research Centre, School of Animal and Veterinary Sciences, Adelaide University, Australia*
11:10-11:30	**Pig production in Vietnam: Improvement of performance by quantitative genetics and genomic information** *Assoc. Prof. Dr. Do Duc Luc* *Vietnam National University of Agriculture*
11:30-13:00	**Lunch**
	Afternoon Session
	Chairman: Prof. Nguyen Xuan Trach & Prof. Chung Ki-Yong
13:30-13:50	**National Hanwoo breeding and genetic improvement system of Korea** *Roh Seung-Hee* *Deputy General Manager Livestock Support Dept., National Agricultural Cooperative Federation, Korea*
13:50-14:10	**Husbandry and feeding systems for H'Mong cattle in Cao Bang province** *Dr. Hoang Xuan Truong*

Time	Contents
	National Institute of Animal Science
14:10-14:30	**Current and prospects of precision management in south Korea beef production** *Prof. Chung Ki-Yong* *Korea National University of Agriculture and Fisheries, Korea*
14:30-14:50	**Lumpy skin disease from a localized infection to a global threat** *Dr. Farhid Hemmatzadeh* *The University of Adelaide Australia*
14:50-15:10	**Tea break**
15:10-15:30	**MicroRNA profile and levels in colostrum and calf blood before and after receiving different colostrum sources** *Dr. Do Thi Hue* *The University of Adelaide Australia*
15:30-15:50	**Plant extract-loading Fe_3O_4 nanosystems to inhibit viruses for sustainable livestock production** *Le Thi Thu Huong* *Vietnam National University of Agriculture*
15:50-16:10	**Fermentative and nutritive quality of fruit by-product silage** *Dinh Thi Yen* *Vietnam National University of Agriculture, PhD student at Universitas Gadjah Mada, Indonesia*
16:10-17:00	**Closing ceremony**
17:00-20:00	**Gala dinner**

CONTENTS

PART I. ABTRACTS

Vietnam-Korea Livestock Higher Education Research Institute (VKLI)
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GENOMIC APPROACHES TO THE CONSERVATION AND IMPROVEMENT OF KOREAN NATIVE CHICKENS

Minjun Kim[1], Eunjin Cho[2], Jaewon Kim[1], Roshani Fernando[1], Jinhyeong Kim[1] & Jun Heon Lee[1, 2*]

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ABSTRACT

Understanding the genomic basis of indigenous livestock is essential for both conservation and sustainable improvement. Korean native chickens (KNCs), although representing a small fraction of the poultry industry in Korea, are distinguished by their unique meat quality, robustness, and adaptability. Recent genomic studies have investigated their genetic diversity, evolutionary history, and economically important traits. High-density SNP arrays and population structure analyses have clarified the distinct identity of KNC lines, while runs of homozygosity provided insights into inbreeding, conservation progress, and functional loci. Selection signature analyses identified candidate genes related to growth, metabolism, reproduction, and immune function, reflecting line-specific adaptation. Genome-wide association studies further identified variants associated with taste-active compounds, fatty acid composition, and growth traits, offering a foundation for genomic selection. Moreover, research on disease-related genes such as major histocompatibility complex B genes has documented substantial genetic variability in KNCs, establishing important genomic resources for subsequent studies on avian immunity and pathogen response. Together, these findings highlight KNCs as a valuable reservoir of genetic variation with implications for both conservation and breeding. More broadly, the genomic insights obtained from KNCs provide a cautious yet informative model for indigenous livestock worldwide, demonstrating how genomic tools can support sustainable breeding programs that balance biodiversity preservation with productivity.

Keywords: Korean native chickens, Genetic diversity, Selection signatures, Association study, Disease-resistance genes.

OVERVIEW OF H'MONG CATTLE - A VALUABLE LIVESTOCK GENETIC RESOURCE

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ABSTRACT

H'Mong cattle are considered to have several advantages over other local Yellow cattle in Vietnam, serving as a valuable livestock genetic resource. This breed is not only a primary livelihood but also a source of pride deeply tied to the cultural identity of the H'Mong people. Several research and development projects have been undertaken to utilize this cattle breed. This paper reviews available research findings to provide an overview of the breed's origins, actual strengths and weaknesses, and proposes sustainable solutions for its utilization.

Keywords: H'Mong cattle, genetic resource, meat productivity, beef quality

A STUDY ON HANWOO (KOREAN NATIVE CATTLE) IMPROVEMENT SYSTEM

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ABSTRACT

Hanwoo is a culturally and emotionally important livestock in Korea. Historically, it served as a key means of transportation and draft animal during the agrarian period, and with industrialization, it was improved as a beef breed. Hanwoo is known for its calm temperament, tolerance to low-quality feed, and relatively high content of oleic acid, an unsaturated fatty acid. The Hanwoo population declined significantly after the Korean War, but government policies and the roles of improvement agencies laid the foundation for population recovery and genetic improvement. The improvement of Hanwoo began with a registration program in 1969. After about 57 years of breeding efforts, progeny-tested steers showed an annual increase in yearling weight of 4.47 kg, reaching 399.7 kg, and in 24-month body weight of 7.98 kg, reaching 751.5 kg. Genetic progress in carcass traits was observed with annual improvements of 4.2548 kg in carcass weight, 3.4472 cm^2 in eye muscle area, a decrease of 0.071 mm in backfat thickness, and an increase of 0.0881 points in marbling score. These results are attributed to the selection of superior sires through contemporary and progeny testing combined with genomic selection technologies.

Keywords: Hanwoo, performance test, progeny test, genomic selection, young bull, proven bull.

MICRORNA PROFILE AND LEVELS IN COLOSTRUM AND CALF BLOOD BEFORE AND AFTER RECEIVING DIFFERENT COLOSTRUM SOURCES

Do T. Hue,[1,2*] Kiro Petrovski,[1] John L. Williams, [1,3] Tong Chen,[1] Kelly Ren,[1] Wai Yee Low,[1] Thien D. Van,[1] Cynthia D. K. Bottema,[1]

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ABSTRACT

MicroRNAs (miRNAs) are short non-coding RNA, but they play critical roles in regulatory gene expression and are involved in various biological processes of animals. In this study, miRNA profile was analysed in colostrum and calf blood before and after colostrum ingestion. Dam colostrum was fed to their own calves (Group A) and foster calves (Group B) within 4 hours after birth and every 12 hours after birth. Pooled colostrum that collected from multiple cows days 0 – 4 postpartum was used as the first feed for Group C calves, then these calves were fed bulk tank milk from many cows after 5 days postpartum. Total RNA from calf blood within 2 hours after birth and before receiving colostrum (day 0), and 24 hours after feeding colostrum (day 1) was extracted using miRNeasy Mini Kit, sequenced by Illumina-compatible Next-Generation Sequencing, and then analysed by using a bioinformatics pipeline. Levels of miRNA were validated in colostrum and calf blood (days 0 and 1) by the reverse transcription polymerase chain reaction (RT-qPCR). The large number of miRNAs were detected at high levels in calf blood at both days 0 and 1, which was generally 4-fold higher than in colostrum. Total of 303 miRNAs detected in colostrum (296 known and 7 novel miRNAs), whereas 1,198 miRNAs (1,004 known and 194 novel) were identified in calf blood. A similar miRNA profile was found in dam and pooled colostrum with 76% of the miRNAs expressed in dam colostrum also found in pooled colostrum, however, only four miRNAs had significantly higher levels in dam than in pooled colostrum.

94% miRNAs were detected in the calf blood at both days 0 and 1, and only 22 miRNAs had significantly different levels between the two time points. Of these 22 miRNAs, three miRNAs had higher levels at day 1 after two colostrum feeds (let-7a-3p, miR-1260b and miR-12042), however, after validating by RT-qPCR, only miR-1260b showed higher levels in calf blood day 1 compared to day 0. In addition, these three miRNA levels in the calf blood were not correlated with the levels in the corresponding colostrum by both RNA seq and RT-qPCR results. These findings suggest that miRNAs in the colostrum are not likely to be absorbed by the calves to any great extent.

MODELING GROWTH CURVES TO ESTIMATE LIVE WEIGHT, WEIGHT GAIN, AND OPTIMAL SLAUGHTER AGE IN INDIGENOUS HUONG PIGS

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ABSTRACT

The Huong pig is an indigenous Vietnamese breed known for its adaptability and meat quality, making it important for sustainable smallholder farming. This study aimed to determine the most suitable nonlinear model to describe growth patterns in Huong pigs and estimate live weight, weight gain, and optimal slaughter age. A total of 240 pigs (120 castrated males and 120 females) were monitored monthly from birth to 9 months of age. Eight nonlinear growth models (von Bertalanffy, Bridges, Janoschek, Gompertz, Logistic, Lopez, Richards, and Weibull) were fitted to body weight data using nonlinear regression analysis in R. Goodness-of-fit was assessed based on R^2, Akaike's Information Criterion (AIC), Bayesian Information Criterion (BIC), and standard error of regression (SER). The Gompertz model provided the best fit for both sexes, with high R^2 values (>99%) and low AIC and SER. Based on the Gompertz function, the optimal slaughter age was estimated at 9.42 months (51.45 kg) for castrated males and 9.93 months (53.68 kg) for females. These findings support the application of growth curve modeling for improving the economic efficiency of Huong pig production and may guide breeding and management strategies for other native breeds.

Keywords: Bodyweight, breeding, Huong pigs, growth curve, slaughter age

EFFECTS OF DRINKING WATER SOURCES ON GROWTH PERFORMANCE AND CARCASS TRAITS OF DUCKS

Nguyen Thi Phuong Giang[1], Bui Huy Doanh[1], Bui Thi To Nga[2], Ha Xuan Bo[1], Nguyen Thi Chau Giang[1], Cu Thi Thien Thu[1], Nguyen Cong Oanh[1], Nguyen Van Thong[1], Nguyen Thi Vinh[1]*

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ABSTRACT

This study was conducted to evaluate the effects of drinking water sources on the growth performance, carcass yield and quality of commercial Cherry Valley ducks raised in the coastal area of Thai Thuy (formerly Thai Binh province). A total 225 Cherry Valley ducks (81 males and 144 females) were randomly assigned to 3 treatments corresponding to different drinking water sources (filtered water, tap water, and pond water), with three replicates of 25 ducks each. Results showed that water source significantly influenced final body weight and average daily gain, with ducks receiving filtered or tap water performing better than those given pond water; however, weight gain, feed intake, and feed conversion ratio were not affected. Carcass yield was generally unaffected by drinking water source, except for thigh weight, while meat quality traits such as pH and color varied notably across different water sources. Sex had a clear effect on growth and meat quality, with male ducks showing faster growth and higher thigh pH, while females exhibited greater breast water loss. The interaction between water source and sex also influenced final body weight, growth rate, and several meat quality traits (L*, a*, pH15, b*).

Keywords: Drinking water source, growth performance, carcass traits

EFFECT OF BANANA PEEL POWDER ON GROWTH PERFORMANCE, INTESTINAL MORPHOLOGY, CARCASS YIELD, AND MEAT QUALITY OF BROILER CHICKENS

Duong Thu Huong#, Tran Bich Phuong#, Nguyen Van Thong, Dao Thi Ngoc Anh, Bui Huy Doanh, Nguyen Thi Phuong Giang, Nguyen Thi Vinh*

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ABSTRACT

Banana peel is a readily available agricultural by-product with potential use in poultry feeding. This study investigated the effects of banana peel powder (BPP) on growth performance, intestinal morphology, carcass yield and meat quality of broilers. A total of 126 one-day-old chicks were randomly assigned to three dietary treatments: control (BPP0, corn – soybean basal diet), BPP7 (7% banana peel), and BPP10 (10% banana peel), with three replicates of 14 birds each, and reared for 35 days. Survival rate was not significantly different among groups (P > 0.05), although BPP10 showed the highest value (96.97%). The inclusion of 7% and 10% in the diets did not significantly affect initial weight, average daily gain, feed intake, or feed conversion ratio (P > 0.05). However, broilers fed the 10% BPP diet showed numerically higher final weight and weight gain, with both parameters reaching statistical significance (P = 0.05). There are no statistically significant differences were observed in villus height, crypt depth, or the villus height to crypt depth ratio. Carcass traits were not influenced by diet (P > 0.05). However, several meat quality traits were significantly affected (P <0.05). In thigh meat, yellowness (b*) decreased in VC7 and VC10. In breast meat, lightness (L*) increased and yellowness (b*) decreased with banana peel inclusion (P < 0.05). In conclusion, inclusion of 10% banana peel powder tended to enhance growth and altered meat color without adverse effects on FCR or carcass yield, supporting its potential as a sustainable feed ingredient in broiler production.

Keywords: Banana peel, broiler performance, agricultural by-products, sustainable poultry production.

PART II. PRESENTATION

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1. STATE MANAGEMENT OF LIVESTOCK BREEDING

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DEPARTMENT OF LIVESTOCK AND ANIMAL HEALTH

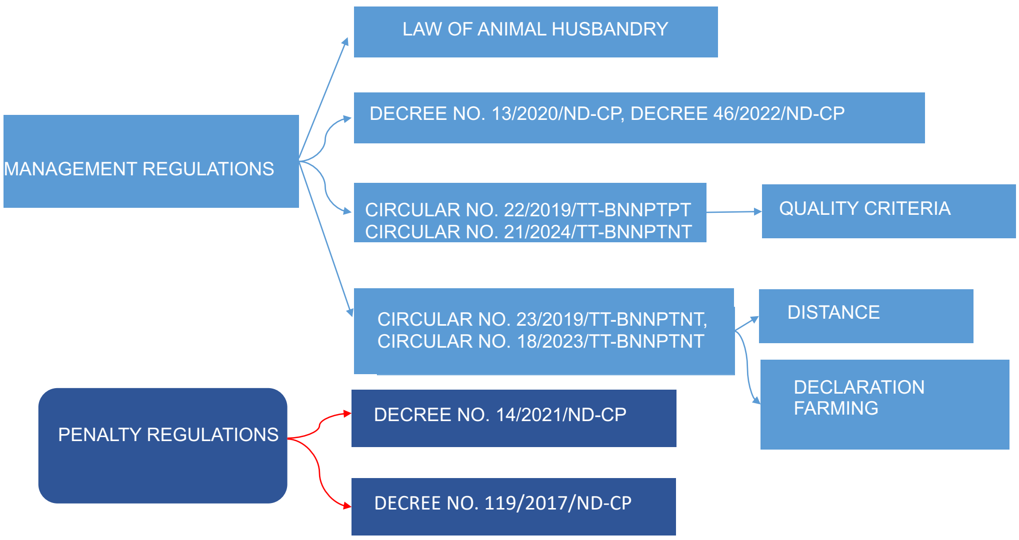
DISCUSSION REPORT

STATE MANAGEMENT OF LIVESTOCK BREEDING

Hanoi , October 17 , 2025

REPORT OUTLINE

I. STATE MANAGEMENT DOCUMENT SYSTEM ON LIVESTOCK BREEDS



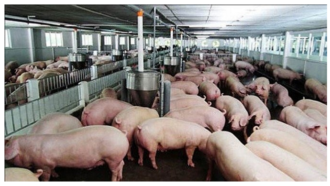
I. STATE MANAGEMENT DOCUMENT SYSTEM ON LIVESTOCK BREEDS

	Content	As provided in the article, clause
1	The State support for preserving genetic resources of rare and precious livestock breeds and indigenous breeds	Clause 1, Article 4, Law of Animal Husbandry
2	The State supports livestock recovery activities after natural disasters and epidemics.	Clause 2, Article 4, Law of Animal Husbandry
3	High technology, advanced technology, new technology and high - tech products are prioritized and encouraged to be applied in the field of livestock breeding.	Clause 1, Article 7, Law of Animal Husbandry
4	International cooperation in exchanging high-yield, high-quality livestock breeds that adapt to climate change .	Clause 3 , Article 10, Law of Animal Husbandry
5	Building a Database on Livestock Breeds	Clause 2, Article 11, Law of Animal Husbandry; Article 4 of Circular 20/2019/TT-BNNPTNT
6	It is strictly forbidden to destroy or appropriate livestock genetic resources.	Clause 5, Article 12, Law of Animal Husbandry
7	Prohibition of illegal export of genetic resources of precious and rare livestock breeds	Clause 6, Article 12, Law of Animal Husbandry

I. STATE MANAGEMENT DOCUMENT SYSTEM ON LIVESTOCK BREEDS

	Content	As provided in the article, clause
8	Management genetic resources	Clause 1, Article 13 of Law of Animal Husbandry
9	Collecting, preserving, exploiting and developing livestock genetic resources	Article 14, Law of Animal Husbandry
10	Exchange of genetic resources of precious and rare livestock breeds	Article 15, Article 16, Law of Animal Husbandry, regulations; Article 3, 4 Circular 22/2019/TT-BNNPTNT dated November 30, 2019 guiding a number of articles of Law of Animal Husbandry on management of livestock breeds and breed products
11	Genetically modified animals and animal cloning	Article 17 of the Law of Animal Husbandry
12	Breeds and livestock breed products circulating on the market	Article 18 of the Law of Animal Husbandry





I. STATE MANAGEMENT DOCUMENT SYSTEM ON LIVESTOCK BREEDS

	Content	As provided in the article, clause
13	Livestock breeds that need to be preserved and banned to export	Article 19, Law of Animal Husbandry
14	Import of livestock breeds and livestock breed related products	Article 20, Law of Animal Husbandry; Article 5 of the Circular Circular 22/2019/TT-BNNPTNT
15	Export and international exchange of livestock breeds and livestock breed products	Article 21, Law of Animal Husbandry; Article 6 of the Circular Circular 22/2019/TT-BNNPTNT
16	Conditions for production and purchase livestock breeds	Article 22, Law of Animal Husbandry



I. STATE MANAGEMENT DOCUMENT SYSTEM ON LIVESTOCK BREEDS

	Content	As provided in the article, clause
17	Production, sale of semen, embryos, breeding eggs, larvae, artificial insemination services, and embryo transfer ; Regulations on Certificate of artificial insemination and embryo transfer training.	Article 23, Law of Animal Husbandry; Article 3 of the Circular Circular 23/2019/TT-BNNPTNT
18	Quality requirements of male and female breeds; Mandatory quality standards for male and female breeds	Article 24 Law of Animal Husbandry; Article 7 of the Circular Circular 22/2019/TT- BNNPTNT
19	Rights and obligations of business on producing and trading in livestock breeds	Article 25 Law of Animal Husbandry
20	Animal breed testing	Article 26, 27, Law of Animal Husbandry
21	Animal breed inspection	Article 28, Law of Animal Husbandry
22	Naming new livestock breeds	Article 29 Law of Animal Husbandry



I. STATE MANAGEMENT DOCUMENT SYSTEM ON LIVESTOCK BREEDS

	Content	As provided in the article, clause
23	Recognition of new livestock breeds and lines	Article 30 Law of Animal Husbandry
24	Rights and obligations of livestock breed testing facilities	Article 31 Law of Animal Husbandry
25	Management bird's nest production	Article 64 Law of Animal Husbandry, Article 25 of the Decree Decree 13/2019/ND-CP
26	Honey bee management	Article 65, Law of Animal Husbandry
27	Dog and cat management	Article 66, Law of Animal Husbandry



I. STATE MANAGEMENT DOCUMENT SYSTEM ON LIVESTOCK BREEDS

	Content	As provided in the article, clause
28	Sika deer farming management	Article 67 Law of Animal Husbandry, Article 26 of the Decree Decree 13/2019/ND-CP dated January 21, 2020 Guidance detailed instructions Law Blanket feed
29	Animal wel-fare	Articles 69, 70, 71, 72 Law of Animal Husbandry
30	Animal export	Article 77 Law of Animal Husbandry
31	Animal import	Article 78 Law of Animal Husbandry
32	Collecting, preserving, exploiting and developing livestock genetic resources	Article 5 of Decree 13/2019/ND-CP dated January 21, 2020, providing detailed guidance on Law of Animal Husbandry
33	Animal breeds list need to preserve	Article 6 of the Decree Decree 13/2019/ND-CP dated January 21, 2020 Guidance detailed instructions Law of Animal Husbandry

I. STATE MANAGEMENT DOCUMENT SYSTEM ON LIVESTOCK BREEDS

	Content	As provided in the article, clause
34	List of livestock breeds prohibited to export	Article 7 of the Decree Decree 13/2019/ND-CP
35	Update livestock breeds need to be preserved	Article 8 of the Decree Decree 13/2019/ND-CP
36	List of other animals allowed to be raised	Article 17 of the Decree Decree 13/2019/ND-CP
37	Regulations on import of live animals	Article 29 of the Decree Decree 13/2019/ND-CP
38	Import, production and supply of livestock breeding products	Clause 3, Article 1 of the Decree Decree 46/2022/ND-CP

I. STATE MANAGEMENT DOCUMENT SYSTEM ON LIVESTOCK BREEDS

	Content	As provided in the article, clause
39	Appraisal for granting license to exchange genetic resources of livestock breeds, 850,000 VND 01 genetic source/time. Appraisal for granting license to import male breeds, semen, and embryos of livestock breeds for the first time, 250,000 VND 01 breed/time. Appraisal for granting license to export livestock breeds and livestock breed products in the list of livestock breeds banned from export for scientific research, exhibitions, and advertising purposes 850,000 VND 01 breed/time. Recognition of new livestock breeds and lines, 750,000 VND 01 breed/time	Information Circular No. 24/2021/TT-BTC dated March 31, 2021 Regulations on collection levels, collection, payment, management and use of fees in animal husbandry



II. BREEDING QUALITY AND LIVESTOCK BREEDS MANAGEMENT




Foreign sows, crossbred foreign x foreign (80%); *Domestic sows , crossbred foreign x domestic (20%)*

sows: ~ 3.0 million (10.4% of total herd),
GGP, GP: 137 thousand heads (4.5% of total herd) -
(GGP 15% and GP accounts for 85%)

Boar breeding pigs : 74.9 thousand, AI (53%) - 39.7 thousand heads; DI (47%) - 35.2 thousand heads

II. BREEDING QUALITY AND LIVESTOCK BREEDS MANAGEMENT

a. Commercial pork (foreign x foreign)
ADG from 750-950 grams/head/day
TLN from 54-60 %;
FCR from 2.3 -2.5 kg

b . Commercial pork group (domestic and foreign) ADG from 550-700 grams/head/day;
TLN from 48-52%; high quality meat
FCR from 2.6 - 2.8 kg .

II. BREEDING QUALITY AND LIVESTOCK BREEDS MANAGEMENT

The high quality indigenous chicken breeds *:* Survival rate 90-95%. Egg productivity increased 25.4-53.8%, FCR decreased 10-15%.

II. BREEDING QUALITY AND LIVESTOCK BREEDS MANAGEMENT

Lines of colored feathers LV, VP1, VP2, VP3, VP4, VP5, TP1, TP2, TP3, TP4, TN1, TN2 and TN3

BW 8 weeks old: (female-male) from 902.7-1161.4 grams,
Egg productivity until 64 weeks old: 156-186 eggs,
FCR /10 eggs:1.89 - 2.5 kg.

II. BREEDING QUALITY AND LIVESTOCK BREEDS MANAGEMENT

The egg-line are Egypt, HA1, HA2, VCN/BT-AG1, GT1, GT2, GT3, VCN-G15, RA, GT, GT12, VCZ16

Egg production: 200 – 269 eggs/hen/72 weeks old, FCR /10 eggs from 1.73 – 2.30 kg

II. BREEDING QUALITY AND LIVESTOCK BREEDS MANAGEMENT

Egg-strain duck breeds *:*
TC : 280-290 eggs/hen/year ,
Cỏ breed: 250-260 eggs/hen/year

Dual-purpose duck breeds *:* PT duck , 2 lines of Sea duck . production from 240 - 250 eggs/hen/year.

Meat duck breeds *:* duck lines T 5, T6, V5, V6, V52, V57, TS132 , TS142, CT1, CT2, CT3, CT4,
male duck 3.69 - 3.72 kg,
Female duck: 3.33 – 3.34 kg (24 weeks old)
TP duck 49 days old reaches 3.2-3.5kg



II. BREEDING QUALITY AND LIVESTOCK BREEDS MANAGEMENT

Musk duck *V5, V7, VS, RT9, RT11*

Four ostrich lines *BV1, BV2, BV3, BV4*


II. BREEDING QUALITY AND LIVESTOCK BREEDS MANAGEMENT

Boer-VCN goat: BW75-80 kg/male, 65-70 kg/female, meat yield : 50-55%;
Saanen dairy goats 2.8-3.2 liters/day.

Suffort-VCN, Dopper-VCN sheep and cross breed have 20-25% higher productivity than Phan Rang sheep.

II. BREEDING QUALITY AND LIVESTOCK BREEDS MANAGEMENT

Crossbred dairy cow: milk yield of 5200 - 5500 kg/cycle. Purebred HF cows have been raised in most regions of the country.

Crossbred beef cattle : Zebu crossbred: fattening cattle gain 800 g/head/day.
Crossbreeding between BBB and Vietnamese cow creates high-yielding hybrids.

II. BREEDING QUALITY AND LIVESTOCK BREEDS MANAGEMENT

The BW of mature buffalo reaches over 800 kg/male, over 600 kg for female buffalo.

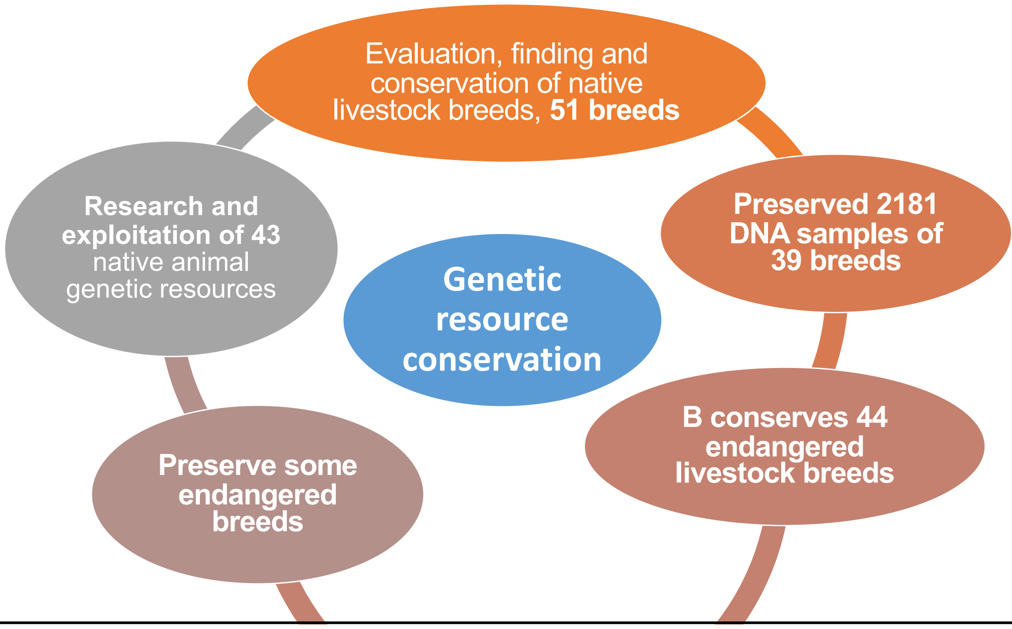
II. BREEDING QUALITY AND LIVESTOCK BREEDS MANAGEMENT

Foreign bee *Apis mellifera* . Create hybrid bee colonies for average honey yield of 40-45kg/hive/year

Silkworm breed:

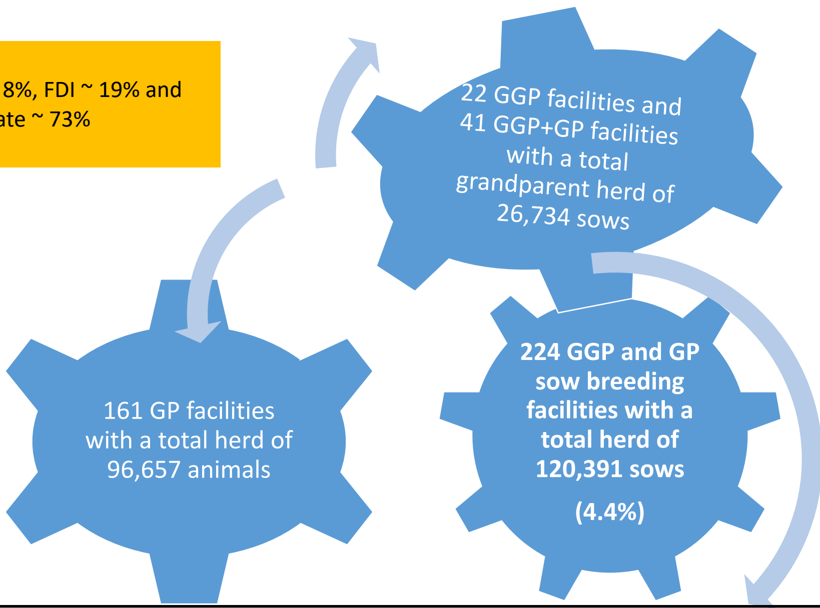
Creating a white cocoon dual-system silkworm breed with a yield of 90% compared to the cocoon yield of Chinese dual-system silkworms.

II. BREEDING QUALITY AND LIVESTOCK BREEDS MANAGEMENT



II. BREEDING QUALITY AND LIVESTOCK BREEDS MANAGEMENT

State-owned: 8%, FDI ~ 19% and Private ~ 73%



II. BREEDING QUALITY AND LIVESTOCK BREEDS MANAGEMENT

GENERAL ASSESSMENT

- State management documents
- Import breed
- Selective Breeding
- Breeding quality management
- Breeding project

II. BREEDING QUALITY AND LIVESTOCK BREEDS MANAGEMENT

EXIST

- Breeding monitoring and management system
- Lack of specialized staff
- Regional Center for quality assessment
- VC facility
- Inspector, Check
- Announcement basic standard

III. LIVESTOCK DEVELOPMENT STRATEGY TO 2030

Target

2026 – 2030 :

3 - 4% / year

2025: 5.0 - 5.5 million tons of meat
Pork 63 - 65 % ; poultry 26 - 28 % , grass-fed cattle 8 - 10 %

2030 : 6.0 - 6.5 million tons of meat
Pork 59 - 61 %, poultry 29 - 31 %, grass-fed cattle 10 - 11 %

Export 15 - 20% of pork production, 20 - 25% poultry meat and eggs.

2030: About 23 billion eggs and 2.6 million tons of milk.

Average livestock products/person/year until 2030: 58 - 62 kg of all kind of meat, 220 - 225 eggs and 24 - 26 kg of fresh milk

III. LIVESTOCK DEVELOPMENT STRATEGY TO 2030

PROJECT FOR DEVELOPING LIVESTOCK BREEDING INDUSTRY

- 90% of pig breeding supply, 80% poultry breeding supply, 100% duck breeding supply, 70% beef cattle breeding supply
- Building brands and geographical indications for native breeds
- Import of great-grandparent and grandparent livestock breeds
- 6 industrial-scale livestock breeding facilities
- Exploitation and development of native livestock genetic resources
- Management and production of livestock breeds in pyramid form with identification codes

MINISTRY OF AGRICULTURE AND ENVIRONMENT
DEPARTMENT OF LIVESTOCK AND ANIMAL HEALTH

THANKS FOR YOUR ATTENTION

2. RECENT RESEARCH PROGRESS FOR THE KOREAN NATIVE CHICKEN

PROF. LEE JUN-HEON
PRESIDENT OF KSAST, KOREA

Seminar in Vietnam National University of Agriculture

Genomic studies using Korean native chicken

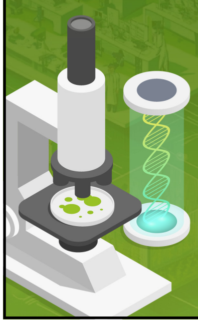
Jun Heon Lee, PhD

Department of Animal and Dairy Science,
Department of Bio-AI Convergence,
Chungnam National University, Korea

2025. 10. 17

ANIMAL MOLECULAR GENETICS LAB.

Chungnam National University



Presentation outline

Introduce myself

+ Jun Heon Lee, PhD

Professor in Animal Molecular Genetics
College of Agriculture and Life Sciences
Chungnam National University, Daejeon, Korea

- Bachelors & Master's Degree in the Department of Animal Science, at Chungnam National Univ, Korea (1987-1995)
- PhD degree (Majoring in Animal Molecular Genetics) in the Department of Animal Science at the Univ of Sydney, Australia (1997-2001)
- Dean for College of Agriculture and Life Sciences, at Chungnam National University (2023-2025)
- Post Doc in the Department of Animal Science at Univ of Illinois, USA (2001-2002)
- JSPS (Japanese Society for Promotion of Science) Research Fellow in the Kobe University, Japan
- Visiting Research Fellow in the Dept of Pathology at the Univ of Michigan, USA (2009)
- President of Korean Society of Animal Science and Technology and Korean Society of Animal Breeding and Genetics, President for ISAG2025 LOC (Local Organising Committee)

Previous research projects in CNU, Korea

1. 2003-2007: BioGreen 21 (Development of economic trait genes of Korean native chickens using proteomics)
2. 2008-2010: FTA Project (Research on the production of high-quality chicken for domestic poultry genetic resources)
3. 2011-2013: FTA Project (Research on the development of domestic breeds using national and private seeds and the enhancement of marketability)
4. 2011-2014: Next-generation BioGreen 21 Project (Research on genome selection technology for the development of high-quality meat breeds)
5. 2013-2021: GSP Golden Seed Project
   (Step 1: Development of large-scale analysis of genetic markers of the collected samples and the mating lines)
   (Step 2: Development of a new native breed and establishment of a breeding system – Development of molecular markers for identification of native chickens and establishment of verification system)
6. 2014-2015: Agenda Project (Development of domestic seed stocks for white meat duck and industrialization of native duck: early termination due to AI outbreak)
7. 2019-2021: Basic research by the National Research Foundation of Korea (MHC haplotype analysis related to immunity and disease resistance of chickens)
8. 2022-2024: Internationalization Foundation Project (Deep learning modeling for genomic prediction to increase accuracy of breeding value in Korean and Israeli cattle populations)
9. 2023-2024: Development of a National Breeding Platform Project (Development of technology for the trait improvement based on the livestock dip-data (Establishment of genomic selection for Korean native ducks))

- **Mostly Poultry Genetics using native chicken breeds**
- **Some collaboration Projects for Korean native pigs (not listed)**

Ongoing research projects in CNU, Korea

1. 1. 2021-2025: 2025 Advanced Technology for Addressing Livestock Issues (Development of genomic selection technology to improve meat quality Woorimatdag)
2. 2022-2025: Basic research by the National Research Foundation of Korea (MHC haplotype analysis related to immunity and disease resistance of Asian chicken population)
3. 2025-2027: National Breeding Platform Development for Public Benefit (Development of an AI-based breeding platform for improving egg production traits using livestock deep data)
4. 2025-2027: National Breeding Platform Development for Public Benefit (Construction of deep-data-based growth and meat quality databases)
5. 2025-2028 : Mid-Career Research Program by the National Research Foundation of Korea (Establishment of a foundation for breeding disease-resistant chicken lines through analysis of MHC gene surface expression levels)

- **Basic researches for chicken MHC, candidate genes, QTLs**
- **Development of commercially available new native chicken breeds**

Research directions for Korean Native Chickens (KNC)

1. Growth and Production Traits
- Slower growth rate compared to commercial broilers
- Smaller body size, however adapted to local environment

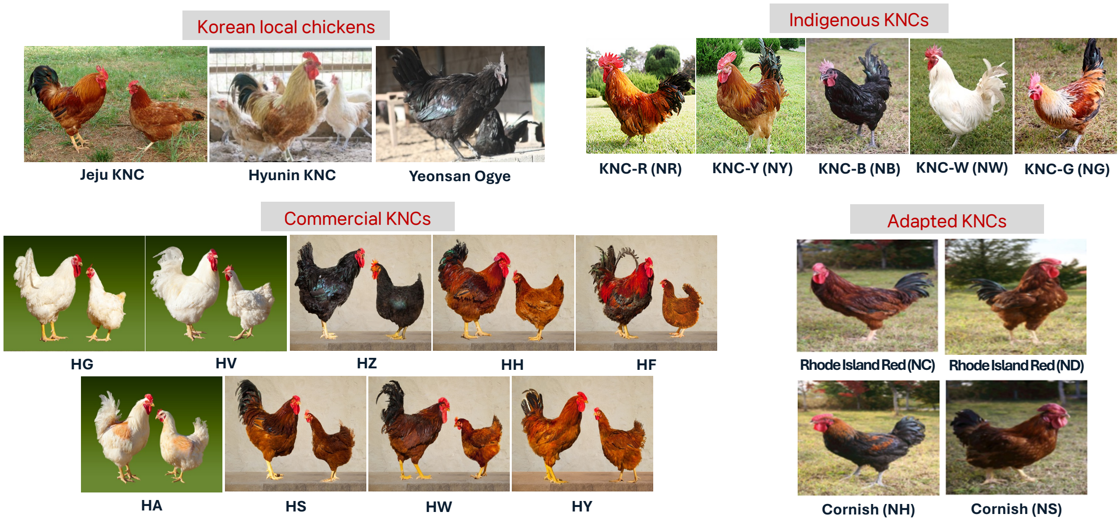
2. Meat Quality and Culinary Value
- Superior meat texture and flavor
- High protein content with lower fat levels

3. Health and Disease Resistance
- Potentially higher resistance to common poultry diseases
- Valuable genetic resource for breeding programs

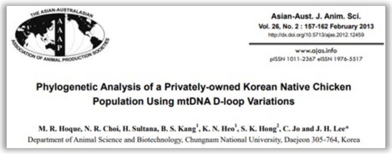
4. Importance for Research
- Preserving genetic diversity of native chicken populations
- Basis for improving disease resistance and meat quality through breeding

Korean Native Chicken (KNC) breeds in Korea

+ 21 Korean native chicken populations



1. Genetic diversity analyses and breed identification using Korean native chickens


Asian-Aust. J. Anim. Sci.
Vol. 26, No. 2 : 157-162 February 2013

Phylogenetic Analysis of a Privately-owned Korean Native Chicken Population Using mtDNA D-loop Variations

M. R. Hoque, N. R. Choi, H. Sultana, B. S. Kang[1], K. N. Heo[1], S. K. Hong[2], C. Jo and J. H. Lee*
Department of Animal Science and Biotechnology, Chungnam National University, Daejeon 305-764, Korea

+ KNC diversity analysis with mtDNA D-loop diversity

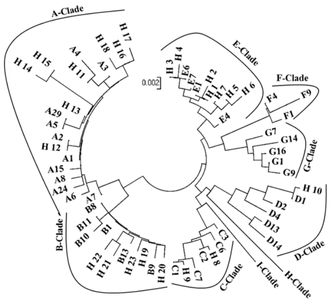


Figure 1. NJ phylogenetic analysis of Korean native chicken populations using D-loop variations and the Kimura 2-parameter method.

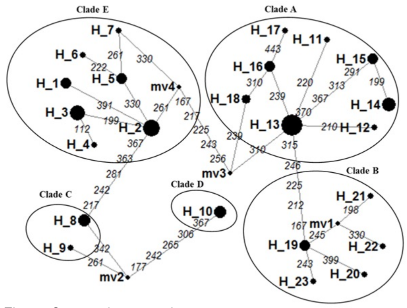


Figure 2. Identification of phylogenetic tree through network analysis of D-loop variations in Korean native chicken populations.

- It was confirmed that KNC populations belong to five of the nine phylogenetic groups of Red Jungle Fowl.
- Most KNC populations are classified into A, B, and E groups, which are distributed across the Eurasian continent and these results suggest that KNC populations have diverse maternal origins.

+ SNP (Single Nucleotide Polymorphism)-based diversity analysis: using Illumina 600K chip

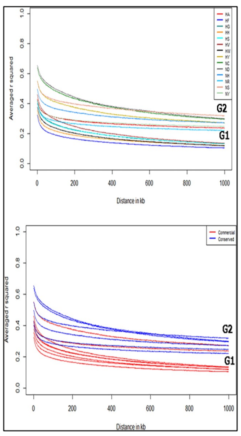
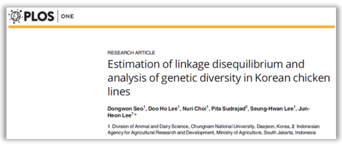


Figure 1. LD decay analysis results (r^2 values of Correlation between the closest markers)

The results indicated that commercial native chickens have less calculated LD (average, r^2 = 0.13–0.26) and purebred native chickens have more calculated LD (average, r^2 = 0.24–0.37) across the entire genome.


PLOS | ONE

RESEARCH ARTICLE

Estimation of linkage disequilibrium and analysis of genetic diversity in Korean chicken lines

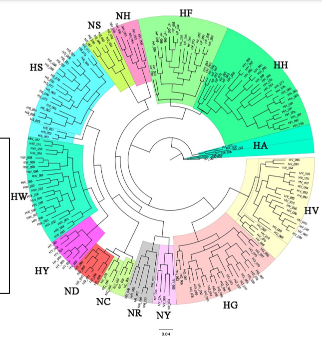
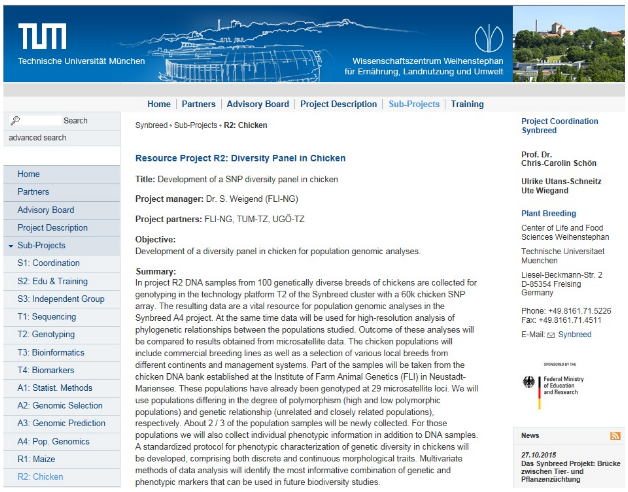


Figure 3. Phylogenetic analysis results for the 14 native chicken lines

+ SYNBREED genetic diversity study

❖ Comparison analysis with 600K chip data


Technische Universität München

Wissenschaftszentrum Weihenstephan für Ernährung, Landnutzung und Umwelt

Home | Partners | Advisory Board | Project Description | Sub-Projects | Training

Search

advanced search

Home
Partners
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Project Description
Sub-Projects
S1: Coordination
S2: Edu & Training
S3: Independent Group
T1: Sequencing
T2: Genotyping
T3: Bioinformatics
T4: Biomarkers
A1: Statist. Methods
A2: Genomic Selection
A3: Genomic Prediction
A4: Pop. Genomics
R1: Maize
R2: Chicken

Synbreed › Sub-Projects › R2: Chicken

Resource Project R2: Diversity Panel in Chicken

Title: Development of a SNP diversity panel in chicken

Project manager: Dr. S. Weigend (FLI-NG)

Project partners: FLI-NG, TUM-TZ, UGÖ-TZ

Objective:
Development of a diversity panel in chicken for population genomic analyses.

Summary:
In project R2 DNA samples from 100 genetically diverse breeds of chickens are collected for genotyping in the technology platform T2 of the Synbreed cluster with a 60k chicken SNP array. The resulting data are a vital resource for population genomic analyses in the Synbreed A4 project. At the same time data will be used for high-resolution analysis of phylogenetic relationships between the populations studied. Outcome of these analyses will be compared to results obtained from microsatellite data. The chicken populations will include commercial breeding lines as well as a selection of various local breeds from different continents and management systems. Part of the samples will be taken from the chicken DNA bank established at the Institute of Farm Animal Genetics (FLI) in Neustadt-Mariensee. These populations have already been genotyped at 29 microsatellite loci. We will use populations differing in the degree of polymorphism (high and low polymorphic populations) and genetic relationship (unrelated and closely related populations), respectively. About 2 / 3 of the population samples will be newly collected. For those populations we will also collect individual phenotypic information in addition to DNA samples. A standardized protocol for phenotypic characterization of genetic diversity in chickens will be developed, comprising both discrete and continuous morphological traits. Multivariate methods of data analysis will identify the most informative combination of genetic and phenotypic markers that can be used in future biodiversity studies.

Project Coordination Synbreed

Prof. Dr. Chris-Carolin Schön

Ulrike Utans-Schneitz
Ute Wiegand

Plant Breeding

Center of Life and Food Sciences Weihenstephan

Technische Universitaet Muenchen

Liesel-Beckmann-Str. 2
D-85354 Freising
Germany

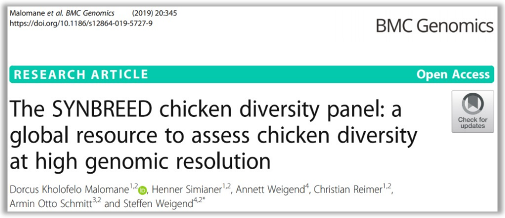
Phone: +49.8161.71.5226
Fax: +49.8161.71.4511

E-Mail: Synbreed

SPONSORED BY THE Federal Ministry of Education and Research

News

27.10.2015
Das Synbreed Projekt: Brücke zwischen Tier- und Pflanzenzüchtung


Malomane et al. BMC Genomics (2019) 20:345
https://doi.org/10.1186/s12864-019-5727-9

BMC Genomics

RESEARCH ARTICLE Open Access

The SYNBREED chicken diversity panel: a global resource to assess chicken diversity at high genomic resolution

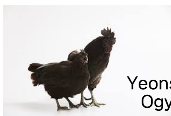
Dorcus Kholofelo Malomane[1,2], Henner Simianer[1,2], Annett Weigend[4], Christian Reimer[1,2], Armin Otto Schmitt[3,2] and Steffen Weigend[4,2*]

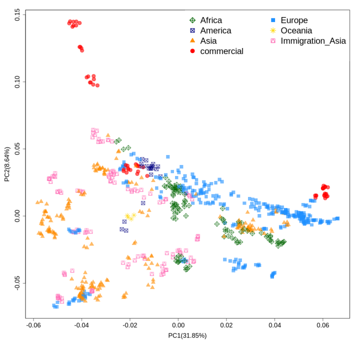
Dr. Steffan Weigend

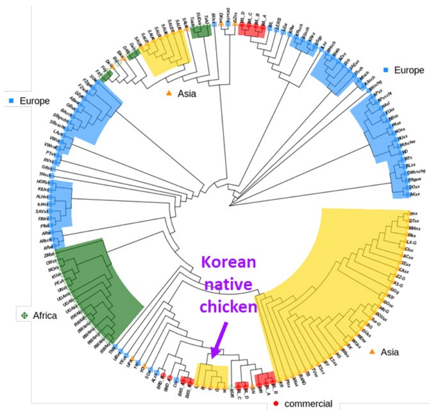
Cho *et al.*
Unpublished data

+ SYNBREED genetic diversity study (Cont.)

❖ Worldwide chicken SYNBREED data (174 breeds) + KNC chicken data (6 breeds)







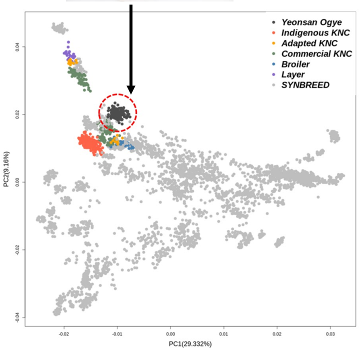


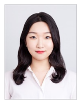
Fig. 2. Results of principal component analysis of 600K single nucleotide polymorphism genotype data.

Note that Yeonsan Ogye (within the red circle) is distinct from the other Korean breeds, and the foreign SYNBREED populations (Malomane et al., 2019). KNC, Korean native chicken.

- The total data were divided into 4 main clusters from a single continent and 2 sub-clusters with a multi-continent.

Chapter 1 Genetic Diversity Analyses in Korean native chicken

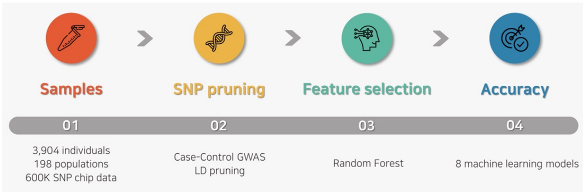
+ SNP Markers combinations for classifying Yeonsan Ogye Using Machine Learning

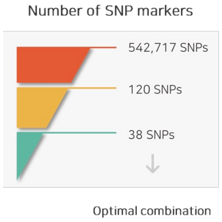



JAST

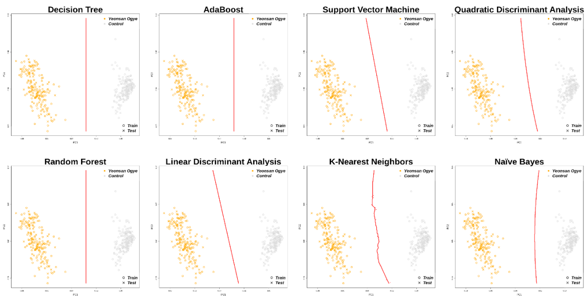
RESEARCH ARTICLE

Single nucleotide polymorphism marker combinations for classifying Yeonsan Ogye chicken using a machine learning approach





- Utilize machine learning-based feature selection techniques to select optimal and minimal markers.
- A total of 38 SNP marker combinations were confirmed through the selection process.



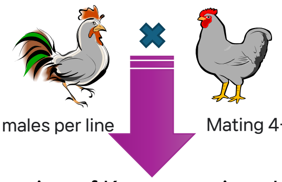
- Utilize machine learning-based feature selection techniques to select optimal and minimal markers.
- A total of 38 SNP marker combinations were confirmed through the selection process.

2. A study on the QTL and GWAS of Korean native chickens

+ QTL mapping for economically important traits for KNC

❖ Construction of reference population for QTL mapping

Within line mating



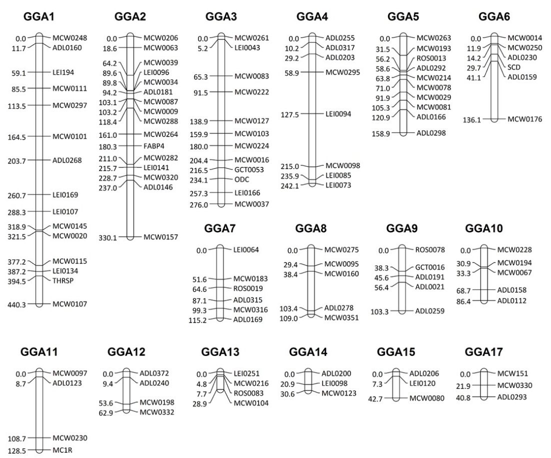
3 males per line

Mating 4-5 females per male

F1 generation of Korean native chicken (596)

Gray (110) Black (90) Red (135) White (126) Yellow (135)

+ Genome-wide linkage map (using MS markers) for Korean native chicken



Measurement of phenotypic traits for a total of 91 traits

- Color related: 2 traits (feather color, skin color)
- Growth related: 3 traits
- Meat quality: 9 traits
- Fatty acid related: 20 traits
- Volatile compounds: 43 traits
- Nucleic acid related: 4 traits
- Physiological function related: 2 traits
- Clinical measurement: 8 chemical traits

Open Access
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Vol. 29, No. 1 : 43-50 January 2016
http://dx.doi.org/10.5713/ajas.15.0193
www.ajas.info
pISSN 1011-2367 eISSN 1976-5517

Variance Component Quantitative Trait Locus Analysis for Body Weight Traits in Purebred Korean Native Chicken

Muhammad Cahyadi[1,2,a], Hee-Bok Park[1,a], Dong-Won Seo[1], Shil Jin[1], Nuri Choi[1], Kang-Nyeong Heo[3], Bo-Seok Kang[3], Cheorun Jo[4], and Jun-Heon Lee[1,*]
[1] Division of Animal and Dairy Science, Chungnam National University, Daejeon 305-764 Korea

Livestock Science 182 (2015) 145–150
Contents lists available at ScienceDirect
Livestock Science
journal homepage: www.elsevier.com/locate/livsci

QTL analyses of general compound, color, and pH traits in breast and thigh muscles in Korean native chicken

D.W. Seo[a,1], H.B. Park[a,1], S. Jung[a], M. Cahyadi[a,b], N.R. Choi[a], S. Jin[a], K.N. Heo[c], C. Jo[d], J.H. Lee[a,*]

LOD = 6.30
(Nominal P = 7.21E-08)

Figure 2 .Fullsib ... contents.

Position (cM)
QTL on GGA5

Mol Biol Rep (2016) 43:601–605
DOI 10.1007/s11033-016-3994-y

SHORT COMMUNICATION

Genome scan linkage analysis identifies quantitative trait loci affecting serum clinical–chemical traits in Korean native chicken

Dong-Won Seo[1] · Hee-Bok Park[1] · Shil Jin[1] · Muhammad Cahyadi[1,2] · Nuri Choi[1] · Kang-Nyeong Heo[3] · Cheorun Jo[4] · Jun-Heon Lee[1]

191 cM
= 2.64
= 0.00072)

...ine and breast IMP contents.

+ QTL mapping for Shank color variation

- Diverse shank color variations were observed in KNCs

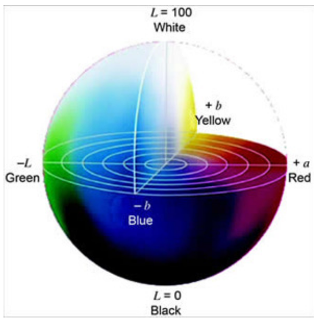


Table 3. The shank color variations and heritability values in five lines of Korean native chicken.

	G	L	R	W	Y	Average	h^2
L^*	54.05	46.67	56.02	55.09	56.14	53.59	0.87
a^*	-0.76	0.04	0.95	-0.31	0.52	0.09	0.71
b^*	2.70	3.78	11.31	8.15	13.77	7.94	0.70

Lightness (L^*), **Yellowness** (b^*), **Redness** (a^*)

Spectrophotometer (Minolta CM-3500d, Japan)

QTL mapping for Shank color variation

- Genome-wide scan at 1 cM intervals for linkage with variation in shank color (b*) in KNC

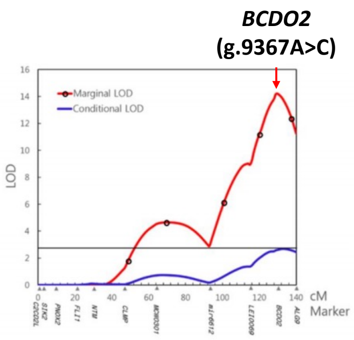
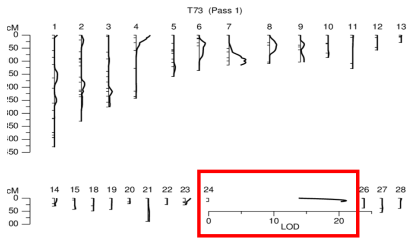


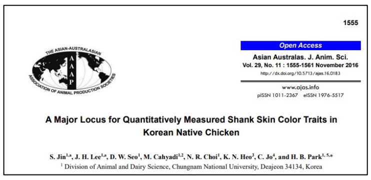
Figure 2. Test statistic (LOD score) curve for linkage with Variation in shank color(b*) in KNC



OPEN ACCESS Freely available online PLOS GENETICS

Identification of the *Yellow Skin* Gene Reveals a Hybrid Origin of the Domestic Chicken

Jonas Eriksson, Greger Larson, Ulrika Gunnarsson, Bertrand Bed'hom, Michele Tixier-Boichard, Lina Strömstedt, Dominic Wright, Annemieke Jungerius, Addie Vereijken, Ettore Randi, Per Jensen, Leif Andersson



1555

Open Access

Asian Australas. J. Anim. Sci. Vol. 29, No. 11 : 1555-1561 November 2016

A Major Locus for Quantitatively Measured Shank Skin Color Traits in Korean Native Chicken

S. Jin, J. H. Lee, D. W. Seo, M. Cahyadi, N. R. Choi, K. N. Heo, C. Jo, and H. B. Park

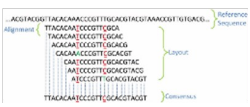
Division of Animal and Dairy Science, Chungnam National University, Daejeon 34134, Korea

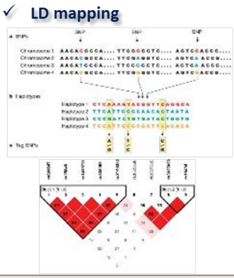
Seo *et al.* Unpublished data

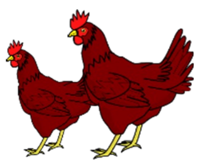
Development of customized SNP chip for selection of Korean chicken genome

- SNP Selection - Association study using High density SNP array

Reference Mapping and SNP Annotation	Estimation of Heatmap and LD	Low Density SNP Combination	KNC Genomic Prediction
✓ KNC 12 lines 120 sample reference mapping (GRCg6a Reference) ✓ SNP annotation	✓ Heatmap analysis ✓ LD mapping	✓ Low density SNPs imputation and calculation of accuracy ✓ Development of low-density SNP panel	✓ Genomic prediction by GEBV





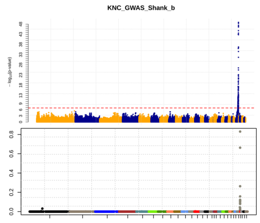


Seo *et al.* (2021)
Unpublished data

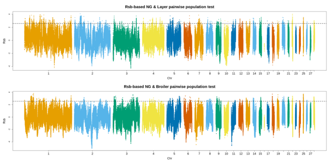
✚ Development of customized SNP chip for selection of Korean chicken genome

❖ SNP array design plan

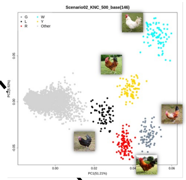
GWAS QTL markers



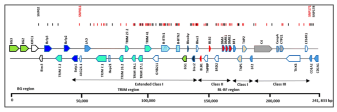
Signature of selection markers



Breed Identification markers



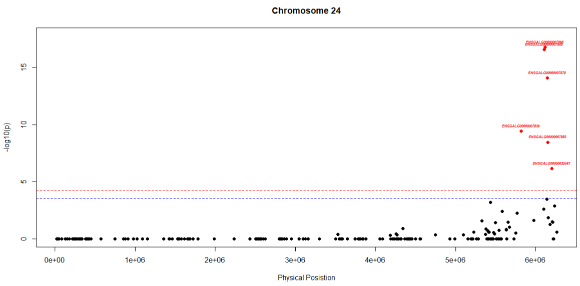
MHC markers



New KNC 50K SNP chip

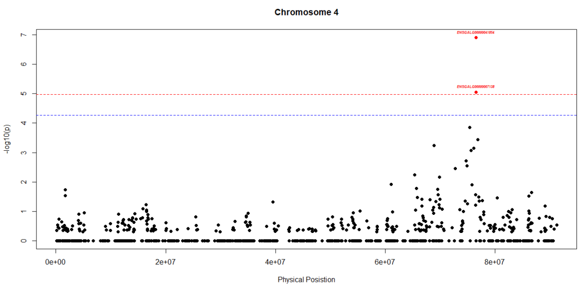
Cho *et al.*
Unpublished data

Shank color a*, b* GGA24



Marker	hgnc_symbol	start_position	end_position
ENSGALG00000007878		6145627	6148525
ENSGALG00000007848	PTS	6106022	6108646
ENSGALG00000007868	BCDO2	6110301	6130965
ENSGALG00000007839		5780707	5862536
ENSGALG00000007885		6148581	6155989
ENSGALG00000032467	C11orf52	6200315	6206582
ENSGALG00000021271		5436226	5442088
ENSGALG00000007833		5765420	5775028
ENSGALG00000007699	RPS25	5634320	5636087
ENSGALG00000043837		6097140	6100099

Growth 20w, Slaughter GGA4



Marker	hgnc_symbol	start_position	end_position
ENSGALG00000041854	FAM184B	76488439	76523293
ENSGALG00000007138	MED28	76527539	76530570
ENSGALG00000034621	KCNIP4	75415551	75452371

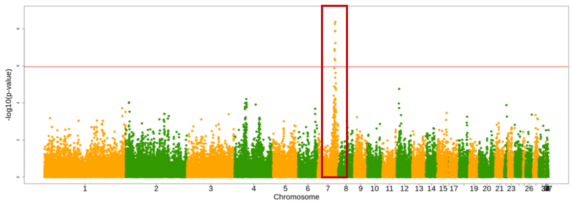
The same QTL locations were observed and SNP markers were identified using SNP chip

Chapter 2 A study on the QTL and GWAS of Korean native chickens

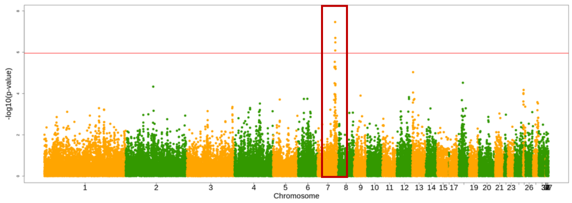
✚ GWAS results of taste-active compounds in chicken breast meat

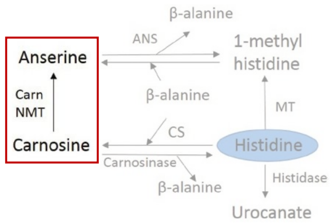
❖ Peptides - related to the meat flavor in chickens (Carnosine, Anserine)

Carnosine



Anserine

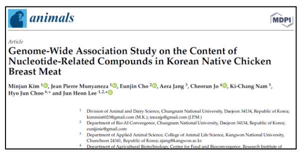




Carnosine and Anserine synthesis pathway
(S. M. Andersen, *et al.* (2016))

- Carnosine and Anserine shared significant genomic region
- Those traits were directly related in a synthesis pathway
- *HNMT* and *HNMT-like* genes were associated with the pathway

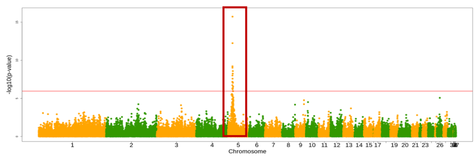
Chapter 2 A study on the QTL and GWAS of Korean native chickens



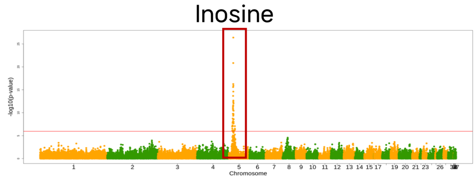
✚ GWAS results of taste-active compounds in chicken breast meat

❖ Nucleotide- related with meat flavor (IMP, Inosine, Hypoxanthine)

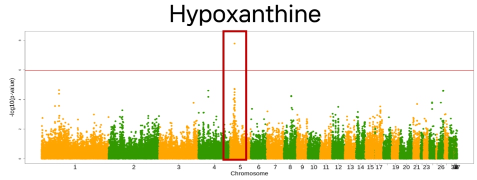
IMP

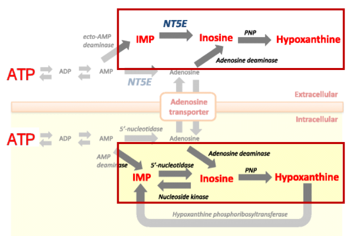


Inosine



Hypoxanthine

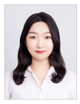




IMP degradation pathway in skeletal muscle
(Uemoto, Y. *et al.* (2017))

- Nucleotide-related compounds shared significant genomic region
- Amount of ATP in the muscle was related with all three traits
- Genes including *IGF2* and *DUSP8* were associated with the ATP contents in a muscle

➔ These genetic markers can be utilized for genomic selection to improve the taste of Korean native chicken meat.

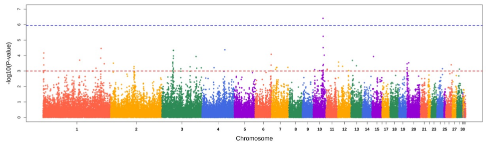


Cho *et al.* (2024)
Unpublished data

+ Machine learning application in significant SNP detection for GWAS

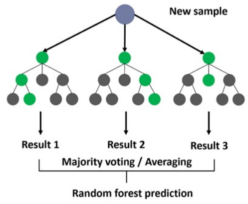
Background

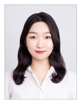
- GWAS have been utilized to enhance meat quality through genomic selection
- But, how can we accurately define significant SNPs in GWAS results?
- How about using machine learning methods?



Materials & Methods

- 829 KNC-R birds
- 6 traits (IMP, Alanine, Aspartic acid, Glutamic acid, Glycine, Valine)
- 44,638 SNPs from Illumina 60K Chip
- GWAS using GCTA-MLMA model
- Feature selection using RF regression based on the threshold $-\log_{10}(P\text{-value}) \geq 3$
- Functional annotation using candidate genes

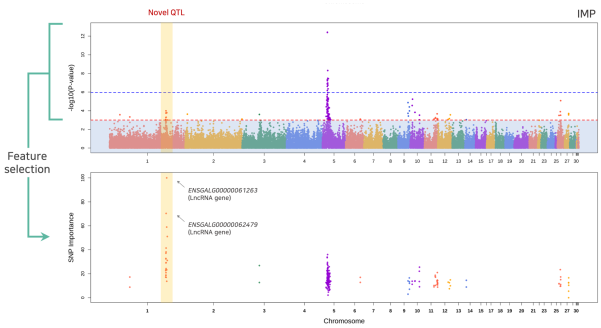


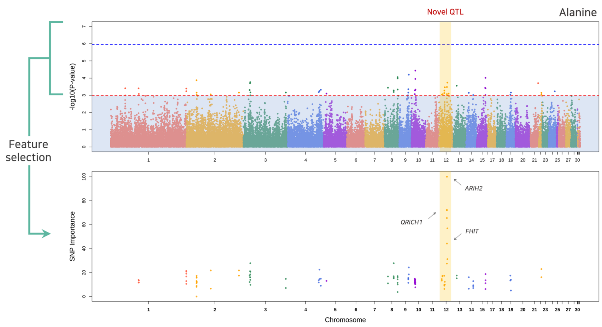


Cho *et al.* (2024)
Unpublished data

+ Machine learning application in significant SNP detection for GWAS

Results

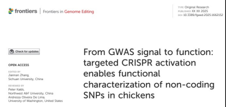




Conclusions

- ✔ Feature selection process revealed novel QTL regions for complex traits
- ✘ SNP interactions could not be verified due to the black box of the model

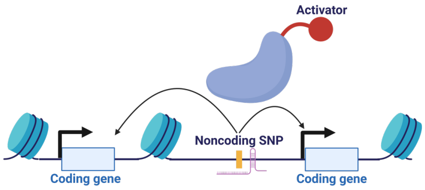
Functional validation of non-coding GWAS SNP regions using CRISPR toolkit



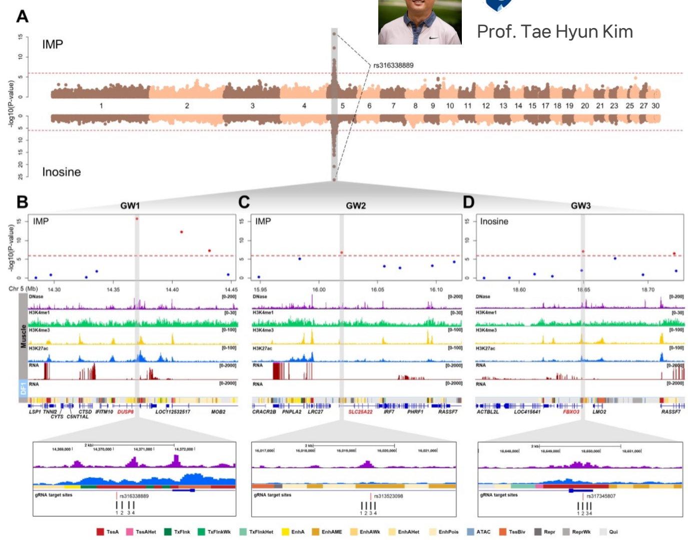
PennState

Prof. Tae Hyun Kim

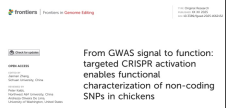
- Most SNPs identified through GWAS are located in non-coding regions, making it difficult to interpret their functional roles.
- CRISPR activation (CRISPRa) increases the expression of genes located near target regions.
- We used CRISPRa to activate SNP regions linked to nucleotides (IMP and inosine) and analyzed transcriptomic changes to identify associated functional phenotypes.



CRISPR activation

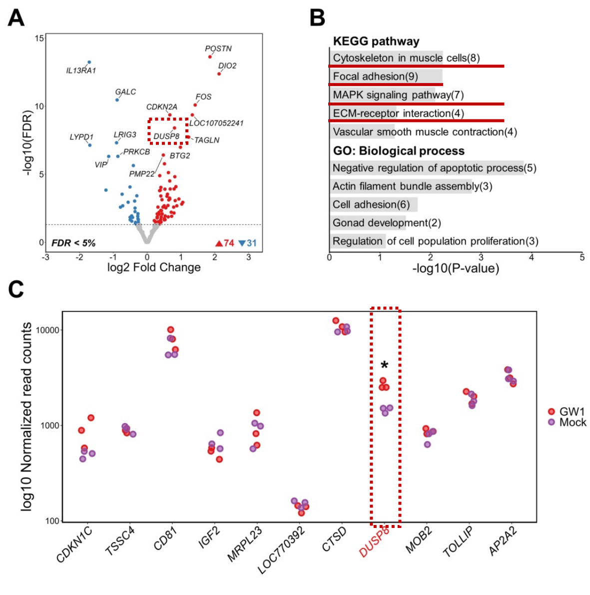


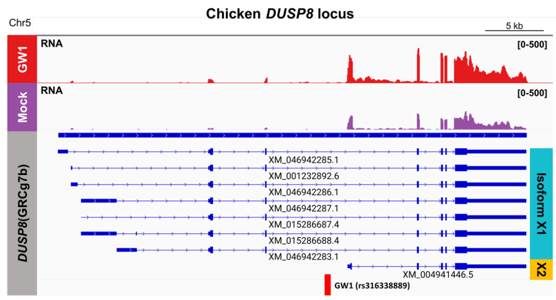
Functional validation of non-coding GWAS SNP regions using CRISPR toolkit



PennState

Prof. Tae Hyun Kim





- The most significant SNP was located in an intron of *DUSP8*, and its activation increased DUSP8 expression.
- Transcriptomic changes in muscle-related pathways which may indirectly affect purine metabolism.
- The most significant SNP increased transcripts of an isoform rather than the canonical transcript, suggesting that this region functions as an alternative promoter.

3. Selection signature studies in Korean native chickens

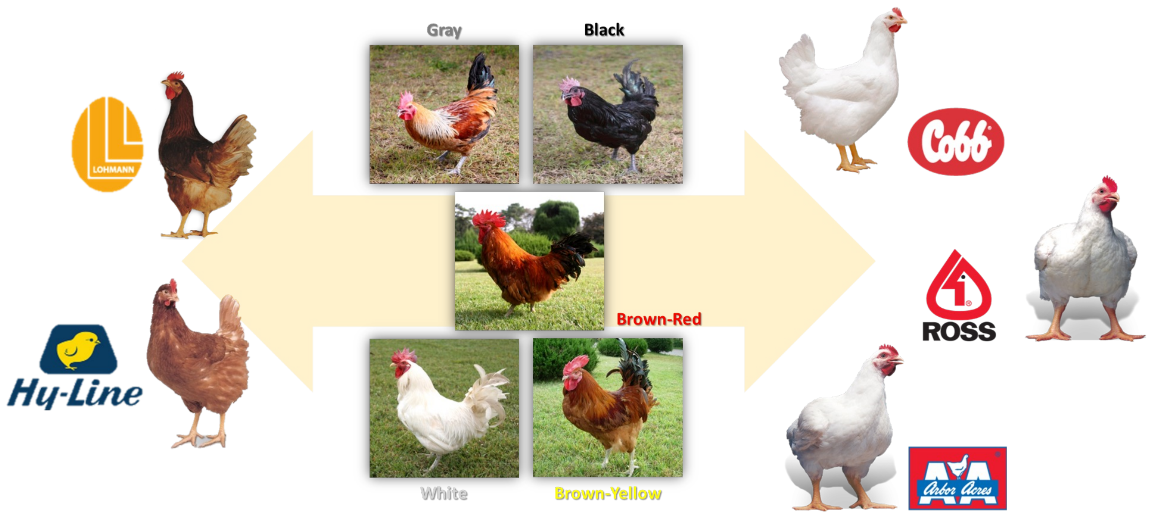
+ Selection Signal Analysis of KNC and Commercial Chickens

genes MDPI

Article

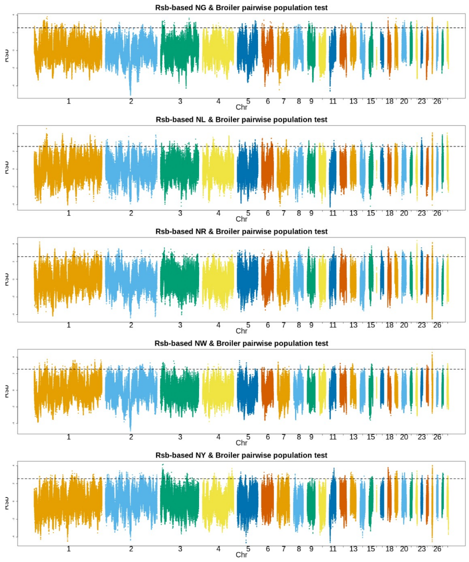
Comparison of Selection Signatures between Korean Native and Commercial Chickens Using 600K SNP Array Data

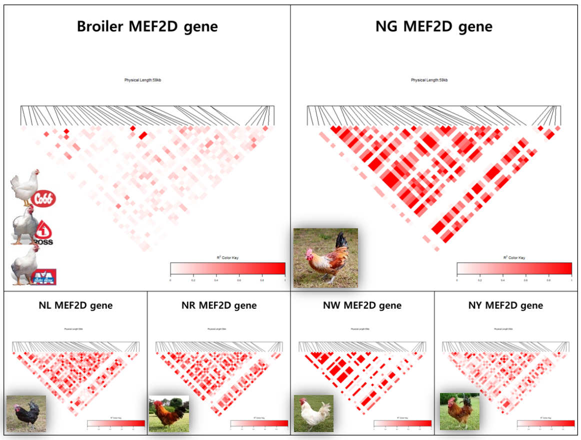
Sunghyun Cho [1], Prabuddha Manjula [1], Minjun Kim [1,2], Eunjin Cho [1], Dooho Lee [1], Seung Hwan Lee [1,2], Jun Heon Lee [1,2] and Dongwon Seo [1,2,*]



Commercial Layers | Korean native chicken | Commercial Broilers

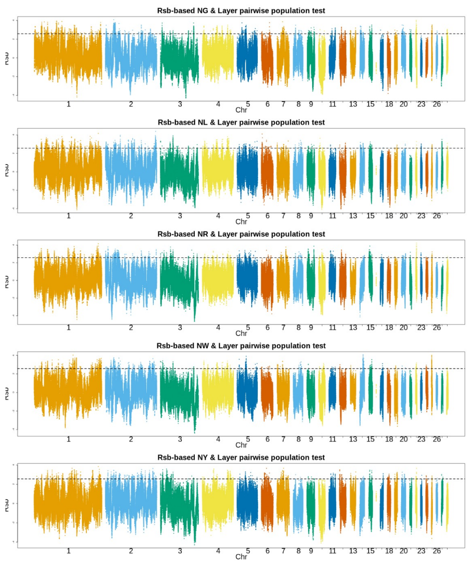
✚ Selection Signal Analysis of KNC and broiler

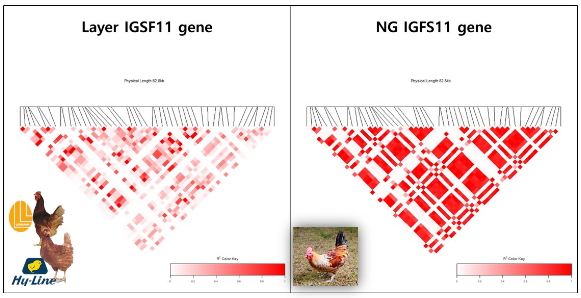




- This study confirmed the association of a selection signal with the MEF2D gene (Chr 25: 1,557,867–1,620,174 bp) in all KNC lines, in which a strong LD block was present compared with the broiler population
- The myocyte-specific enhancer-binding factor 2D (MEF2D) gene is a member of the MEF2 family and acts as a major regulator in the production of various muscles.

✚ Selection Signal Analysis of KNC and layer

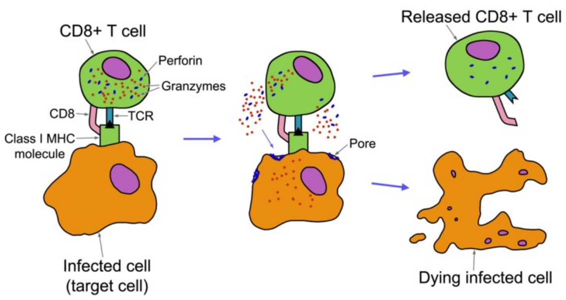




- Among the candidate selection signal genes immunoglobulin superfamily member 11 (IGSF11) genes have been associated with immune responses and disease sensitivity (Chr 1: 80,838,084 – 80,925,757 bp) .
- The IGSF11 gene is a member of the immunoglobulin superfamily and is mainly expressed in the brain and reproductive organs

4. MHC diversity study in Korean native chickens

+ What is MHC ?



(Wikimedia Commons, the free media repository)

- The Major Histocompatibility Complex (MHC) is a gene region encodes membrane bound glycoprotein molecules - Discriminating self/ non-self antigens
- Many of the genes within the MHC contribute to immunity (humoral/ cell mediate)

Xenotransplantation
Official Journal of the International Xenotransplantation Association

Characterization of the swine major histocompatibility complex alleles at eight loci in Westran pigs

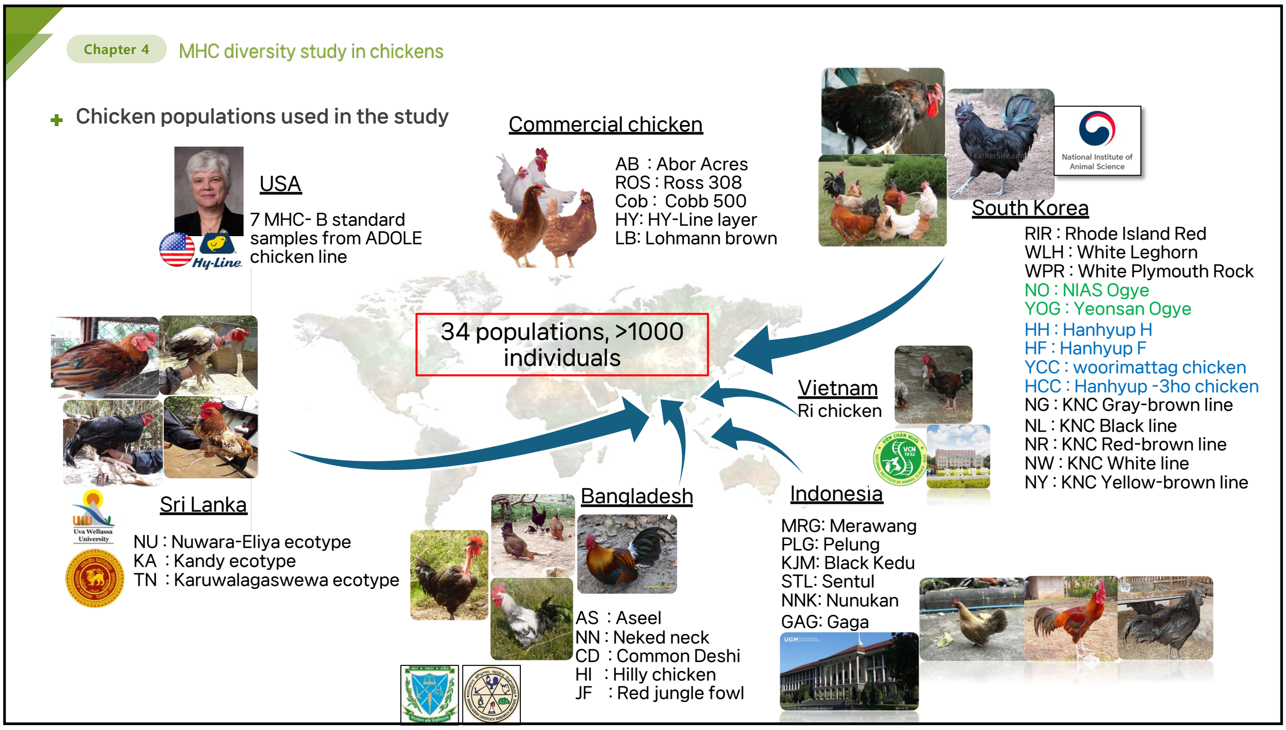
Jun-Heon Lee, Denbigh Simond, Wayne J. Hawthorne, Stacey N. Walters, Anita T. Patel, Douglas M. Smith, Phillip J. O'Connell, Chris Moran

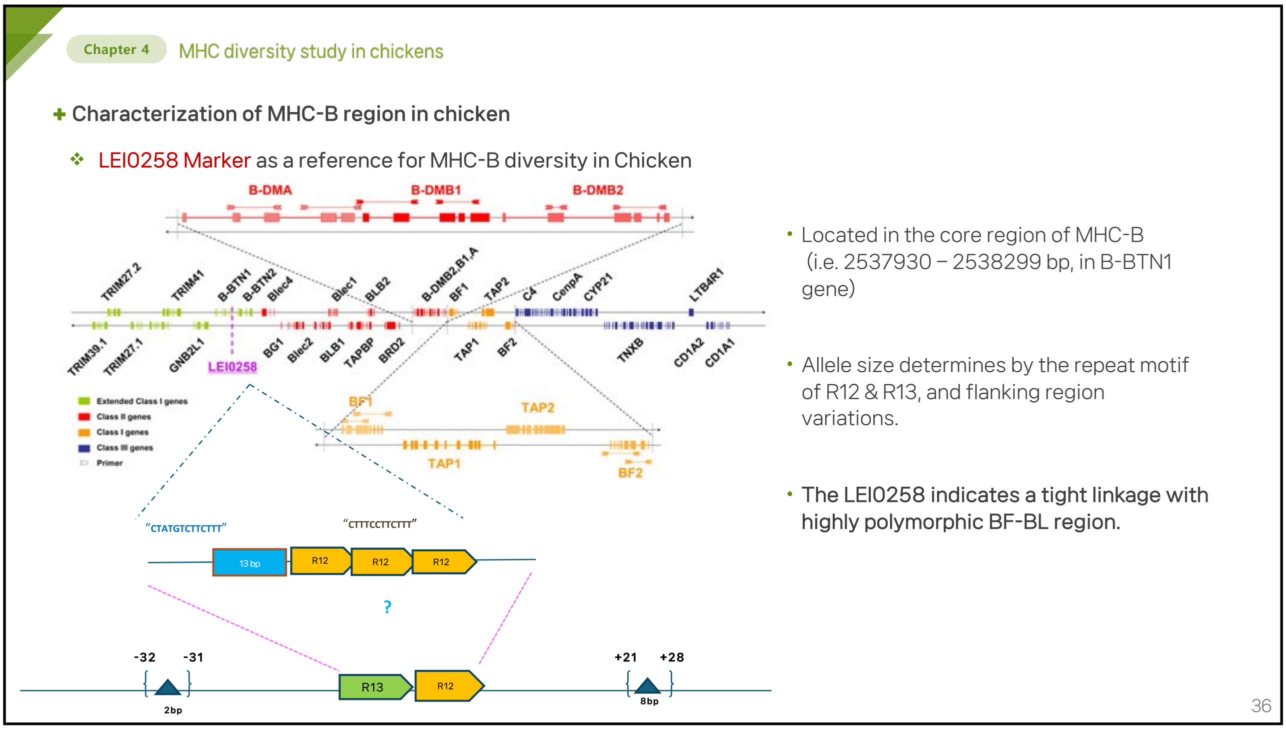
First published: 24 May 2005 | https://doi.org/10.1111/j.1399-3089.2005.00231.x | Citations: 42

MHC associated with;
- Xenotransplantation and immunity
- Design of effective vaccines
- Reproductive success
- Kin recognition
- Production traits of domestic animals

Every vertebrate animals contain MHC

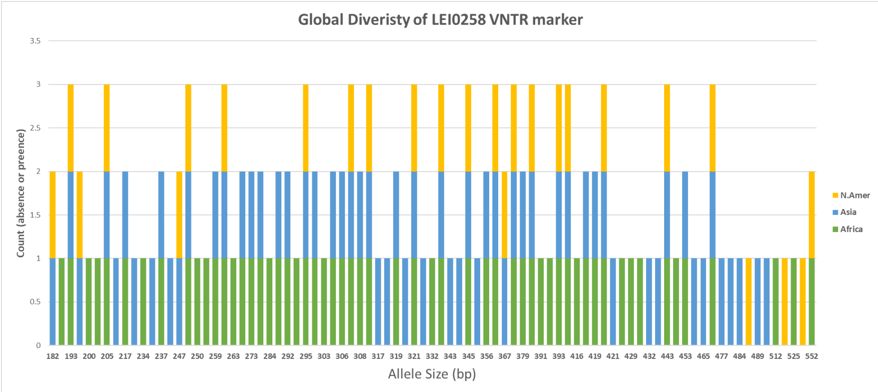
- Humans MHC – HLA
- Mouse MHC – H-2
- Rat MHC – H-1
- Chimpanzee MHC – ChLA
- Swine MHC – SLA
- Chicken – gaga MHC (B complex)

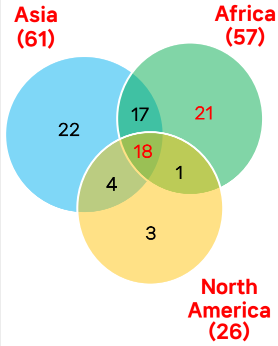

Chapter 4
MHC diversity study in chickens
Chicken populations used in the study
USA
7 MHC- B standard samples from ADOLE chicken line
Hy-Line
Commercial chicken
AB : Abor Acres
ROS : Ross 308
Cob : Cobb 500
HY: HY-Line layer
LB: Lohmann brown
National Institute of Animal Science
South Korea
RIR : Rhode Island Red
WLH : White Leghorn
WPR : White Plymouth Rock
NO : NIAS Ogye
YOG : Yeonsan Ogye
HH : Hanhyup H
HF : Hanhyup F
YCC : woorimattag chicken
HCC : Hanhyup -3ho chicken
NG : KNC Gray-brown line
NL : KNC Black line
NR : KNC Red-brown line
NW : KNC White line
NY : KNC Yellow-brown line
34 populations, >1000 individuals
Vietnam
Ri chicken
Sri Lanka
NU : Nuwara-Eliya ecotype
KA : Kandy ecotype
TN : Karuwalagaswewa ecotype
Bangladesh
AS : Aseel
NN : Neked neck
CD : Common Deshi
HI : Hilly chicken
JF : Red jungle fowl
Indonesia
MRG: Merawang
PLG: Pelung
KJM: Black Kedu
STL: Sentul
NNK: Nunukan
GAG: Gaga


Chapter 4
MHC diversity study in chickens
Characterization of MHC-B region in chicken
LEI0258 Marker as a reference for MHC-B diversity in Chicken
B-DMA
B-DMB1
B-DMB2
TRIM27.2
TRIM41
B-BTN1
B-BTN2
Blec4
Blec1
BLB2
B-DMB2.B1.A
BF1
TAP2
C4
CenpA
CYP21
LTB4R1
TRIM39.1
TRIM27.1
GNB2L1
LEI0258
BG1
Blec2
BLB1
TAPBP
BRD2
TAP1
BF2
TNXB
CD1A2
CD1A1
Extended Class I genes
Class II genes
Class I genes
Class III genes
Primer
BF1
TAP2
TAP1
BF2
"CTATGTCTTCTTT"
"CTTTCCTTCTTT"
13 bp
R12
R12
R12
?
-32
-31
2bp
R13
R12
+21
+28
8bp
Located in the core region of MHC-B (i.e. 2537930 – 2538299 bp, in B-BTN1 gene)
Allele size determines by the repeat motif of R12 & R13, and flanking region variations.
The LEI0258 indicates a tight linkage with highly polymorphic BF-BL region.
36

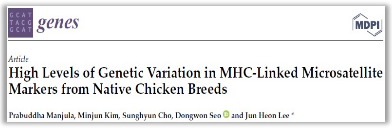
+ Global diversity LEI0258 locus

❖ LEI0258 allele size distribution in Africa, Asia, North American populations (Based on the LEI0258 sequence information)





- 86 alleles (182 -565 bp) > more alleles reported previously (181-552 bp)
- Variation in repeat motif units (R12 & R13), and flanking sequence polymorphism such as indels and SNPs are account for the high diversity of this marker


genes MDPI

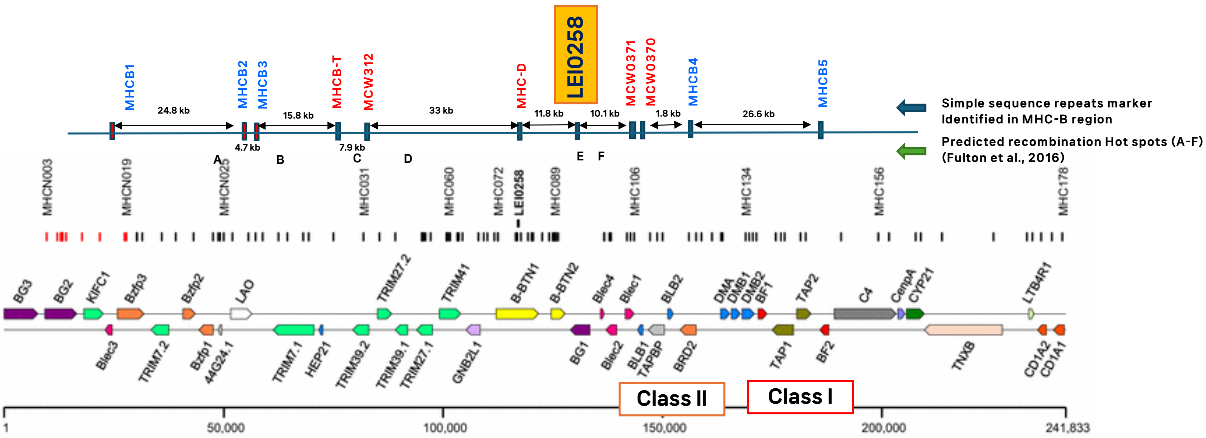
Article

High Levels of Genetic Variation in MHC-Linked Microsatellite Markers from Native Chicken Breeds

Prabuddha Manjula, Minjun Kim, Sunghyun Cho, Dongwon Seo and Jun Heon Lee *

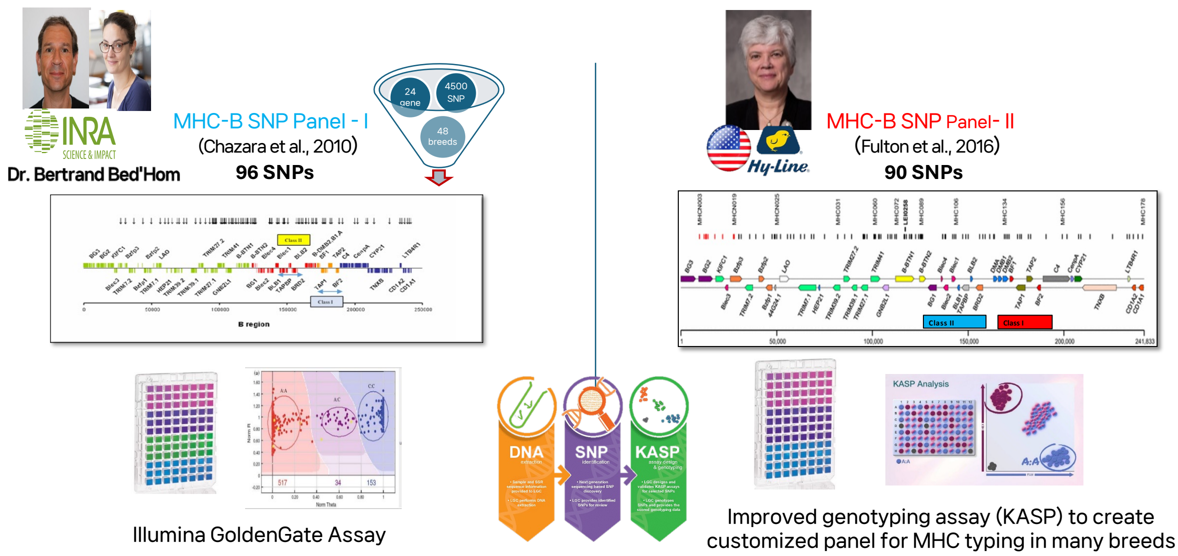
+ Updated MHC-B linked microsatellite markers

❖ Search for new MHC-B linked microsatellite markers – to identify accurate MHC allele variations



- Markers in blue color are identified using a in-silico tools, markers in red color are reported in literature and confirmed by In-silico tool. LEI0258 marker is reported in the core region of MHC-B.

+ Assessing the MHC diversity in chicken using a dedicated SNP panel



+ MHC-B SNP haplotype segregation based on Panel-I SNPs

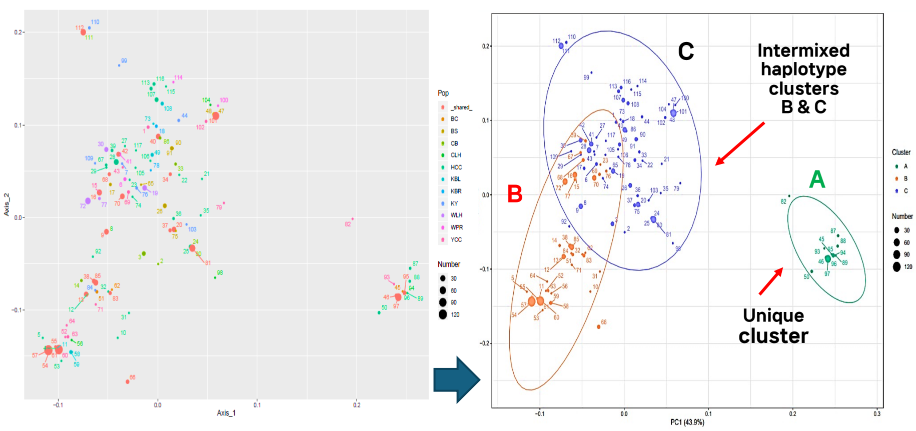


Figure. MHC-*B* SNP Haplotype principal component analysis plot: represents the SNP diversity of the 117 unique haplotypes (labels represent their MHC ID) by PCA

- Pop: color corresponds to private haplotypes for each breed, and shared haplotypes. Size of points corresponds to the counts of haplotype in each breed or in all populations (together for shared haplotypes).

✚ MHC-B haplotypes diversity in Six KNC strains – Using SNP panel-II (90 SNPs)

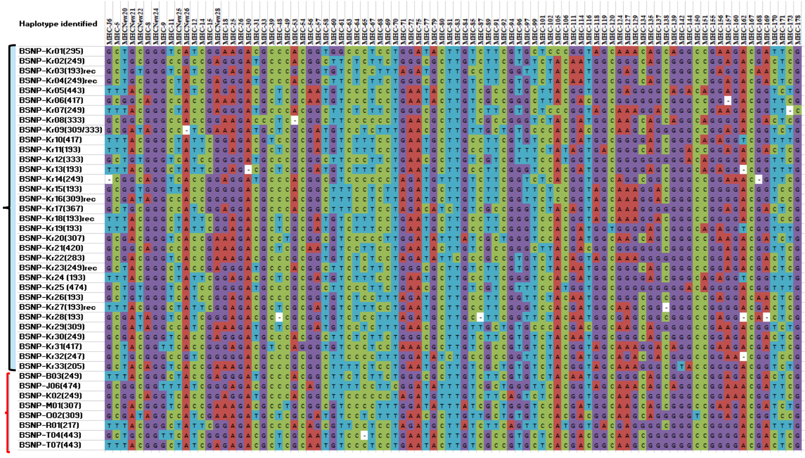
(Standard haplotype) SNP base Haplotype nomenclature (Novel haplotype)

MHC-B region, Holotype Family, Identification order → BSNP-AXX (LEI0258 size, *B*-Serotype)

MHC-B region, Origin, Identification order → BSNP-KrXX (LEI0258 size)

Novel haplotypes in KNC

Previously identified Standard Haplotypes in KNC



Roshani Fernando
Unpublished data

✚ Identification and Comparative Analysis of Novel Major Histocompatibility Complex-B Haplotypes in Indonesian Native Chickens

Colalboration with Prof
Dyah Maharani

Background

- The Major Histocompatibility Complex (MHC) is crucial for immune response and disease resistance in chickens
- Indonesian native chickens possess unique genetic traits providing valuable insight into:
  - Genetic diversity
  - Adaptation to local environments

Objectives

- Assess MHC-B genetic diversity within Indonesian native chicken populations
- Compare the Indonesian chicken MHC-B genetic diversity with standard reference haplotypes

Materials & Methods

- Six (06) populations of Indonesian native chicken: Merawang, Pelung, Black Kedu, Sentul, Nunukan and Gaga
- 90 SNPs from the high-density MHC-B SNP panel
- Applied kompetitive Allele-Specific PCR (KASP) for genotyping
- Haplotype Diversity Analysis: computational approach using the PHASE 2.1 programme
- MrBayes programme was used to investigate evolutionary relationships

Chapter 4 MHC diversity study in chickens

Results

Table. Numbers of individuals used from each population and summary of the obtained haplotypes

Population	Number of individuals	Number of haplotypes		
		Unique	Shared	Total
Merawang	25	38	2	40
Pelung	17	25	0	25
Black Kedu	30	16	3	19
Sentul	16	20	1	21
Nunukan	14	10	1	11
Gaga	20	12	0	12

No. of shared haplotypes = 03

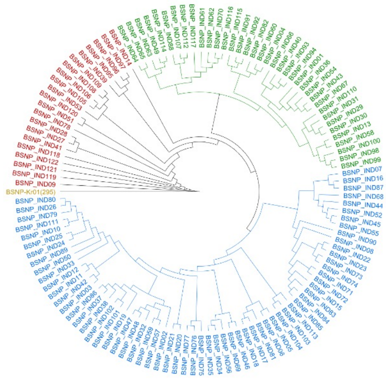


Figure. Bayesian approach-based circular cladogram for BSNP haplotypes of Indonesian chickens. Three subclades were identified.

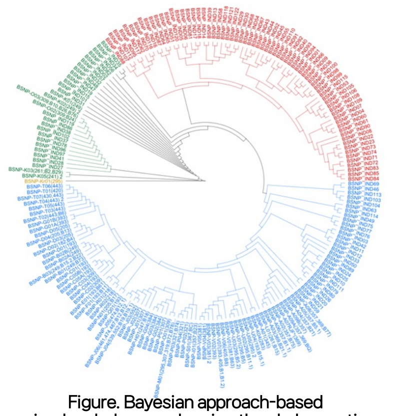


Figure. Bayesian approach-based circular cladogram showing the phylogenetic relationships among BSNP Haplotypes of Indonesian chickens and standard reference haplotypes.

Conclusion

- The present study discovered a set of unique MHC-B haplotypes in Indonesian native chicken at the local level, suggesting that the observed populations are diverse for MHC-B region
- A comparison with standard reference haplotypes revealed no 100% matches, suggesting that these haplotypes are novel and specific to the Indonesian population

Chapter 4 MHC diversity study in chickens

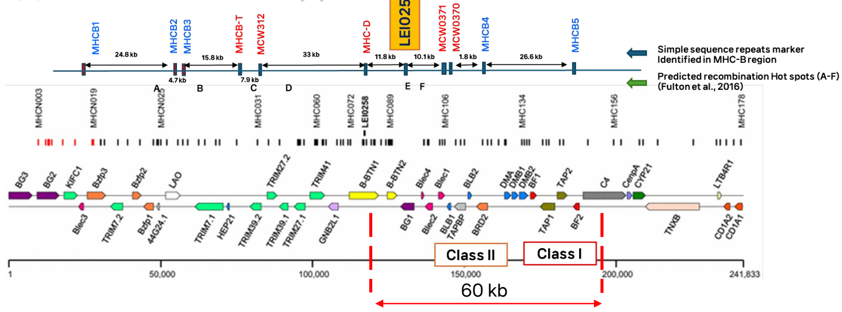
frontiers | Frontiers in Genetics

Application of next-generation sequencing for the high-resolution typing of MHC-*B* in Korean native chicken

Thisarani Kalhari Ediriweera[1], Prabuddha Manjula[2], Eunjin Cho[1], Minjun Kim[3] and Jun Heon Lee[1,3]*

+ High resolution Genotyping of MHC-B region of KNC lines

- This study aim to genotype the MHC-B region of Korean Native Chicken (KNC)
- Chickens homozygous for MHC-B linked 90 SNPs panel and LEI0258 marker were used
- Five KNC lines and the Ogye breed was studied for their MHC regions
- Chicken microchromosome 16
- MHC-B region
- Genes: from BG1 – C4
- Approximately 60 kb region



Map of the MHC-*B* region based on [GenBank: AB268588, and NC_006103.5]

44

+ Long range PCR (LR-PCR) & NGS base haplotyping of Target gene of MHC-B

- Provides high resolution application for MHC haplotyping
- Details variation in the stable Class I and Class II genes can be evaluate in comparison with standards haplotypes

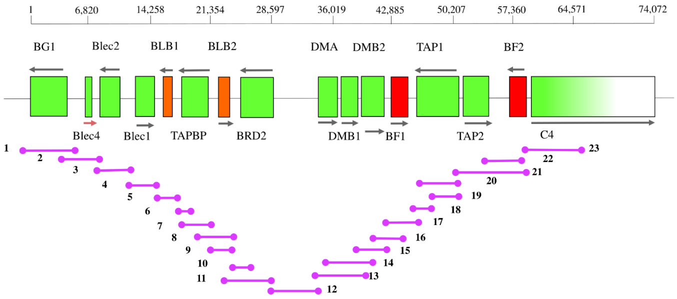
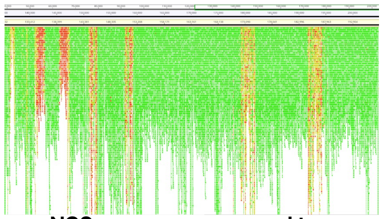
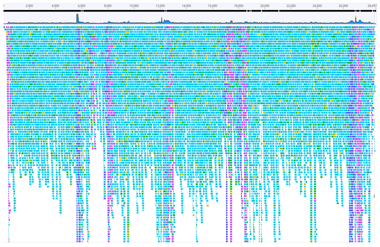


Figure. Map for the LR-PCR primers used to amplify the MHC-*B* region



NGS sequences mapped to reference

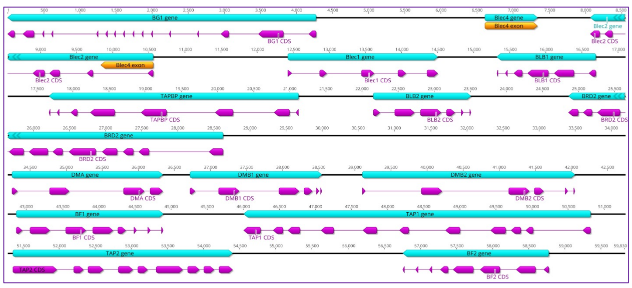


De novo assembly of NGS sequences

- Use of LR-PCR to perform NGS on large genomic regions have benefits, especially when the entire gene regions including introns are of interest

+ Genes and Exons annotations for MHC-B region of KNC

- The consensus sequence for MHC-B region (BG1 – BF2) of all the 5 KNC lines and the Ogye breed were generated
- The generated consensus sequences were annotated for their genes (and pseudogenes) and exons
- The final results were submitted to the GenBank



A visualization of the MHC genes, pseudogenes and exons

```
##Assembly-Data-START##
Assembly Method        :: Geneious Prime v. 2022.0.1
Assembly Name          :: Gallus gallus - Korean Native Chicken
                       (KNC_Black line) _ BG1-BF2 of MHC-B region
Coverage               :: 61,070
Sequencing Technology :: Illumina
##Assembly-Data-END##
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                     /db_xref="taxon:9031"
                     /country="South Korea"
                     /breed="Korean Native Chicken (KNC)"
   gene              complement(542..4807)
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   CDS               complement(join(542..633,750..899,1018..1038,1143..1163,
                     1771..1791,1895..1918,2014..2034,2138..2158,2269..2289,
                     2394..2414,2525..2545,2775..2795,3163..3183,3492..3596,
                     4013..4354,4708..4807))
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                     /codon_start=1
                     /product="lectin like natural killer cell surface protein"
```

An example of a GenBank annotation prepared

Agulto *et al.* (2025)
Unpublished data

✚ Genetic Characterization of MHC I Genes in KNC

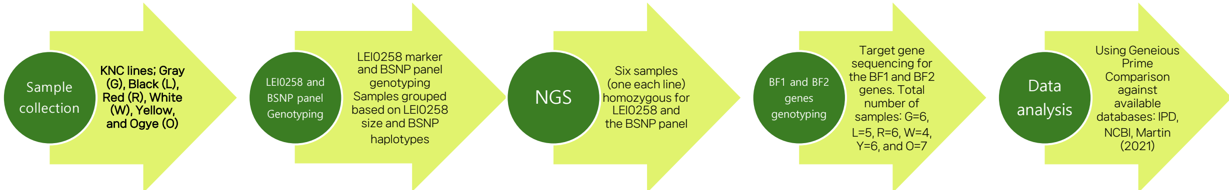
Background

- The Class I BF2 gene in the MHC region, particularly the B21 haplotype, is linked to immune responses against diseases such as Marek's disease
- However, the existing LEI0258 microsatellite marker and 90-SNP panel for MHC do not fully capture the high polymorphism of the BF1 and BF2 genes

Objective

- To genetically characterize the MHC class I, BF1 and BF2 genes in Korean native chicken (KNC) breeds in relation to the LEI0258 marker and the 90-SNP panel (BSNP)

Materials and Methods



Chapter 4 MHC diversity study in chickens

Results and Discussion

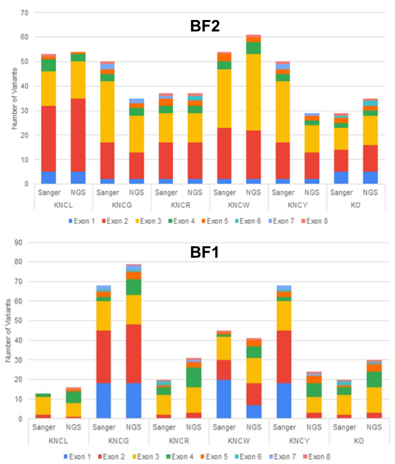


Figure 1. Variant Distribution: NGS vs. Sanger. Alignment to the reference sequence (accession no. AB268588); most variants found in exons 2 & 3 (peptide-binding regions).

Figure 2. MHC Class I Exon 2 and 3 Clusters. Exon 2 & 3 regions extracted and aligned with data from Martin (2021); KNC samples properly clustered into the BF2 clade, with four haplotypes remaining to be unique.

Conclusion

- The KNC population showed strong genetic diversity in the BF2 gene, giving insight into their possible immune response to diseases.
- This data can help guide breeding programs to select BF2 haplotypes that may improve disease resistance in KNC populations

Chapter 4 MHC diversity study in chickens

Ongoing research for Genetic Characterization of MHC Genes

- Chungnam National University hosted CCAT2025 conference
- CCAT2025 : **CNU Conference of Advanced Technology 2025 (Sep 24-26, 2025)**

- A session is hosted in the Department of Animal science, called "Animal Bio Big Data"

A telomere-to-telomere pangenome reveals structural variations as key drivers of complex traits in chickens

Ranran Liu
liuranran@caas.cn

- Provide long-read 8 Chinese native chicken samples
- Plan to generate long-read Korean native chicken samples
- Can be used for the structural variation in the MHC region

Summary

1. Genetic Diversity – The KNC population exhibits unique genetic characteristics based on diversity analyses.
2. GWAS Findings – Genome-wide association studies identified QTLs related to shank color and meat quality traits in KNC.
3. Functional Validation – CRISPR validation confirmed that GWAS-identified SNP regions associated with gene expression linked to the phenotype.
4. Selection Signatures – KNC population show genetic similarities to both meat-type and layer-type breeds through selection signature analyses.
5. MHC Study – The MHC analysis suggests that KNC may possess unique genetic variants contributing to disease resistance.

Conclusion

- **These findings provide valuable insights for the conservation and genetic improvement of native chicken populations**
- **Future studies will expand on these results using high-resolution sequencing data rather than SNP chip.**

Chungnam National University

National Institute of Animal Science

ANIMAL MOLECULAR GENETICS LAB.

Acknowledgements

AMG lab members in Chungnam National University

Thank you.

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3. OVERVIEW OF H'MONG CATTLE - A VALUABLE LIVESTOCK GENETIC RESOURCE

PROF. NGUYEN XUAN TRACH
VIETNAM NATIONAL UNIVERSITY OF AGRICULTURE

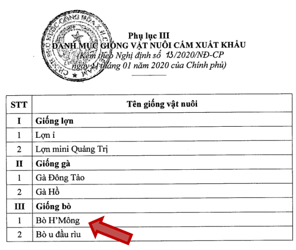
H'MONG CATTLE
A VALUABLE LIVESTOCK GENETIC RESOURCE

by
Prof. Dr. Nguyen Xuan Trach

VNUA, 2025

INTRODUCTION

- H'Mong cattle (also known as Meo cattle, Cao Bang humped cattle, Dong Van cattle, or highland yellow cattle) are commonly raised by the H'Mong people and other ethnic minorities in highland areas.
- Serving as a livelihood and a cultural symbol of the H'Mong people.
- Considered to have significant advantages over other local Vietnamese cattle.
- H'Mong beef is famous for its fragrance, tenderness, and fine texture.
- The breed is listed in the government's prohibited export category.



Phụ lục III
DANH MỤC GIỐNG VẬT NUÔI CẤM XUẤT KHẨU
(Kèm theo Nghị định số 13/2020/NĐ-CP ngày [illegible] tháng 01 năm 2020 của Chính phủ)

STT	Tên giống vật nuôi
I	**Giống lợn**
1	Lợn ỉ
2	Lợn mini Quảng Trị
II	**Giống gà**
1	Gà Đông Tảo
2	Gà Hồ
III	**Giống bò**
1	Bò H'Mông
2	Bò u đầu rìu

INTRODUCTION

- Several projects have been developed to promote H'Mong cattle farming.
- Some businesses have invested in branding H'Mong beef.

- *What are the actual advantages and limitations of this breed?*
- *What are the solutions for sustainably utilizing this genetic resource?*

CONTENTS

- ORIGIN OF H'MONG CATTLE
- APPEARANCE AND BODY SIZE
- MEAT PRODUCTIVITY
- REPRODUCTIVE PERFOMANCE
- DRAFT POWER
- ADAPTABILITY
- R & D ORIENTATION
- CONCLUSIONS
- Q & A

ORIGIN OF H'MONG CATTLE

- **Historical Background**
  - ✓ H'Mong people migrated southward for a long history.
  - ✓ Nowadays, the H'Mong primarily reside in rugged mountainous regions stretching from Southwest China to Vietnam, Northern Laos, Northeast Thailand, and Northeeast Myanmar.
  - ✓ H'Mong people arrived in Vietnam in three major waves:
    1. Late 17th - Early 18th century: Following the failure of the "Reformation of Local Rule" policies.
    2. 1796-1820: After the unsuccessful resistance against Emperor Qianlong and Gia Khanh.
    3. 1840-1868: After the collapse of the Taiping Rebellion.

❖ The H'Mong cattle followed the H'Mong people migrating from China to Vietnam?

ORIGIN OF H'MONG CATTLE

- **Historical Background**
  - ✓ In Vietnam:
    - Alternative names: Miao, Miêu, Mèo, Mẹo, Lao Sung
    - Population: Nearly 1.4 million people
    - Distribution: Mountainous Northern region, Northern Central region, and Central Highlands.

❖ *The H'Mong cattle is an indigenous breed created by the H'Mong people after they arrived in Vietnam?*

ORIGIN OF H’MONG CATTLE

- **Historical Background**

Which cattle breeds are raised by newly migrated H’Mong people in the Central Highlands?

- ✓ They use local cattle breeds provided by the Government, such as the Vang and Laisind breeds.
- ✓ Cattle raising is their main activity, and they take better care of their cattle compared to the local ethnic groups.
- ✓ They buy cattle from H’Mong people in Thailand, Laos, and Cao Bang to raise as fighting bulls → CULTURE.

➔ Wherever there are H’Mong people, there are H’Mong cattle (not only in Vietnam).

ORIGIN OF H’MONG CATTLE

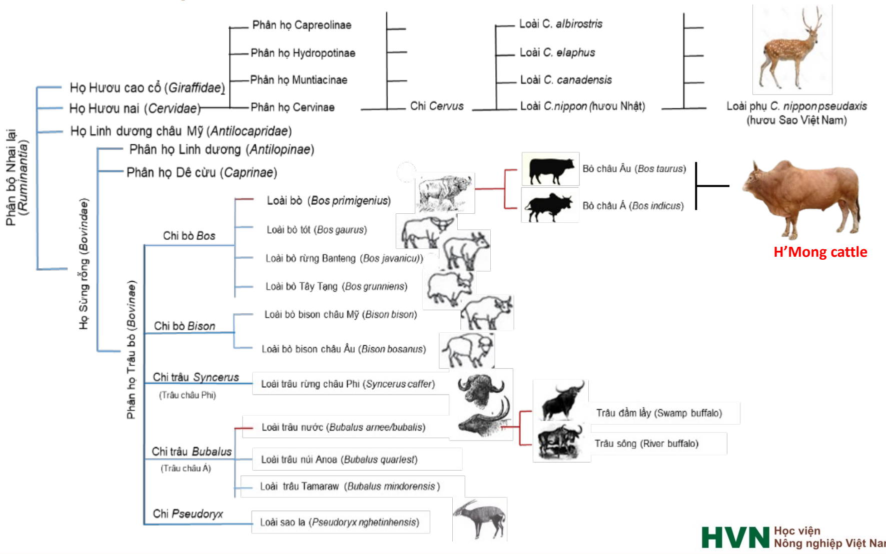
- **Genetic evidence**

- ✓ Phạm Doan Lan et al. (2008): The H’Mong cattle have a homogeneous genetic structure and a high level of genetic diversity.
- ✓ Berthouly et al. (2010):
  - All individuals carry a zebu-type Y chromosome, while there is a mixture of taurine and zebu maternal lineages.
  - H’Mong cattle are positioned between the taurine and zebu genetic groups in the neighbor-joining (NJ) phylogenetic tree.
- ✓ Le Trung Thanh et al. (2013): H’Mong cattle are genetically distinct from other local breeds, indicating a separate genetic origin.
- ✓ The presence of both taurine and zebu maternal lineages resembles the genetic pattern of cattle in southern China (Cai et al., 2006; Lei et al., 2006).

⇒ The H’Mong cattle originated from southern Chinese cattle as a result of historical crossbreeding (*Bos indicus* × *Bos taurus*).

ORIGIN OF H'MONG CATTLE

- **Taxonomy**



PHYSICAL CHARACTERISTICS

- **Apperance:**
  - ✓ Small ears growing horizontally; slightly curved back; long rump; tall legs; slightly convex or flat forhead; broad dewlap.
  - ✓ Bulls have a fairly high shoulder hump, a long body, a robust physique, and well-developed muscles; cows have a smaller shoulder hump but a large udder.
  - ✓ The coat color varies: light yellow, chestnut brown, dark red, or jet black.
  - ✓ Eyes and eyelashes are slightly yellowish, with a bright yellow ring around the eye corners.

- ➢ H'Mong cattle share similarities with the Southern Yellow cattle group.
- ➢ They are intermediate between European cattle (*Bos taurus*) and Indian humped cattle (*Bos indicus*).

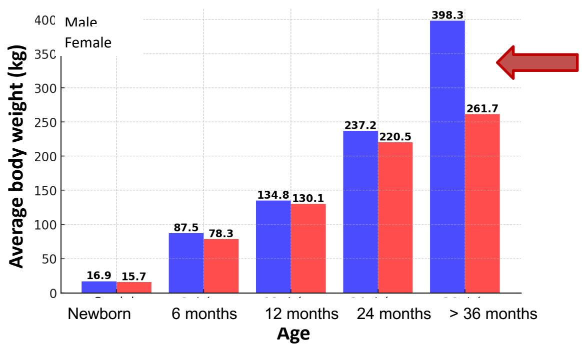
PHYSICAL CHARACTERISTICS

- **Body size**

Age	Male (kg)	Female (kg)	Source
Newborn	15-16	15-16	Viện Chăn nuôi (2004)
	17-18	14-16	Đào Lan Nhi (2012)
	17.34	16.87	Trần Văn Thăng & cs. (2014)
	16.25	15.72	Nguyễn Thị Ngoan & cs. (2015)
6 months	90.45	78.34	Trần Huê Viên (2016)
	87.45	78.34	Trần Văn Thăng & cs. (2014)
12 months	141.41	137.92	Nguyễn Thị Ngoan & cs. (2015)
24 months	233-275	216-225	Đào Lan Nhi (2012)
	321.3	267.4	Trần Huê Viên (2016)
≥36 months	397.83	261.86	Nguyễn Thị Ngoan & cs. (2015)
	380-390	250-270	Viện Chăn nuôi (2004)
	400-450	250-280	Nguyễn Văn Niêm & cs. (2001)
	382-388	250-270	Đào Lan Nhi (2012)

PHYSICAL CHARACTERISTICS

- **Body size**



- **Local Yellow Cattle**: Birth weight 12-15kg, Mature weight (male: 200-250kg, female: 160-200kg).
- **Sindhi Crossbred Cattle**: Birth weight 17-19kg, Mature weight (male: 350-450kg, female: 250-300kg).

➢ *Bigger than Yellow cattle, comparable to Sindhi crossbred cattle*

HVN Học viện Nông nghiệp Việt Nam

MEAT PRODUCTIVITY

- **Average daily gain (ADG)**

Age period	ADG (g/head/day)	Source
Birth to 6 months (male)	406.16	Trần Văn Thăng & cs. (2014)
Birth to 6 months (female)	341.50	Trần Văn Thăng & cs. (2014)
18 – 24 months of age	294	Nguyễn Đàm Thuyên (2012)
24 - 36 months of age	135	Nguyễn Đàm Thuyên (2012)
Fattened at 2 years of age	540	Hoàng Xuân Trường (2018)
Fattened at 3 years of age	387	Hoàng Xuân Trường (2018)
Fattened at 4 years of age	323	Hoàng Xuân Trường (2018)

➢ *Comparable to local Yellow cattle but lower than Sindhi crossbred cattle.*

MEAT PRODUCTIVITY

- **Meat Yields**

Parameter	Value (%)	Source
Dressing percentage	52.12	Nguyễn Văn Niêm & cs. (2001)
	50-52	Đào Lan Nhi (2012)
	55	Hoàng Xuân Trường (2018)
Meat percentage	40.33	Nguyễn Văn Niêm & cs. (2001)
	38-40	Đào Lan Nhi (2012)
	45	Hoàng Xuân Trường (2018)
Class 1 meat	>45	Trần Huê Viên (2016)

➢ *Higher than local Yellow cattle, similar to Sindhi crossbred cattle.*

MEAT PRODUCTIVITY

- **Meat quality**

Parameter	Age at fattening (years)		
	2	3	4
Chemical composition			
Dry mater (%)	25.35	25.03	25.10
Protein (% DM)	77.48	3.68	3.78
Ash (% DM)	3.67	77.24	77.12
Fat (% DM)	7.18	7.55	7.96
pH			
after 45 minutes	6.62	6.87	6.82
after 24 hours	5.57	5.72	5.67
after 48 hours	5.61	5.59	5.56

Source: Hoàng Xuân Trường (2018)

MEAT PRODUCTIVITY

- **Meat quality** (cond.)

Parameters	Age at fattening (years)		
	2	3	4
Colour (after 48h)			
Lightness (L*)	42.57	39.34	37.05
Redness (a*)	21.11	20.73	20.82
Yellowness (b*)	10.14	10.88	11.03
Water loss after preservation/processing (%)			
after 24h	1.9/37.0	1.8/32.6	1.40/31.18
after 48h	2.4/38.5	1.7/35.5	1.52/34.45
Toughness (N)*			
after 24h	65.10	70.00	86.50
after 48h	64.21	69.04	84.31

Source: Hoàng Xuân Trường (2018)

- ➢ *More tender than Yellow cattle and Zebu hybrids.*
- ➢ *Comparable to tropical beef breeds.*

REPRODUCTIVE PERFORMANCE

- **Cows**

Parameters	Average	Source
Age at first calving (months)	33.44	Trần Xuân Vũ (2012)
	33-35	Đào Lan Nhi (2012)
	36.78	Trần Huê Viên (2016)
Days open (months)	3.58	Trần Huê Viên (2016)
Conception after first insemination (%)	45.28	Trần Xuân Vũ (2012)
Calving interval (months)	17.23	Trần Xuân Vũ (2012)
	12.79	Trần Huê Viên (2016)
1 calving/year (%)	47.09	Nguyễn Thị Ngoan (2015)
	60	Hoàng Xuân Trường (2018)
2 calvings/3 years (%)	42.38	Nguyễn Thị Ngoan (2015)
	35	Hoàng Xuân Trường (2018)

REPRODUCTIVE PERFORMANCE

- **Bulls**

Parameters	Average	Source
Semen volume (V, ml)	4.37	Trần Xuân Vũ (2012)
	4.43	Trịnh Xuân Bình (2013)
	4.50 (Summer-Fall) 6.10 (Winter-Spring)	Trịnh Quang Phong & Phan Văn Kiểm (2006)
Sperm activity (A, %)	67.98	Trần Xuân Vũ (2012)
	68.97	Trịnh Xuân Bình (2013)
	70 before freezing, 30 after thrawing in Summer-Fall; 80 before freezing, 35 after thrawing in Winter-Spring	Trịnh Quang Phong & Phan Văn Kiểm (2006)
Sperm concentration (C, bil./ml)	0.84	Trần Xuân Vũ (2012)
	0.85	Trịnh Xuân Bình (2013)
	0.85 (Summer-Fall) 0.98 (Winter-Spring)	Trịnh Quang Phong & Phan Văn Kiểm (2006)
Total active sperms (bil.)	2.5	Trần Xuân Vũ (2012)
Abnormal sperms (%)	16.26	Trần Xuân Vũ (2012)
	16.57	Trịnh Xuân Bình (2013)
Active sperms after thrawing (%)	83.47	Trịnh Xuân Bình (2013)
Semen pH	6.74	Trần Xuân Vũ (2012)

R & D ORIENTATION

- Genetic conservation
- Protection of genetic resource
- Research on genetics
- Selection and breeding for meat production
- Improvement of feeding practices
- Market linkage and value chain development

R & D ORIENTATION

- Genetic conservation
  - ❖ **Purpose:** To conserve and sustainably develop the genetic resources of H'Mong cattle, aiming to increase productivity, product quality, and efficiency in cattle raising and to enhance farmers' incomes.
  - ❖ **Solutions:**
    - ✓ ***In-situ* conservation**:
      Maintain and develop the breed in its native habitat: traditional farming supports, training local farmers in selective breeding techniques, community-based purebreeding programs, and link local production to markets.
    - ✓ ***Ex-situ* conservation**:
      Preserve genetic resources through the storage of semen, embryos, and live specimens in research and breeding centers.

R & D ORIENTATION

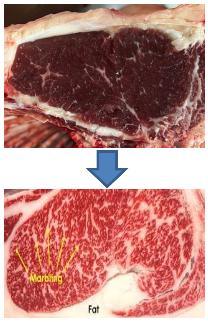
- **Protection of genetic resource**
  - ❖ **Objective:** To safeguard against genetic dilution, it is important to regulate crossbreeding with other breeds.
  - ❖ **Strategies:**
    - ✓ Establishing a registration and certification system for purebred H'Mong bulls;
    - ✓ Implementing AI programs using semen from genetically confirmed bulls;
    - ✓ Developing designated breeding areas or "nucleus herds" exclusively for maintaining pure H'Mong cattle.

R & D ORIENTATION

- **Research on genetics**
  - ❖ **Objective:** Provide scientific basis for the conservation, selection, and breeding of H'Mong cattle.
  - ❖ **Methods:** Microsatellites, single nucleotide polymorphisms (SNPs), mitochondrial DNA, and quantitative genetics.
  - ❖ **Contents:**
    - ✓ DNA sequencing;
    - ✓ Identification of marker genes related to important traits;
    - ✓ Assessment of genetic diversity through heterozygosity and allelic richness;
    - ✓ Determination of inheritability of important traits;
    - ✓ Determination of genetic structure of populations and inbreeding risks;
    - ✓ Monitoring genetic changes over time resulting from selection pressures or admixture with other breeds.

R & D ORIENTATION

- **Selection and breeding for meat production**
  - ❖ **Objectives:**
    - ✓ *Genetic improvement*: Enhance traits related to meat production, including marbling, growth rate, carcass weight, and feed efficiency.
    - ✓ *Conservation of native traits*: Safeguard the breed's unique genetic identity and its adaptation to mountainous environments.
    - ✓ *Productivity enhancement*: Improve overall farm profitability.

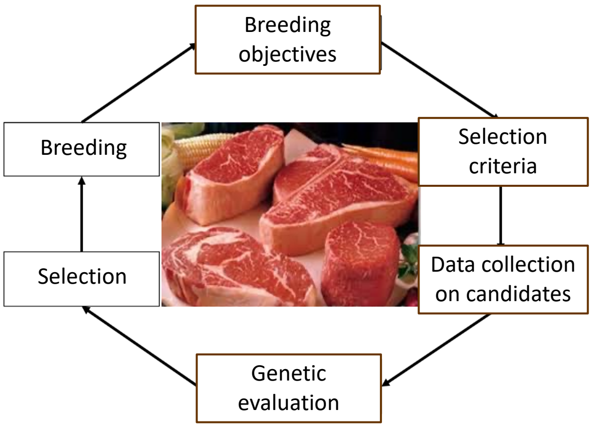


R & D ORIENTATION

- **Selection and breeding for meat production**
  - ❖ **Approaches:**
    - ✓ *Performance recording*: Systematic collection of phenotypic data through body measurements, ultrasound imaging, and carcass grading after slaughter.
    - ✓ *Estimated breeding values (EBVs)*: Selection based on traits such as growth rate, FCR, carcass quality, eye muscle area, intramuscular fat, and backfat thickness.
    - ✓ *Genomic selection*: Application of SNP-based markers to predict performance and breeding value at an early stage.
      - ➢ Develop infrastructure (artificial insemination, embryo transfer).
      - ➢ Establish a central genetic database.
      - ➢ Develop a complete breeding program.

R & D ORIENTATION

- **Selection and breeding for meat production**



Breeding program for meat production

R & D ORIENTATION

- **Improvement of feeding practices**
  - ❖ **Objective:** Optimize beef productivity, improve feed utilization efficiency, and enhance meat quality—particularly tenderness, marbling, unsaturated fatty acid content, and flavor.
  - ❖ **Solutions:**
    - ✓ *Enhanced utilization of local feed resources* such as grass, corn, silage, and by-products.
    - ✓ *Supplementation*: to overcome nutritional deficiencies or imbalances.
    - ✓ *Development of sustainable feeding systems:*
      - o Develop feeding standards for each production stage (breeding, growing, finishing).
      - o Determine optimal slaughter weight and age.
      - o Formulate **cost-effective rations** using locally available feed resources, complemented by commercial feeds when necessary.

R & D ORIENTATION

- **Market linkage and value chain development**
  - **Objectives:**
    - ✓ Enhance income and livelihood security for upland farmers;
    - ✓ Incentivize genetic and nutritional improvements;
    - ✓ Preserve the breed through economic relevance;
    - ✓ Meet growing domestic demand for high-quality, traceable beef.

R & D ORIENTATION

- **Market linkage and value chain development**
  - **Solutions:**
    - ✓ *Strengthening producer organizations*
    - ✓ *Enhancing market linkages and aggregation systems*
    - ✓ *Product differentiation and branding*
    - ✓ *Value-added processing and quality assurance*
    - ✓ *Access to market information and digital tools*

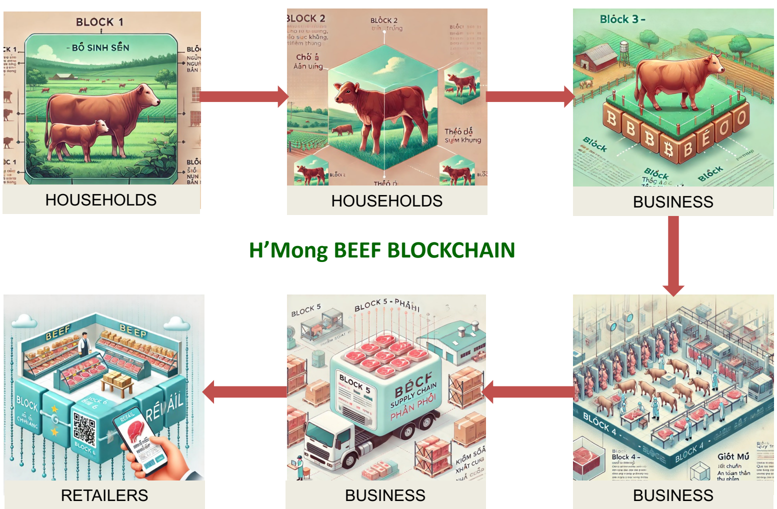
R & D ORIENTATION

- **Market linkage and value chain development**

No.	Stages	Activities	Key actors
1	Cow-calf farming	Free or semi ranging	Contracted households
2	Grower farming (weaning to start of fattening)	Free or semi ranging	Contracted households and/or businesses
3	Fattening	Intensive farming	Businesses
4	Slaughter & processing	Slaughtering, meat cutting and packaging in slaughterhouses	Businesses
5	Meat distribution	Transporting beef products to wholesalers, retailers, and restaurants	Businesses
6	Retail & consumption	Selling beef products in supermarkets, butcher shops, and restaurants	Retailers & consumers

R & D ORIENTATION

- **Market linkage and value chain development**



CONCLUSIONS

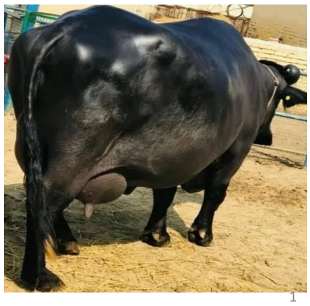
- ✓ H'Mong cattle serve as an essential livelihood and a cultural feature of the H'Mong people.
- ✓ Their morphological traits resemble the Southern Yellow cattle group.
- ✓ They likely originated in China, accompanying the migration of H'Mong communities to Vietnam.
- ✓ Their body size and dressing percentage are comparable to native Yellow cattle and comparable to Sindhi crossbreds.
- ✓ Their growth rates, feed conversion efficiency, and reproductive performance are generally low.
- ✓ Their meat shows normal pH, color, and water-holding capacity, with tenderness superior to that of native Yellow cattle and zebu crossbreds, and comparable to tropical beef breeds, though intramuscular fat remains limited.
- ✓ They exhibit strong adaptability to high-altitude conditions and cold weather.
- ✓ It is necessary to conserve and protect this genetic resource, conduct research to improve genetic quality towards beef production, in parallel with improving feeding regimes and developing a value chain for specialty H'Mong beef products.

4. BUILDING CLIMATE-SMART BUFFALO ENTERPRISES THROUGH PRECISION FARMING, ARTIFICIAL INTELLIGENCE, AND GENOMIC SELECTION

DR. MEHAR KHATKAR
DAVIES LIVESTOCK RESEARCH CENTRE, SCHOOL OF ANIMAL AND VETERINARY SCIENCES, ADELAIDE UNIVERSITY, AUSTRALIA

Building Climate-smart Buffalo Enterprises Through Precision Farming, Artificial Intelligence, and Genomic Selection

Mehar Khatkar



Outlines

- Precision livestock farming- Introduction
- Buffalo precision farming project
- Buffalo genomic resources and 1000 buffalo project
- Breeding for low emission buffaloes

Precision Livestock Farming (PLF)= Data driven management

PLF uses technology and data-driven techniques to monitor and manage livestock.

Enhance animal well-being, improve re/production, and reduce environmental impact.

Utilizes a range of sensors and cameras tailored for livestock management.

Animal welfare improvement, reduced carbon footprint, precise reproduction timing, and efficient resource use.

Why Precision Livestock Farming Now?

- **Technological Maturity:** Advancements in sensor technology, Artificial Intelligence and data analytics make PLF more effective and affordable than ever.

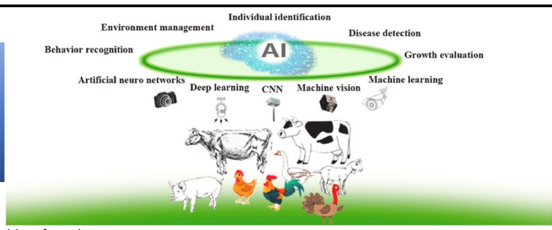
- **Environmental Imperative**: With growing concerns about climate change, PLF offers a way to reduce the carbon footprint of livestock farming.

- **Market Demands**: Consumers are increasingly seeking products that are sustainably produced and ethically sourced, which PLF can deliver.

- **Operational Efficiency:** The ongoing challenges of disease management, feed optimization, and waste reduction make PLF an immediate necessity for sustainable farming.

- **Innovation & Youth Engagement:** As part of the SmartBuffalo Project, the integration of modern technology in farming attracts a younger generation to agricultural professions, rejuvenating the industry.

Species Where PLF Has Been Applied



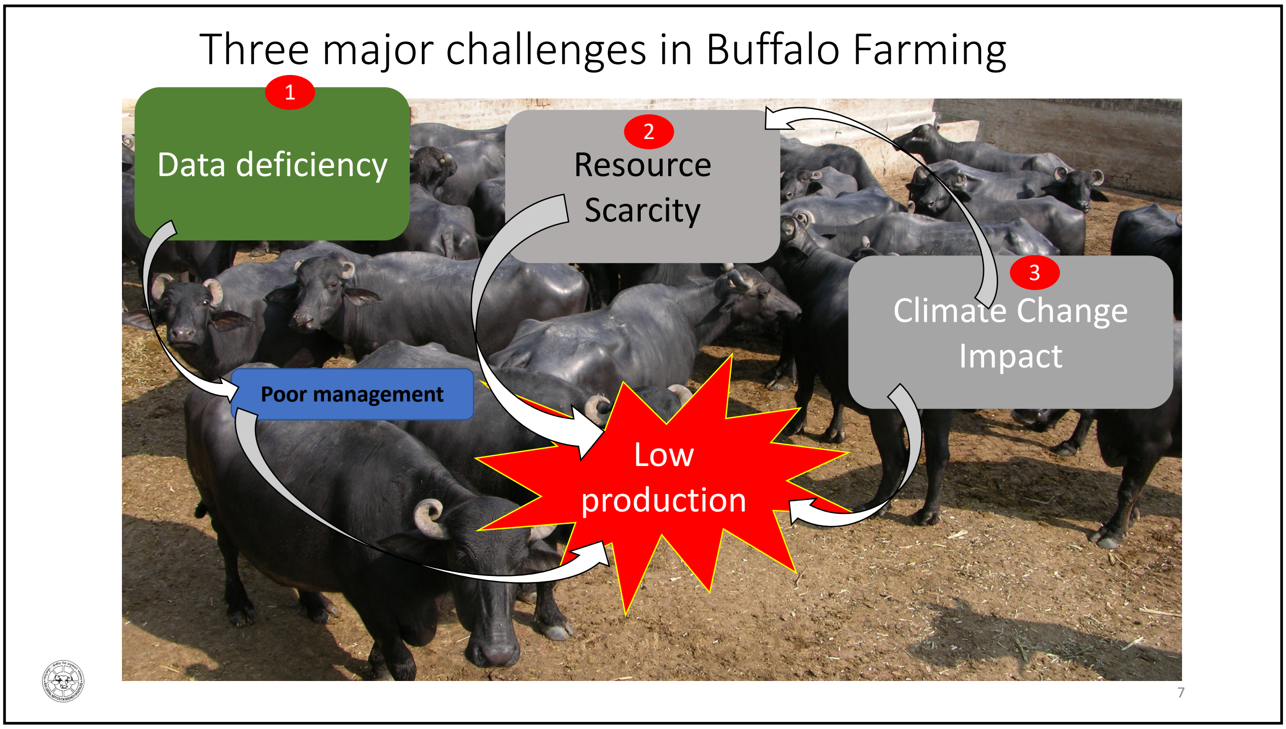
- **Cattle:** Monitoring of rumen pH, estrous cycles, and overall health in both dairy and beef cattle.
- **Poultry**: Sensors for temperature, humidity, and behaviour to optimize egg production and broiler growth.
- -**Swine:** Health monitoring of sows, disease detection, and feeding optimization in pig farming.
- **Sheep and Goats:** Management of grazing patterns, lambing events, and flock health.
- **Aquaculture:** Water quality parameters like pH, temperature, and oxygen levels are monitored in fish farming.
- **Equine:** Monitoring of vital signs and activity levels for health management and training.
- **Camels and Alpacas:** Optimized feeding and health monitoring, particularly in regions where they are primary livestock.
- - **Pets:** Monitoring of activity levels, nutrition, and health metrics, particularly for dogs and cats.

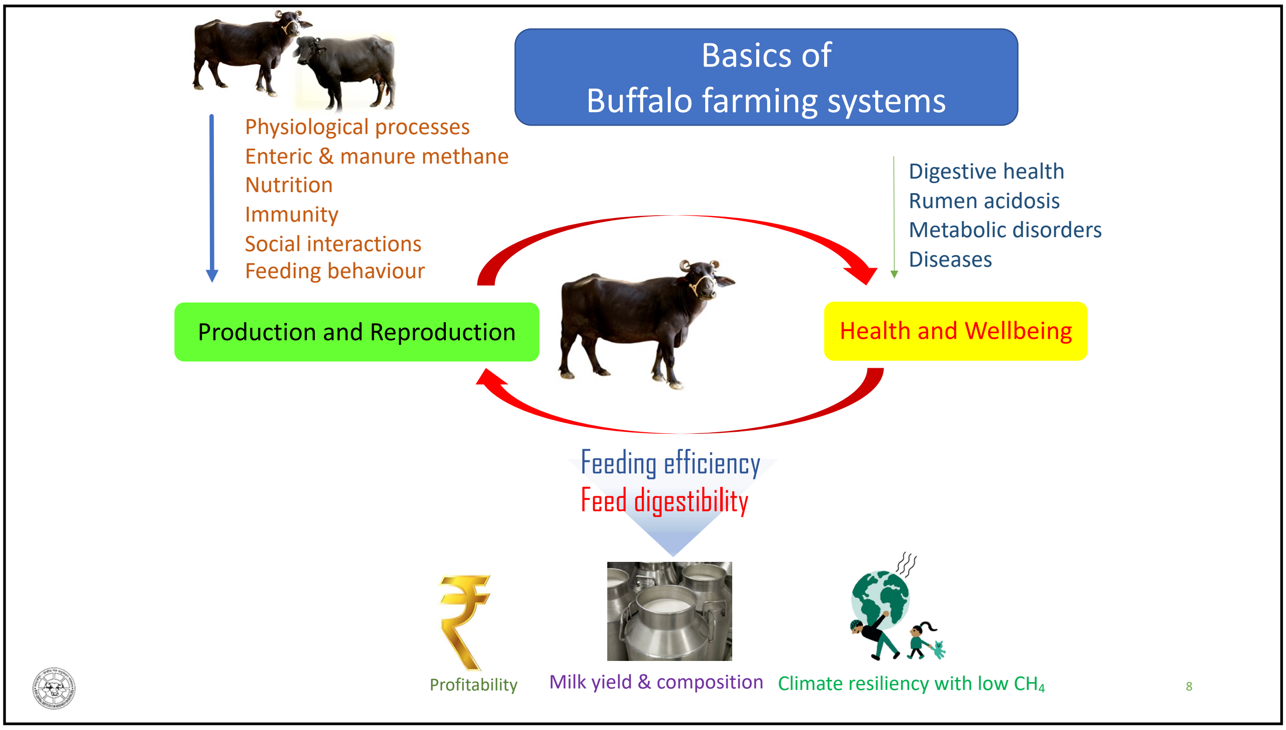
International Collaborative project

Climate smart buffalo farming using digital support systems

Lead Institute
ICAR- Central Institute for Research on Buffaloes,
Hisar -125001, India

Collaborating Institutes
Indian Institute of Technology, Roorkee, India
&
University of Adelaide, Australia


Three major challenges in Buffalo Farming
1
Data deficiency
2
Resource Scarcity
3
Climate Change Impact
Poor management
Low production
7


Basics of
Buffalo farming systems
Physiological processes
Enteric & manure methane
Nutrition
Immunity
Social interactions
Feeding behaviour
Digestive health
Rumen acidosis
Metabolic disorders
Diseases
Production and Reproduction
Health and Wellbeing
Feeding efficiency
Feed digestibility
Profitability
Milk yield & composition
Climate resiliency with low CH_4
8

 are not  !

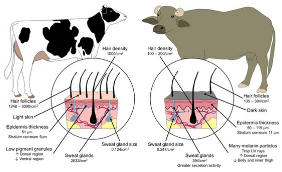
Different Body Conformation & Movement Pattern
Algorithms designed for cows do not accurately interpret buffalo movement data

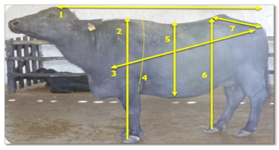
Buffaloes More Aggressive and Physically Stronger
rubbing against objects and each other

Unique Reproductive Physiology
pedometers do not work , silent heat and subdued estrus behavior

Different Feeding & Ruminating Patterns
more time ruminating while resting in a lying posture

Resistance to External Devices:
Love freedom - higher sensitivity and discomfort towards external attachments





Buffalo Husbandry Practices are different

No sensors for tied animals ?

Climate smart buffalo farming using digital support systems

Objectives

I. Building a sensor-based infrastructure for automated, IoT based generation of animal related data

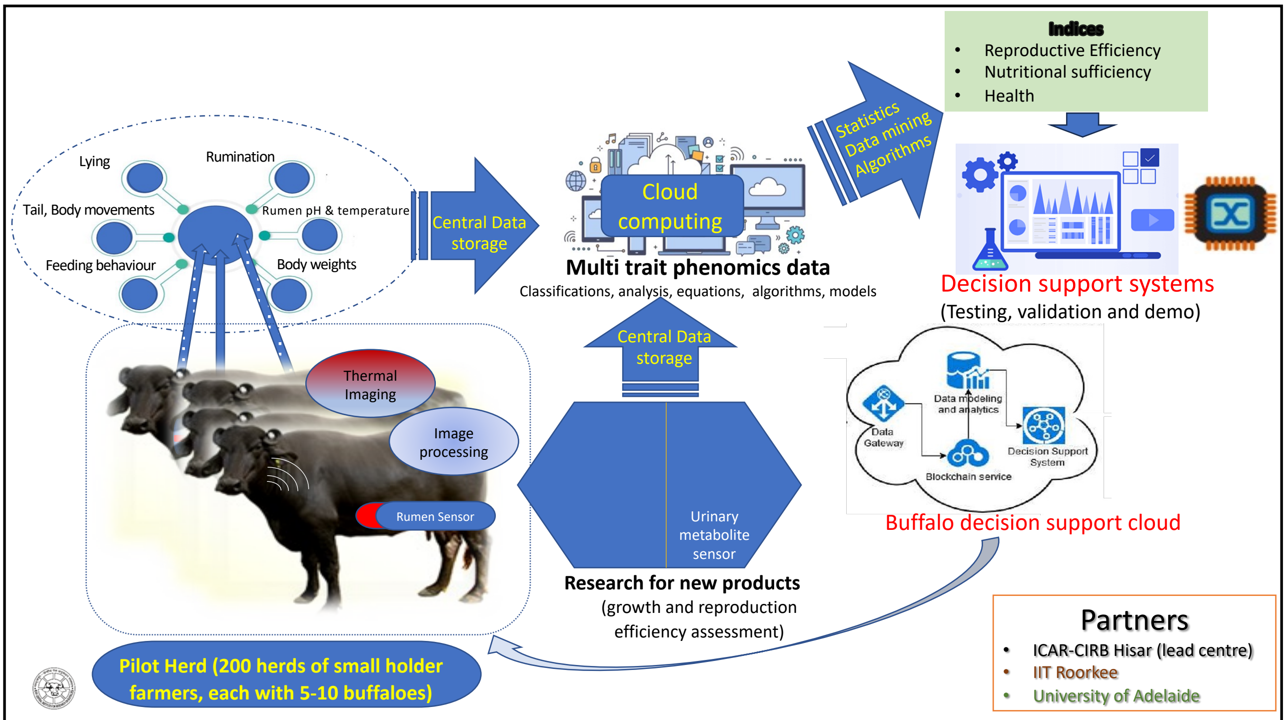
II. Developing buffalo management tools for nutrition, reproduction, health and welfare

III. Demonstration and capacity building in climate smart sensor-based buffalo management

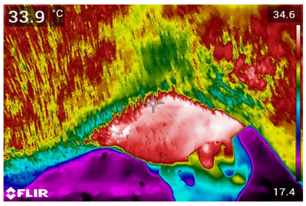
Duration : 5 years

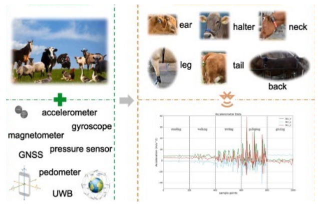
Start – April 1st 2024 End – March 31st 2029

11



How do we plan to get biological data ?



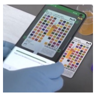


Biosensors
(Molecules in Biofluids)

Photo Sensors
(Body conformations/linear traits)

Thermal Sensors
(Variations in surface temperatures)

Activity Sensors
(Sense physical activities)



Colour derived quantitation

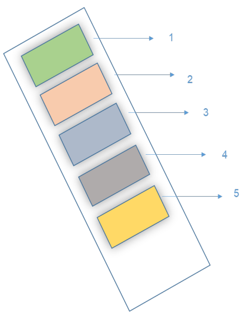
Data on various biological activities affecting animal production and health

Index for performance e.g. Reproductive fitness index, Nutritional sufficiency index, Stress index

Decision support systems

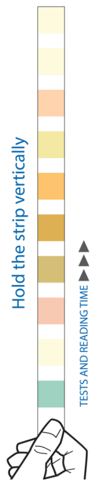
Lab-on-Paper device for assessment of physiological status in buffaloes

(IoT device to follow)

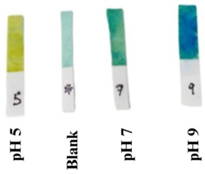


- pH
- Specific gravity
- urea
- blood
- Bilirubin

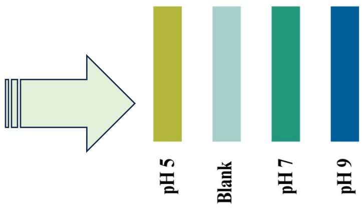
- **pH, specific** : General Health
- **Urea:** Energy balance in body
- **Blood & Bilirubin:** Disease



Urinary pH Paper strips



Original colour

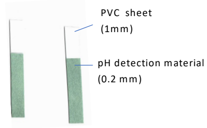


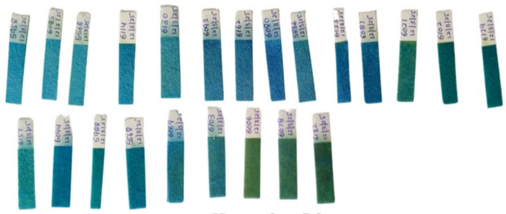
Corresponding RGB colour

Why urine pH is important ?

- Transition nutrition monitoring
- Calcium balance context-to reduce hypocalcemia risk around calving
- Reproductive functions

In-house developed 4 - dye based





pH range from 7-9

pH above 9

Actual field testing

Field Testing results
- N = 151
- Accuracy = 95%

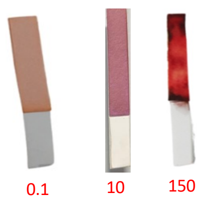
POC : Paper strip-based Milk urea estimation

As an indicator of nutritional sufficiency in buffaloes

Steps involved in development of paper strips for urea estimation in milk:

- Mixing dye with colouring agent (single reagent)
- Incubation (10 hours at 37^{o}C)
- Coating on PVC strip + glue + Whatman filter paper
- Testing and validation in standards and field samples

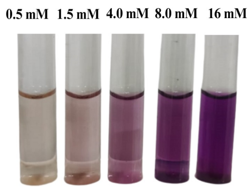
Field Testing results
- N = 89
- Accuracy = 80%



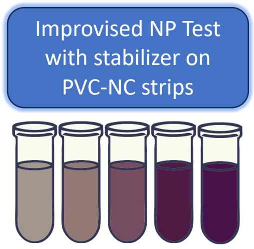
Broad range Urea estimation strips in buffalo milk (conc. in mg/dl)

Normal milk urea conc. = 10 -120 mg/dl

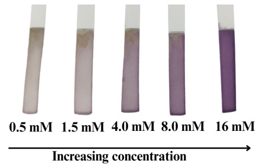
POC : strips for ketosis detection



Wet lab test results



RGB colour coding



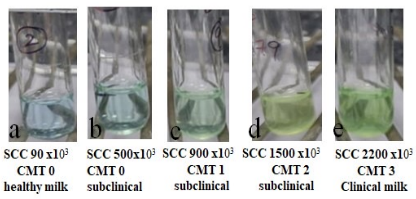
Transformed test on paper strips

POC : ALP Strip test for SCC count & Mastitis detection

- A milk enzyme based
- Useful in diagnosis Subclinical Mastitis and stage of lactation
- Novel method - Combination of 3 reagents (all at room temperature)
- No requirement of any specific instrument
- Test completed in 10 minutes at room temperature
- Patent application (due)

Raw Milk

Casein removal



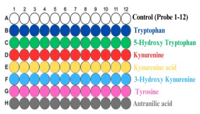
Actual Test results (n=100)

POC : Strip test for detection of bilirubin

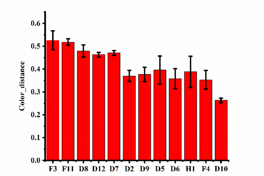
- Urine based
- Novel method – single reagent based ; long storage stability
- Highly sensitive method – can detect bilirubin levels to as low as 1mg/dL
- Eye reading - No requirement of any specific instrument
- Immediate reading (less than 1 minute)
- Patent application (ready to file)

Colorimetric array for assessment of multiple metabolites

Dye + Metal + Metabolite Multiplexed (DM^3) analysis of urinary metabolites

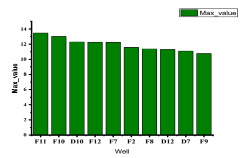


RGB ratio of colour developed in each well



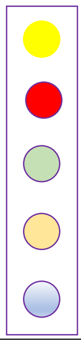
Top 10 Wells recording highest RGB selected for further titration studies

Absorbance values (350 -800 nm)

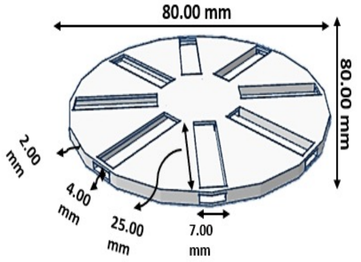


Top 10 Wells recording highest RGB

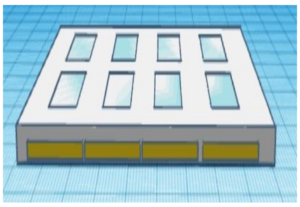
Replicating on real urine samples



Multiplex Paper Sensor card



Circular Disc

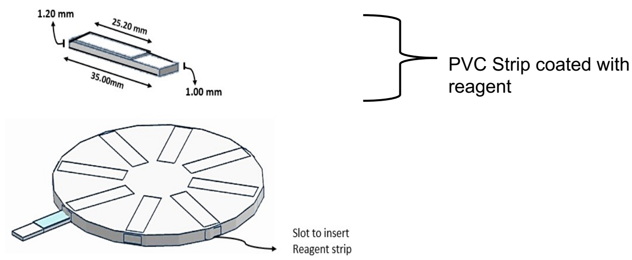


Rectangular

ChromaSense UA ®

RGB-Based Biosensor device

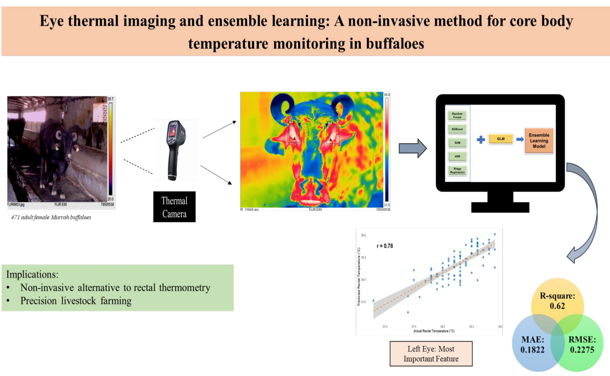
(Patent application to be filed)



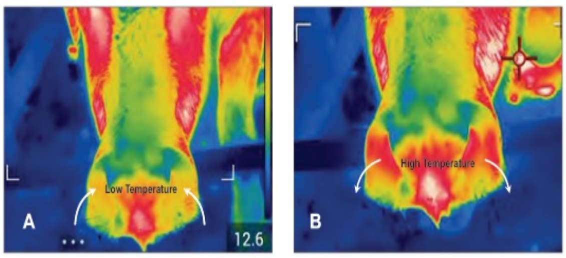
- ✅ Removes redundancy and uniformity in colour reading
- ✅ Low-cost , Portable & Efficient colour reading
- ✅ Multi colour, Multi test (1-8 test readings possible)
- ✅ Help in developing App based Indices
- ✅ Increases App based Color Sensitivity

Automating Recording of Physiological parameters

(Core body Temperature and Respiration Rate)



Manuscript submitted to Computers and Electronics (under review)



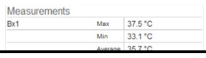
Radiometric images showing inhalation (A) and exhalation (B) through the nostrils

Eye thermal imaging and ensemble learning: A non-invasive method for core body temperature monitoring in buffaloes

a.

b.

c.

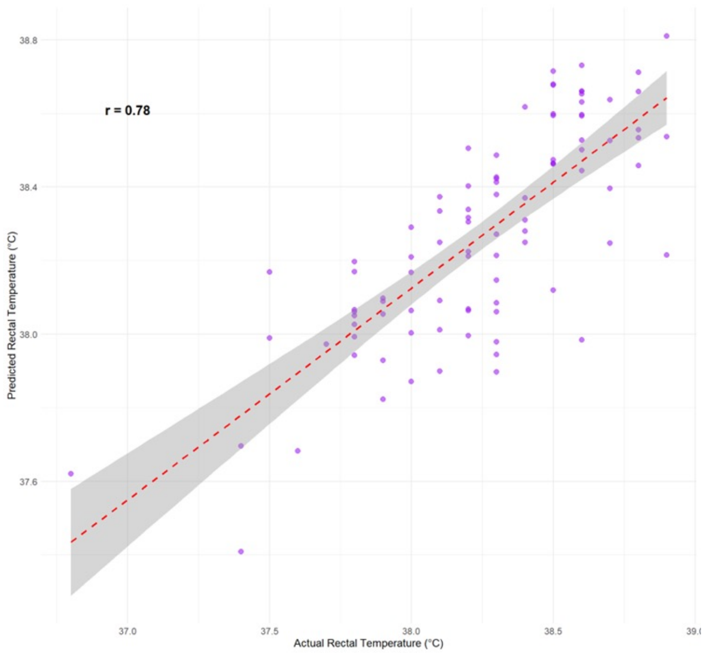


- Infrared thermal images on **471** adult female Murrah breed buffaloes were captured using a hand held thermal camera.
- Extract eye's medial canthus temperatures from thermal images

Ground truth: **Rectal temperature**

Ekta Hooda[1], AK Balhara[1], Gurpreet[1], Promila Sharan[1], AK Boora[1], SK Phulia[1], Sanjay Kumar[1], Yash Pal[1], MS Khatkar[2] and Sunesh Balhara

https://papers.ssrn.com/sol3/papers.cfm?abstract_id=5222085



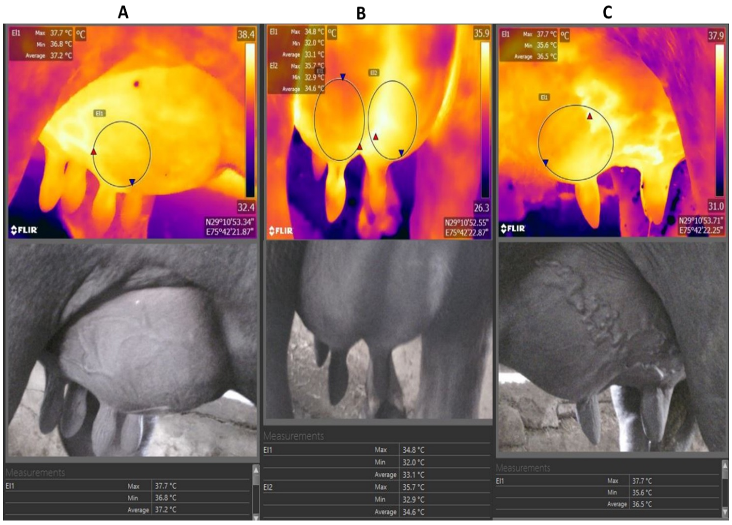
Prediction Accuracy of predicting rectal temperature from thermal imaging data.

- Both eyes: Cor= 0.78

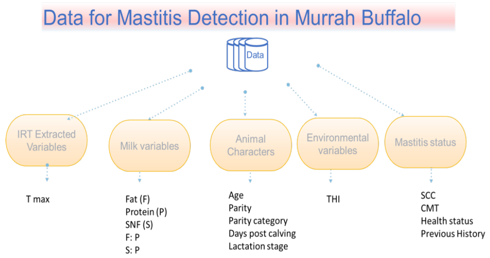
- Left eye only: Cor = 0.78

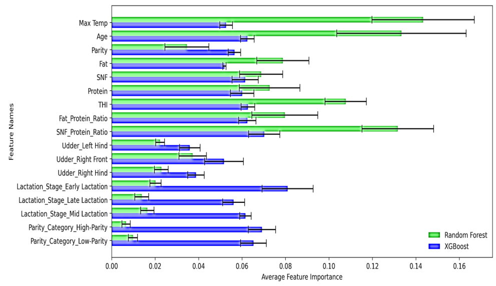
- Right eye only: Cor= 0.67

Machine Learning for Mastitis detection



Extraction of udder skin surface temperatures for machine learning

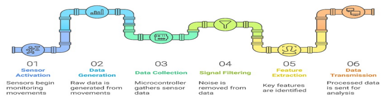


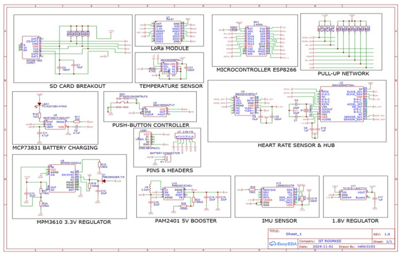


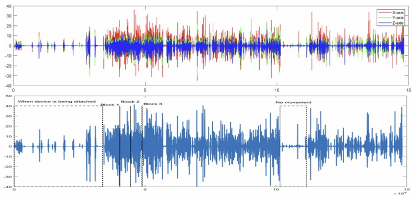
IoT enabled Tail Mounted Physical Activity Sensor

Design submitted for patent (ICAR-CIRB & IIT R)

- 20 devices with complete setup will be ready for testing at CIRB Hisar
- Work on Mobile App & Gateway initiated

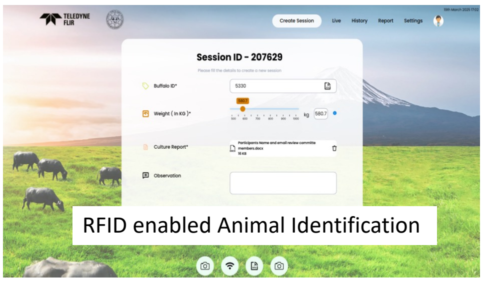






Accelerometer data (device on tail)

Automated IR Thermal Imaging

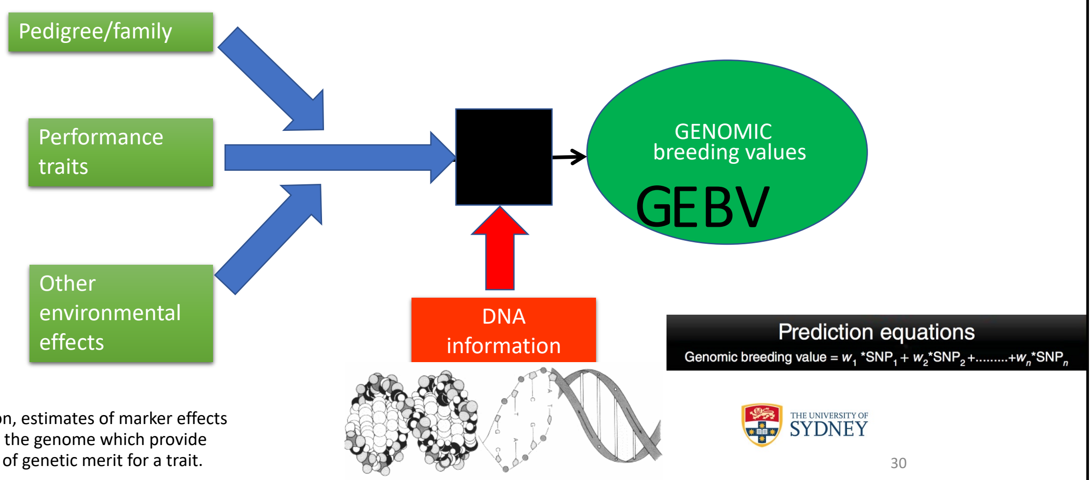


RFID enabled Animal Identification

Buffalo genomic resources

Genomic Selection

Integration of DNA information in breeding



In Genomic Prediction, estimates of marker effects are combined across the genome which provide accurate predictions of genetic merit for a trait.

THE UNIVERSITY OF SYDNEY

1000 BUFFALO GENOMES PROJECT

SCAN ME!

https://1000buffalogenomes.github.io/

to provide information on the genetics of buffalo populations worldwide to establish the foundational resources to utilize genomic prediction tool to breed more productive buffalos.

There is need for effective selection programs to improve milk and meat production of buffaloes

Problem:
Limited genetic resources and genotyping tools

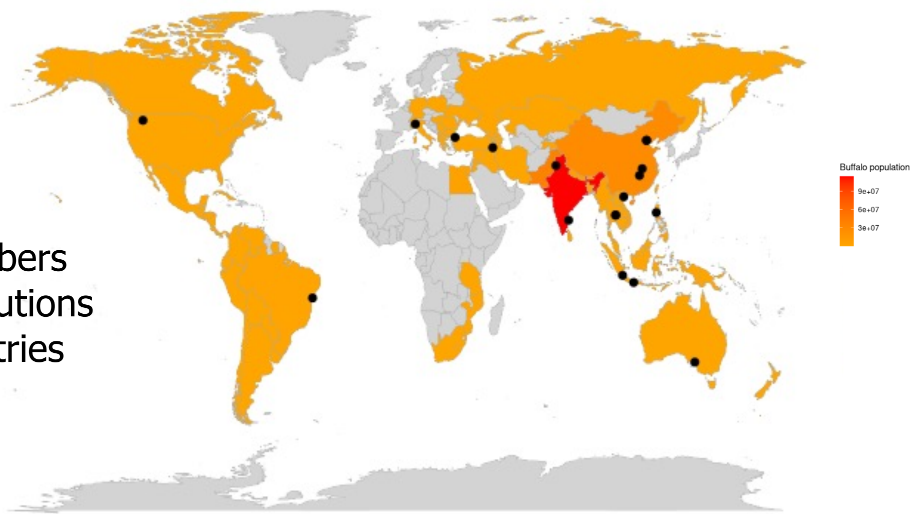
Increased milk and meat

Feed efficiency

Sustainability **Uplift livelihood** **Food security** **Reduced methane**

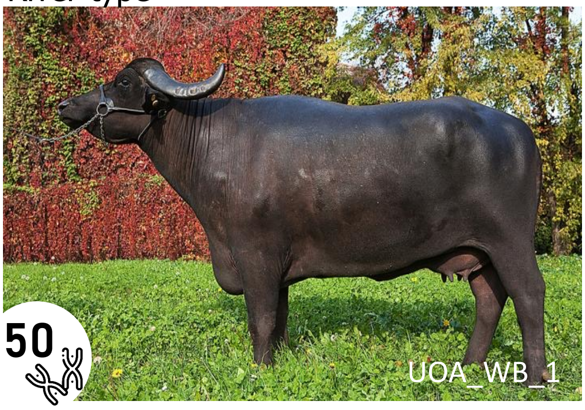
A collaboration around the world

30 members
22 institutions
13 countries



The water buffalo (Bubalus bubalis)

River-type



Swamp-type

https://1000buffalogenomes.github.io/

Data

- 273 river and 267 swamp short-reads WGS
- River buffalo genome
  UOA_WB_1
- Swamp buffalo genome
  PCC_UOA_SB_1v2

https://1000buffalogenomes.github.io/

Water buffalo assemblies

Assembly	Origin	Type	Size (Gb)	No. of contigs	N50 (Mb)	Reference
PCC_UOA_SB_1v2	Philippines	Swamp	2.90	500	85.5	Pineda et al, 2024
Wang_2023	China	Swamp	2.68	173	72.2	Wang et al., 2023
UOA_WB_1	Italy	River	2.65	953	18.8	Low et al., 2019
NDDB_SH_1	India	River	2.63	1132	9.5	Ananthasayam et al., 2020
CUSA_SWP	China	Swamp	2.63	2003	8.8	Luo et al., 2020
CUSA_RVB	China	River	2.65	3482	3.1	Luo et al., 2020

Disentangling river and swamp buffalo genetic diversity: initial insights from the 1000 Buffalo Genomes Project

Paulene S Pineda, Ester B Flores, Lilian P Villamor, Connie Joyce M Parac, Mehar S Khatkar, Hien To Thu, Timothy P L Smith, Benjamin D Rosen, Paolo Ajmone-Marsan, Licia Colli ... Show more

GigaScience, Volume 13, 2024, giae053, https://doi.org/10.1093/gigascience/giae053

https://1000buffalogenomes.github.io/

Results

141 animals

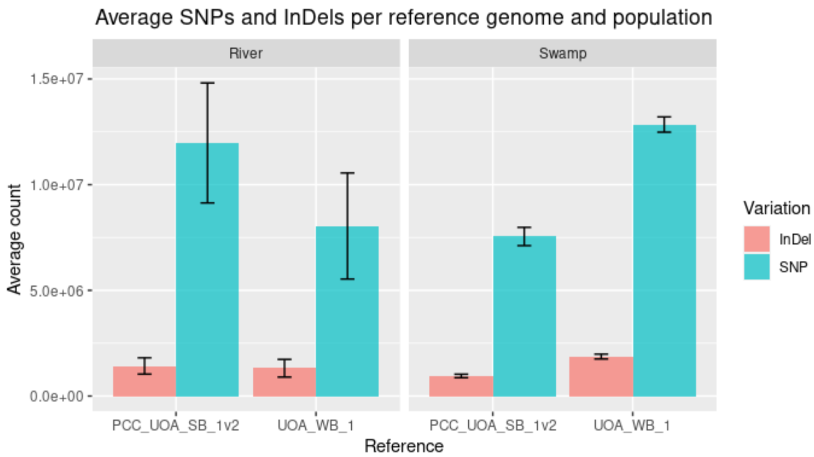
80 swamp type
61 river type

River buffalo as reference:

41,071,165 SNPs

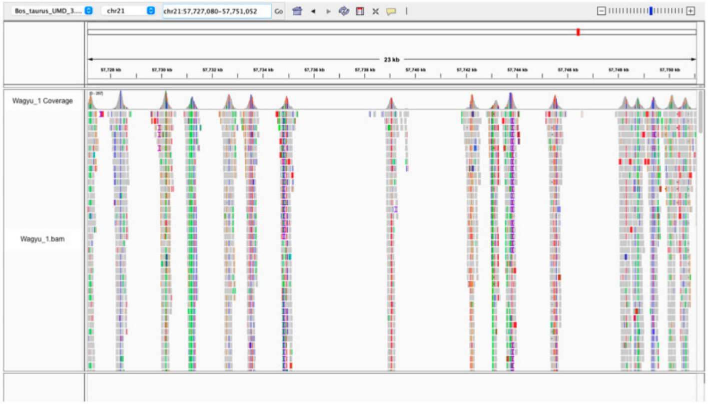
Swamp buffalo as reference:

41,632,997 SNPs



https://1000buffalogenomes.github.io/

Genotyping using probe capture sequencing



Ren Y, Khatkar MS, MacPhillamy C, Wang H, McEwin RA, Chen T, Pitchford WS, Low WY. Evaluating the Efficacy of Target Capture Sequencing for Genotyping in Cattle. Genes (Basel). 2024 Sep 18;15(9):1218. doi: 10.3390/genes15091218. PMID: 39336809; PMCID: PMC11431841.

Cost-Effective Genotyping Using Low-Coverage Sequencing and Imputation

- **Low-Coverage Sequencing (e.g., 1X):** Dramatically reduces sequencing costs by generating sparse genetic data.
- **Imputation of missing genotypes:** Accurately fills in missing genotypes using a high-quality reference panel (e.g., Beagle): .
- **High-Confidence Genotypes:** Achieves dense and accurate genetic data, comparable to more expensive methods.
- **Overall Benefit:** Enables large-scale genomic studies to be more affordable and feasible.
- **Limitation:** High cost of data storage and intensive computational power for processing and imputation remain significant challenges.

Reducing Methane Emissions in Buffaloes through Genomic Selection- Proposal

Measure & Manage Data: Standardise methane measurement protocols, record emissions in project buffaloes, and develop an integrated data platform.

Develop Genomic Tools: Design and deploy a low-cost, buffalo (Murrah)-specific SNP panel for genotyping bulls and cows.

Estimate **genetic parameters**, identify **key genes** for methane emission, and develop **genomic prediction** models for methane and economic traits.

Construct a **genomic selection index** balancing methane with economic traits and establish its efficiency in routine use in Indian buffalo breeding programs.

From Barrier to Breakthrough in Precision Buffalo Farming

Data Scarcity: A critical lack of large, standardized datasets for buffalo health, production, and behavior.

Algorithm Gap: A shortage of AI/ML algorithms specifically trained and validated for unique buffalo physiology.

International Data Consortium: Create a global partnership to collect, standardize, and share buffalo-specific data, overcoming the scarcity barrier.

Unique Opportunities for Novel Data Collection and Algorithm Development in Agriculture

- **Fewer Ethical Constraints**: Unlike human health and social settings, agriculture offers a more lenient ethical landscape for data collection.

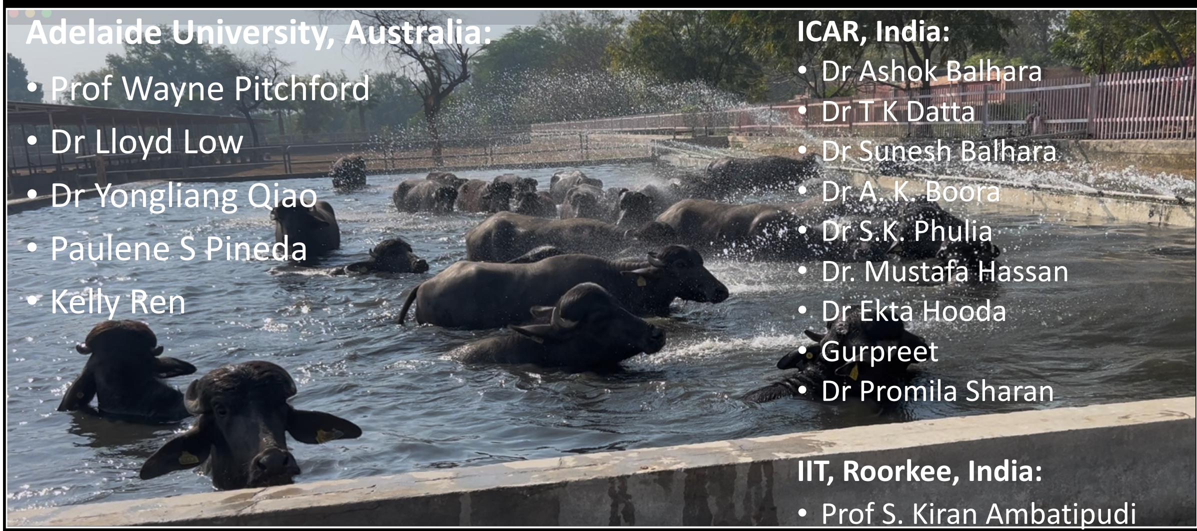
- **Privacy Risks:** Lower privacy concerns in the agricultural context make it easier to amass large datasets required for training deep learning models.

- **Novel Data Availability:** Agriculture, particularly livestock farming, provides unique opportunities to collect novel types of data, such as rumination sounds or thermal images.

- Algorithmic Innovation: The availability of diverse and rich data from PLF paves the way for developing novel deep learning algorithms tailored for specific applications.

- **Untapped Potential:** PLF offers a promising avenue for data scientists and machine learning engineers to apply and test new algorithms, offering a faster route to applications in other domains.

Thanks



Adelaide University, Australia:

- Prof Wayne Pitchford
- Dr Lloyd Low
- Dr Yongliang Qiao
- Paulene S Pineda
- Kelly Ren

ICAR, India:

- Dr Ashok Balhara
- Dr T K Datta
- Dr Sunesh Balhara
- Dr A. K. Boora
- Dr S.K. Phulia
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- Dr Ekta Hooda
- Gurpreet
- Dr Promila Sharan

IIT, Roorkee, India:

- Prof S. Kiran Ambatipudi
- Prof P M Pradhan
- Dr Puneet Kumar

Adelaide University

5. PIG PRODUCTION IN VIETNAM: IMPROVEMENT OF PERFORMANCE BY QUANTITATIVE GENETICS AND GENOMIC INFORMATION

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VIETNAM NATIONAL UNIVERSITY OF AGRICULTURE

HỌC VIỆN NÔNG NGHIỆP VIỆT NAM
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PIG PRODUCTION IN VIETNAM IMPROVEMENT OF PERFORMANCE BY QUANTITATIVE GENETICS AND GENOMIC INFORMATION

International Symposium Transformation To Sustainable Livestock Production
Hanoi, 17 October 2025

DO DUC LUC
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Important of livestock sector in Vietnam

- 11.88% GDP from Agriculture (Crop Production, Animal Production, Sylviculture, Aquaculture) in total GDP
- 25-28% GDP of animal production in Agriculture's GDP

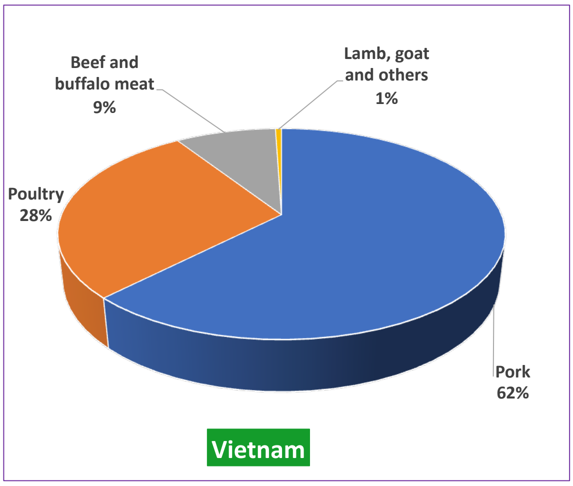
Livestock population from 2014 to 2024

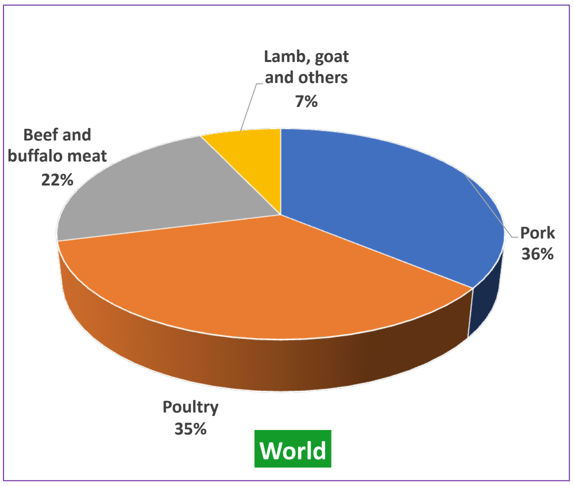
Year	Buffalo ($\times 10^6$ head)	Cattle (dairy cow) ($\times 10^6$ head)	Pig (sow) ($\times 10^6$ head)	Poultry (chicken) ($\times 10^6$ head)
2014	2.59	5.38	27.8 (3.9)	353.9
2015	2.63	5.75 (0.275)	28.9 (4.1)	369.5
2016	2.64	6.22 (0.283)	30.9 (4.2)	395.5
2017	2.61	6.29 (0.290)	29.1 (4.0)	407.1
2018	2.49	6.33 (0.294)	29.8 (4.0)	435.9 (316.9)
2019	2.39	6.28 (0.318)	20.2 (2.5)	480.3 (382.6)
2020	2.33	6.33 (0.317)	22.0 (2.6)	512.7 (409.5)
2021	2.26	6.39 (0.317)	23.2 (3.0)	524.1 (424.2)
2022	2.23	6.35 (0.352)	24.7 (3.0)	547.0 (444.8)
2023	2.14	6.33 (0.375[2])	25.5 (3.1)	559.4
2024	**2.03**	**6.21 (0.330[3])**	**26.5 (3.1)**	**584.1**
2030			**30.0 (2.5)[1]**	

[1]Livestock Department (2024), [2]https://microbelift.vn/tong-quan-ve-nganh-chan-nuoi-bo-sua-o-nuoc-ta/, GSOV (2025)
[3]Nguyen Xuan Duong (2025)

HVN Học viện Nông nghiệp Việt Nam

How is important of pork in Vietnam

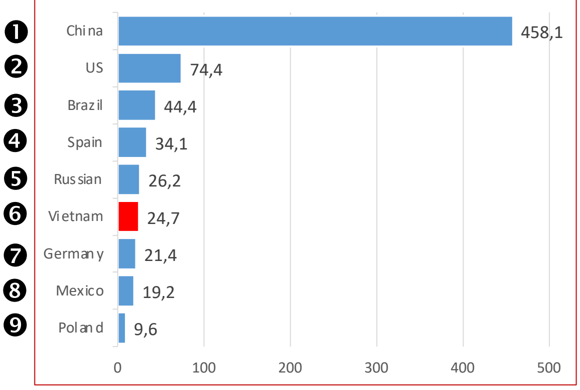




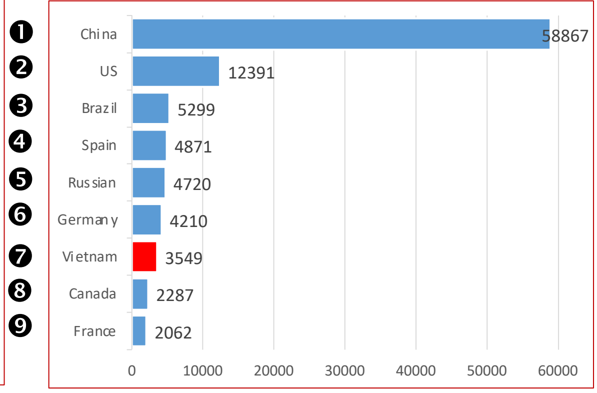
adapted from Vo Trong Thanh (2022)

Ranking

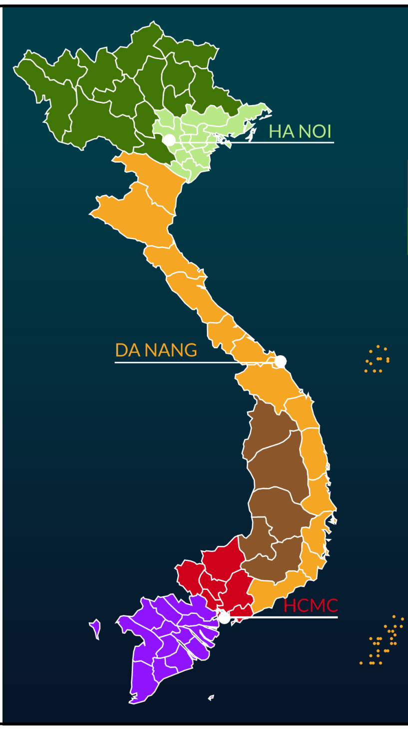
6 in herd population (×10^6 head)



7 in meat production (×10^3 ton)



FAOSTAT (2024)

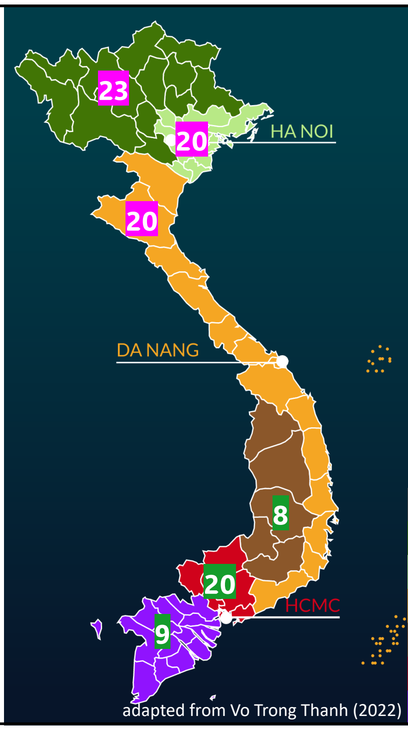


Six socio-economic zones in Viet Nam

Region	Number of locality
Northern midland and mountainous region	14
Red River Delta region	11
North central coast and central coast	14
Central Highlands	5
Southeast region	6
Mekong Delta region	11

(*According to the Government's resolution No. 138/NQ-CP on the national master plan for the 2021-2030 period which was submit to the National Assembly for approval)

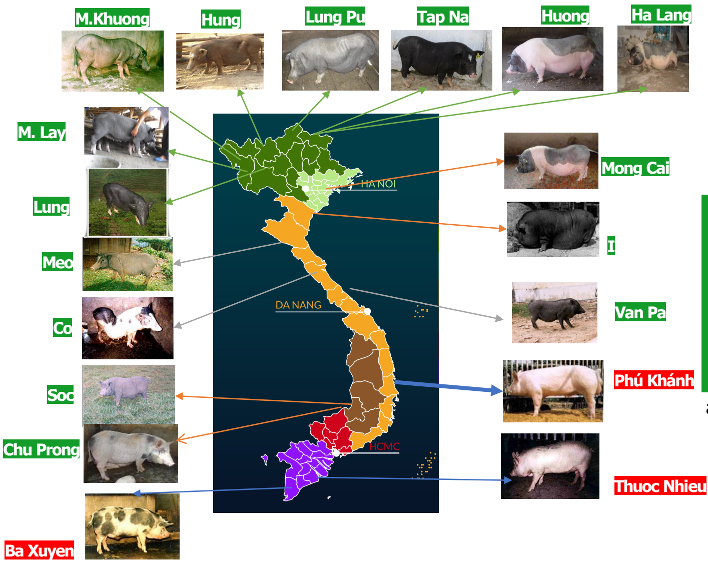
VGP VIETNAM.GOV.VN



adapted from Vo Trong Thanh (2022)

Pigs distribution

Region	Number of locality
Northern midland and mountainous region	14
Red River Delta region	11
North central coast and central coast	14
Central Highlands	5
Southeast region	6
Mekong Delta region	11



North: 55.55%

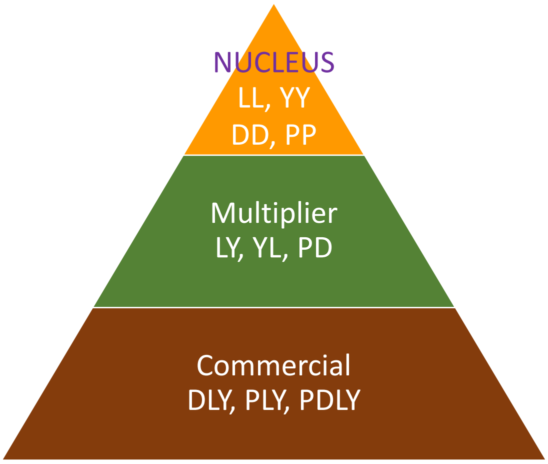
Centre and Tay Nguyen: 33.34%

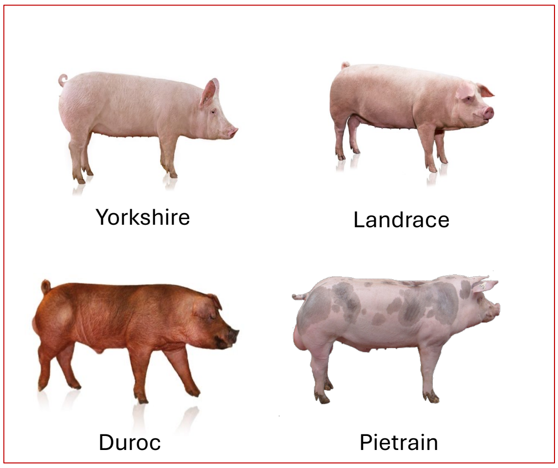
South: 11.11%

adapted from Vu Dinh Ton (2023)

Origin and Distribution of Indigenous pig breeds in Vietnam

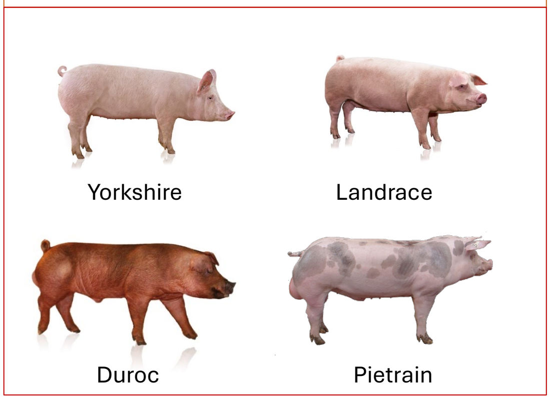
Herds



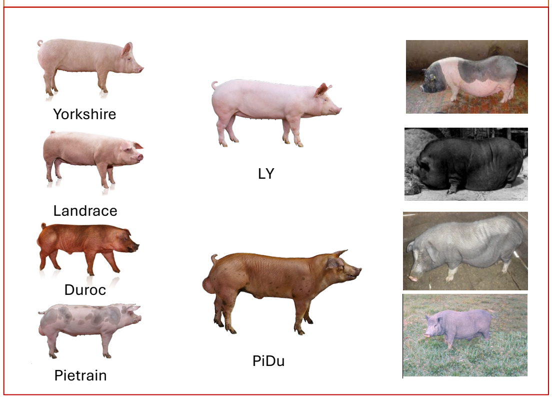


Pig breeds in Vietnam

Industry



Household



Pig population

Population	GGP and GP herd

• **26.6**×10^6 head (population)
• **3.1**×10^6 sows (11,65%)
• **467** breeding units/ bases
	• **240** units for GGP and GP
	• **135k** sows (4,21%)
	  • **20.3k** GGP (15%)
	  • **114.7k** GP (85%)

Improvement of performance

- Importation
- Boars control
- Gilts and sows control

- Quantitative genetics
- Genetic information
  - Genetic markers
  - Genomic selection

Importation

Country	GGP and GP

• **France**
• **Denmark**
• **Canada**
• **US**
• **Taiwan**
• Cooperl, Axiom, Danbred, Genesus, PIC, Hypor…
	• **11%** importation (2015-2020)
	• **4.181** heads ~ **2.66**$\times 10^6$ USD (2015)
	• **43.806** head ~ **27.42**$\times 10^6$ USD (2020)
	• **4.088** head (2024)[1]
	  • **32567** gilts
	  • **832** boars

Livestock Department(2022)
[1]*AgriMonitor.vn*

Performance of imported pigs

Initial population	Imported
• Weaned/ sow/ year: 34.4 – 47.3 • Weaned/ litter: 15.3 – 18.9 • ADG: 800 – 1200g • FCR: 1.89 – 2.50kg • Lean meat: 60.5 – 65%	• Weaned/ sow/ year: • Weaned/ litter: 13.3 – 14.9 • ADG: 742 – 959g • FCR: 2.44 – 2.65kg • Lean meat: 60.5 – 65%

Artificial Insemination (AI)

AI	Boar control

• AI in all industrial farms
• Boars on sow farms (ASF)
• 50 - 100 sows/ boars
• Fresh semen
• Boar stations
  • Household
  • Industry
	• Testicle control by ultrasound
	  • Young boars
	  • Adult boars
	• CASA system to control semen quality
	• Performance testing

Gilts and sow control

By ultrasound

- Pregnancy control
- Backfat control
- Body condition control

Quantitative genetics

Quantitative genetics

Data records

- Database
  - Belong to each company
  - No exchange between companies
- Records within company
  - Indepedent
  - Intergration with imported company

Traits/ Phenotypes

Reproduction	Production	Meat quality
• Total born/ litter	• ADG	• IMF
• Born alive/ litter	• Age to 100kg	• pH
• Weaned/ litter	• Backfat thickness	• Color
• Weaned/ sow/ year	• Muscle thickness	• Drip loss
• Number of teats	• Lean meat	• Cooking loss
• Birth weight	• FCR	• Tenderness
• Maternal behavior		• Odor
• Semen quality		

Herds management and Calculation

Management

- Inbreeding control
  - Manually
  - Imported company
  - PigPen
  - MateSel
- Database
  - Excel
  - Imported company
  - PigPen
  - Clouds farm

Calculation

- Selection
  - Phenotype(s)
  - Estimated breeding value
  - Selection index
- Calculation
  - Independent
  - Imported company
- Software
  - PEST, VCE, BLUPF90, HiBLUP
  - Imported company

Genetic markers

Genetic markers

Reproduction
- ESR
- PRLR
- FSHB
- RNF4
- RBP4
- VRTN

Production
- MC4R
- GH
- IGF2

Disease/ stress
- FUT1
- MUC4
- Hal
- ASF?

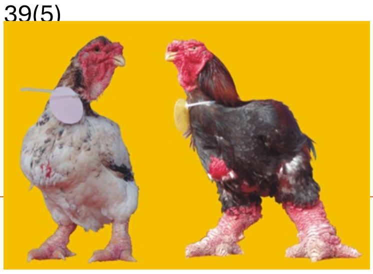
Quality
- PIT1
- H-FABP
- PIC3K3
- CAST
- MYOG
- Hal
- RN
- HFABP
- FAPB3

Genomic selection

Genomic selection (completed)

Chicken

- Biodiversity (2012-2013)
  - Selection for sustainable conservation of **Ho chicken** breed
  - High-resolution genomic analysis of four local Vietnamese chicken breeds (2021). *Journal of Animal Breeding and Genetics* 139(5)



Pig

- Disease (2020-2023)
  - Study on natural resistance to **AFS** of surviving pigs in outbreak areas in Vietnam
  - Unpublish: SNPs related to survivor pigs infected by ASF virus

Genomic selection (in progress)

Pig

- Pig production (2024-2026)
  - Improving reproductive and productive performance of Landrace pigs using genomic information
- Project information
  - Support by ARES-CCD (Belgium)
  - VNUA, ULiege, BAF

Partner

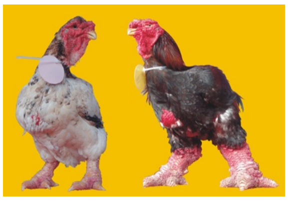
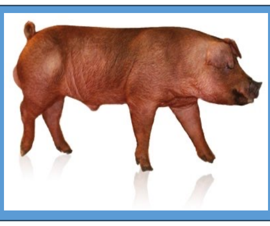
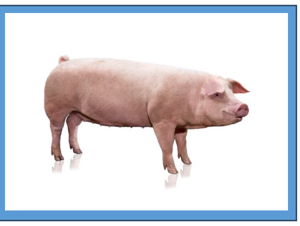
ARES ACADÉMIE DE RECHERCHE ET D'ENSEIGNEMENT SUPÉRIEUR

BAF NÂNG TẦM CHẤT LƯỢNG CUỘC SỐNG

LIÈGE université

Genomic selection (future project)

Exotic and indigenous

Future project

- Pigs companies
  - BAF
  - Dabaco
  - Green Feed
  - Hoa Phat
  - Massan
  - CP
  - Xuan Thien

AAAP 2026

The 21st AAAP (Asian-Australasian Association of Animal Production) Animal Science Congress

2026

National Convention Center
Hanoi, Vietnam
28 to 31 October

2024

Melbourne Convention and Exhibition Centre
Australia

2022

ICC JEJU, Jeju, Korea

https://aaap2026.org/

ddluc@vnua.edu.vn

Q A

6. NATIONAL HANWOO BREEDING AND GENETIC IMPROVEMENT SYSTEM OF KOREA

ROH SEUNG-HEE
DEPUTY GENERAL MANAGER LIVESTOCK SUPPORT DEPT., NATIONAL AGRICULTURAL COOPERATIVE FEDERATION, KOREA

NEW Korea NACF

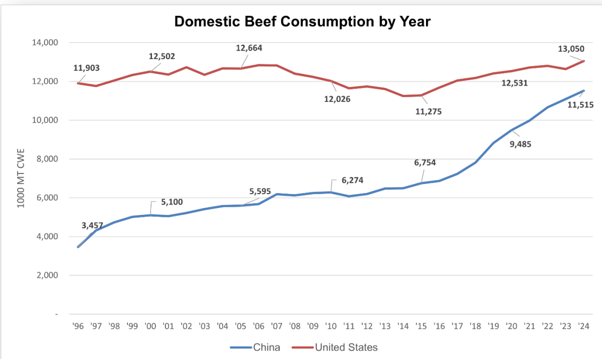
National Hanwoo Breeding and Genetic Improvement System of Korea

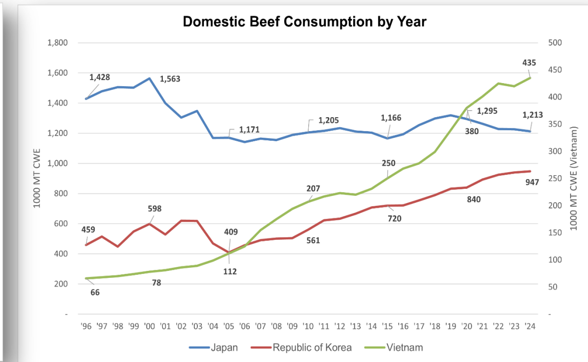
National Agricultural Cooperative Federation Agribusiness Group(NACF),
Republic of Korea.

Seung Hee, Roh (Ph.D)
(E-mail : jinsweet@empal.com)

Domestic Beef(included Veal) Consumption by Year

NEW Korea NACF





(Source : USDA)

▣ America and Asia Country

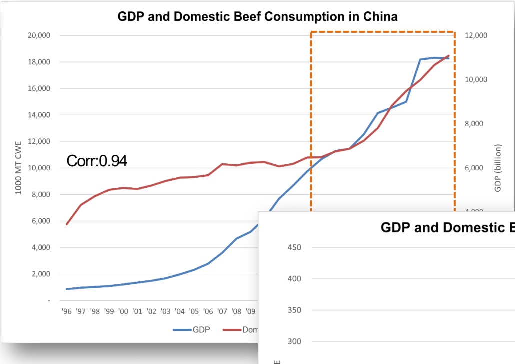
- USA : ('96 year) 11,903 → ('05) 12,664 → ('15) 11,275 → ('24) 13,050 (9.6% ↑)
- China : ('96 year) 3,457 → ('05) 5,595 → ('15) 6,754 → ('24) 11,515 (233.1% ↑)

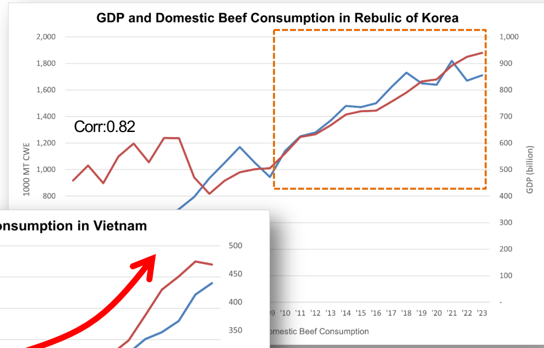
▣ Asia Country

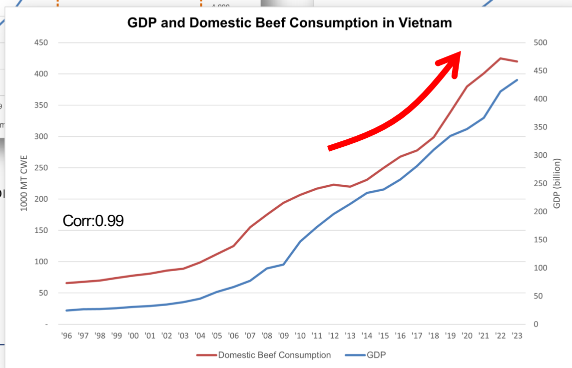
- Japan : ('96 year) 1,428 → ('05) 1,171 → ('15) 1,166 → ('24) 1,213 (15.1% ↓
- Rep. of Korea : ('96 year) 459 → ('05) 409 → ('15) 720 → ('24) 947 (106.3% ↑
- Vietnam : ('96 year) 66 → ('05) 112 → ('15) 250 → ('24) 435 (559.1% ↑

GDP and Domestic Beef Consumption

NEW Korea NACF







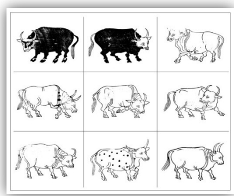
(Source : World Bank Group)

▣ The relationship between GDP and Do

- China : GDP began to increase in 2008,
- Korea : Since 2009, the increase in GDP

The history of Hanwoo

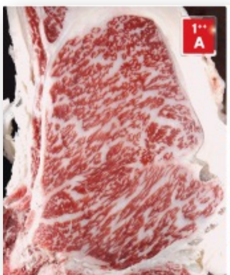
NEW Korea NACF



Ancestor of Hanwoo
(~ 1900 years)

Work Cattle
(1900 years ~ 1970 years)

Beef Cattle
(1980 years ~ present)



The best beef in the world

▣ The number of Hanwoo in Korea

(Unit : Heads)

Type	Cow	Bull(included steer)	Total
Hanwoo	2,441,425	1,284,242	3,725,667
Brindle Hanwoo	1,508	598	2,106
Jeju black Hanwoo	332	157	489
Total	2,443,265	1,284,997	3,728,262

As of the end of February 2025

The improvement structural of Hanwoo

NEW Korea NACF

Character test and registration of Hanwoo ('63 year)

Pure breed and cross breed system (Hanwoo+Charolais) ('70 years)

Performance test for Pure breed ('80 years)

The object change from Quality breeding to Quantity breeding ('90 years)

Promotion of Hanwoo improvement through cow performance testing (2000 years)

The main traits of Hanwoo

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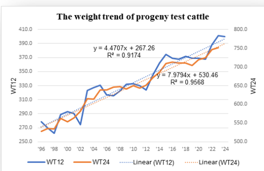
Growth performance
(Birth weight, Weaning weight, Yearling weight etc.)



Slaughter performance
(Carcass Weight, Eye muscle area, Backfat thickness, Marbling score etc.)

Main Traits

Growth Traits

Carcass Traits

Repro-ductive Traits

Ultra-sound Traits

Reproductive Performance
(Pregnancy rate, Calving rate, Calving interval etc.)

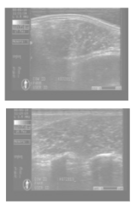
BCS (Body Condition Score)

1 Very thin

…

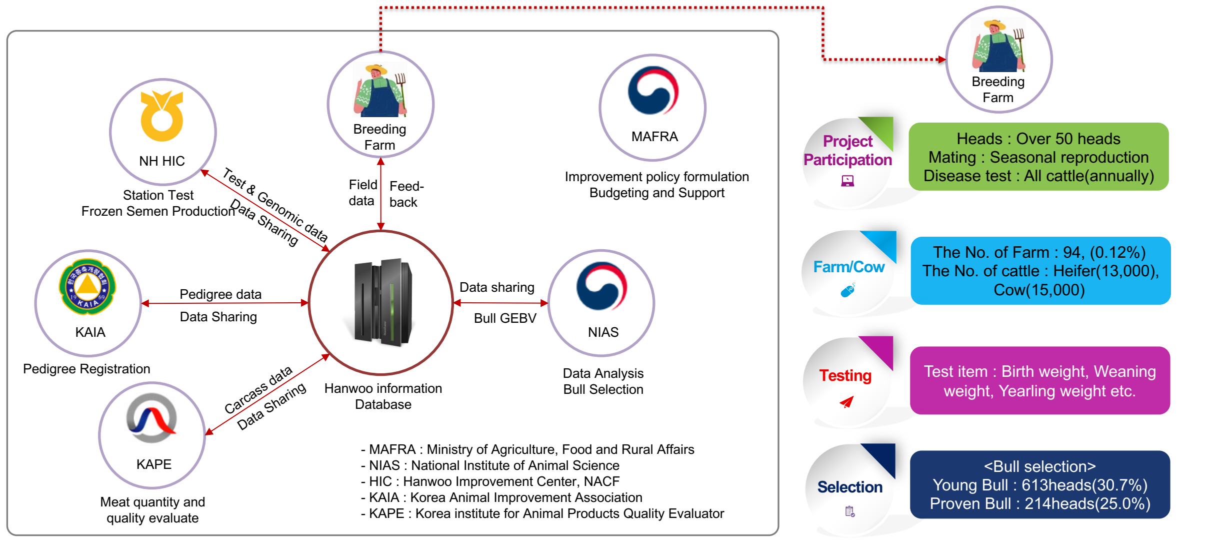
5 Very fat

Realtime carcass performance
(Eye muscle area, Backfat thickness, %IMF etc.)



National breeding institution

NEW Korea NACF



7

National breeding program structure of Hanwoo

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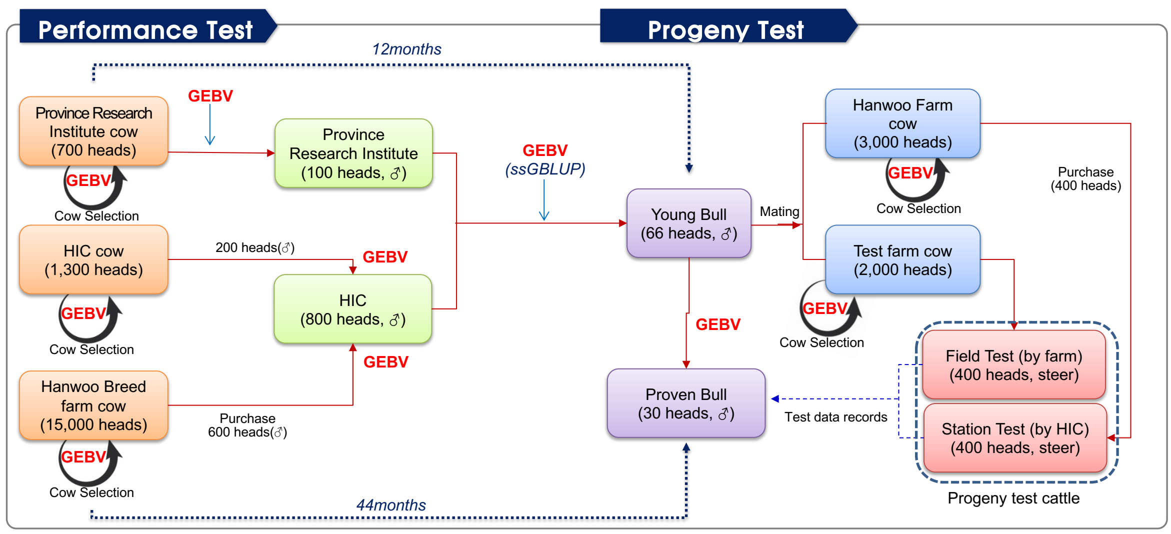


* The reproductive traits will be added in future

8

National breeding program of Hanwoo

NEW Korea NACF

Test records content

◆ Performance Test

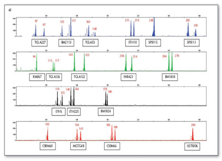
- Growth Traits : Weights at birth, 6, 9, 12 months of age
- Appearance examination
- Body Measurements(12M) : Body height, Hip length, Body length, Chest girth, Chest width, Chest depth, Rump length, Hip width, Thurl width, Pin bone width

◆ Progeny Test : The castration at 6 months of age and slaughtering at 24 months of age

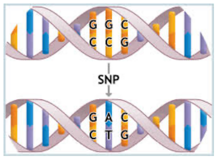
- Growth Traits : Weights at birth, 6, 12, 18, 24 months of age
- Appearance examination
- Body Measurements(12M, 18M, 24M) : Body height, Hip length, Body length, Chest girth, Chest width, Chest depth, Rump length, Hip width, Thurl width, Pin bone width
- Carcass Traits : Carcass Weight, Eye muscle area, Backfat thickness, Marbling score
- Proximate analysis : Moisture, Crude fat, Crude protein, Crude ash
- Fatty acid analysis : Unsaturated fatty acid(Myristic, Palmitic, Stearic acid), Saturated fatty acid(Oleic, Palmitoleic, Vaccenic, Linoleic, γ-Linoleic, Linolenic, Eicosenoic, Arachidonic, Eicosapentaenoic, Docosatetraenoic, Docosahexaenoic acid)
- Meat percent : Primal cut(10 position)

Applied Technology


Embryo transfer


Microsatellite typing

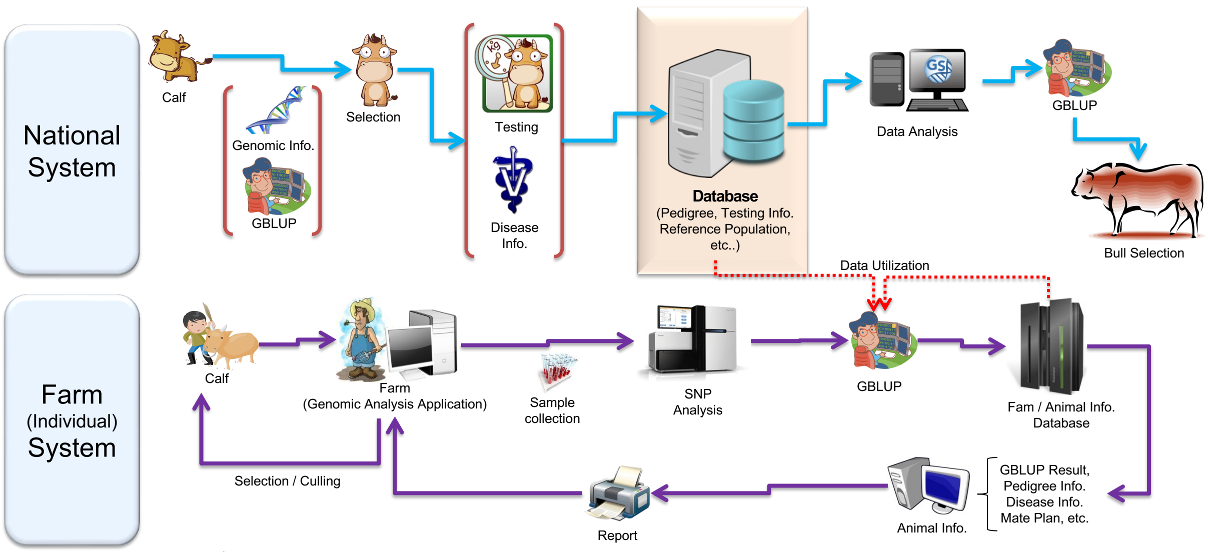

Ultrasound scanning



Genomic Selection

Genomic Selection System

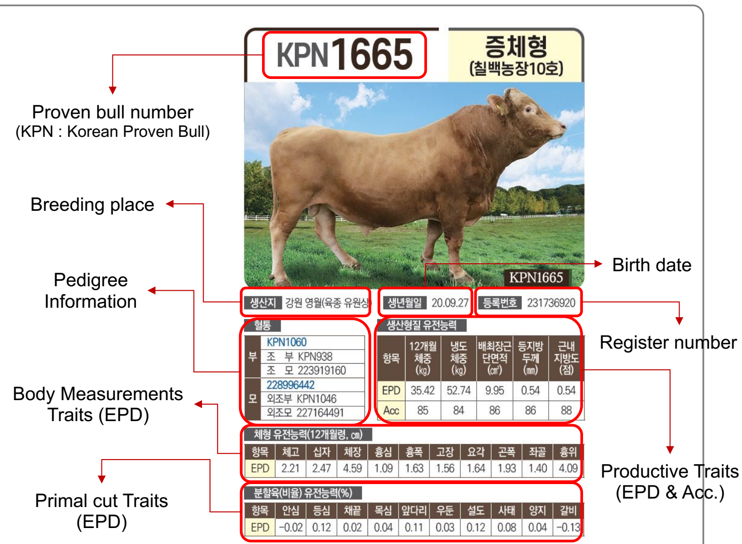
NEW Korea NACF



◆ ssGBLUP

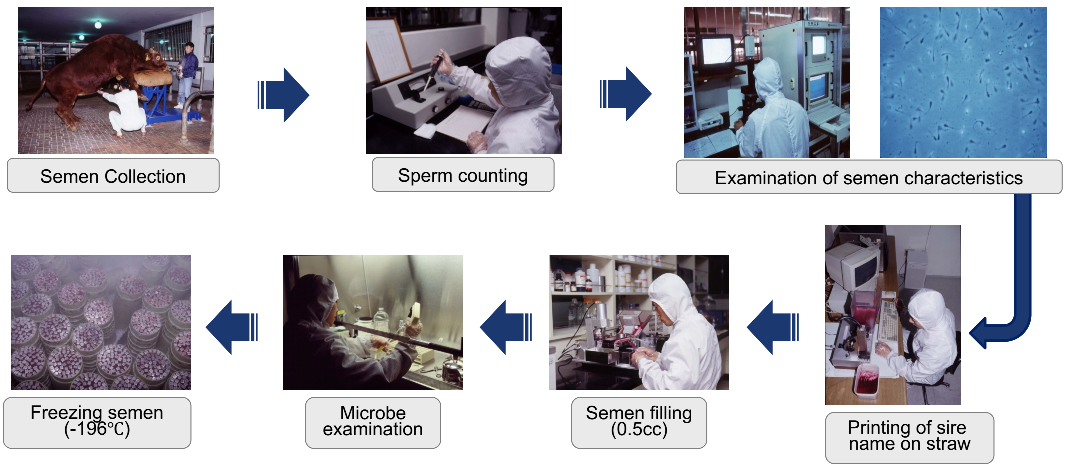
$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + H^{-1}\alpha \end{bmatrix}\begin{bmatrix}\hat{b}\\ \hat{a}\end{bmatrix} = \begin{bmatrix}X'y\\ Z'y\end{bmatrix}, \quad \alpha = \frac{\sigma_e^2}{\sigma_a^2}, \quad H^{-1} = A^{-1} + \begin{bmatrix}0 & 0\\ 0 & G^{-1} - A_{22}^{-1}\end{bmatrix}$$

Hanwoo Sire Summary



Frozen semen production & distribution system

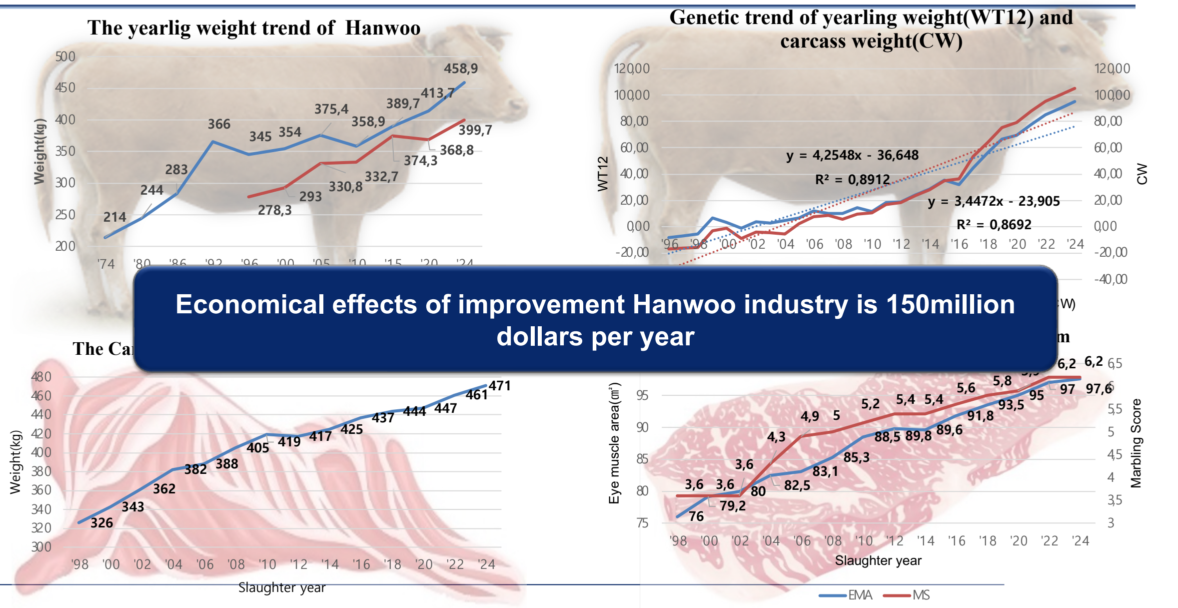
NEW Korea NACF



Frozen semen (2 million straws/year) for artificial insemination are produced through a perfect sanitary system and distributed to the Hanwoo farm.

The Result of Hanwoo Improvement

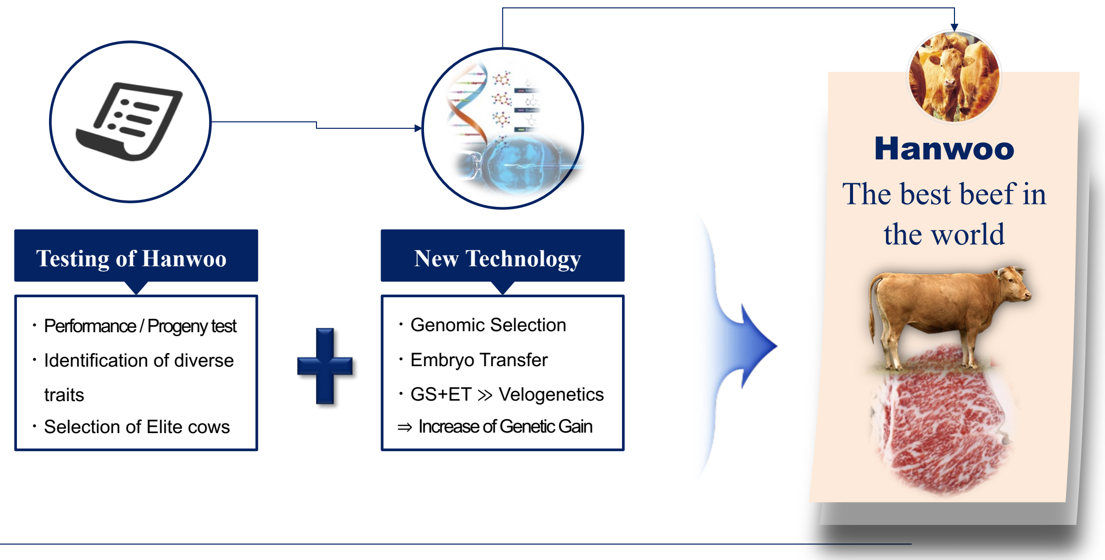
NEW Korea NACF

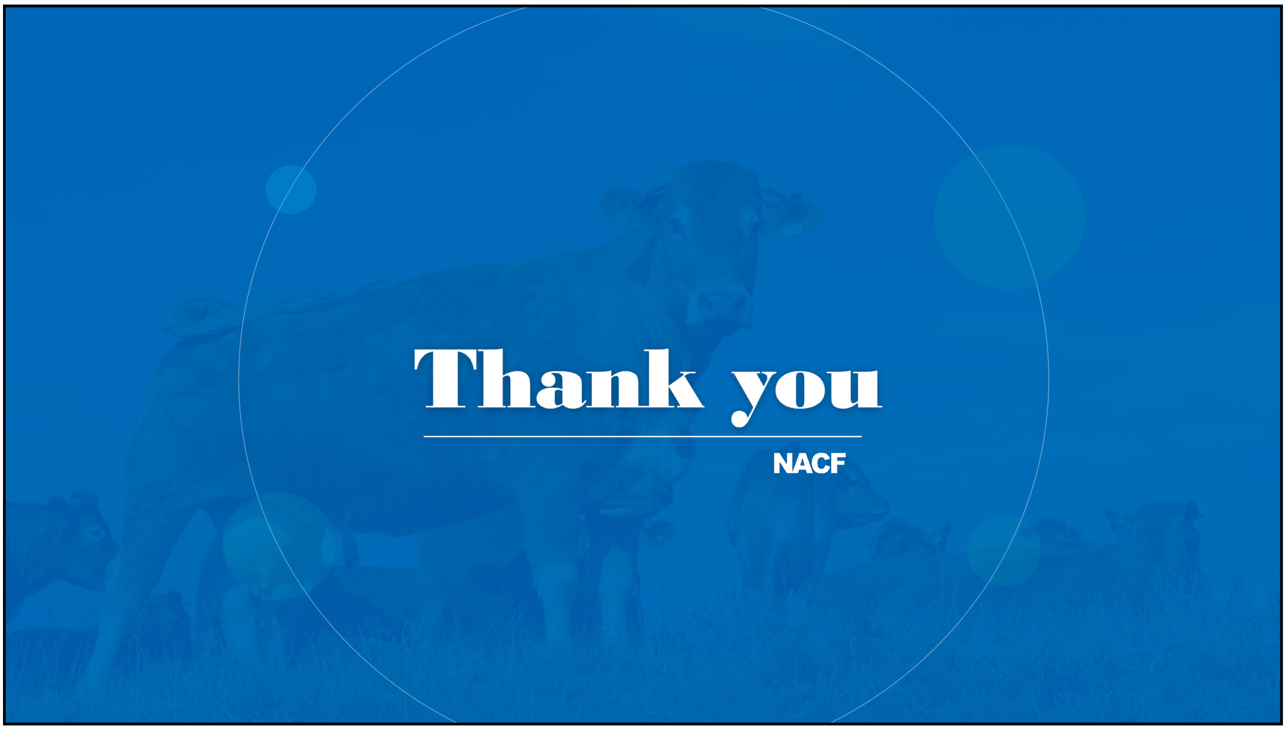


Economical effects of improvement Hanwoo industry is 150million dollars per year

The future of Hanwoo Improvement System

NEW Korea NACF




Thank you
NACF

7. HUSBANDRY AND FEEDING SYSTEMS FOR H'MONG CATTLE IN CAO BANG PROVINCE

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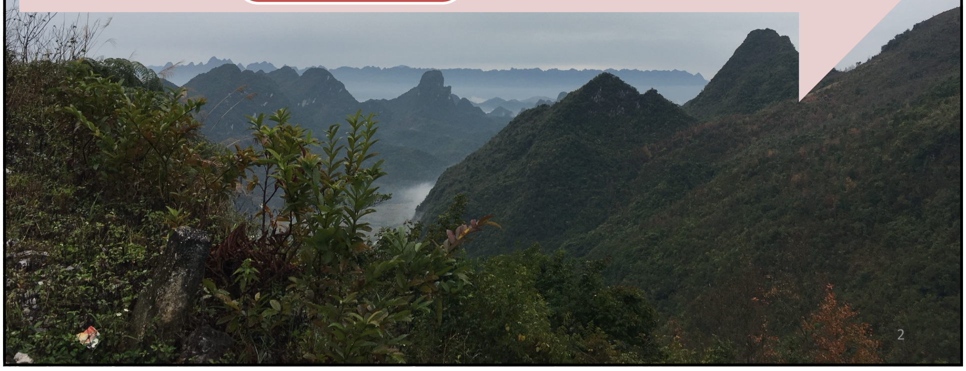
Centre for Agrarian Systems Research and Development (CASRAD)

HUSBANDRY AND FEEDING SYSTEMS FOR H'MONG CATTLE IN CAO BANG PROVINCE

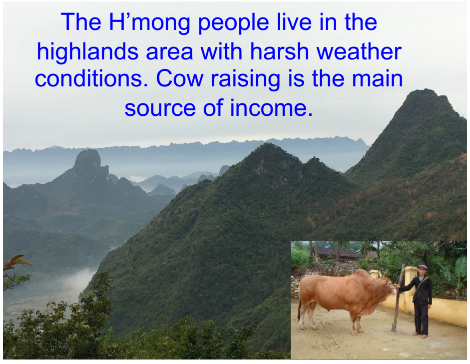
by Dr. Hoang Xuan Truong

CONTENTS

- Introduction
- Methodology
- Results and Discussion
- Conclusions and Recommendations



INTRODUCTION



During the winter-spring season, the Hmong people often raise and fatten cows with many types of forestry plants.

Indigenous knowledge and experience in raising and fattening cows have helped the Hmong people survive and develop in mountainous areas where there is little arable land and harsh natural conditions.
To better understand some indigenous knowledge of the Hmong people, it is necessary to conduct the study on ***"Husbandry and feed systems for H'mong cattle"***

OBJECTIVES

- ✓ Analyze and evaluate the H'mong cattle husbandry systems
- ✓ Identify the main feeds of H'mong cattle

1. H’mong Cattle Husbandry System Analysis

Literature review

Primary data

Questionnaire
Discussions

Survey
(60 households)

Secondary documents

Information Collection
Data Processing

Analysis methods:
- *Comparison*
- *ANOVA analysis*
- *Correlation analysis*

Research categories:
- *Farming scale*
- *Husbandry system characteristics*
- *Fertility*
- *Efficiency of animal husbandry*

2. Research on Green feed Sources in Winter Season for Raising and Fattening H'mong cattle

Field survey and interview **30 households**

↓

Analyzing, Samples sorting, and Data processing;
Using morphologically comparison method, hand held magnifying glass, and taxonomic documents;
Specimens kept at the Vietnam Museum of Nature.

↓

30 households scores each type of feed according to 3 levels:
Most favorite feed (3 scores); Favorite feed (2 scores);
Additive feed (1 score)

↓

Selecting 6 favorite feeds → Conducting analysis for chemical composition and nutritional value at the Institute of Animal Husbandry

RESULTS AND DISCUSSION

1. H’mong Cattle Husbandry Systems in Cao Bang

Characteristics of the cattle husbandry systems of the H’mong people in Cao Bang

2 systems

- Semi-grazing

- Confined raising

H’mong Cattle Breeds at the Research Site

2-year-old: 405 kg

3-year-old: 425 kg

4-year-old: 460kg

- There are 2 main types: (1) high hump (popular) (2) low hump (less popular)
- Diverse coat colors: red, brown, yellow...

- Average weight: male 400-500kg, females 220–260 kg.

Cow Barn

- **100% of households have cow barns** separating from the house, 100% wooden floors.

- **Wooden floor, 0.8-1.2 m above ground**, area from 8-36 m^2 and usually divided into 2-6 cages, each cage 4-6 m^2.
- A cow barn can last over **50 years** with a system of ironwood flooring, investing from 40-50 mil VND.
- The H'mong people's cow barn style comes from the experience of their ancestors of fighting wild animals. → ***Indigenous knowledge in cow barn construction→ Effective management of breeding stock → Reducing disease***

Livestock Production Scale in Surveyed Households (n=60)

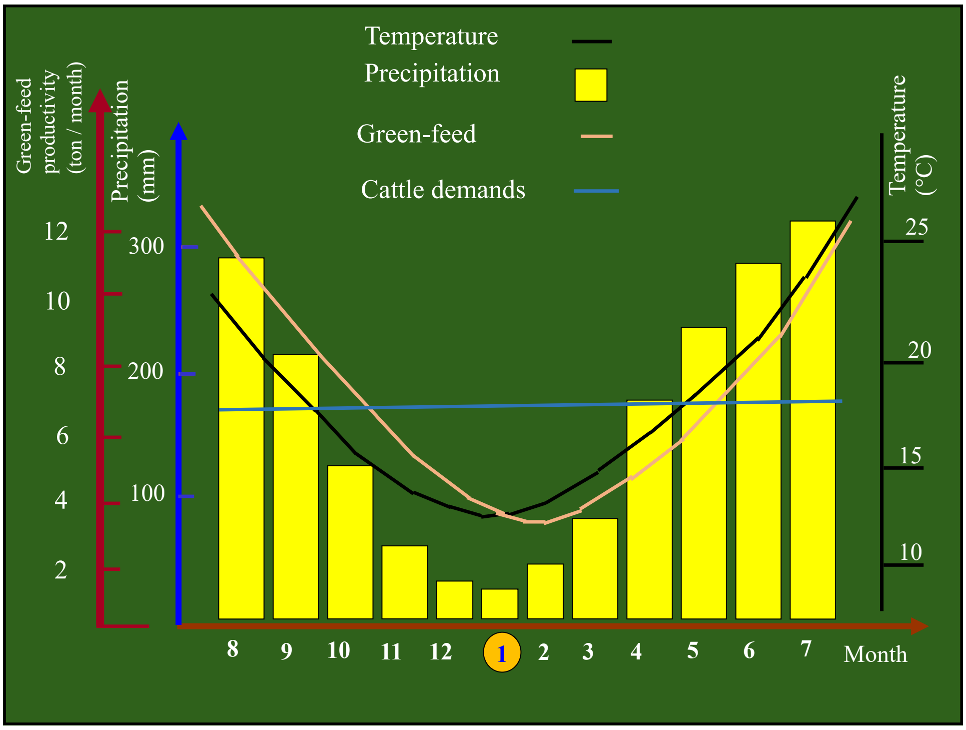
Categories	Scale		
	1-2 cows	3-5 cows	≥ 6 cows
No. of households	51	6	3
Percentage (%)	**85**	10	5
Cow/household	1.60	3.66	9.00

Feeding and Fattening H'mong Cattle

Green-feed:
Natural feed plants in the forest; natural grass, cultivated grass, agricultural by-products

Processed feed:
Corn flour

Cooking congee and mix to feed 2-3 times a day.



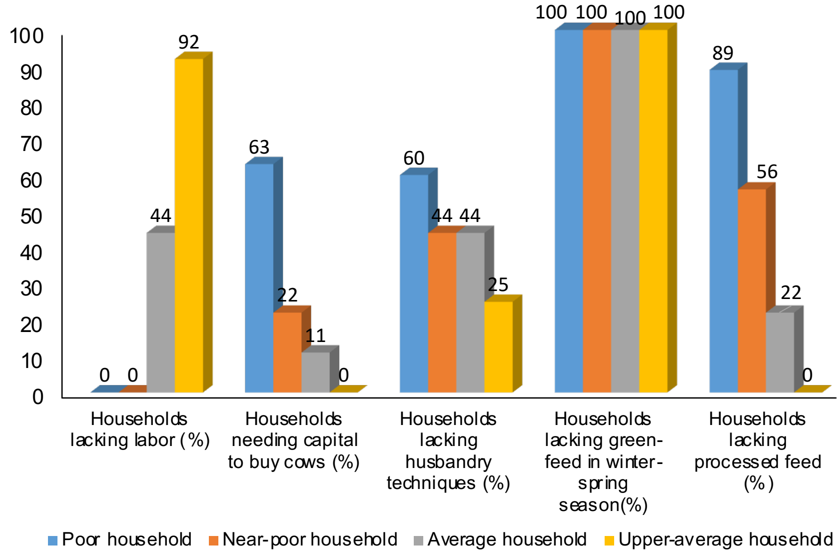
Marketing

- Cao Bang has 9 wholesale markets, Ha Quang district has 3 markets. For the past 3 years, Tra Linh cattle market has 1000 cattles/session with 400 cows.
- Many households have information about the price of cattle before selling. They are free to sell cattle to whomever they want.
- 60% of cows are sold at home and 40% are brought to market.
- Collectors and interest group members rented trucks to transport cows to the market, 2-6 cows/trip and the rental price was 500,000 VND/trip.
- Large male cows in Cao Bang are mainly sold to China, small cows are sold locally and in Thai Nguyen province.

H'mong Cattle Husbandry Efficiency

No.	Indexes	Dual-purpose Cow (Farmers)	SE	Fatten cows (Collectors)	SE
I	Income/cow	**34.287**		**28.288**	
1.1	Income from soil ploughing	1.172	41	0	
1.2	Income from selling cow	30.484	616	28,133	733
1.3	Value from cow dung	2.631	73	155	6.3
II	Cost/cow	**23.814**		**27.399**	
2.1	Breed	9.145	185	25.333	843
2.2	Processed feed	850	40	990	56.9
2.3	Household labor cost	13.047	126	800	50.6
2.4	Veterinary	57	3	50	1.3
2.5	Depreciation of fixed assets	715	24	225	18
III	Net profit/cow	**10.497**	458	**890**	90
IV	Net profit/Household labor	80%		111%	
V	Number of sold cows (cow/household/year)	0,86		12,5	
VI	Mixed income estimated/household/year	**20.247**	-	**21.122**	-

Difficulties in Cattle Husbandry of the H’mong People (N=60)



H’mong Husbandry Culture

The H’mong people have indigenous knowledge that many other ethnic groups do not have:

- Barn and floor are solid, wooden, invested with 40-50 mil VND, and stand over 50 years.
- Good breeds, good breeding stock management
- Households with many cows and big cows are always respected.
- Sharing cows for raising if there are many → **This is a typical community culture of the H’mong people that has existed for a long time.**
- **Fattening techniques for cattle in winter-spring season using native food plants**
- Being able to actively participate in the market, know how to evaluate and price cattle before selling

2. Evaluation of Feed Sources For H'mong Cattle Husbandry in Cao Bang

Classification Results of Feed Plants Used by H’mong People for Cattle in Winter

No.	Scientific name	Common name	Local name	Living form	Parts for usage
	Acanthaceae	Acanthus family			
1	Strobilanthes dalzielii (W.W. Smith) Benoist		Cuoc gia	BUI	Whole plant
	Araceae	Araceae			
2	Rhaphidophora decursiva (Roxb.) Schott	Giant climbing philodendron	Cau Tong	COL	Leaves
	Araliaceae	Ginseng family			
3	Brassaiopsis glomerulata (Blume) Regel		Cau ta cai	BUI	Leaves
4	Schefflera elliptica (Blume) Harms	Ivy Tree	Bay La	BUI	Leaves
	Arecaceae	Palm family			
5	Arenga pinnata (Wurmb) Merr.	Sugar palm		CAU	Leaves
...41					

Specimens of these 41 plants are being kept at the Vietnam Museum of Nature.

06 Favorite Feed Plants of H'mong Cattle

No.	Scientific name	Common name	Local name	Scores
1	Rhaphidophora decursiva (Roxb) Schott	Giant Rhaphidophora	Cau tong	**90**
2	Ficus obscura Blume			60
3	*Ficus vasculosa* Wall.ex Miq	Vascular-leaved Fig		60
4	*Pseudostachyum polymorphum* Munro	Polymorph Bamboo		**90**
5	*Oreocnide kwangsiensis* Hand.Mazz		May roi	**90**
6	*Acer tonkinense* Lecomte	Tonkin Maple	Sau san	**90**

Pictures of 06 Favorite Feed Plants

Rhaphidophora decursiva (Roxb.) Schott; Lân tơ uyn; Cầu tong

Pseudostachyum polymorphum Munro
Hóp thân tái

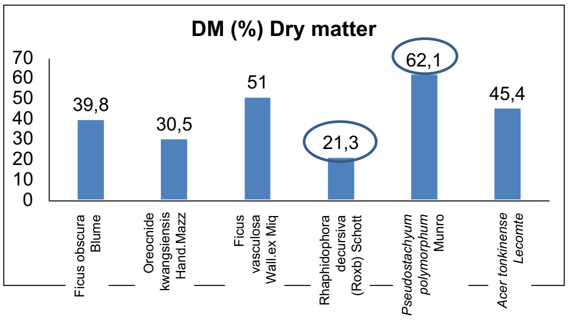
Acer tonkinense Lecomte;
Thích Bắc Bộ, Sâu Sắn

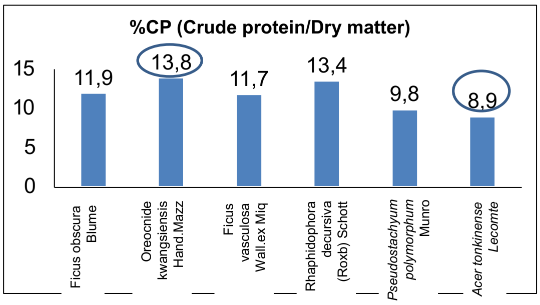
Ficus vasculosa Wall. ex Miq.
Đa lá bóng

Ficus obscura Blume
Sung

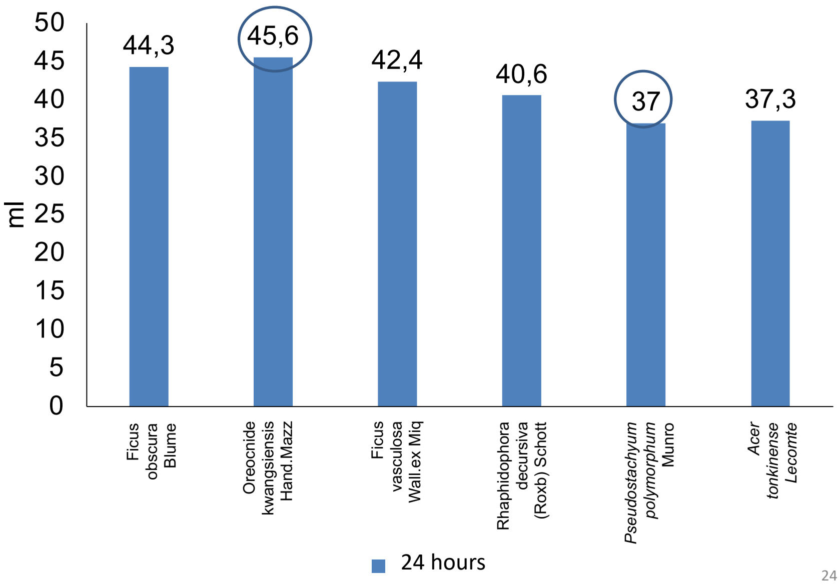
Oreocnide kwangsiensis Hand.Mazz
Chéo béo, Quảng tây, Mảy roi

% Dry matter and % Crude Protein of 06 Favorite Feed Plants

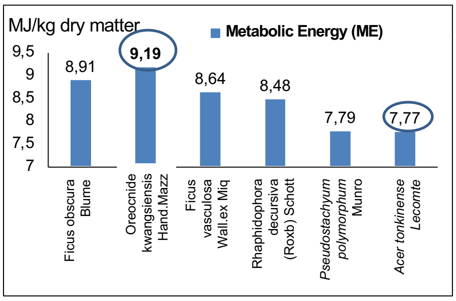


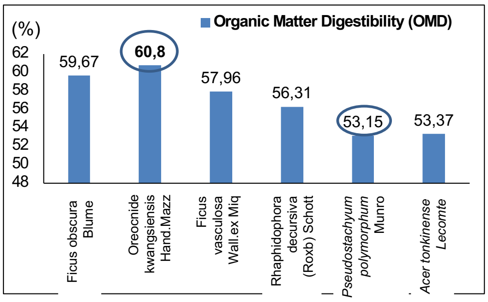


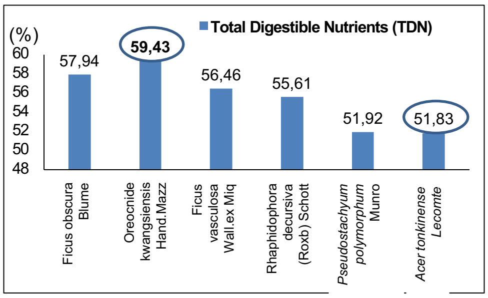
Accumulated Gas Volume During In Vitro Fermentation at 24 Hours of Incubation of Feed Plant Samples (ml)



Metabolic Energy (ME), Organic Matter Digestibility (OMD) và Total Digestible Nutrients (TDN) of 06 Favorite Feed Plants







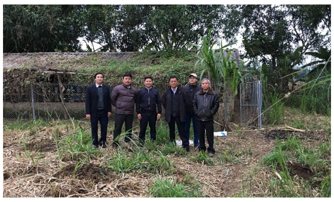
CONCLUSIONS AND RECOMMENDATIONS

CONCLUSIONS

- Dual-purpose cattle husbandry is the dominant husbandry practice of H'mong households in Ha Quang, Cao Bang.
- There are 41 different types of plants used as feed for cattle.
- There are 6 types of favorite groups, 6 types of plants can be mixed to ensure the diet for fattening cattle in the winter.
- The basic nutritional value of favorite feed plants has been analyzed.

RECOMMENDATIONS

- Maintaining the H'mong cattle husbandry systems with indigenous knowledge of the H'mong people
- For livestock farms and households, fattening cattle at 24 months of age should be done with diet 2 (DM: 47.63%; Crude protein: 12.07g and ME: 9.9 MJ).
- Conducting study on the potential for scaling up the cultivation of the six preferred feed plants.
- Establishing Geographical Indication for H'mong beef products in the mountainous region of Northern Vietnam.



THANK YOU!

8. CURRENT AND PROSPECTS OF PRECISION MANAGEMENT IN SOUTH KOREA BEEF PRODUCTION

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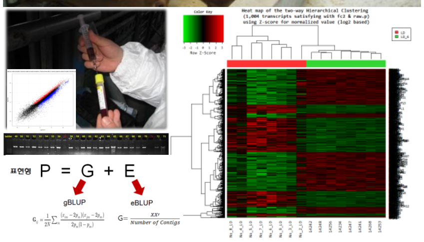
Korea National University of Agriculture and Fisheries

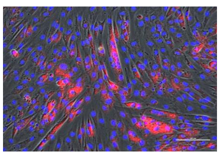
Current and Prospects of Precision Management in South Korea Beef Production

Korea National University of Agriculture and Fisheries
Department of Livestock

CHUNG, KI YONG

목차





Contents

1. Global Issue of Beef Cattle

Green Revolution and Food Production

26 People/1 Farmer
(1900 year)

155 People/1 Farmer
(1960 year)

265 People/1 Farmer
(2050 year)
Population 96 bill U.N. report

Precision Agriculture Prescriptive planting : 처방농업

○ Target of global frontiers (Monsanto/US, Wagennigen/Nethaland, Pitech/Israel)
- Big data, AI, Deep learning Tech
- Reduce environmental facts (Land, Insect, Temperature, Broadcasting etc.)
- Perfect growth control for individual corps(efficiency rate 30% improvement)

※ Relative to high global level 73% technically delayed 4.2 years (RDA report)

1. Global Issue of Beef Cattle

World wide beef cattle breedtype

애버딘 앵거스(Aberdeen Angus) 샤로레(Charolais) 헤어포드(Hereford) 시멘탈(Simmental)

레드앵거스(Red angus) 리무진(Limousine) 겔브비(Gelbvieh) 브란거스(Brangus)

Brahman

Nelore

Hanwoo

Chikso

Jeju Black Cattle

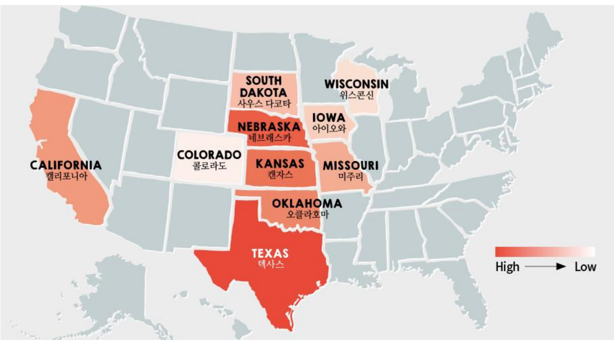
High Quality Meat is …

Angus

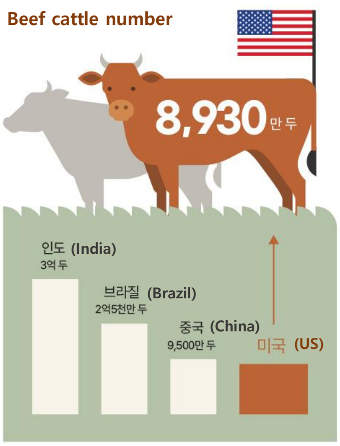
Hanwoo

Japan Wagyu

Beef product area and process in US



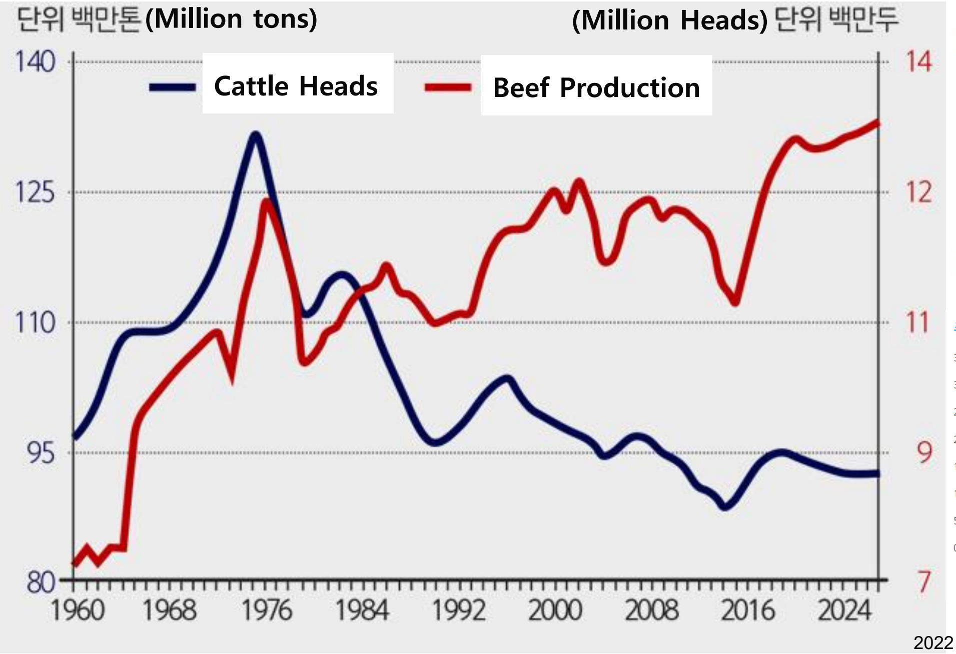
Beef Industry Information(202 3)

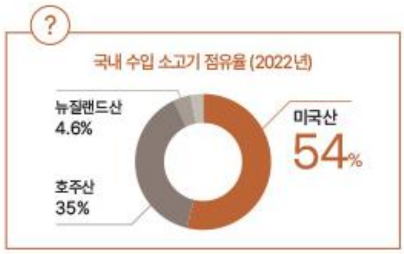


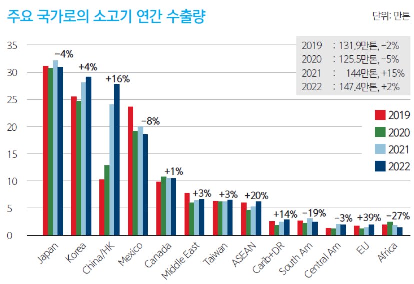
2022 USMEF

1. Global Issue of Beef Cattle

Beef cattle number and Beef product







2022 USMEF

2. History of Hanwoo Cattle Industry

History of Hanwoo

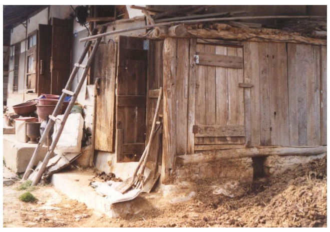
Domestic Work Cattle(1500years~)

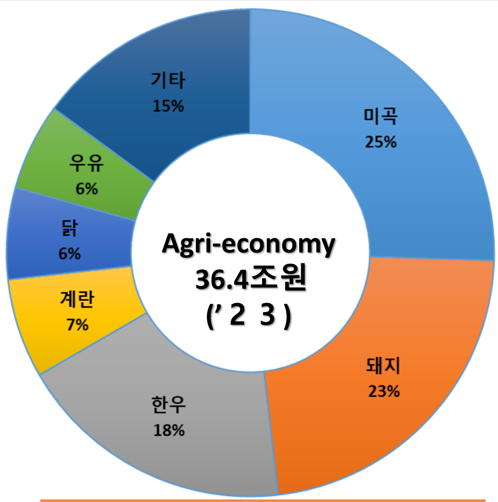
2nd World War
1.5 million Reduce

Korean War
0.17 million Reduce

Work cattle → Beef cattle
Genomic improvement 70 years

Beef Carcass Grading System('92)
→ 3.4 million hd('25)



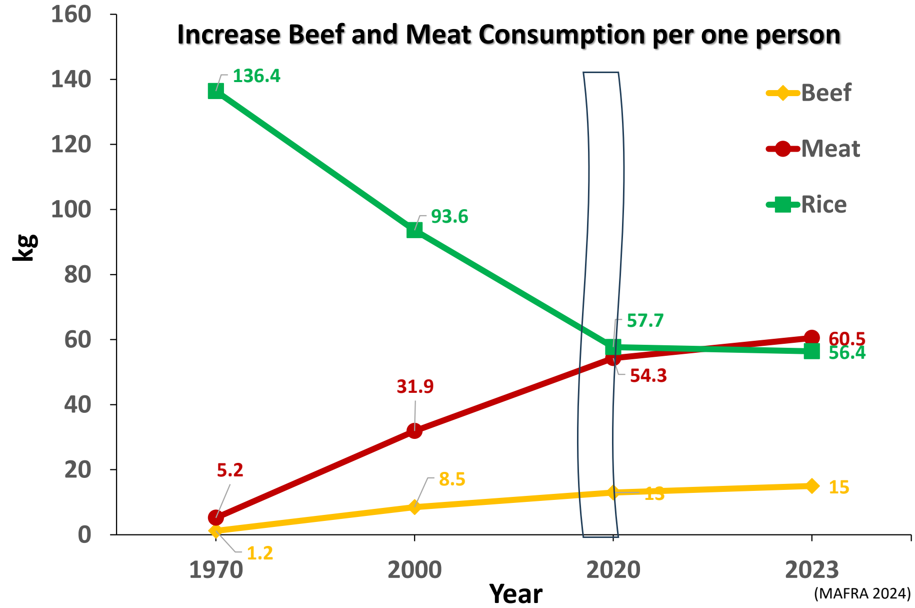


Livestock Industry (Prod. '23 MAFRA)

Rice > pig > **Hanwoo(3rd place)**

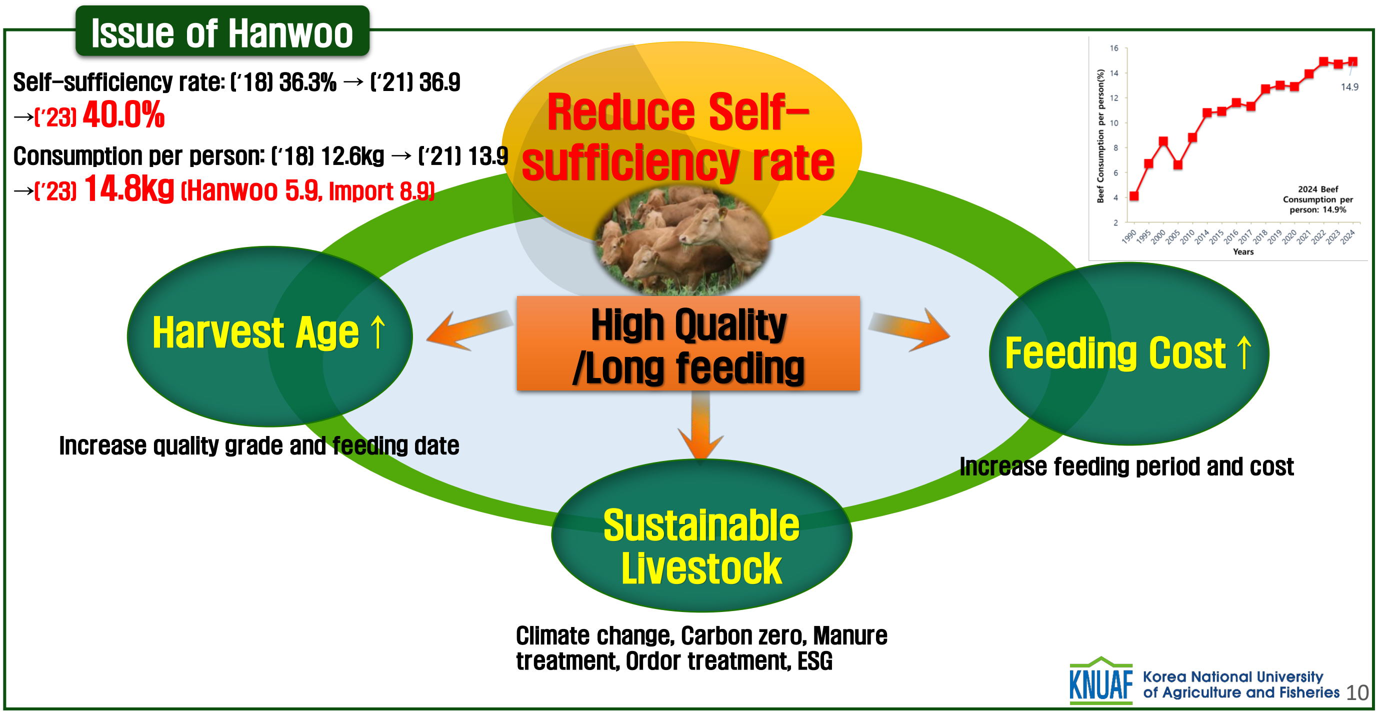
2. History of Hanwoo Cattle Industry

Current Hanwoo Industry Issue and Next



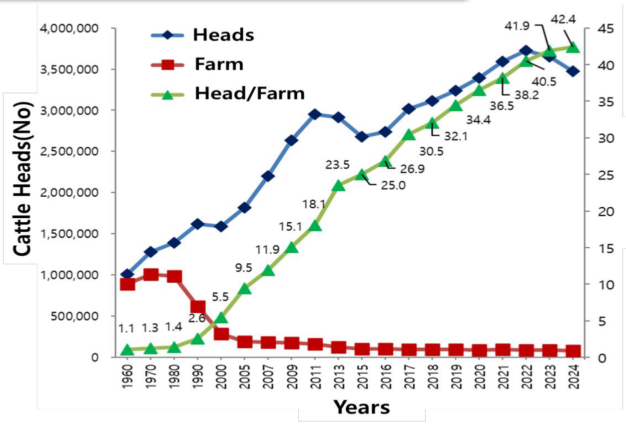
Change rate per years	Consumtion per person(kg)		
	Beef↑	Meat↑	Rice↓
1970-2000	0.24	0.89	1.43
2000-2020	0.23	1.12	1.80

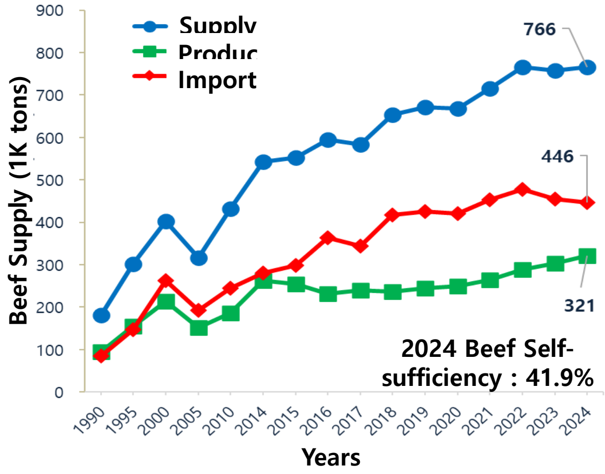
2. History of Hanwoo Cattle Industry



2. Current Issue of Hanwoo Industry

Hanwoo heads per farm(Large scale)





○ **Requied Improved Precision Management System**

Head/Farm ('10)15.1hd→('16)29.9→('20)36.5→('24)42. 2
Farm('10)163,000farm→('16)97,000→('20)93,000 →('24) 8 2,000

Over 100hd Farm
('10)4,600→('16)6,400→('20) 8 ,500 →('24)9,000

(Now) High energy diet based group management → (Next) Genomic based individual adapted precision management

2. History of Hanwoo Cattle Industry

Total Feeding Cost

Calf (male) price
4,000,000won

Feeds etc
4,000,000won

Carcass Price: 8,000,000won
High 1⁺⁺A, 11,280,000 ~ Low 3C, 3,660,000
= 7,600,000 diff. ('24)

The way to Increase Income

2. History of Hanwoo Cattle Industry

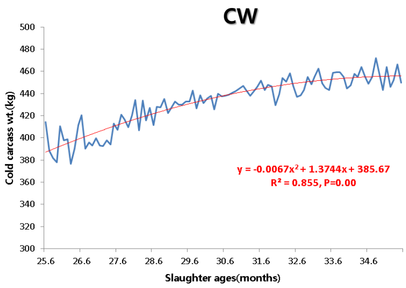
Total Feed Amount

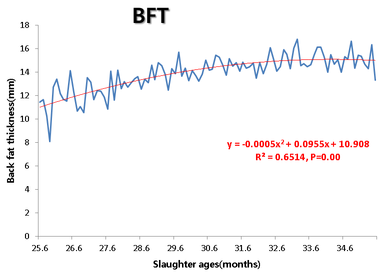
품목	농협사료 (안심한우)	협회OEM (대한한우)	서울축산농협 (한우마춤+)	퓨리나 (맥스-효율형)	천하제일 (상상플러스-대형)	선진 (원더풀)
Feeding Periods	22	22	23	22	23	22
Target WT	750	750	765	785	800	763
Feed Amounts	5137.6	5152.8	5198.4	4894.4	5213.6	5350.4

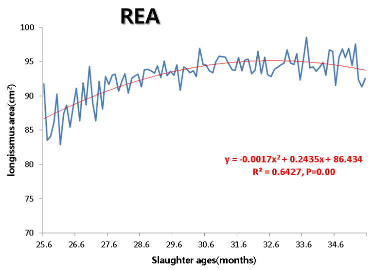
Total Feed Amounts

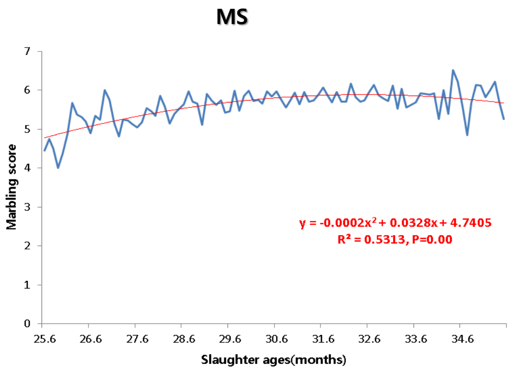
X 206 box = 5,145kg

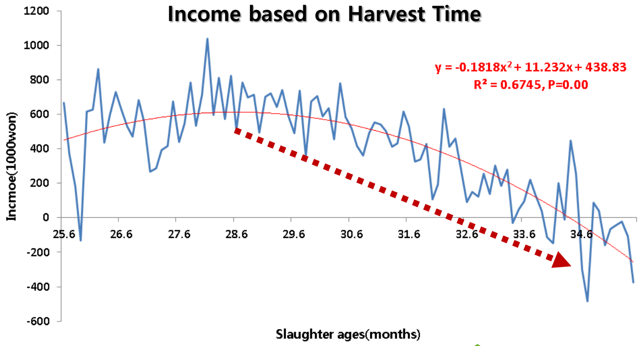
2. History of Hanwoo Cattle Industry









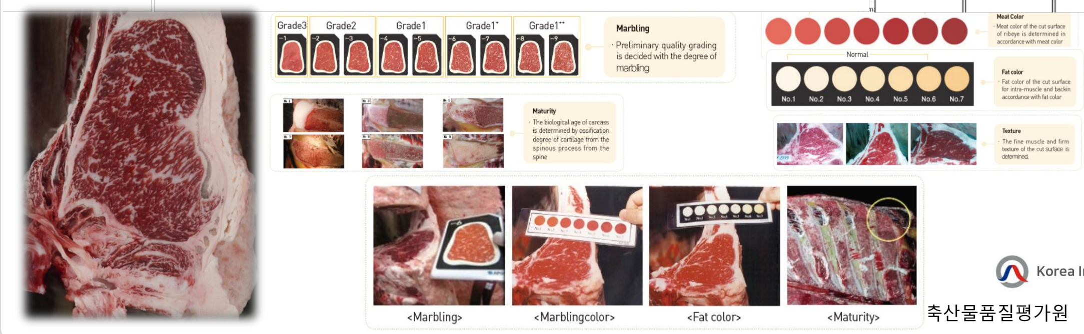


NIAS, 2016

2. History of Hanwoo Cattle Industry

Hanwoo Quality Grading System

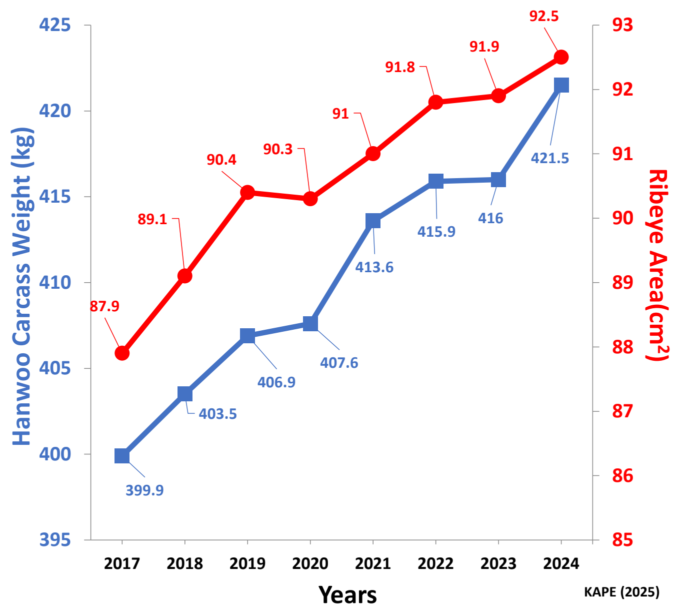
Korea	1⁺⁺							1⁺		1		2		3
BMS(No)/CF(%)						9/19	8/17	7/15	6/13	5/11	4/9	3/7	2/5	1/<5
Japan	5					4			3		2	1		
BMS(No)/CF(%)	12/32	11/29	10/27	9/25	8/23	7/20	6/18	5/16	4/13	3/11	2/9	1/<6.5		
USA	Prime									Choice			Select	Std
BMS(No)/CF(%)	※ BMS: Bovine Marbling Standard/CF: Crude Fat								Ab/10	Ab/9	Md/7	Sm/5	Sl/3	Tr/<2



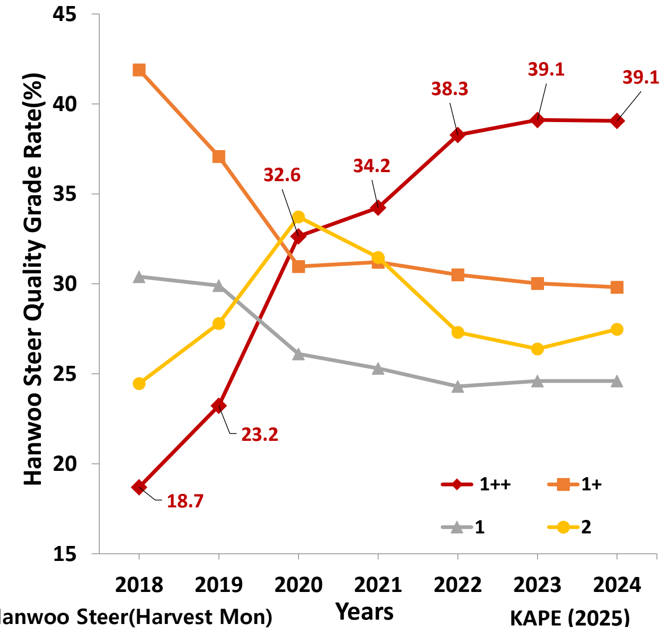
2. History of Hanwoo Cattle Industry

Hanwoo Traceability System

2. History of Hanwoo Cattle Industry



Korea Institute for Animal Products Quality Evaluation (2024)

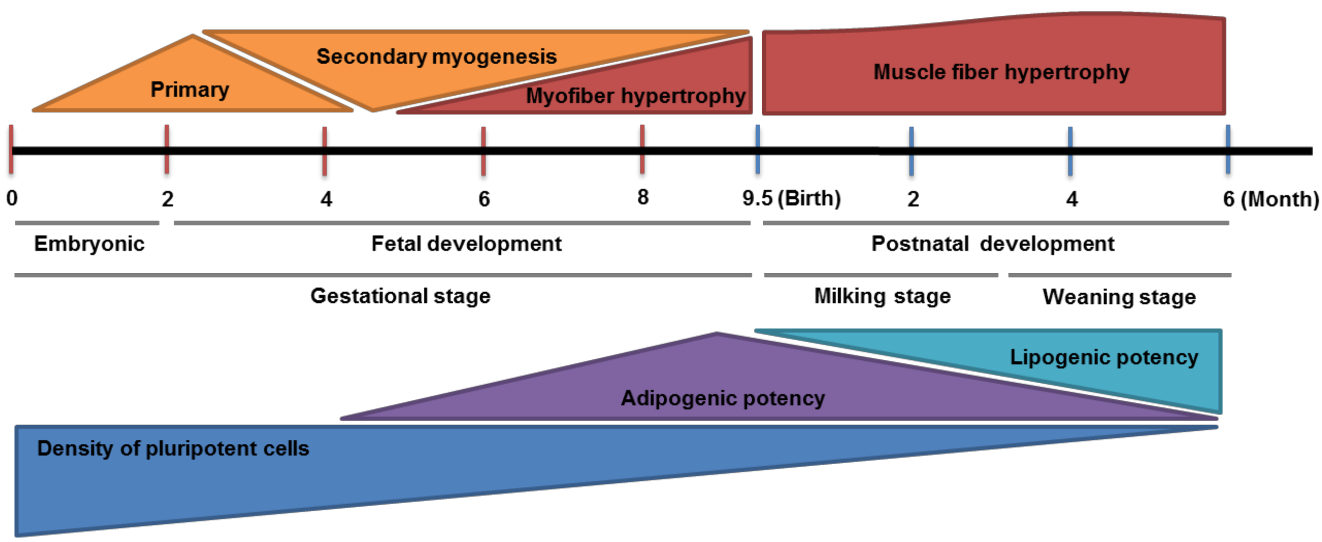


- Hanwoo Steer(Harvest Mon)

'19(30.5)→'20(30.3)→'21(30.4)→'22(30.7)→'23(31.1)→'24(31.6)

3. Genomic Data based Agriculture

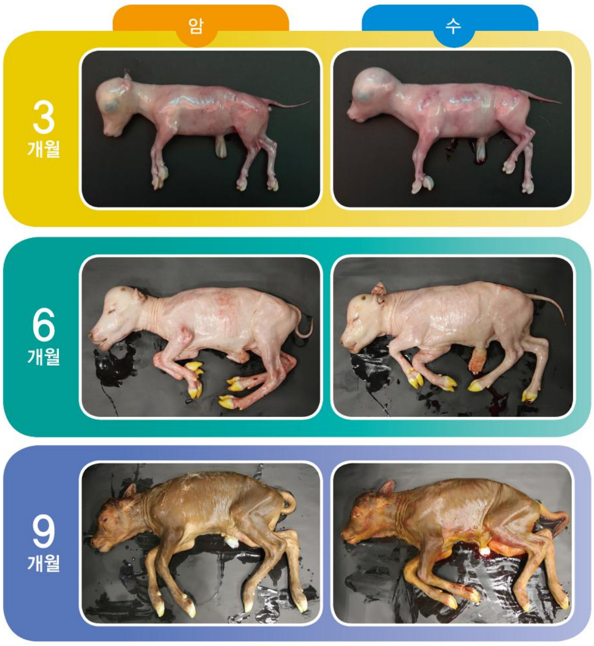
Fetal Programming of Muacle and Adipose Development

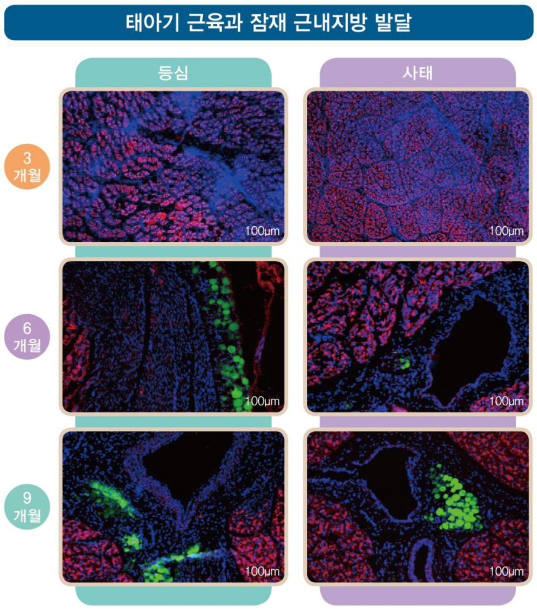


<M.Do et al., 2019>

3. Genomic Data based Agriculture

Fetal Programming of Muacle and Adipose Development



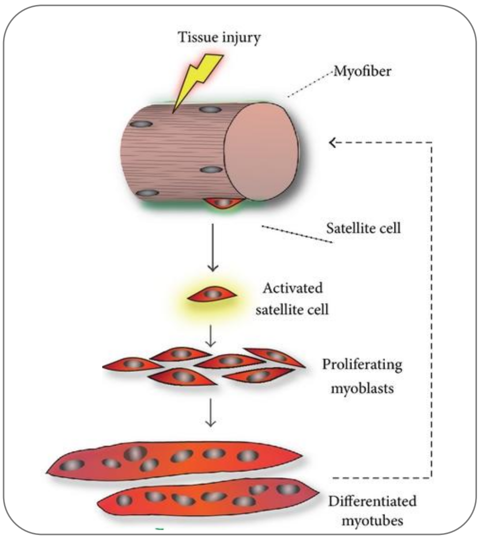


<NIAS, 2020>

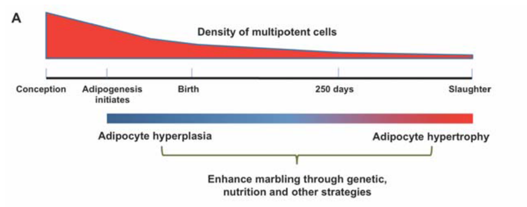
3. Genomic Data based Agriculture

Muscle and Fat Development (Fetal Programming)

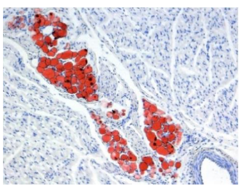
- Muscle satellite cell



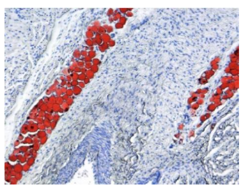
출처 - http://www.hindawi.com/journals/mi/2013/491497/fig1/



M. DU et al., 2010.



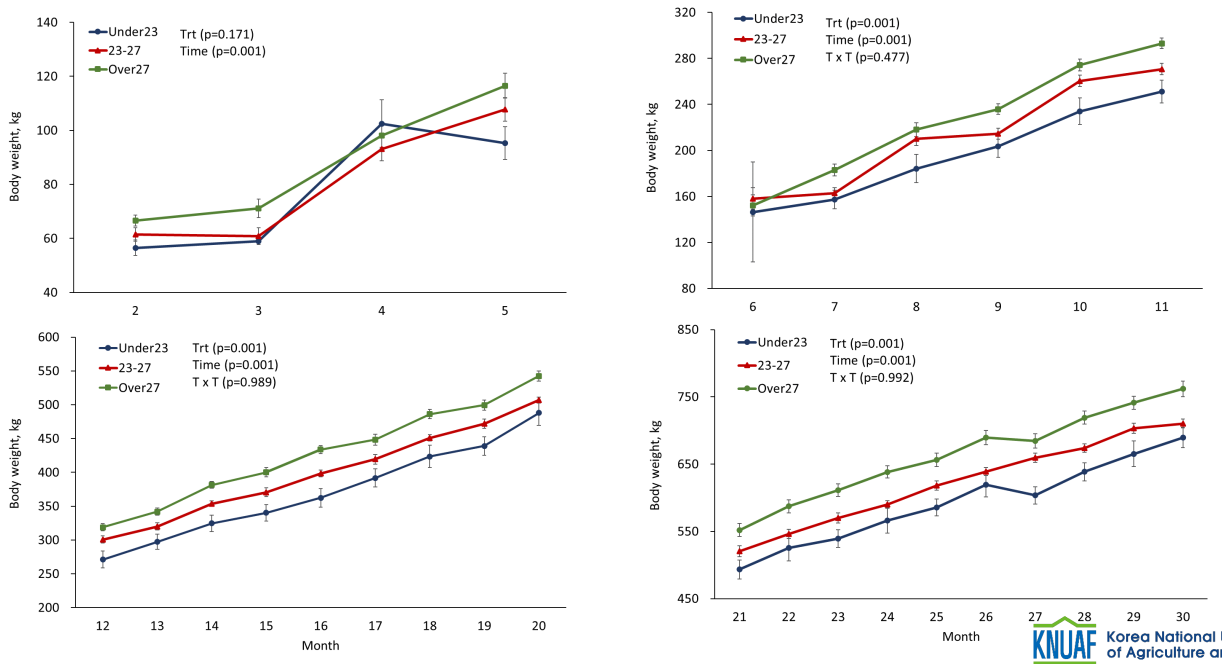
9개월령 태아 한우(수) 등심



9개월령 태아 한우(암) 등심

3. Genomic Data based Agriculture

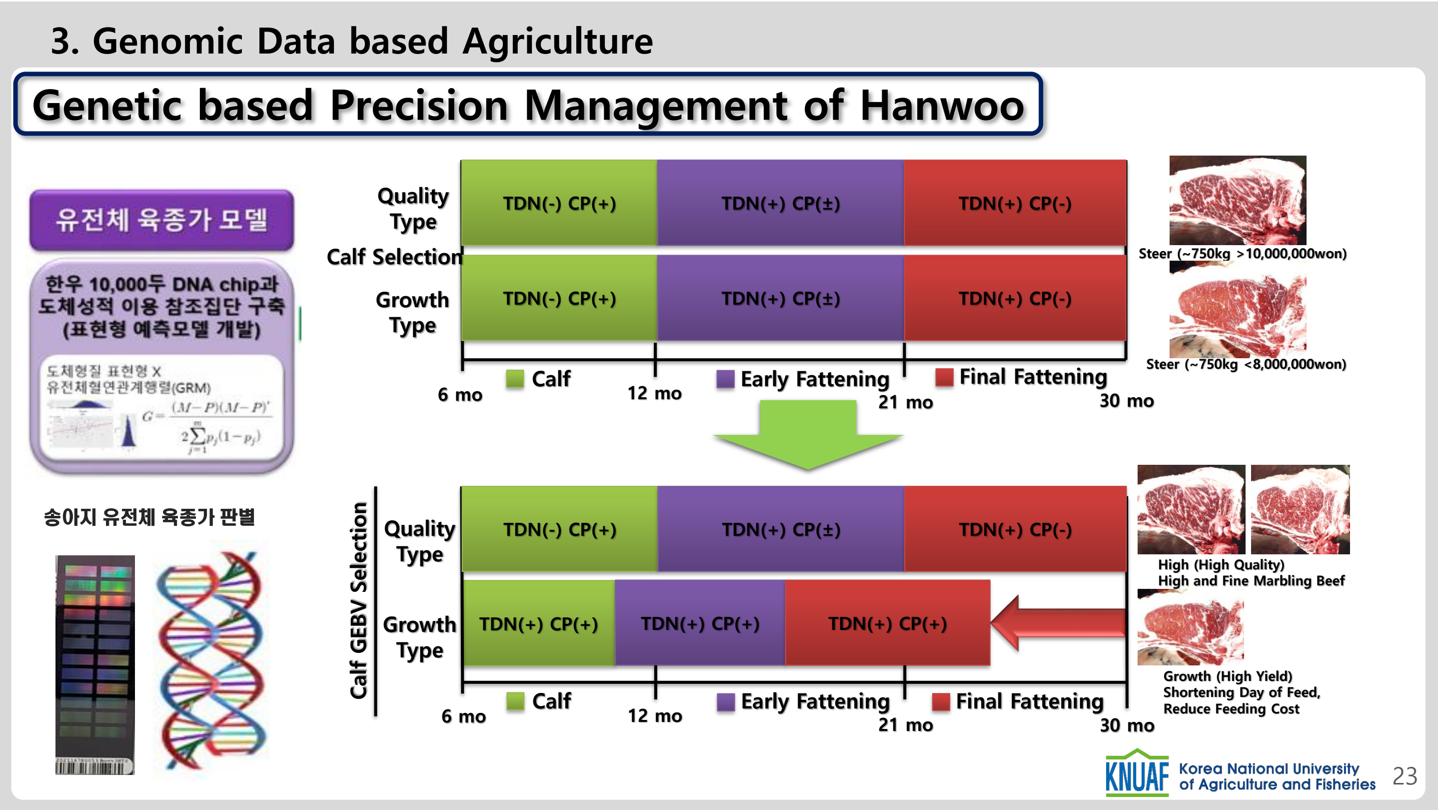
Growth Performance of New Born Cattle (Hanwoo steer 173hd)

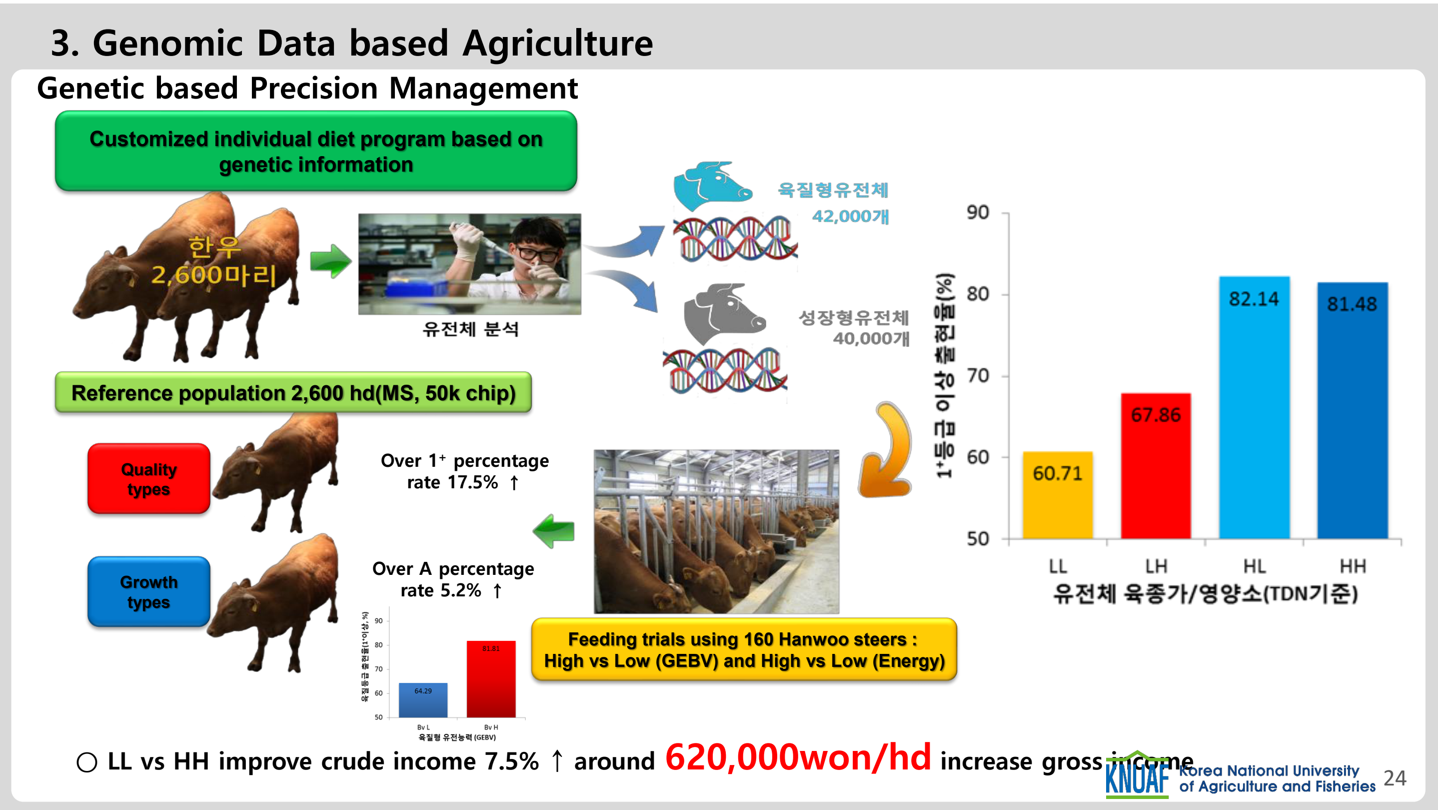


3. Genomic Data based Agriculture

Carcass Characteristics of New Born Cattle (Hanwoo steer 173hd)

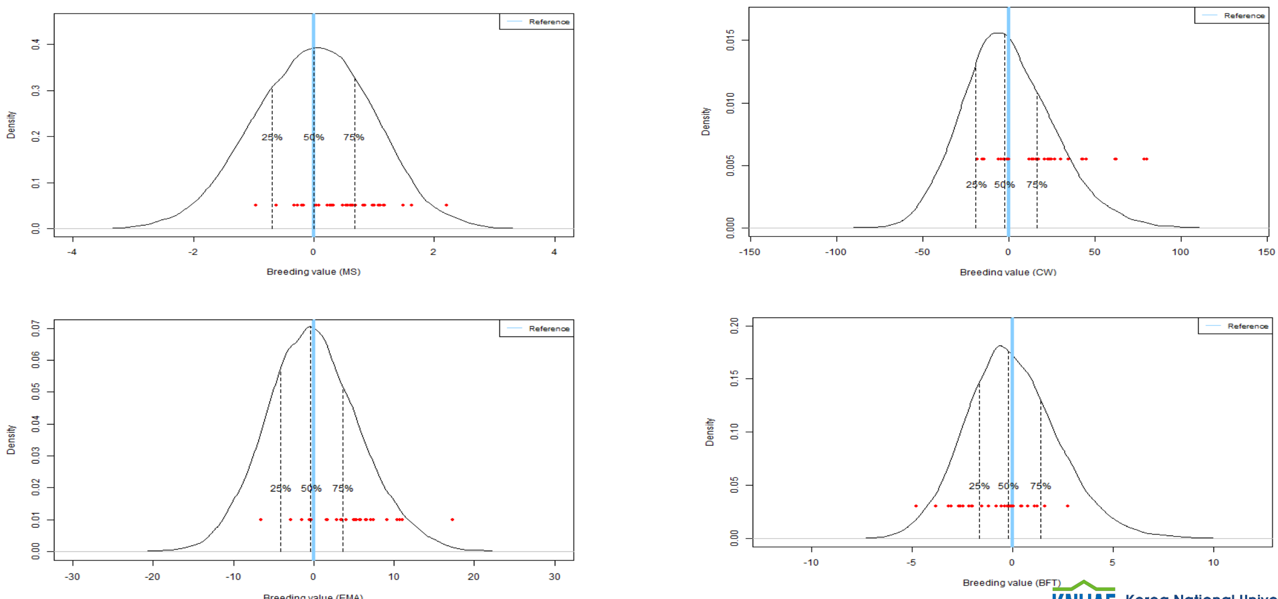
	Under 23	23-27	Over 27	SEM	p-value
Body weight, kg	20.48	25.42	30.22	2.81	0.001
Carcass weight, kg	383.00	400.97	430.19	13.75	0.001
Back-fat thickness, mm	10.33	11.72	12.78	0.71	0.032
Rib-eye area, cm^2	81.07	85.97	89.68	2.49	0.001
Dressing, %	66.29	65.42	64.33	0.56	0.010
Marbling score	5.44	5.50	5.89	0.14	0.407


3. Genomic Data based Agriculture
Genetic based Precision Management of Hanwoo
유전체 육종가 모델
한우 10,000두 DNA chip과 도체성적 이용 참조집단 구축 (표현형 예측모델 개발)
도체형질 표현형 X 유전체혈연관계행렬(GRM)
송아지 유전체 육종가 판별
Quality Type
Calf Selection
Growth Type
TDN(-) CP(+)
TDN(+) CP(±)
TDN(+) CP(-)
6 mo
Calf
12 mo
Early Fattening
21 mo
Final Fattening
30 mo
Steer (~750kg >10,000,000won)
Steer (~750kg <8,000,000won)
Calf GEBV Selection
TDN(+) CP(+)
High (High Quality)
High and Fine Marbling Beef
Growth (High Yield)
Shortening Day of Feed,
Reduce Feeding Cost
KNUAF Korea National University of Agriculture and Fisheries
23


3. Genomic Data based Agriculture
Genetic based Precision Management
Customized individual diet program based on genetic information
한우 2,600마리
유전체 분석
육질형유전체 42,000개
성장형유전체 40,000개
Reference population 2,600 hd(MS, 50k chip)
Quality types
Growth types
Over 1⁺ percentage rate 17.5% ↑
Over A percentage rate 5.2% ↑
Feeding trials using 160 Hanwoo steers : High vs Low (GEBV) and High vs Low (Energy)
1⁺등급 이상 출현율(%)
90
80
70
60
50
60.71
67.86
82.14
81.48
LL
LH
HL
HH
유전체 육종가/영양소(TDN기준)
○ LL vs HH improve crude income 7.5% ↑ around 620,000won/hd increase gross income
KNUAF Korea National University of Agriculture and Fisheries
24

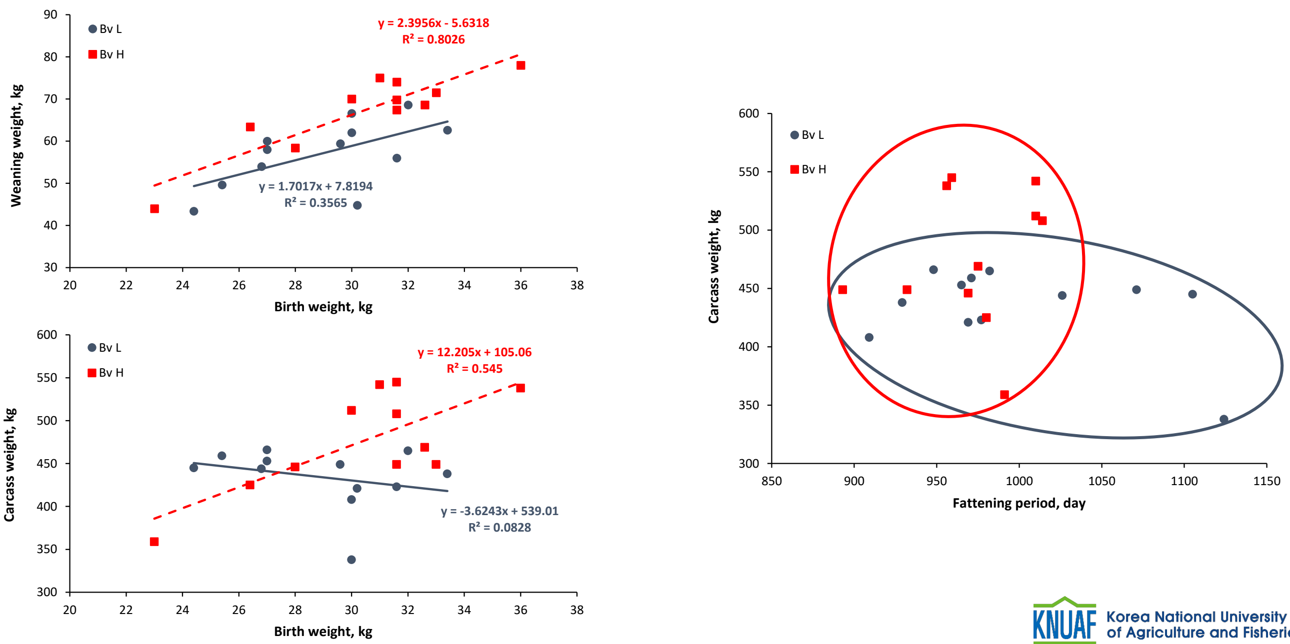
3. Genomic Data based Agriculture

Farm study (2020. Jeju A farm 32 Hanwoo steer)



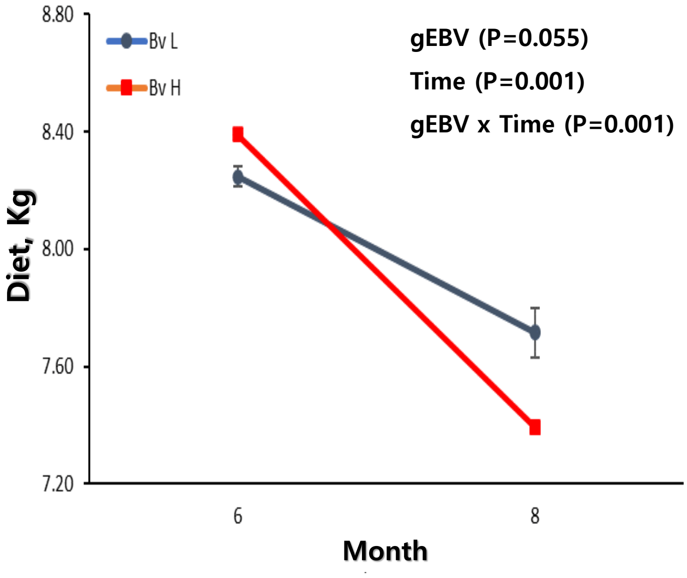
3. Genomic Data based Agriculture

Farm study (2022. Gyunggi B farm 32 Hanwoo steer)



3. Genomic Data based Agriculture-Heat Stress

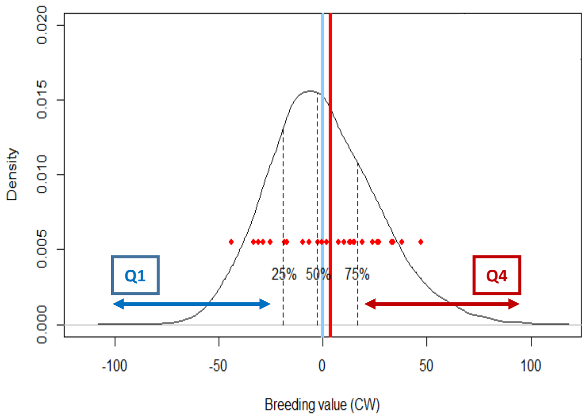
Hanwoo Heat Stress Respond(30 Hanwoo steer)

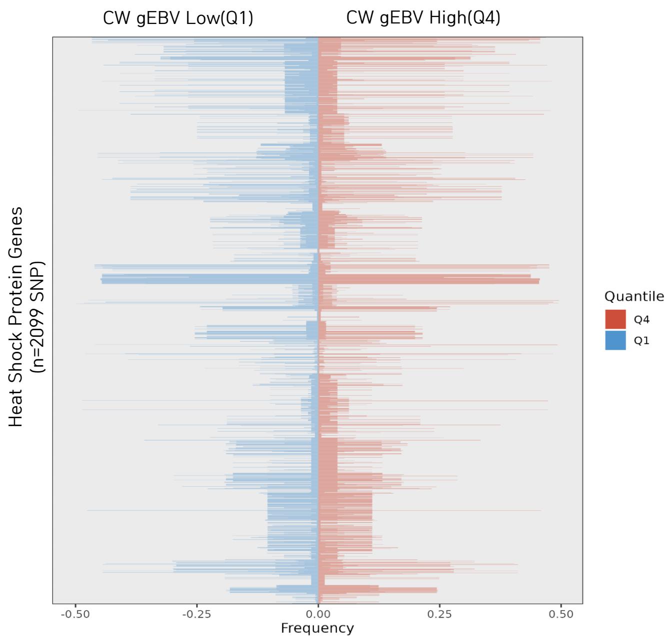


Bv CW	Bv H	Bv L	SEM	P-value
Feeding Periods	378	383	2.32	0.408
Live Weight, kg	768.43	726.57	20.93	0.072
CW, kg	460.07	432.79	13.64	0.051
BFT, mm	13.86	12.43	0.71	0.471
REA, cm^2	94.71	94.29	0.21	0.913
MS	6.64	6.07	0.29	0.321
Quality Grade (1^{++}: 1^{+}: 1 : 2, %)	43 : 36 : 21 : 0	36 : 36 : 28 : 0	.	.
Yield Grade (A : B : C, %)	22 : 64 : 14	43 : 43 : 10	.	.
Auction Price, kg/won	22,909	22,235	337	0.317
Total Price, won	10,603,648	9,718,220	442,7	0.056

3. Genomic Data based Agriculture

HSP 27, 60, 70, 90 SNP 2099 search (Hanwoo reference population 20k)



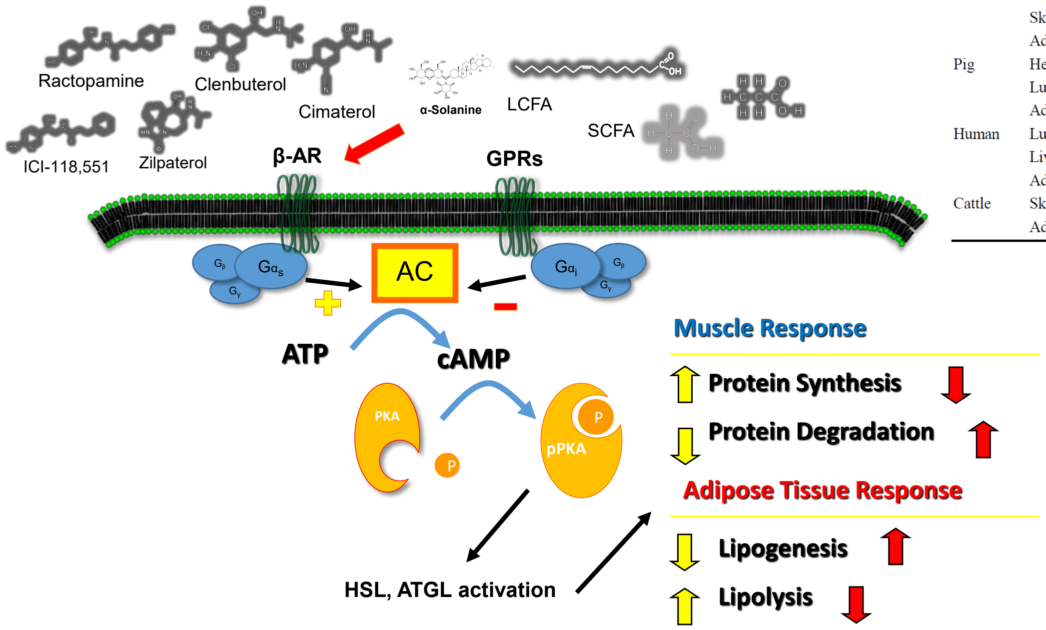


4. Application of Precision Management

Years	Author	Affiliation	Paper Numbers
1970 ~	Allen, R. E.	University of Arizona	59
1980 ~	Dodson, M. V.	Washington State University	52
	Dayton, W. R	University of Minnesota	35
	Greene, E. A	University of Arizona	12
	White, M. E.	University of Minnesota	37
	McFarland, D. C	South Dakota State University	56
1990 ~	Grant, A. L.	Virginia Tech	19
	Gerrard, D. E.	Virginia Tech	12
	Hathaway, M. R.	University of Minnesota	31
	Johnson, S. E.	University of Arizona	29
	Johnson, B. J.	Texas Tech University	51
	Velleman, S. G	Ohio State University	63
2000 ~	M. Du	Washington State University	184
	Kamanga-Sollo, E.	University of Minnesota	18
	Weber, W. J.	University of Minnesota	4

4. Application of Precision Management

Mode of Action Growth Promotant

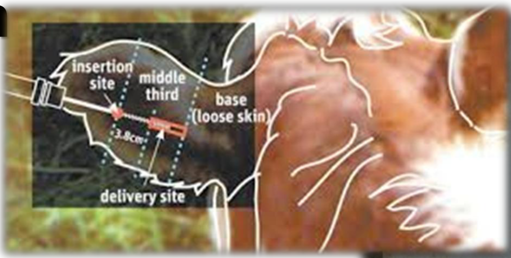


Species	Tissue/organ	Abundance of β-AR subtype
Rat	Heart	$>90\%\ \beta_1$
	Skeletal muscle, lung	$>85\%\ \beta_2$
	Adipose tissue	$>90\%\ \beta_3$
Pig	Heart	$>65\%\ \beta_1$
	Lung	$67\%\ \beta_1$
	Adipose tissue	$73\%\ \beta_1$, $20\%\ \beta_2$, $7\%\ \beta_3$
Human	Lung	$27\%\ \beta_1$
	Liver	$20\%\ \beta_1$
	Adipose tissue	$35\%\ \beta_1$, $65\%\ \beta_2$
Cattle	Skeletal muscle	$>99\%\ \beta_2$
	Adipose tissue	$>90\%\ \beta_2$

Mersmann, 1998

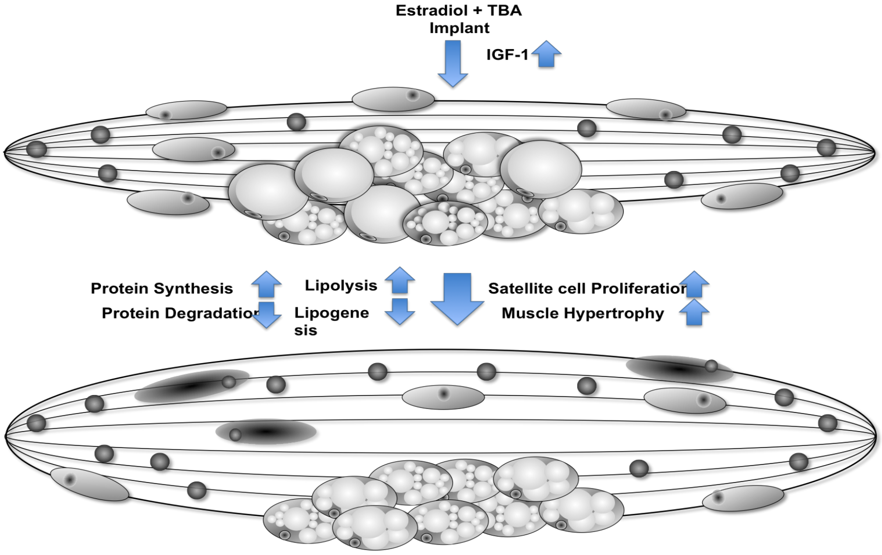
Johnson et al., 2014

Growth Stimulation

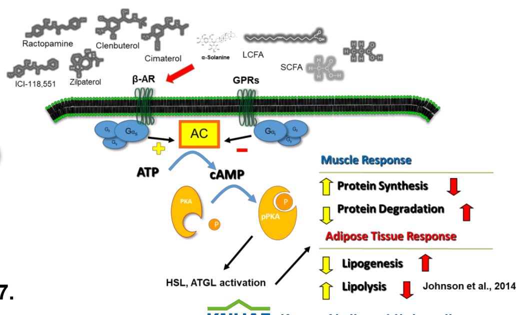


- ○ Muscle injury
- ○ Implants
  - 17β– Estradiol
  - Trenbolone Acetate
- ○ β-Adrenergic agonist
  - Clenbuterol
  - Ractopamin hydrochloride : Optaflexx (Elanco)
  - Zilpaterol hydrochloride : Zilmax (Intervet)

Mode of Action Growth Promotant

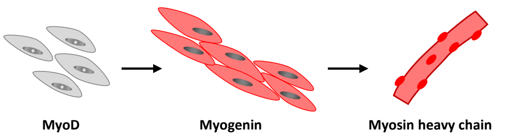


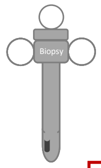
Johnson et al., 1997.

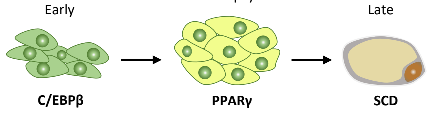


4. Application of Precision Management

- **Muscle (13th rib-eye area) tissue sampling in steers**

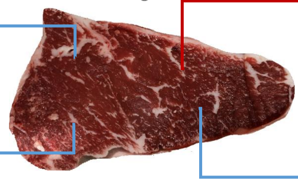






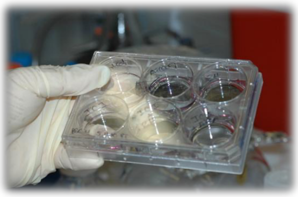
Adipogenic gene
- C/EBP, PPARγ, SCD
- Adipogenesis

Myogenin
- Muscle development & myogenisis

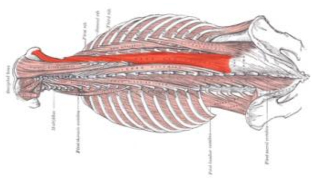


MHC IIX
- Fast glycolytic fiber
- White muscle fiber

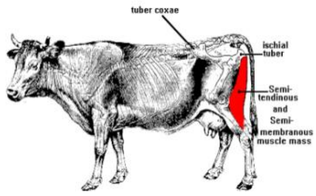
MHC I
- Slow oxidative fiber
- Red muscle fiber



<Primary Cell culture>



<LD(등심) : Longissimus Dorsi>

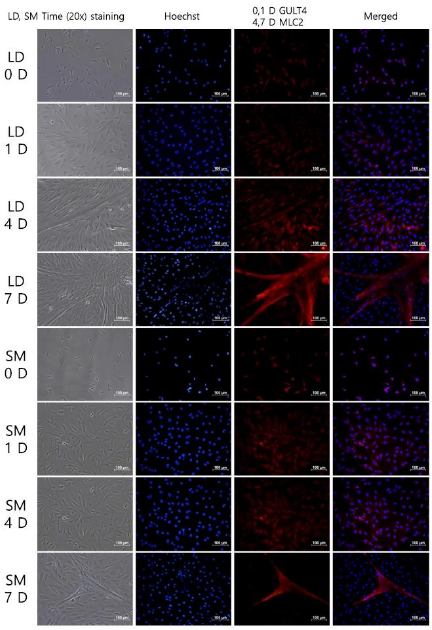


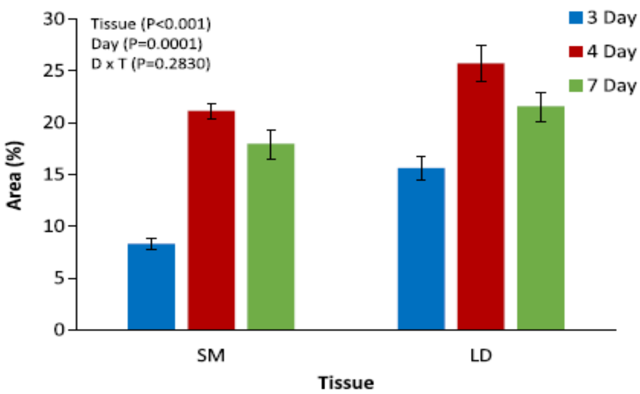
<SM(우둔) : Semimembranosus>

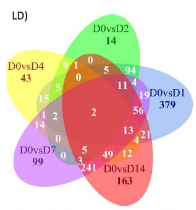
<PRAT(복강지방) : Perirenal AT>

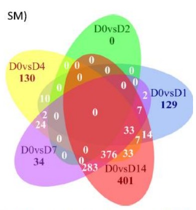
4. Application of Precision Management

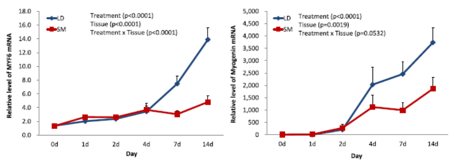
Different between Bovine LD and SM tissue









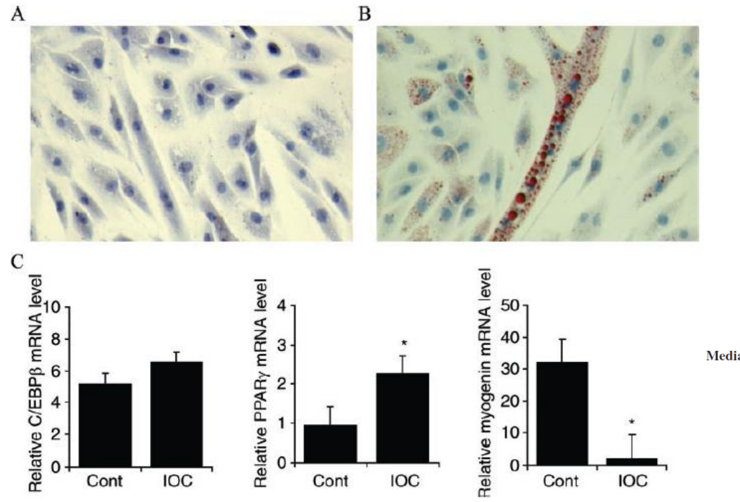


<Sara et al., 2020>

4. Application of Precision Management

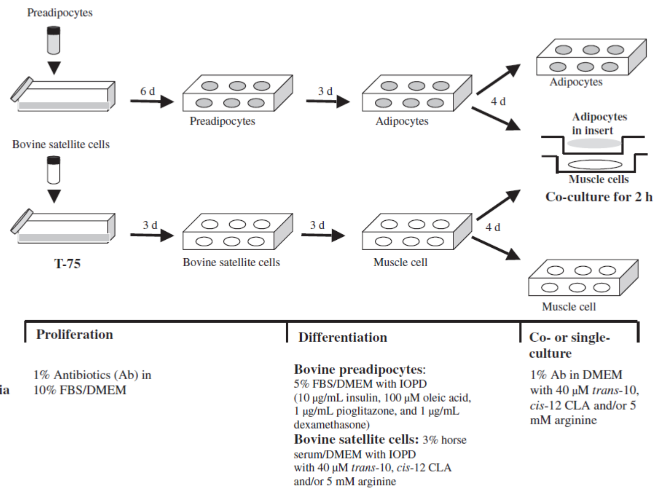
Transdifferentiation from Muscle to Fat

Melengestrol acetate enhances adipogenic gene expression in cultured muscle-derived cells



J. Anim. Sci. 2009. 87:3897–3904
doi:10.2527/jas.2008-1645

Co-culture system of Muscle and Fat

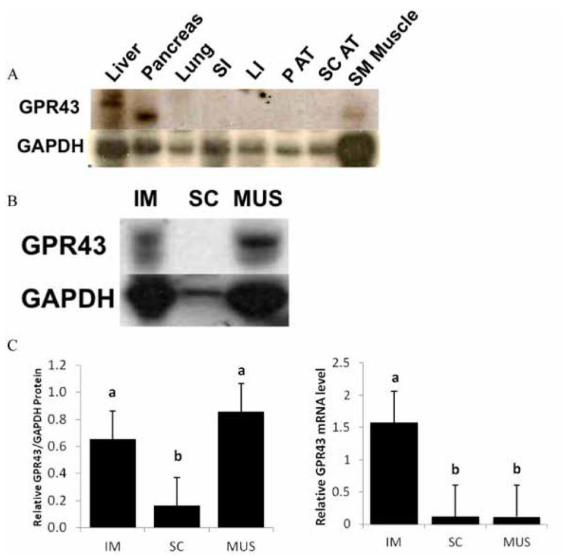


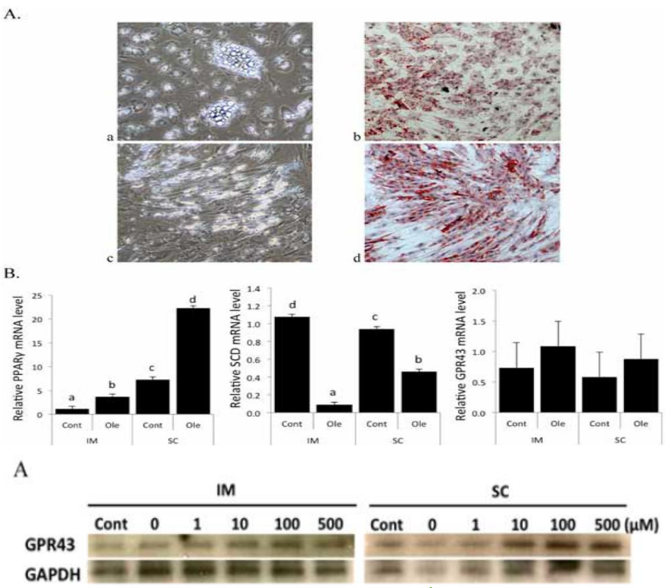
<Choi et al., 2013>

4. Application of Precision Management

Funtional Study of Intramuscular and Subcutaneous Adipose tissues

Oleic acid enhances G protein coupled receptor 43 expression in bovine intramuscular adipocytes but not in subcutaneous adipocytes[1]

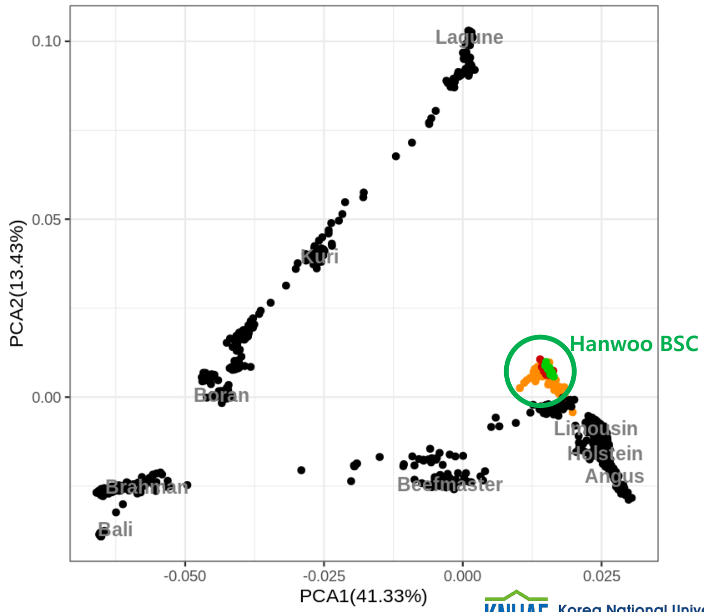




<Chung et al., 2019>

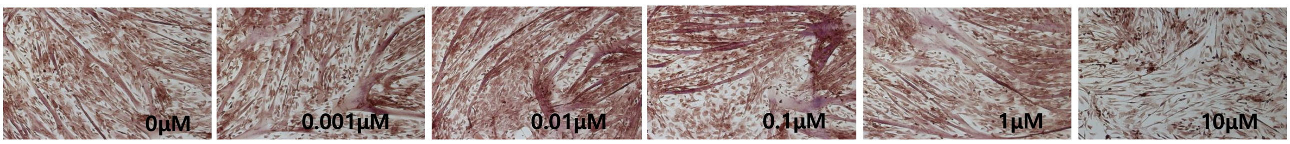
4. Application of Precision Management

Analysis of Hanwoo and Other Breeds



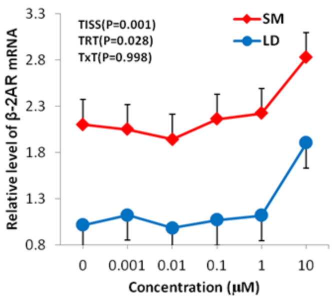
4. Application of Precision Management

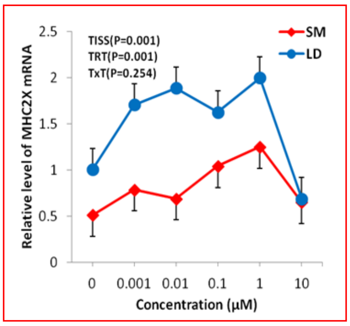
☐ BSC from LD and SM muscle tissue-myogenic gene expression under dose and titlation of Alkaloid compounds.

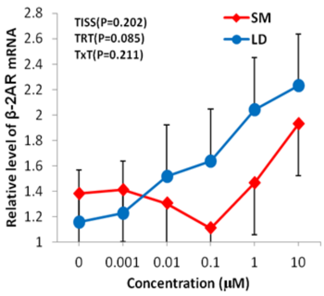


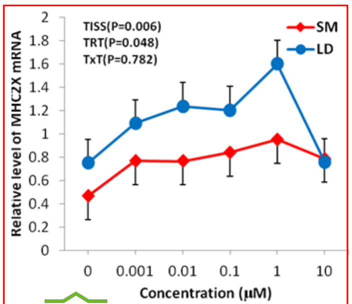
☐ Dose treated α-solanine and α-chaconine affect to BSC differentiation

○ Myogenic related gene (MHC2X and β2-AA) expression increased



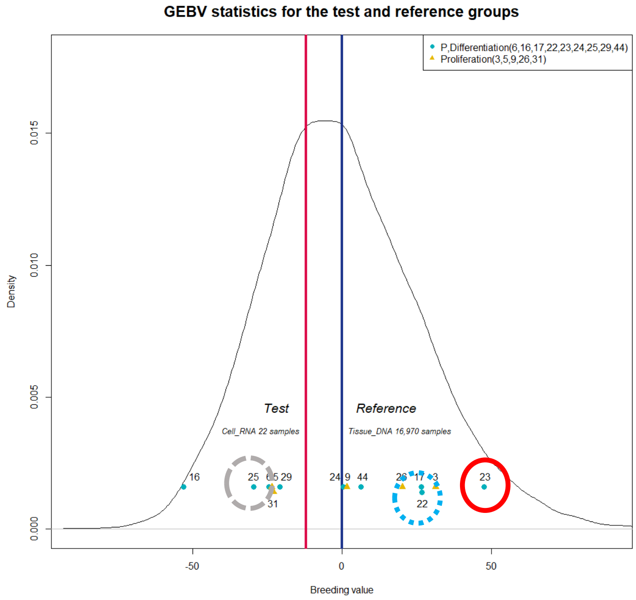


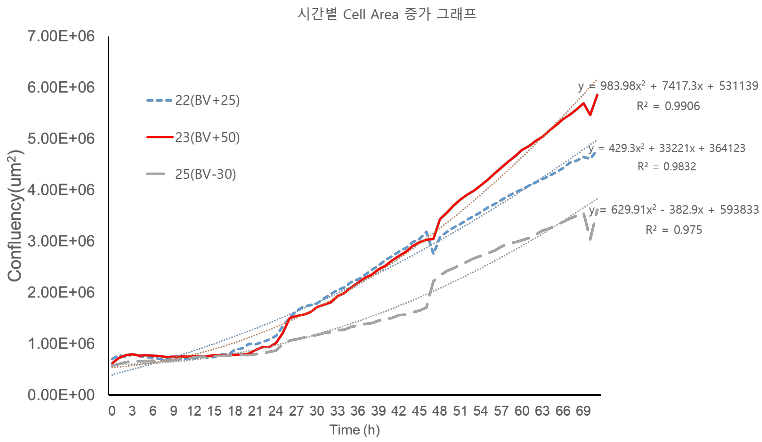




4. Application of Precision Management

Proliferation and Differentiation of Hanwoo BSC



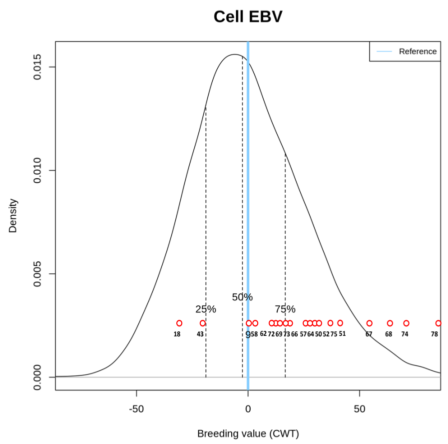


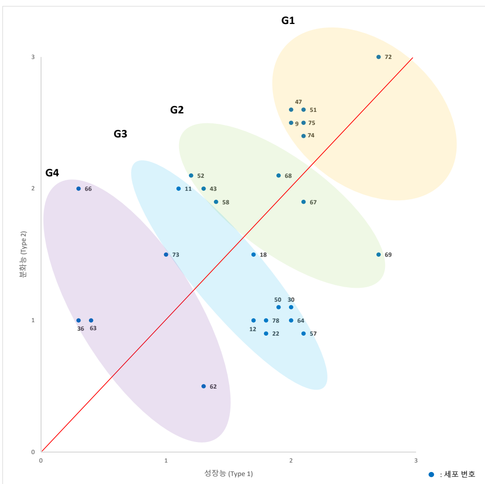
5. Next Goal

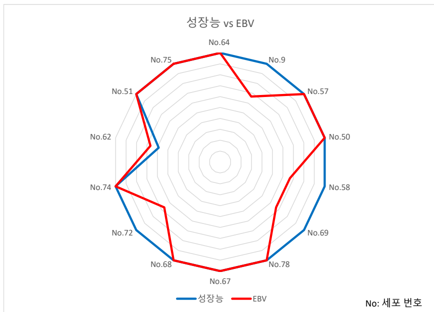
Non-animal Research System

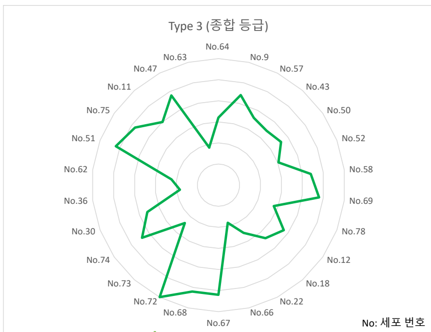
☐ **Genomic Breeding Value (4 Phenotypes) applied Hanwoo BSC selection**

- ○ **Preliminary test of customized functional substances (Material Screening)**
- ○ **During the animal test, the results are used intellectual property rights (IP)**



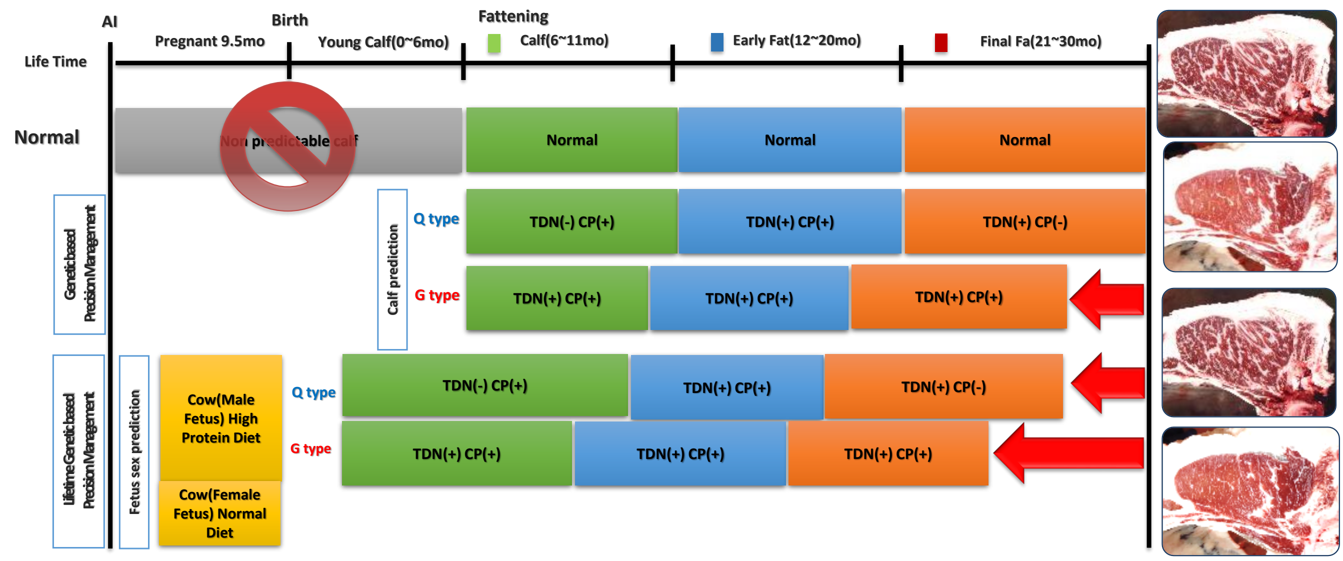




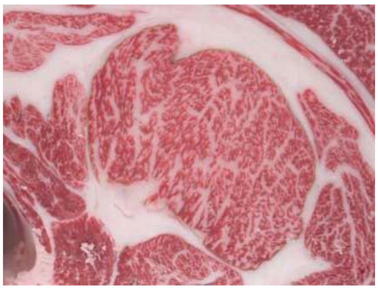
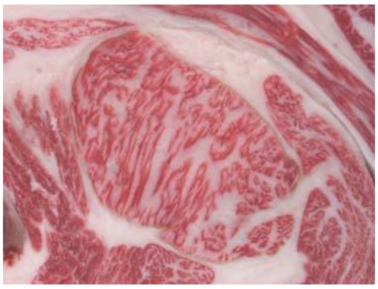


5. Next Goal

Genetic based Lifetime Precision Management System

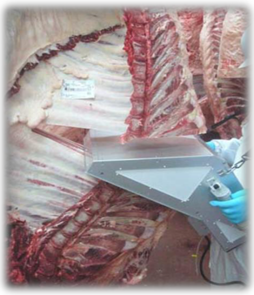
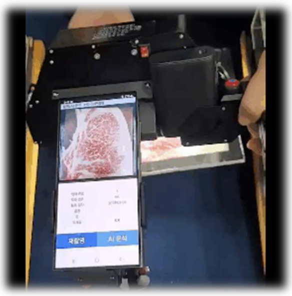


5. Next Goal

No. 8 | BMS | No. 8
79.6 | FI | 58.6


No. 9(1++) | BMS | No. 9(1++)
2.11 | FI | 3.64

○ Finest Index

$$FI = \frac{L}{\sqrt{REA}}$$

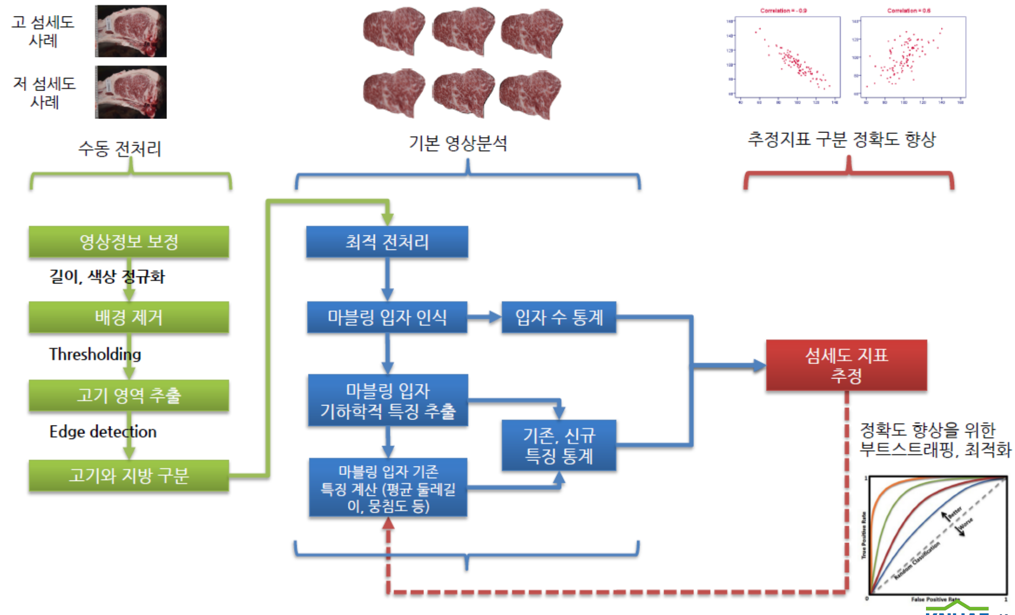
Dr. Kuchida et al 2015

○ JAPAN: rib 6-7

KOREA : rib 13-Lumber 1

○ Korean FI required !

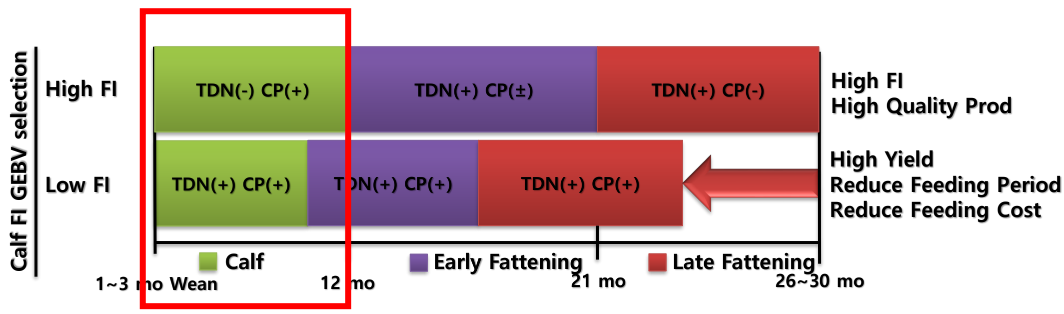
Hanwoo Fine Index (Artificial Intelligence REA Image)



Hanwoo Fine Index based Precision Management

☐ Development of FI GEBV based precision management system

- FI GEBV and castration date (4mo vs 7mo) relationship
- FI GEBV and weaning date (1mo vs 3mo) relationship
- Development of FI GEBV based Individual precision management system



Summary

- **Research for functional gene expression based on GEBV**
  - **Genetic based precise management system**
- **Sustainable farm based individual management system**
  - **Reduce feeding cost, periods, and provide labor intensive system**
- **Development technology for enhancing livestock efficiency**
  - **Multidisciplinary approach of Animal, Food, Engineering Sciences (ex. Traceability system)**

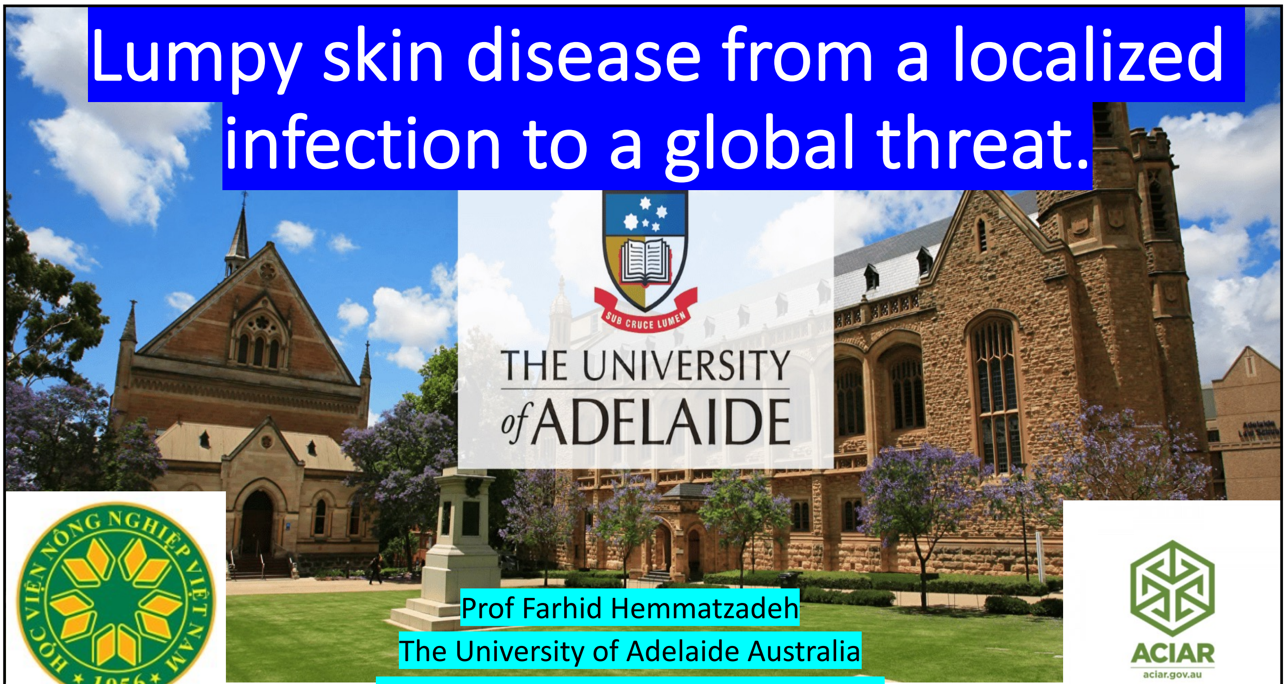
Research collaborators

Dr. Bradley J. Johnson at Texas Tech University
Dr. Stephen B. Smith at Texas A&M University
Dr. Brad Kim at Purdue University
Drs. J. K. Kim and D. H. Kang at Michigan State University
Dr. Takafumi Gotoh at Hokkaido University
Dr. Seung Hwan Lee at Chung Nam University
Dr. Kesinee Gatphayak at Chiang Mai University
Dr. Bo Hye Park at ©Kai Bio and ©Seawith

Thank you

9. LUMPY SKIN DISEASE FROM A LOCALIZED INFECTION TO A GLOBAL THREAT

DR. FARHID HEMMATZADEH
THE UNIVERSITY OF ADELAIDE AUSTRALIA



Lumpy skin disease from a localized infection to a global threat.

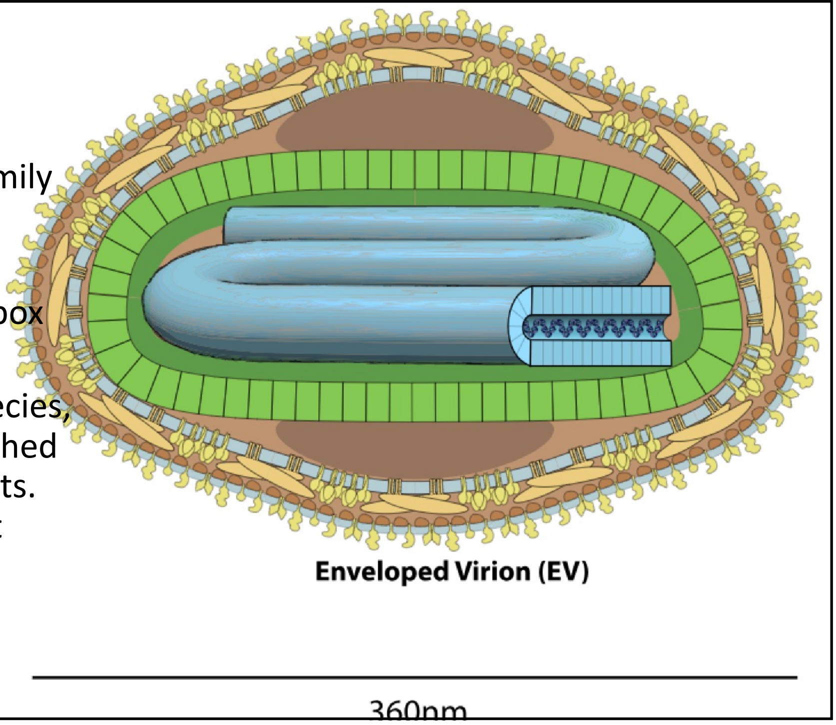
Prof Farhid Hemmatzadeh
The University of Adelaide Australia
farhid.hemmatzadeh@adelaide.edu.au

Lumpy Skin Disease

- High morbidity in cattle.
  - Up to 100%
- Low mortality
  - 1-3% up to 40%
- Very high economic losses
  - Estimated losses is 19 billion USD annually
- loss of condition
- Decreased milk production
- Abortions,
- Infertility and skin Damage

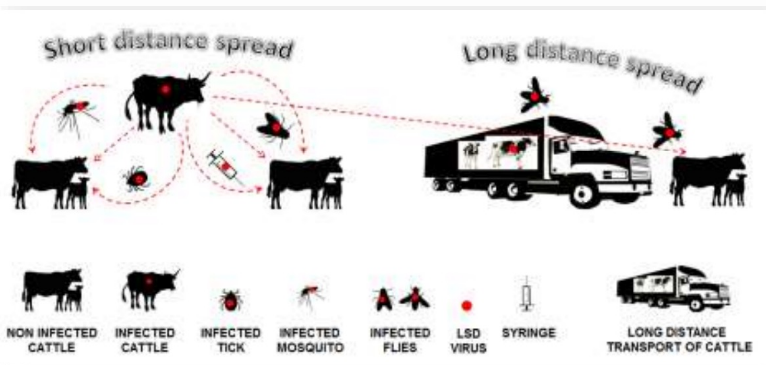
Aetiology

- Capripoxvirus and the family Poxviridae.
- Antigenically related to sheeppox virus and goatpox virus.
- They are distinct viral species, they cannot be distinguished by routine serological tests. There is no evidence that LSDV can infect humans.



Transmission of LSD

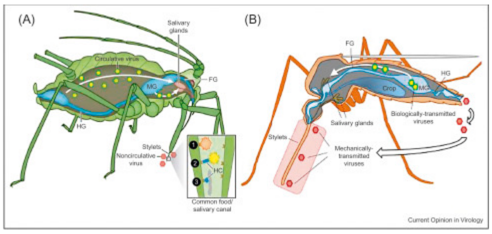
- Long distance :
  - Animal movements is the highest risk for transmission
- Short distance:
  - Insect vector
  - Climate change
- Direct and indirect contact facilitate the transmission.



LSD Viral vectors and reservoirs

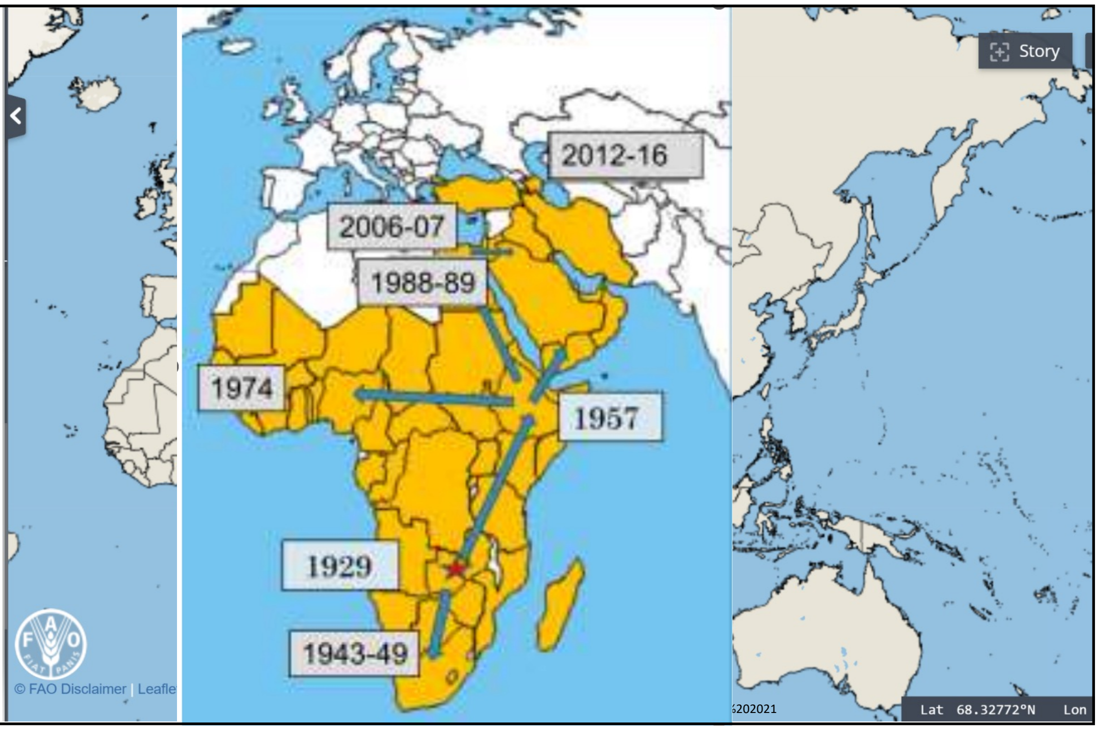
- The main viral vectors are blood-feeding insects
  - Flies

  - Mosquitoes
    - Biological
    - Mechanical



  - Tick

1934-2005



2007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2010


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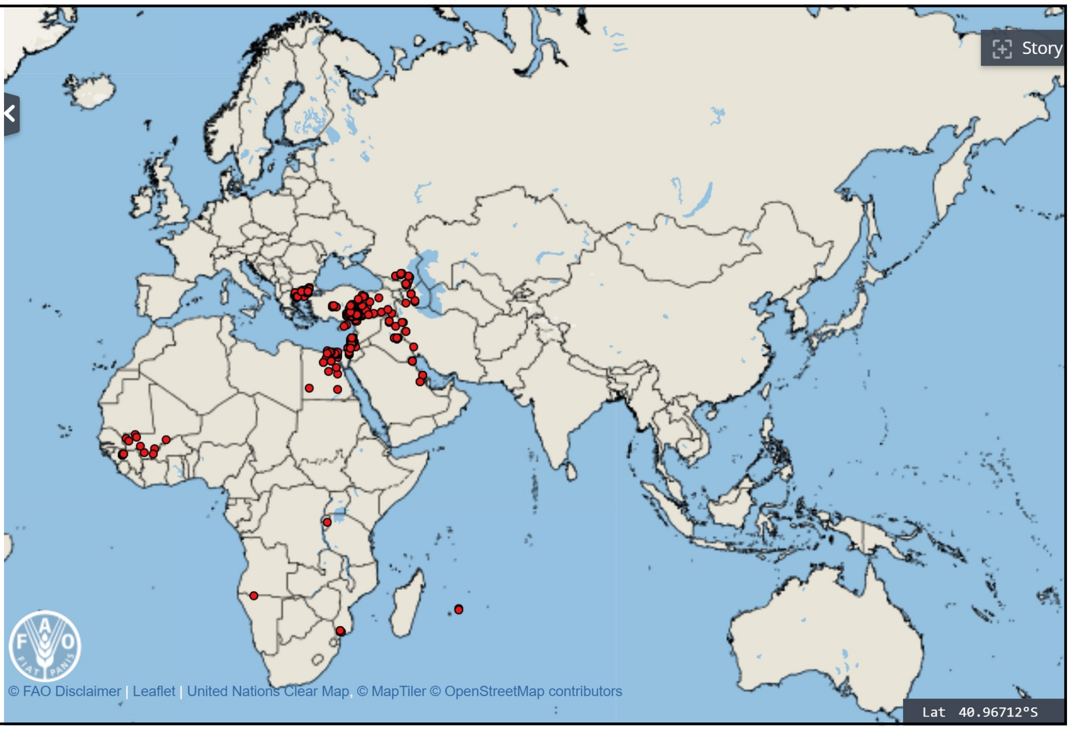
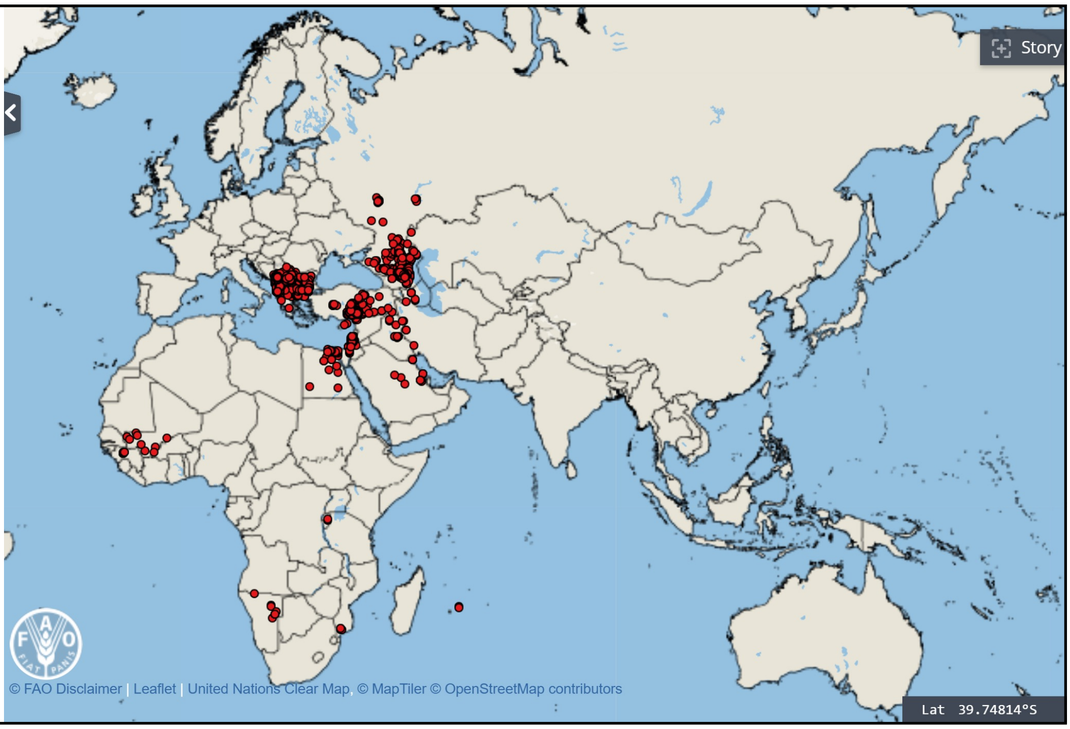
2015

South-Eastern Europe
Albania,
Bulgaria,
Greece
Montenegro
Macedonia
Serbia

2016



2017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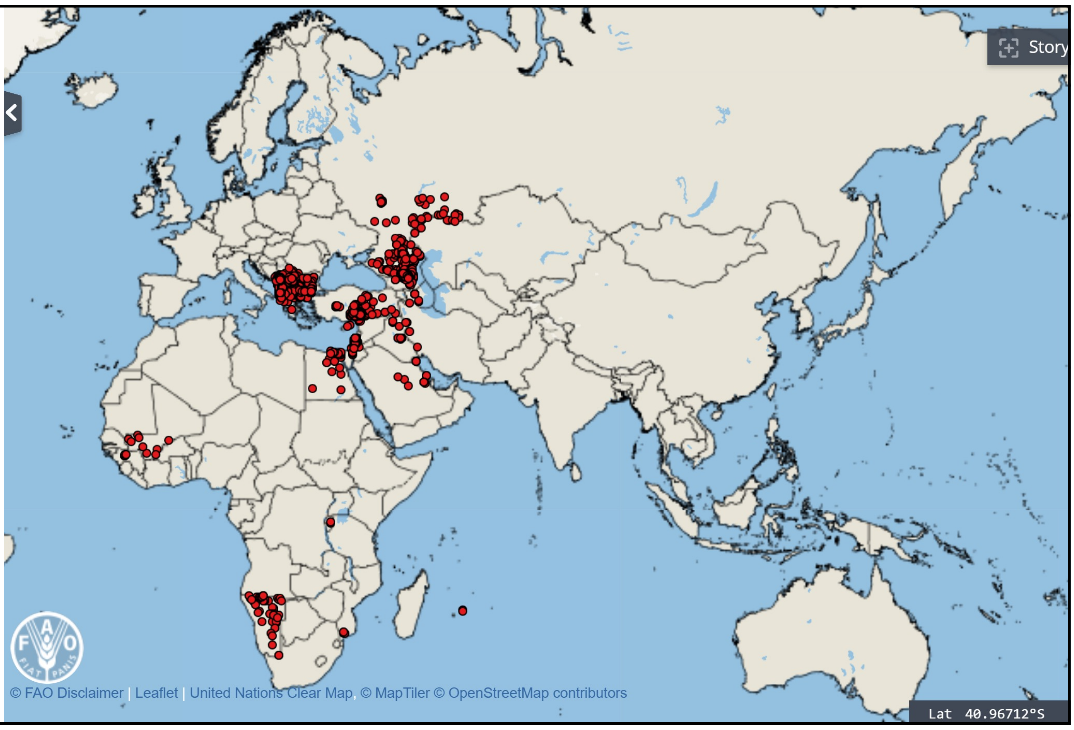
2018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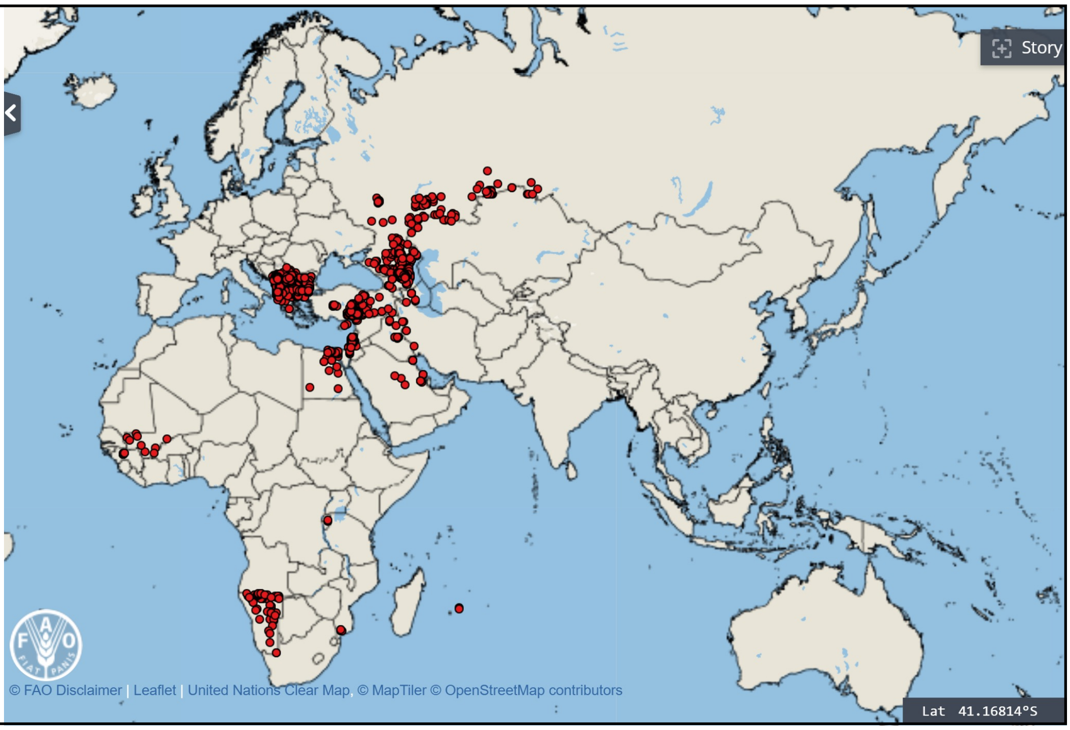
2019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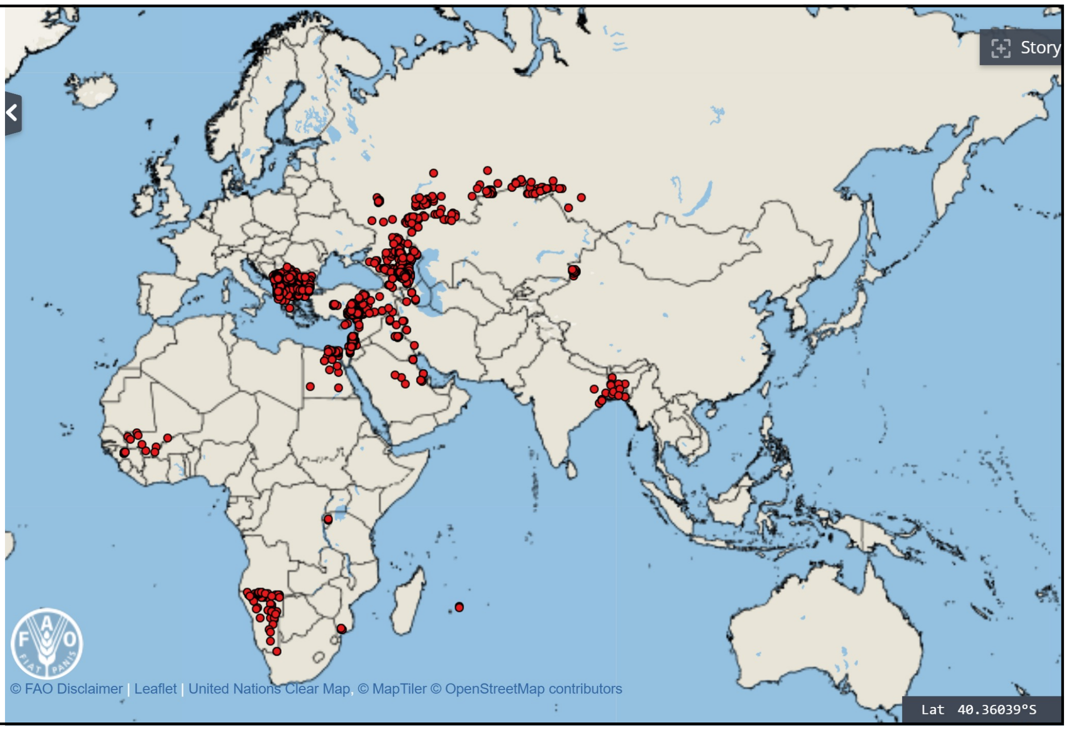
2020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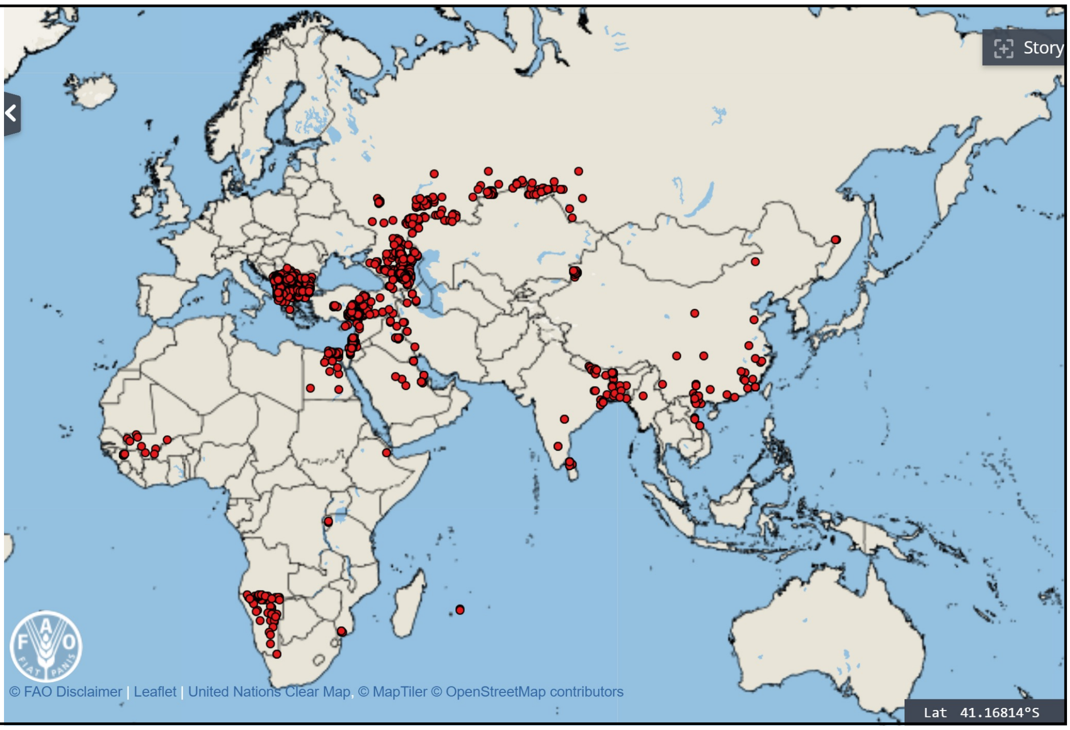
2021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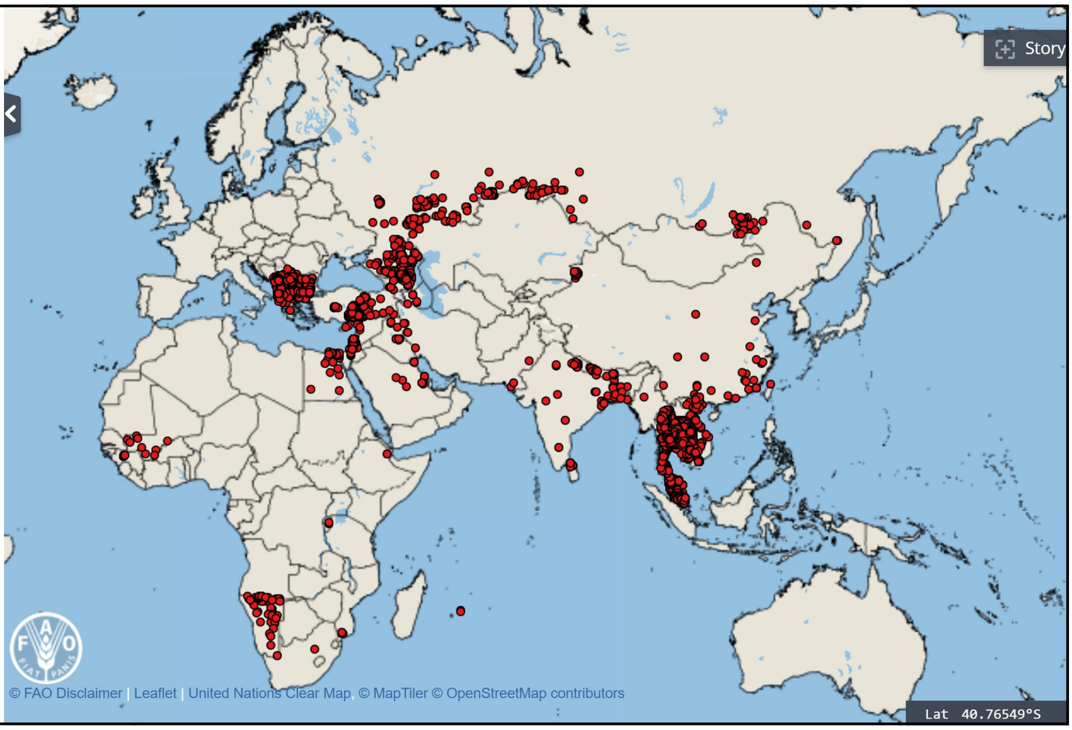
2022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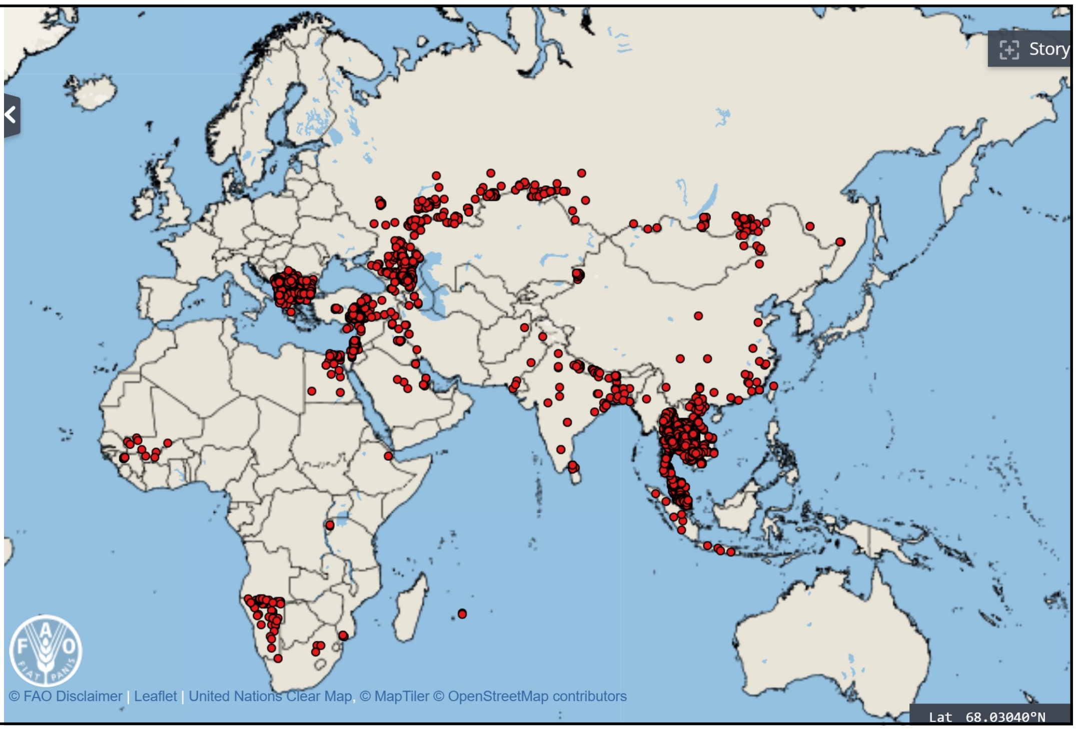
2023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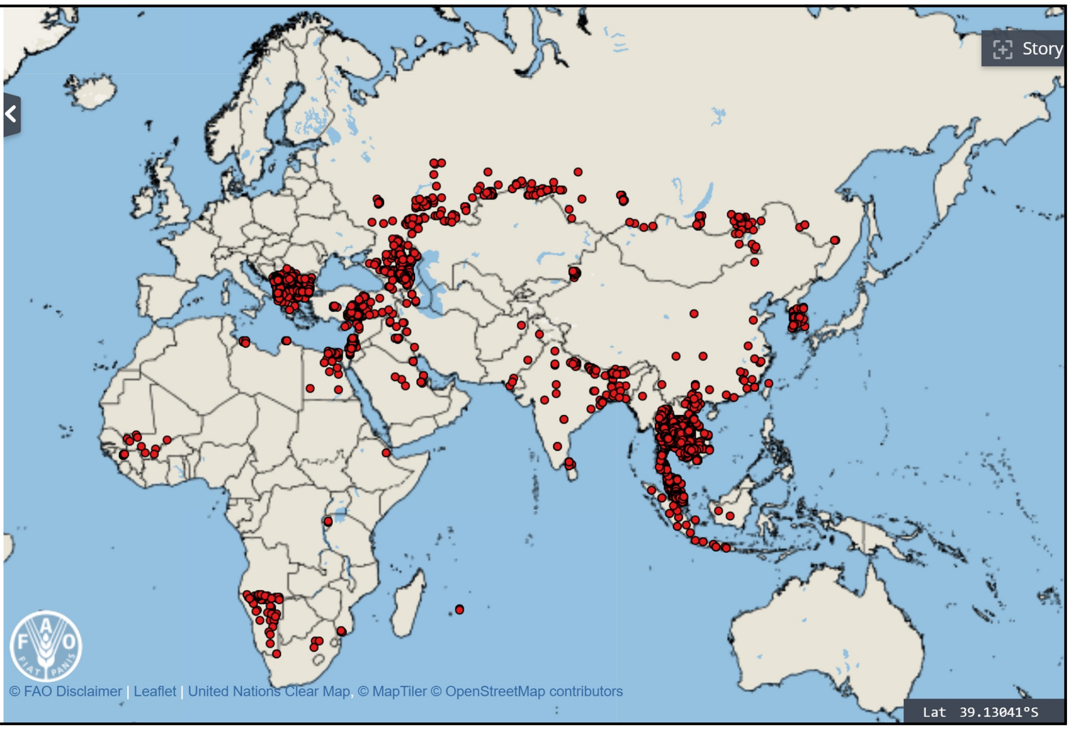
2024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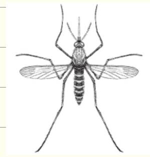
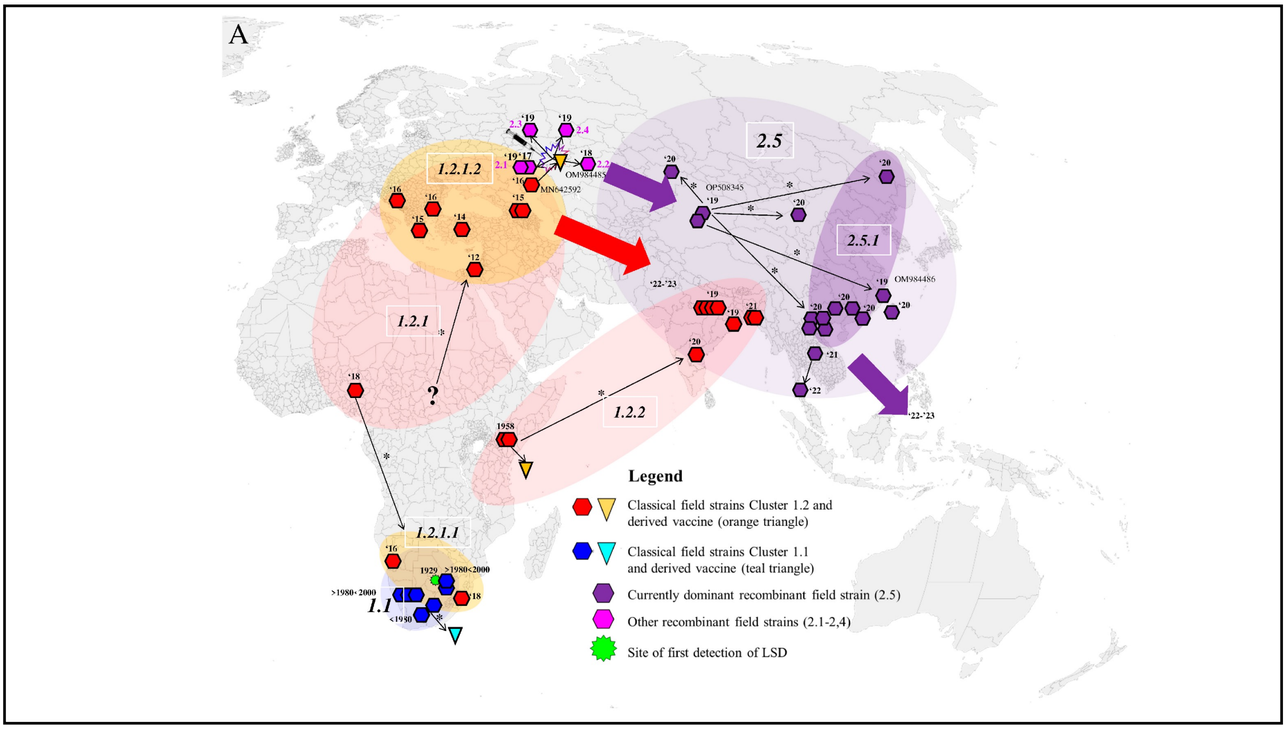
LSD Viral vectors

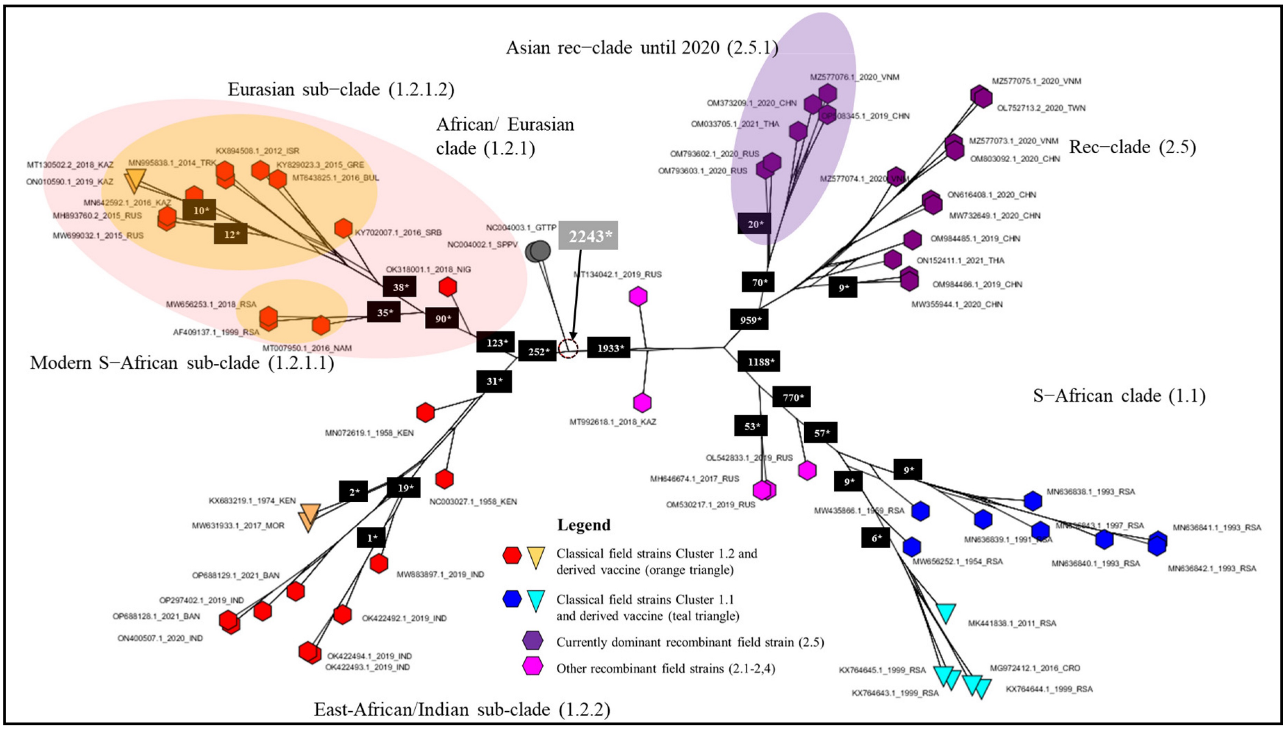
Invertebrate hosts	Countries/Regions	References
Ticks		
Rhipicephalus appendiculatus	South Africa	[9–12]
Amblyomma hebraeum	South Africa	[9–11, 13–15]
Rhipicephalus decoloratus	South Africa	[13, 15]
Glimpses		
Haematopota spp.	South Africa	[16]
Flies		
Stomoxys calcitrans	Belgium, Egypt	[16, 17]
Mosquitoes		
Aedes aegypti	Egypt	[18]
Anopheles stephensi	Egypt	[17]
Culex quinquefasciatus	Egypt	[17]
Culicoides nubeculosus	Egypt	[19]

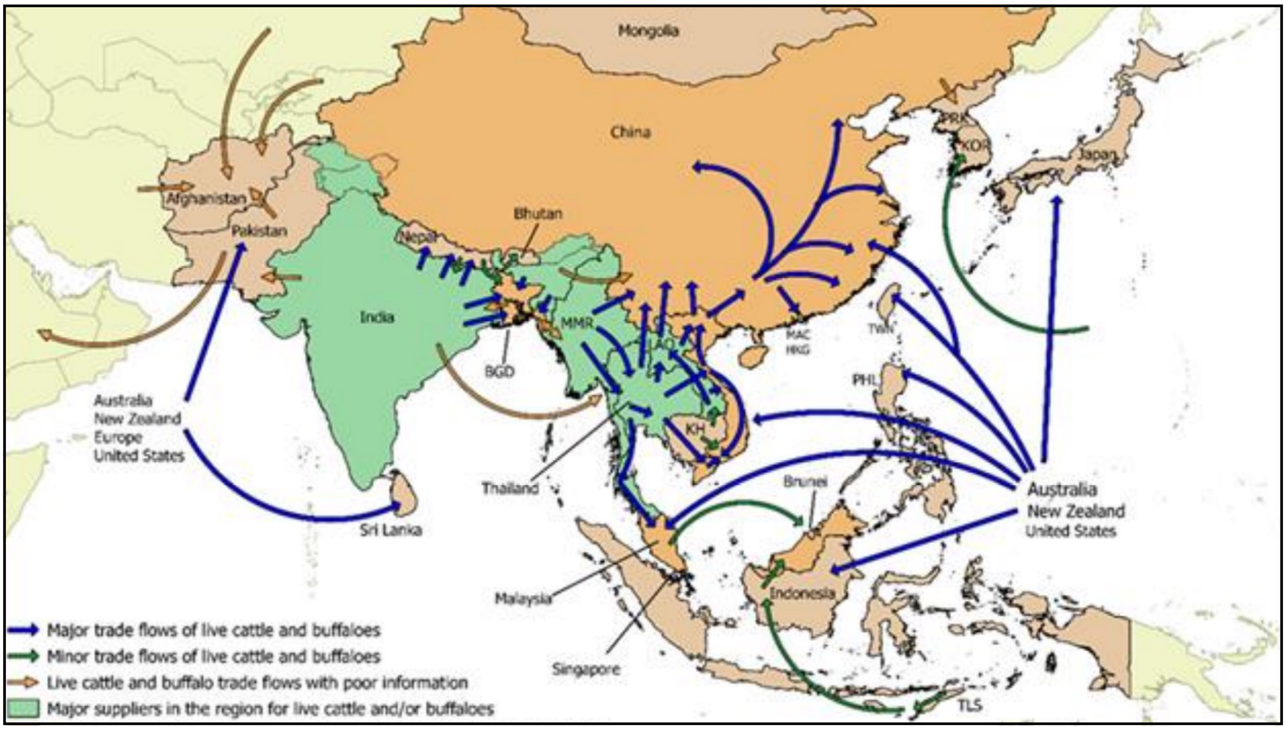


Current situation

- Geographical distribution & Latest situation in our region
- LSD is currently endemic in most of Africa, parts of the Middle East and Turkey. Since 2015, the disease has spread to most of the Balkan countries, the Caucasus and the Russian Federation, where the disease continues to spread, making the risk of an imminent incursion into other unaffected countries very high. Since 2019, several outbreaks of LSD have been reported by Members in Asia (Bangladesh, India, China, Chinese Taipei, Vietnam, Bhutan, Hong Kong (SAR-RPC), Nepal, Sri Lanka, Myanmar, Indonesia Malaysia, Thailand- as of 02/6/2021).

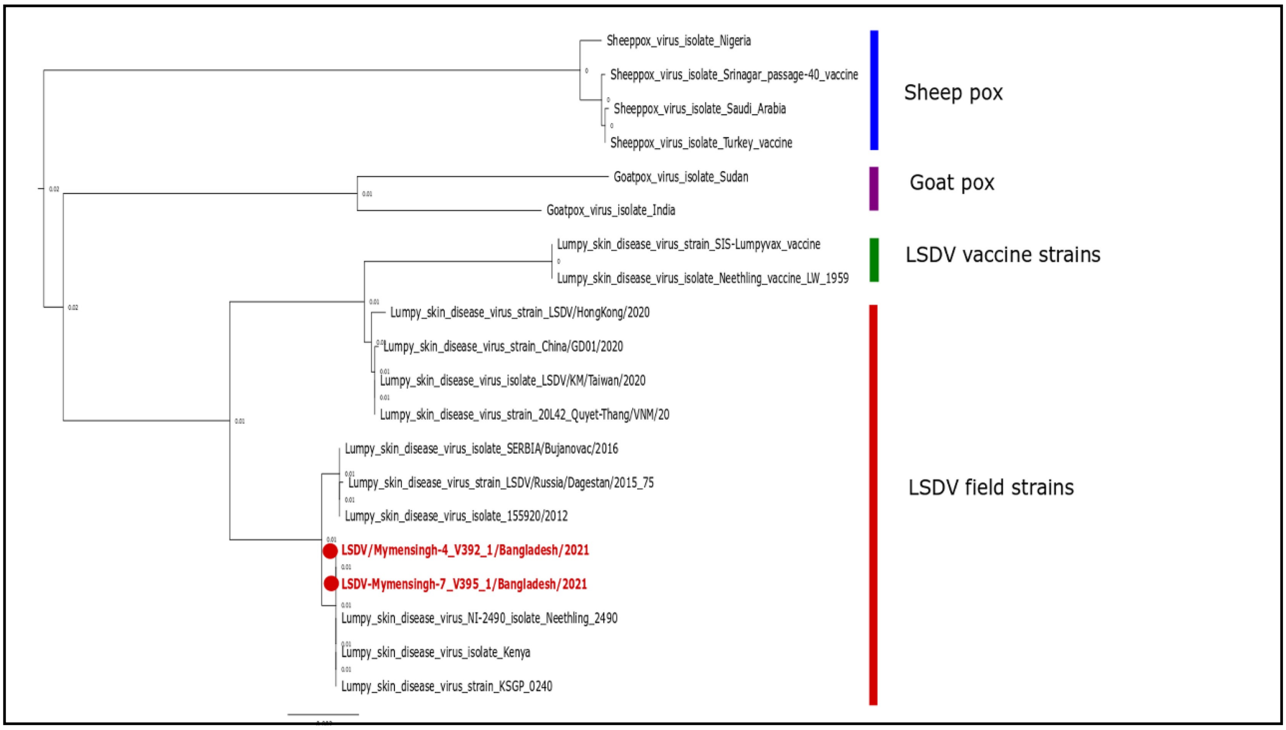

A
1.2.1.2
1.2.1
1.2.2
1.2.1.1
1.1
2.5
2.5.1
?
Legend
Classical field strains Cluster 1.2 and derived vaccine (orange triangle)
Classical field strains Cluster 1.1 and derived vaccine (teal triangle)
Currently dominant recombinant field strain (2.5)
Other recombinant field strains (2.1-2,4)
Site of first detection of LSD


Asian rec−clade until 2020 (2.5.1)
Eurasian sub−clade (1.2.1.2)
African/ Eurasian clade (1.2.1)
Rec−clade (2.5)
Modern S−African sub−clade (1.2.1.1)
S−African clade (1.1)
East-African/Indian sub-clade (1.2.2)
2243*
1933*
1188*
959*
770*
252*
123*
90*
70*
57*
53*
38*
35*
31*
20*
19*
12*
10*
Legend
Classical field strains Cluster 1.2 and derived vaccine (orange triangle)
Classical field strains Cluster 1.1 and derived vaccine (teal triangle)
Currently dominant recombinant field strain (2.5)
Other recombinant field strains (2.1-2,4)



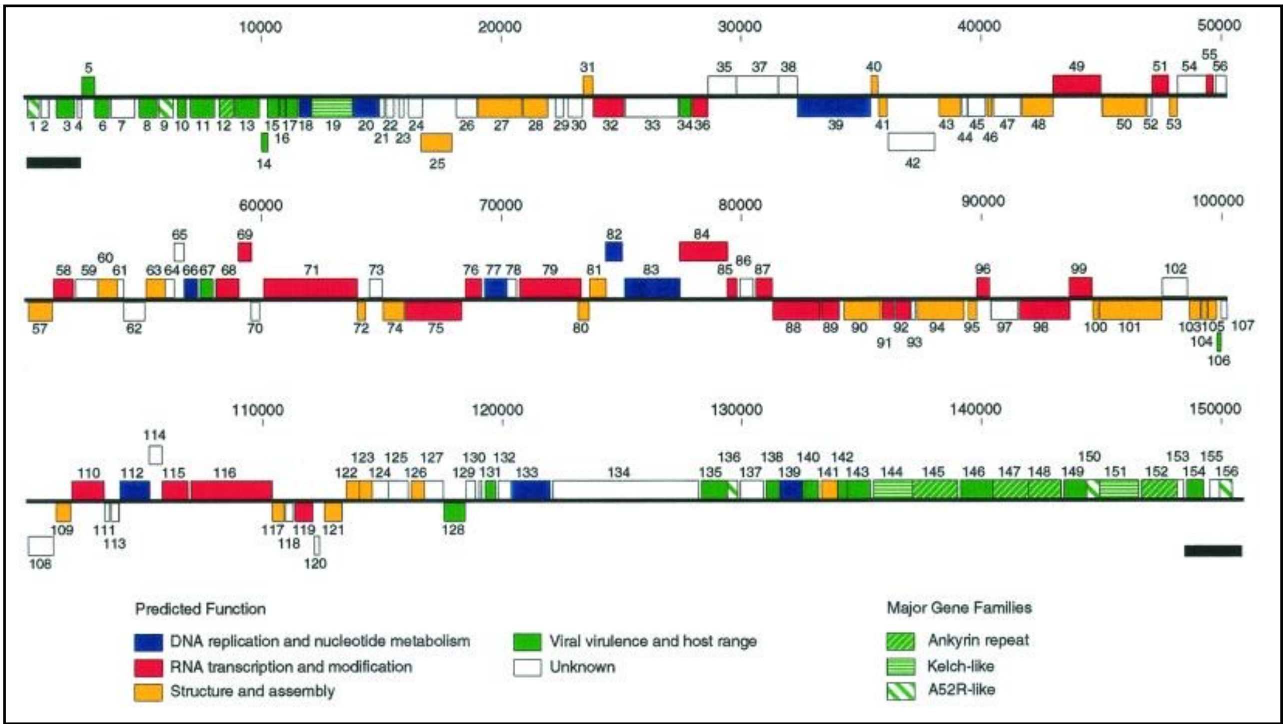
Vaccination

- Live attenuated LSDV vaccines (Neethling vaccines) is the only homologues LSD vaccine
- 80 percent vaccination coverage will break the circulation of the virus in a population
- Regional vaccination campaigns should be preferred to ring vaccination.
- Antigenic homology to LSD
  - SPPV and GTPV vaccines are suitable for the areas where outbreaks are in with LSDV
    - LSD shared 97% identity in the nucleotide sequences with SPPV and GTPV genome
    - Gorgan GTPV is a good alternative in those countries where GTP and LSD overlap (Kazakhstan and Germany)
  - Heterologous immunity always provide less effective protection



Post vaccination monitoring and DIVA

- The ID-Vet antibody ELISA was as specific as the SNT, and therefore, they concluded that this ELISA provides an excellent tool for rapid and simple serological examination of LSDV-vaccinated or infected cattle.
- No Differentiation of Infected from Vaccinated Animals (DIVA) vaccines have been developed against LSD.
- University of Adelaide and BRIN Indonesia
  - DIVA test development project (ACIAR research fund)



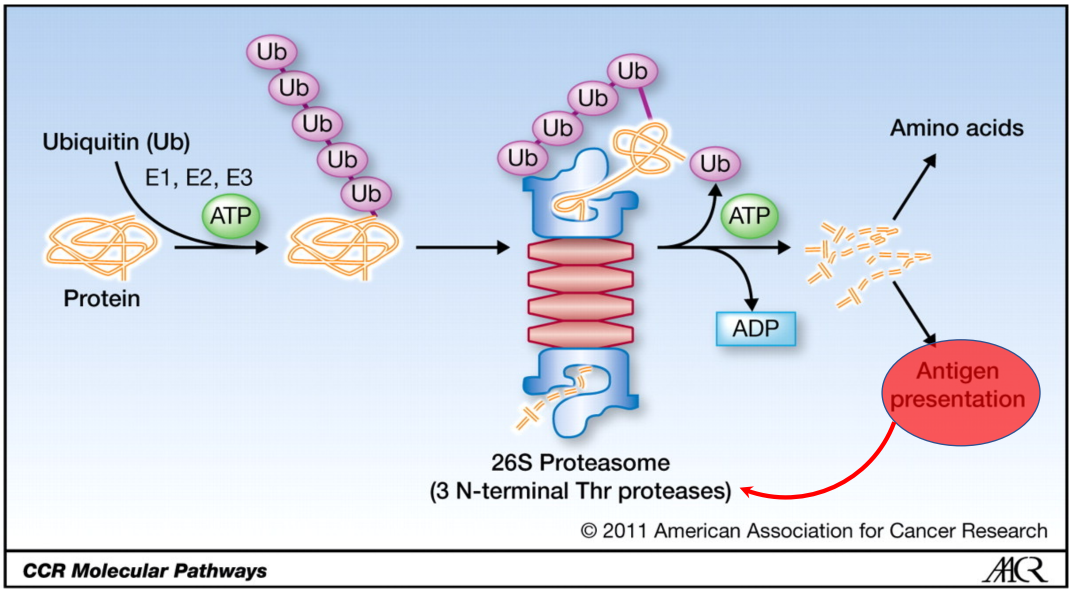
Target genes for Degron Tag attenuation

- KITH_SHEVKThymidine kinase (EC 2.7.1.21)
- VFUS_SHEVKPutative fusion protein (Protein HM2)
- A28_SHEVKEnvelope protein A28 homolog (Protein HM3)
- J1_SHEVKProtein J1 homolog (Protein F7)
- VQ3L_SHEVKG-protein coupled receptor homolog Q2/3L
- VT4_SHEVKT4 protein
- VT3C_SHEVKT3C protein
- VHR2_SHEVKProbable host range protein 2
- PAP1_LSDVNPoly(A) polymerase catalytic subunit (EC 2.7.7.19) (Poly(A) polymerase large subunit) (PAP-L)
- A28_LSDVNEnvelope protein A28 homolog (Protein LSDV118)
- VHR2_LSDVNProbable host range protein 2
- VT4_SHEVNT4 protein
- B14_SHEVNProtein B14 homolog (Protein T3A)
- LAP_LSDVE3 ubiquitin-protein ligase LAP (EC 2.3.2.27) (Leukemia associated protein) (LAP) (RING-type E3 ...

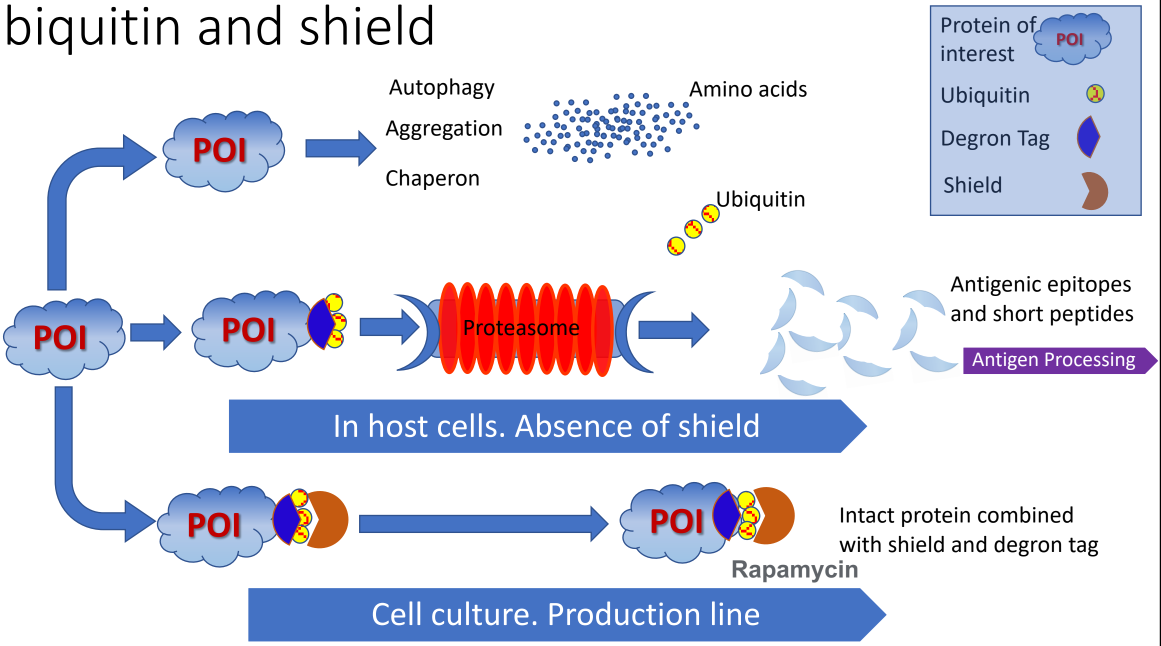
Cell culture for vaccine production

- CAM
- Primary skin fibroblast cells
- MDBK
- GEEP
  - For maintenance and production.

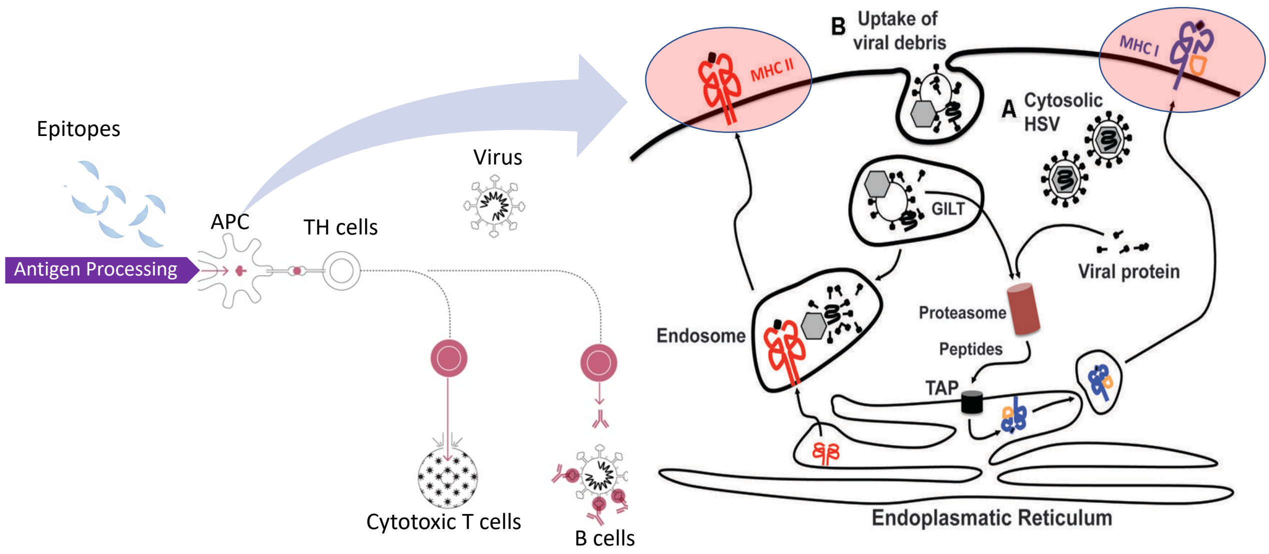
Ubiquitination and Proteasome



Ubiquitin and shield



Cytosolic pathway and immune response in viral infection



Microbiology and Immunology, Volume: 63, Issue: 2, Pages: 51-64, First published: 24 January 2019, DOI: (10.1111/1348-0421.12669)

International collaboration on LSD and ASF vaccines in Vietnam, Indonesia and Thailand

Acknowledgements

- The University of Adelaide
- NHMRC, Australia
- NIH, USA
- University of Illinois
- Indonesian National Research and Innovation Agency (BRIN), Indonesia
- Navetco vaccine production company, Vietnam
- King Mongkut's University of Technology Thonburi, Thailand
- Pasouk vaccine and knowledge-based company, Iran

10. MICRORNA PROFILE AND LEVELS IN COLOSTRUM AND CALF BLOOD BEFORE AND AFTER RECEIVING DIFFERENT COLOSTRUM SOURCES

DR. DO THI HUE
THE UNIVERSITY OF ADELAIDE AUSTRALIA

11. PLANT EXTRACT-LOADING FE3O4 NANOSYSTEMS TO INHIBIT VIRUSES FOR SUSTAINABLE LIVESTOCK PRODUCTION

LE THI THU HUONG
VIETNAM NATIONAL UNIVERSITY OF AGRICULTURE

VIETNAM NATIONAL UNIVERSITY OF AGRICULTURE

INTERNATIONAL CONFERENCE ON TRANSFORMATION TO SUSTAINABLE LIVESTOCK PRODUCTION

Plant extract-loading Fe_3O_4 nano systems to inhibit viruses for sustainable livestock production

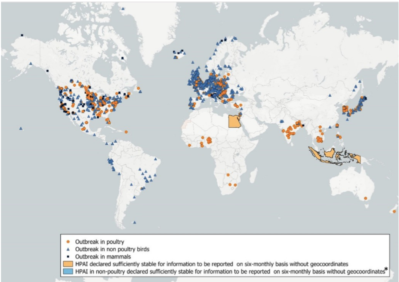
Le Thi Thu Huong
lethithuhuong@vnua.edu.vn

Hanoi, October 2025

Contents

Problem to be solved

Virus diseases cause high loss in livestock production



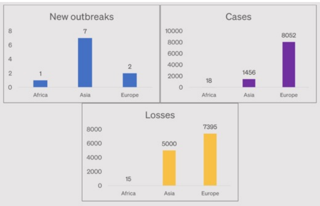


Figure 4. Number of new outbreaks, associated cases and losses (losses include animals dead and killed and disposed of within outbreaks – they do not include culling around outbreaks). It should also be noted that some countries or territories are unable to provide a precise number of cases and leave this field blank in the report.

High pathogenicity avian influenza Situation report 73, WOAH, 7/2025

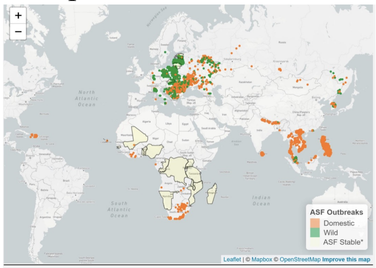


Figure 1. Map of ASF outbreaks which started between 1 January 2022 and31 July 2025 in domestic pigs and wildlife.

Table 1. Summary of the number of outbreaks, cases and animal losses caused by ASF in the different world regions since January 2022.

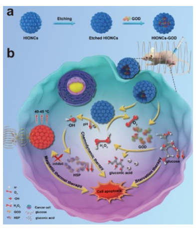
	Outbreaks		Cases		Losses*
	Domestic pigs	Wild boar	Domestic pigs	Wild boar	Domestic pigs
Africa	863	6	119,823	0	113,917
Americas	65	0	467	0	9,412
Asia	6,452	108	315,137	541	558,242
Europe	4,946	24,174	610,593	37,912	1,512,335
Oceania	0	0	0	0	0
Total	12,326	24,288	1,046,020	38,453	2,193,906

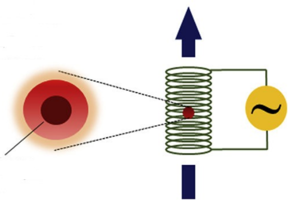
*Losses (deaths + animals killed and disposed of): this figure refers to losses in the establishments affected by the outbreaks and it does not include the animals culled in areas around the outbreak for controlling the disease.

African swine fever Situation report 68, WOAH, 8/2025

Research approaches

- Fe_3O_4 nanoparticles:
  - drug delivery system
  - Inductive heating: thermal treatment + active release
  - Antiviral activity

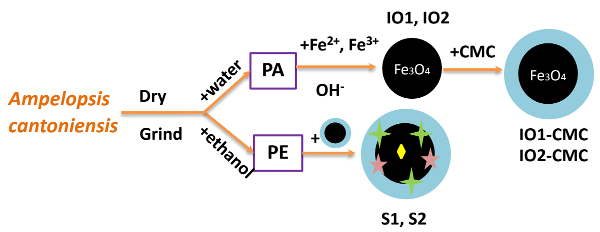




- Plant extract
  - Stabilizer
  - Antiviral activity

Materials and Methods

Synthesis of the Fe_3O_4-plant extract nanosystems

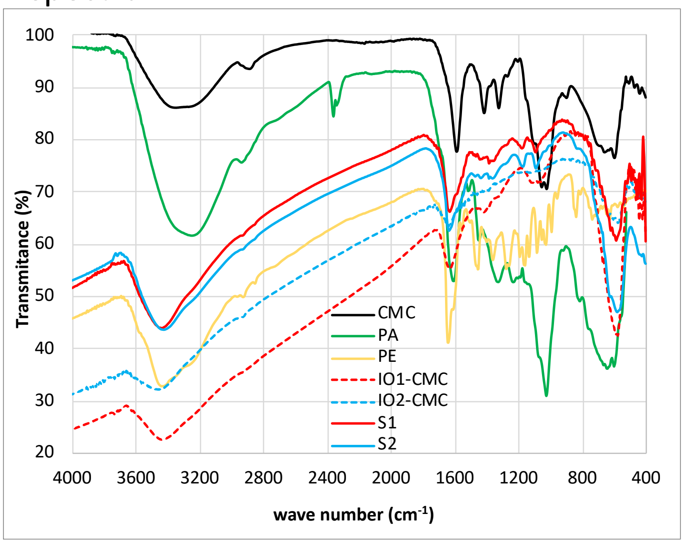


Characterization: FTIR, XRD, FESEM, TGA, VSM, inductive heating, passive and active drug release

In vitro **antiviral activity: H5N1 (MDCK), ASFV (PAM) at 25 and 45 °C**

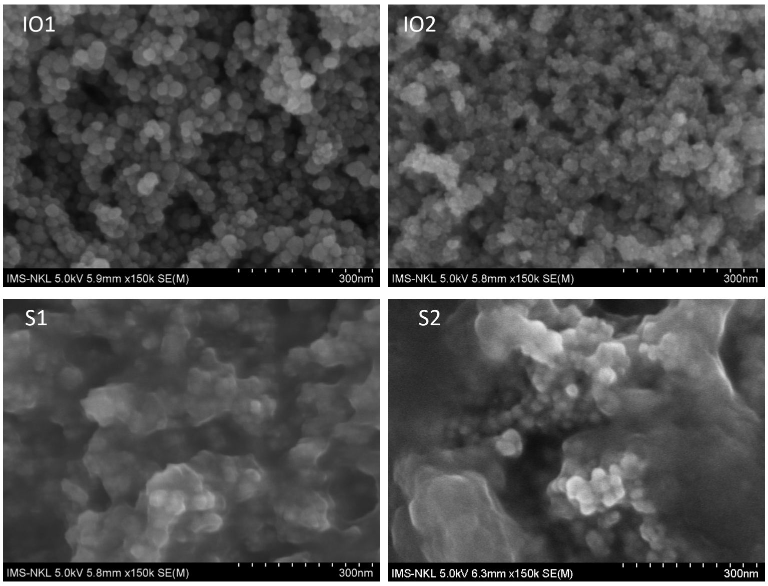
Results and Discussion

- FTIR spectrum



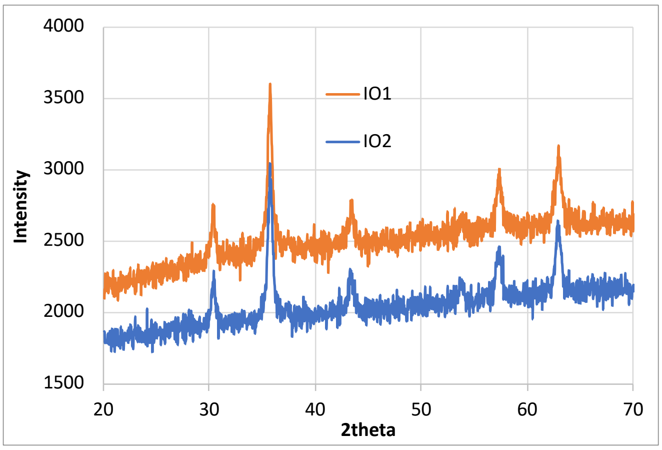
Results and Discussion

- FESEM images



Results and Discussion

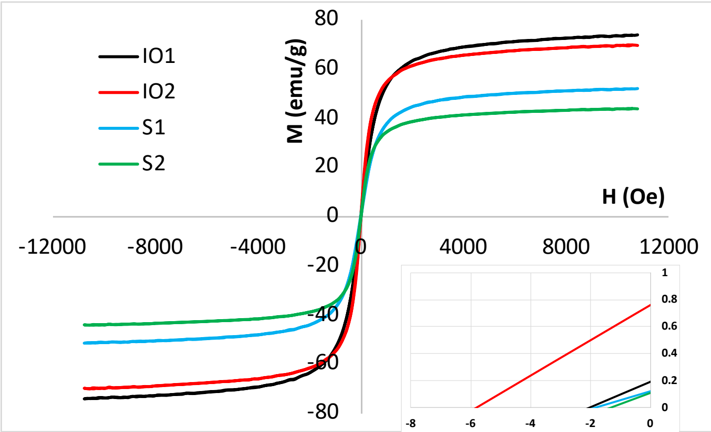
- XRD diagrams



	d (nm)
IO1	20.6
IO2	15.1

Results and Discussion

- Saturation magnetization

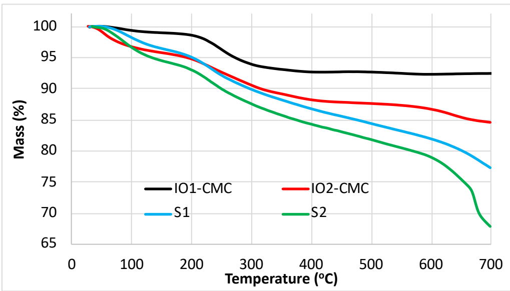


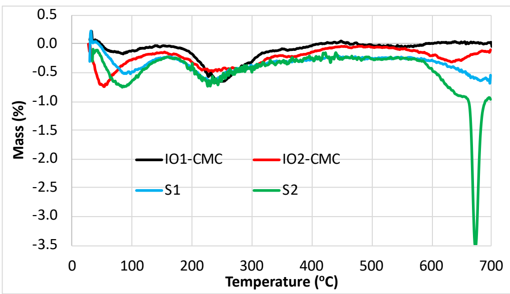
Results and Discussion

- Thermal analysis

Temp. (°C)	<150	200-400	400-700
IO1-CMC	1.02	6.32	0.21
IO2-CMC	4.28	6.5	4.61
S1	3.93	7.69	11.18
S2	5.69	7.28	19.19

	Fe_3O_4 (%)	CMC (%)	CMC + plant extract (%)
IO1-CMC	93.40	6.60	
IO2-CMC	88.39	11.61	
S1	80.36		19.64
S2	71.93		28.07





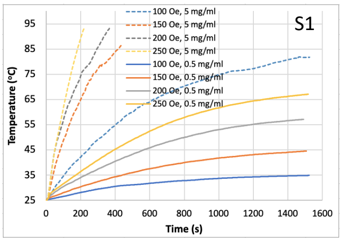
Results and Discussion

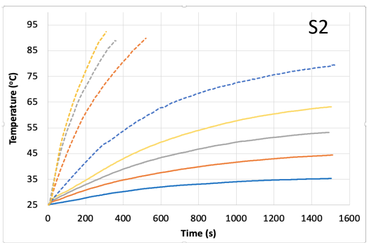
- Loading content

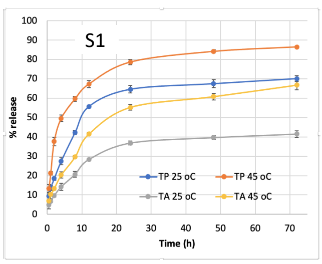
Sample	M_s (emu/g)	LC (%) calculated from TGA	LC (%) (calculated from DHM)	EE (%) (calculated from DHM)
IO1	73.9			
IO2	70.0			
S1	51.7	13.04	11.5 ± 0.4	61.0 ± 1.0
S2	44.1	16.46	15.7 ± 0.5	73.5 ± 1.5

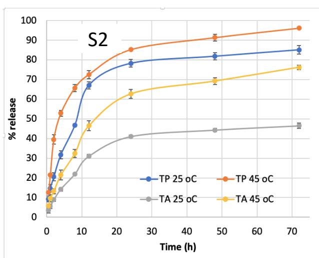
Results and Discussion

- Magnetic inductive heating curves and drug release



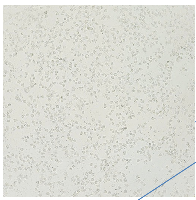






Results and Discussion

- Antiviral activity
- H5N1

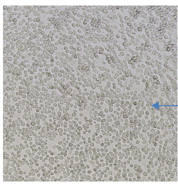


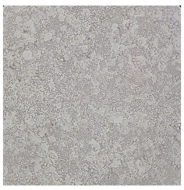
25°C	PA			S1			S2			(+)C		
0												
-1							+	+	+			
-2	+	+	+									
-3					+							
-4												
-5											+	
-6		3.5			3.8			2.5			5.8	
(-)C												

45°C	PA			S1			S2			(+)C		
0												
-1	+	+	+	+	+	+						
-2												
-3												
-4												
-5										+		
-6		2.5			2.5			<=1.5			5.8	
(-)C												

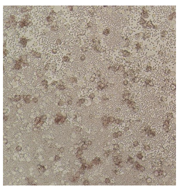
Results and Discussion

- Antiviral activity
- ASFV





normal PAM cells and red blood cells



red blood cells adsorb on the infected PAM cells

25°C	PA			S1			S2			(+)C		
0												
-1												
-2	+	+	+	+	+		+					
-3												
-4											+	
-5												
-6		3.5			3.2			2.8			4.8	
(-)C												

45°C	PA			S1			S2			(+)C		
0												
-1	+	+	+									
-2												
-3										+	+	+
-4												
-5												
-6		2.5			<=1.5			<=1.5			4.5	
(-)C												

Conclusion

- Successfully synthesize Fe_3O_4 nanoparticles (IO1: 20.6 nm, IO2 15.1 nm)
- Successfully synthesize Fe_3O_4–plant extract nanosystems (S1, S2)
- S1 with larger core shows higher Ms, better inductive heating effect but loads lower amount of plant extract than S2
- S1 and S2 show comparable anti-H5N1 and -ASFV activities with the pure extract. S2 better reduces the virus titer than S1
- High temperature induces higher antiviral activity of both S1 and S2.

Fe_3O_4-plant extract nanosystems are potential in antiviral applications.

Acknowledgement

I would like to thank the Postdoctoral Scholarship Programme of Vingroup Innovation Foundation (VINIF)

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Thank you for your listening!

12. FERMENTATIVE AND NUTRITIVE QUALITY OF FRUIT BY-PRODUCT SILAGE

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VIETNAM NATIONAL UNIVERSITY OF AGRICULTURE
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FERMENTATIVE AND NUTRITIVE QUALITY OF FRUIT BY PRODUCT SILAGE

Presented by: Dinh Thi Yen
PhD student, UGM, Indosinesia

MAIN CONTENTS

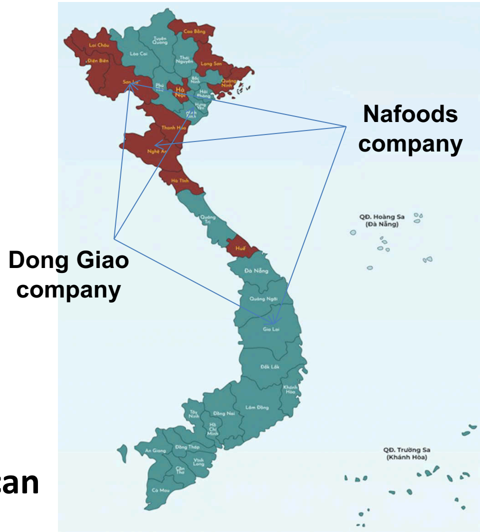
1. Introduction
2. Materials and Methods
3. Results and Discussion
4. Conclusion

Introduction

❖The number of cattle herds increase due to the growing demand for protein-based food sources →The demand for cattle feed is rising as well →need cheap, efficient food sources.

❖Vietnam is a country that produces many kinds of fruits. In the production process, many fruit by-products are created →Pressure on the environment

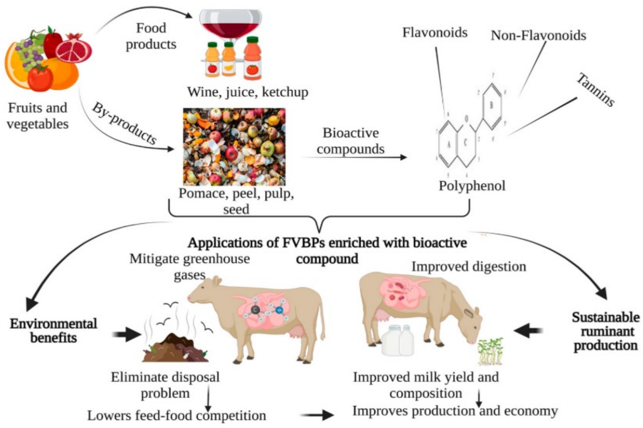
→If properly utilized, these by - products can transform waste into opportunities



Introduction

❑These by-products are highly valuable for ruminant animals

❑Carbohydrate (6 – 64%), protein (10 – 24%), vitamins and minerals, bioactive compound and rich in fiber → Vegetable and fruit by-products are a potential feed source for ruminants



Introduction

Fruit by-products

- ❑ High moisture (>80%)
- ❑ Fruit by-products in processing plants include many types
- ❑ Limited seasonal availability

Processing method: Mix seasonal fruit by-products

+ Dry + **Silage**

- ✓ The drying method is effective, but it causes high production costs
- ✓ **With the goal of utilizing a mix of by-products from processing plants and reducing feed production costs, the silage method is highly suitable**

Research Objectives

- ❖ **General objective**: Evaluation of fermentation quality and nutritional value of fruit silage used in beef cattle farming.
- ❖ **Specific objectives:**
- ✓ 1. Determine chemical composition (DM, CP, EE, NDF, ADF...)
- ✓ 2. Evaluation of fermentation parameters (pH, lactic acid, NH_3–N...)
- ✓ 3. Compare nutritional values between compost recipes.

Materials and Methods

- **Location**: Experiment conducted at the laboratory of the Faculty of Animal Husbandry
- **Time**: From May to October in year 2025
- **Objective**: To evaluate the fermentation quality and nutritional value of fruit silage by-products.
- **Design**: Completely randomized, 4 fermentation formulas, 3 replications.




Materials and Methods

Silage formulars: 5kg of mixture will be put in the plastic box,

- In the summer–autumn season, the proposed silage formulas are as follows:

Treatment 1*: 60% pineapple peel + 25% banana peel + 15% dried rice straw*

Treatment 2*: 60% pineapple peel + 25% banana peel + 15% dried cassava pulp*

Treatment 3*: 60% pineapple peel + 25% passion fruit peel + 15% dried rice straw*

Treatment 4*: 60% pineapple peel + 25% passion fruit peel + 15% dried cassava pulp*

Data collection: at 0, 30, 60 and 90 days after make a silage, 300 g of sample will be collected for the analysis of:

-Fermentation quality: pH, lactic, propionic, acetic, butyric

-Chemical composition: DM, CP,…

-Microbial population: Total arobic bacteria, lactic bacterial, …..

Statistical analysis: Anova one way with formular of silage by SAS (9.4)…

$Y_{ij} = \mu + F_i + e_{ij}$ where: Y_{ij} = all dependent variables; μ = overall mean; F_i = the effect of silage formular ($i = 4$); e_{ij} = random error. Differences among treatments were investigated by Duncan test at $P < 0.05$.

Results and discussion

Table 1. Chemical composition of feed ingredients before silage(Mean)

	By-products of processing plants							SEM	Other ingredients	
Indicators	Pineapple peel	passion fruit peel	banana peel	fresh vegetable soybean peel	Sweet corn cob	Sweet corn stalks	Mango Peel		dried rice straw	dried cassava pulp
DM	19.51[a]	12.20[c]	11.56[c]	17.6[b]	18.83[a]	19.29[a]	18.54[ab]	0.24	87.20	87.89
CP	4.23[c]	9.55[a]	8.14[b]	5.54[c]	8.26[ab]	5.86[c]	3.65[c]	0.29	7.01	2.21
EE	0.42[c]	0.85[c]	5.55[a]	0.82[c]	2.69[b]	0.83[c]	0.86[c]	0.26	1.37	0.38
Ash	3.11[c]	8.26[b]	12.03[a]	7.80[b]	2.39[c]	2.73[c]	2.12[c]	0.28	11.29	3.06
NDF	60.68[a]	40.31[d]	12.54[f]	60.21[a]	44.91[c]	57.55[b]	16.53[e]	0.48	60.79	45.76

Results and discussion

Table 2. Some physical characteristics of silage

Treatment	physical characteristics		
	30 days	60 days	90 days
Treatment 1	3	2.58[b]	2.75
Treatment 2	3	2.75[ab]	2.75
Treatment 3	3	2.91[ab]	2.75
Treatment 4	3	3.00[a]	2.83
SEM	**0**	0.06	0.04

Treatment 1: 60% pineapple peel, 25% banana peel, 15% dry straw;

Treatment 2: 60% pineapple peel, 25% banana peel, 15% cassava residue;

Treatment 3: 60% pineapple peel, 25% passion fruit peel, 15% dry straw;

Treatment 4: 60% pineapple peel, 25% passion fruit peel, 15% cassava residue.

Table 3. Chemical composition of silage formulas for summer - autumn crops (Mean)

Treatment	DM	CP	EE	CF	NDF	ADF	ADL	Ash	Sugar	OM
					0 day					
Treatment 1	$25,15^{b}$	$7,09^{a}$	$3,67^{a}$	$23,23^{b}$	$47,13^{b}$	$23,25^{a}$	4,48	$10,08^{a}$	12,34	$61,47^{a}$
Treatment 2	$27,05^{a}$	$3,91^{c}$	$0,76^{c}$	$25,76^{a}$	$39,91^{d}$	$22,72^{b}$	4,13	$4,74^{b}$	10,11	$38,33^{b}$
Treatment 3	$24,45^{b}$	$6,67^{a}$	$1,08^{b}$	$22,23^{c}$	$48,26^{a}$	$24,67^{a}$	4,01	$9,52^{a}$	9,63	$50,71^{a}$
Treatment 4	$24,71^{b}$	$4,71^{b}$	$0,47^{d}$	$20,77^{d}$	$42,31^{c}$	$29,70^{a}$	4,38	$4,67^{b}$	6,69	$68,18^{a}$
SEM	0,17	0,11	0,05	0,15	0,16	0,55	0,42	0,18	0,43	7,01

Treatment	DM	CP	EE	CF	NDF	ADF	ADL	Ash	Sugar	OM
					30 days					
Treatment 1	$26,24^{a}$	$7,53^{a}$	$2,15^{a}$	$23,72^{c}$	$52,36^{a}$	$27,93^{b}$	$3,34^{b}$	$11,11^{a}$	$1,17^{b}$	135,17
Treatment 2	$22,13^{bc}$	$4,95^{b}$	$1,91^{b}$	$22,34^{d}$	39,78c	$26,69^{b}$	$5,90^{a}$	$6,14^{c}$	$1,67^{b}$	178,06
Treatment 3	$22,10^{c}$	$7,78^{a}$	$0,95^{c}$	$28,22^{a}$	$54,04^{a}$	$31,19^{a}$	5,04a^{b}	$10,13^{b}$	$1,38^{b}$	156,01
Treatment 4	$23,87^{b}$	$5,83^{b}$	$0,47^{d}$	$25,51^{b}$	$41,82^{b}$	$27,54^{b}$	4,25a^{b}	$5,15^{d}$	$2,69^{a}$	182,42
SEM	0,39	0,31	0,04	0,16	0,39	0,42	0,38	0,08	0,19	16,06

Treatment 1: 60% pineapple peel, 25% banana peel, 15% dry straw;

Treatment 2: 60% pineapple peel, 25% banana peel, 15% cassava residue;

Treatment 3: 60% pineapple peel, 25% passion fruit peel, 15% dry straw;

Treatment 4: 60% pineapple peel, 25% passion fruit peel, 15% cassava residue.

Table 3. Chemical composition of silage formulas for summer - autumn crops (Mean)

Treatment	DM	CP	EE	CF	NDF	ADF	ADL	Ash	Sugar	OM
					60 days					
Treatment 1	$25,95^{a}$	$7,99^{a}$	$2,35^{b}$	$23,93^{b}$	$52,13^{b}$	$30,49^{ab}$	$4,49^{b}$	$11,37^{a}$	$1,49^{b}$	$138,77^{b}$
Treatment 2	$17,16^{c}$	$6,10^{b}$	$2,95^{a}$	$20,56^{c}$	$41,33^{c}$	$27,52^{c}$	$5,92^{a}$	$8,45^{c}$	$1,74^{b}$	$229,94^{a}$
Treatment 3	$23,47^{b}$	$5,56^{bc}$	$1,17^{c}$	$26,43^{a}$	$55,10^{a}$	$31,63^{a}$	$4,81^{ab}$	$10,54^{b}$	$1,77^{b}$	$139,69^{b}$
Treatment 4	$24,50^{b}$	$5,26^{c}$	$0,46^{d}$	$24,61^{b}$	$40,17^{c}$	$29,27^{b}$	$5,45^{ab}$	$5,32^{d}$	$5,38^{a}$	$176,60^{ab}$
SEM	0,26	0,14	0,03	0,22	0,36	0,37	0,34	0,09	0,35	16,04

Treatment	DM	CP	EE	CF	NDF	ADF	ADL	Ash	Sugar	OM
					90 days					
Treatment 1	$21,24^{c}$	$8,02^{a}$	$3,83^{a}$	$23,28^{c}$	$48,31^{b}$	28,22	$5,67^{b}$	$12,31^{a}$	$1,27^{b}$	175,83
Treatment 2	$21,38^{c}$	$5,69^{b}$	$2,71^{b}$	$21,27^{d}$	$40,38^{c}$	28,04	$7,96^{a}$	$6,74^{c}$	$3,30^{a}$	197,84
Treatment 3	$25,34^{a}$	$8,03^{a}$	$1,20^{c}$	$27,41^{a}$	$52,32^{a}$	29,66	$4,39^{c}$	$10,32^{b}$	$1,86^{b}$	144,06
Treatment 4	$23,63^{b}$	$5,17^{c}$	$0,45^{d}$	$25,35^{b}$	$41,32^{c}$	30,14	$6,93^{a}$	$5,03^{d}$	$4,50^{a}$	194,88
SEM	0,23	0,08	0,07	0,18	0,28	0,78	0,26	0,11	0,28	15,00

Treatment 1: 60% pineapple peel, 25% banana peel, 15% dry straw;

Treatment 2: 60% pineapple peel, 25% banana peel, 15% cassava residue;

Treatment 3: 60% pineapple peel, 25% passion fruit peel, 15% dry straw;

Treatment 4: 60% pineapple peel, 25% passion fruit peel, 15% cassava residue.

Table 4. Volatile fatty acids and N-NH3 of silage formulations (Mean)

Fermentation time (days)	Treatment	NH_3-N (%)	Organic acids (g/kg DM)			
			Lactic acid	Acetic acid	Propionic acid	Butyric acid
30 days	Treatment 1	2.54	19.07^{a}	13.87^{ab}	n.d	7.25^{a}
	Treatment 2	n.d	19.30^{a}	17.43^{a}	n.d	2.99^{bc}
	Treatment 3	n.d	15.67^{b}	12.37^{bc}	n.d	5.49^{ab}
	Treatment 4	1.10	15.47^{b}	16.60^{a}	n.d	3.34^{b}
	SEM		0.70	0.91		0.61

Fermentation time (days)	Treatment	NH_3-N (%)	Organic acids (g/kg DM)			
			Lactic acid	Acetic acid	Propionic acid	Butyric acid
60 days	Treatment 1	5.60^{c}	19.83^{a}	18.90	n.d	7.15^{a}
	Treatment 2	9.11^{a}	19.57^{a}	19.13	n.d	3.28^{b}
	Treatment 3	7.81^{ab}	15.00^{b}	13.83	n.d	6.23^{a}
	Treatment 4	3.94^{d}	14.50^{b}	15.77	n.d	2.39^{b}
	SEM	0,33	0.72	2.27		0.50

Fermentation time (days)	Treatment	NH_3-N (%)	Organic acids (g/kg DM)			
			Lactic acid	Acetic acid	Propionic acid	Butyric acid
90 days	Treatment 1	4.44^{b}	19.10^{a}	17.60	n.d	8.41^{a}
	Treatment 2	1.12^{c}	16.70^{ab}	17.60	n.d	2.55^{c}
	Treatment 3	5.41^{ab}	15.60^{ab}	13.27	n.d	5.21^{bc}
	Treatment 4	5.96^{a}	14.17^{b}	16.67	n.d	2.64^{c}
	SEM	0.28	0.91	1.36		0.80

Treatment 1: 60% pineapple peel, 25% banana peel, 15% dry straw;

Treatment 2: 60% pineapple peel, 25% banana peel, 15% cassava residue;

Treatment 3: 60% pineapple peel, 25% passion fruit peel, 15% dry straw;

Treatment 4: 60% pineapple peel, 25% passion fruit peel, 15% cassava residue.

Table 5. pH value of silage formulations (Mean)

Treatment	pH value		
	30 days	60 days	90 days
Treatment 1	4.05^{c}	4.13^{b}	4.23^{d}
Treatment 2	4.22^{a}	4.56^{a}	4.51^{b}
Treatment 3	4.15^{b}	4.50^{a}	4.37^{c}
Treatment 4	4.26^{a}	4.68^{a}	4.70^{a}
SEM	0.01	0.06	0.02

Treatment 1: 60% pineapple peel, 25% banana peel, 15% dry straw;

Treatment 2: 60% pineapple peel, 25% banana peel, 15% cassava residue;

Treatment 3: 60% pineapple peel, 25% passion fruit peel, 15% dry straw;

Treatment 4: 60% pineapple peel, 25% passion fruit peel, 15% cassava residue.

Table 6. Microbial composition of silage (Mean)

Fermentation time (days)	Treatment	Total aerobic bacteria log10	LAB log10	Yeast log10	Mold log10	Bacillus log10	Clolotridium log10
30 days	Treatment 1	4.29	3.69	2.53	n.d	3.72	n.d
	Treatment 2	4.30	3.33	n.d	n.d	3.61	n.d
	Treatment 3	4.23	3.48	n.d	n.d	3.37	n.d
	Treatment 4	4.04	3.37	n.d	n.d	3.50	n.d
	SEM	0.71	0.23			0.29	

Fermentation time (days)	Treatment	Total aerobic bacteria log10	LAB log10	Yeast log10	Mold log10	Bacillus log10	Clolotridium log10
60 days	Treatment 1	4.74	3.31	n.d	n.d	4.60	1.77
	Treatment 2	4.58	3.04	n.d	n.d	4.49	1.94
	Treatment 3	4.78	3.09	n.d	n.d	4.55	1.77
	Treatment 4	4.62	3.00	n.d	n.d	4.48	n.d
	SEM		0.21			0.27	0.23

Treatment 1: 60% pineapple peel, 25% banana peel, 15% dry straw;

Treatment 2: 60% pineapple peel, 25% banana peel, 15% cassava residue;

Treatment 3: 60% pineapple peel, 25% passion fruit peel, 15% dry straw;

Treatment 4: 60% pineapple peel, 25% passion fruit peel, 15% cassava residue.

Table 6. Microbial composition of silage (Mean)

Fermentation time (days)	Treatment	Total aerobic bacteria log10	LAB log10	Yeast log10	Mold log10	Bacillus log10	Clolotridium log10
90 days	Treatment 1	4.56	2.94	n.d	n.d	4.52	n.d
	Treatment 2	4.78	2.91	n.d	n.d	4.09	1.72
	Treatment 3	4.00	2.93	n.d	n.d	4.01	n.d
	Treatment 4	4.30	2.79	n.d	n.d	4.25	n.d
	SEM		0.12			0.24	0.20

Treatment 1: 60% pineapple peel, 25% banana peel, 15% dry straw;

Treatment 2: 60% pineapple peel, 25% banana peel, 15% cassava residue;

Treatment 3: 60% pineapple peel, 25% passion fruit peel, 15% dry straw;

Treatment 4: 60% pineapple peel, 25% passion fruit peel, 15% cassava residue.

Conclusion

- ❖Fruit by-products (pineapple peel, banana peel, passion fruit peel, cassava pulp...) have good nutritional value, rich in carbohydrates, vitamins, minerals and fiber - a potential source of raw materials for beef cattle farming.

- ❖Silage method helps preserve by-products effectively, reduces feed production costs and limits environmental pollution.

- ❖**The analysis results show:**
  - ✓ Good fermentation quality: reduced pH, high lactic acid content, low NH_3–N.
  - ✓ Stable nutritional value: DM, CP, NDF and ADF content suitable for beef cattle rations.
  - ✓ The combination of 60% pineapple peel + 25% passion fruit peel + 15% dried cassava pulp gives optimal fermentation and nutritional results.

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2021 - 2030

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Thạc sĩ (2 năm): Chăn nuôi, Chăn nuôi thú y

Đại học (4 năm): Chăn nuôi, Chăn nuôi thú y

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- Cán bộ kỹ thuật
- Chuyên gia kỹ thuật
- Nhân viên kinh doanh
- Cán bộ quản lý
- Tự khởi nghiệp

HỢP TÁC QUỐC TẾ

- Nhiều dự án quốc tế trong đào tạo và nghiên cứu khoa học
- Tiêu biểu: Dự án Việt Bỉ (từ năm 1997 đến nay);
  Dự án KOICA, Hàn Quốc (từ năm 2021 đến 2030)
- Trao đổi sinh viên quốc tế (Đan Mạch, Canada, Hàn quốc, Nhật Bản, Thái Lan, Indonesia,...

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CƠ SỞ VẬT CHẤT

6 phòng thực hành chuyên môn

3 phòng nghiên cứu trọng điểm

- Phòng thí nghiệm trung tâm đạt chứng chỉ ISO/IEC 17025:2017
- Phòng nghiên cứu di truyền động vật

Trung tâm

- Trung tâm nghiên cứu liên ngành và PTNN
- Trung tâm giống vật nuôi chất lượng cao

Mô hình nghiên cứu

- Mô hình chăn nuôi lợn, gà, dê, thỏ
- Mô hình vườn cỏ

CƠ CẤU TỔ CHỨC

6 Bộ môn

- Sinh học động vật
- Hóa sinh động vật
- Chăn nuôi chuyên khoa
- Di truyền - Giống vật nuôi
- Dinh dưỡng và thức ăn chăn nuôi
- Sinh lý và tập tính động vật

Đội ngũ cán bộ

52 cán bộ:

- 31 giảng viên
  (02 Giáo sư, 08 Phó Giáo sư, 16 TS, 03 NCS, 02 ThS)
- 21 cán bộ hỗ trợ

KOICA – VNUA PROJECT

2025
INTERNATIONAL CONFERENCE
TRANSFORMATION TO SUSTAINABLE LIVESTOCK PRODUCTION

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