



Genetic diversity of Philippine native pig populations of Ifugao based on morphometrics & molecular markers

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 2ND PIG GENETIC NETWORKING – PHILIPPINES & TAIWAN
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Rationale



Philippine Native Pig

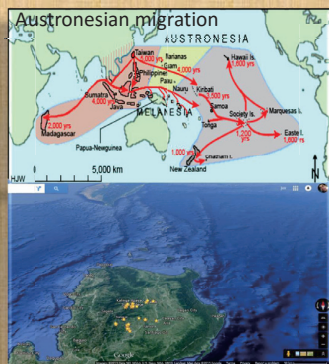


Traditional Ifugao House
 Preservation of culture and tradition

Lechon
 Etag
 Cochinillo
 Production of uniquely Filipino specialty food products

~39~

Rationale



Philippine Native Pig

Lanyu Pig

Purpose

- Determine the genetic diversity;
- Establish phylogenetic relationship between Ifugao and Taiwan native pigs;
- Establish the possible origin of the Philippine native pigs using molecular tools; and
- Provide basic information for possible development of conservation programs for Philippine native pigs

Native pig samples



Methodology

Quota purposive sampling

Establish the morphological characteristics (quantitative and qualitative traits) of Ifugao native pigs

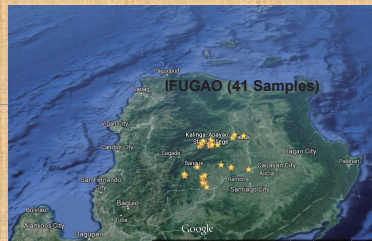
DNA Extraction from ear tissue

mtDNA Amplification

SSR Amplification

~40~

Sampling Area



Qualitative and quantitative traits

QUALITATIVE TRAITS	FREQUENCY	PERCENTAGE	QUANTITATIVE TRAITS	MEAN (cm)
COAT COLOR				
Black	22	54		
Black w/ white hock	11	27	Body length	46.76
Black w/ white belly	7	17	Head length	27.85
Black w/ patches	1	2	Heart girth	74-99
COAT COLOR PATTERN				
Plain	33	83	Tail length	21.35
Patchy	8	17	Ear length	11.70
Spotted	0	0	Height at withers	40-30
SNOUT TYPE				
Long and thin	34	78		
Short & cylindrical	6	15		
Long and cylindrical	0	0		
Short and pointed	3	7		
HEAD PROFILE				
Concave	2	5		
Straight	38	93		
Convex	1	2		
EAR TYPE				
Droopy	2	5		
Semi-lop	9	22		
Lop	0	0		
Erect	30	73		
EAR ORIENTATION				
Forward	2	5		
Backward	39	95		
TAIL TYPE				
Straight	38	93		
Curly	3	7		
BACKLINE				
Straight	13	32		
Swaybacked	28	68		

mtDNA amplification

The D-loop sequence was obtained from the 41 samples from Ifugao and 38 from Kalinga native pigs

Outgroup and other pig sequences were obtained from National Center for Biotechnology Information (NCBI)

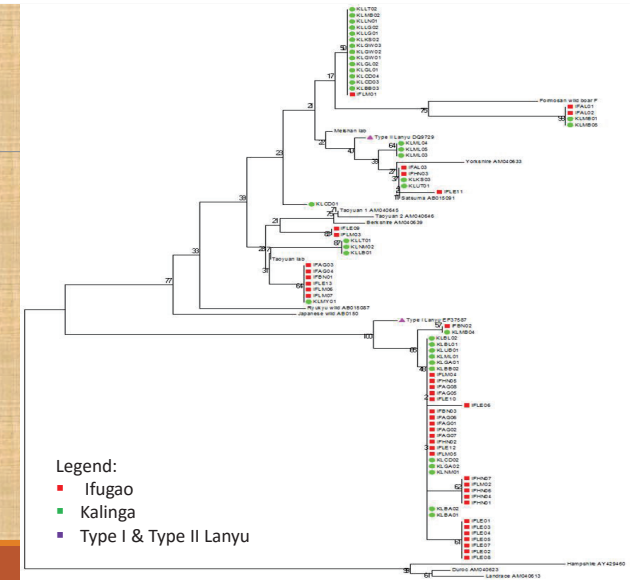
The sequences were puzzled using the EditSeq software

Haplotypes were determined using dnap v 5.10

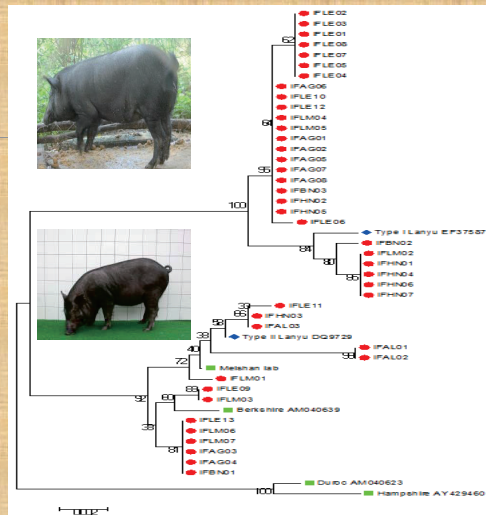
The full length sequences were aligned using MEGAlign software

Phylogenetic tree was constructed using MEGA software

Phylogenetic tree



41



5 Unique Haplotypes of Ifugao Native pig population with Taiwan native pig

Asian

European Breeds

Phylogenetic tree

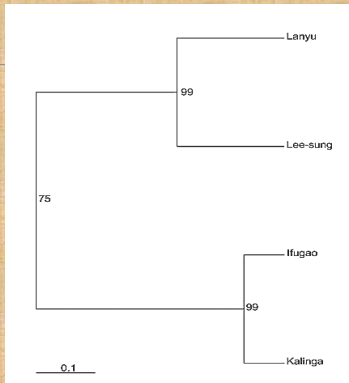
SSR amplification

Nine microsatellite markers recommended by FAO were used to study the genetic variability and genetic structure within and between populations

Samples include Native pigs from Ifugao and Kalinga; Lanyu and Leesung

DNA amplification and microsatellite genotyping

Data analysis for Molecular Characterization (POPGENE, CERVUS, POPULATIONS, TreeView)



UPGMA tree based on Nei (1972) standard genetic distance of Ifugao and Kalinga native pigs (*Sus scrofa* L.) and Taiwan Lanyu and Lanyu derived pig breeds using microsatellite markers. The number at each branch represents the percentage of bootstrap values from 1,000 replications of resampled loci.

Establishment of Nucleus Herd in Ifugao State University



**Thank you for your attention!
Haggiyo!**