



Identification of Close Relatives of Crossbred Dairy Cattle in Ethiopia

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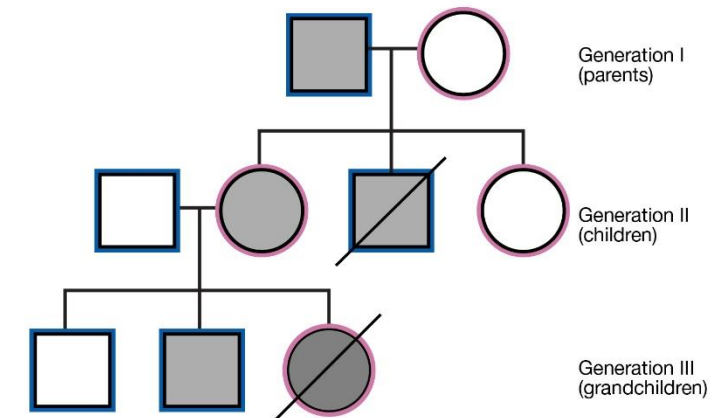
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Introduction

- Correct pedigree is essential to produce accurate genetic evaluation and make informed breeding decision.
- Pedigree error in livestock is common with significant error rated reported in different species (Moore *et al.*, 2019).
- Pedigree recording in smallholder dairy farming system is rare
- Molecular techniques can be used for parentage verification and reassignments to improve the accuracy of pedigree.

PEDIGREE IS KING



Introduction

- McClure et al. (2015) have suggested that a panel with a minimum of 500 SNPs is more appropriate for parentage verification and prediction.
- African Dairy Genetic Gains (ADGG) program supports Ethiopia's national dairy recording center to operate a digital data capture.
 - Vision: African smallholder dairy farmers are continuously accessing more productive and adaptive dairy genetics under tropical environment
- Selected animals were genotyped through ADGG program in collaboration with National Animal Genetic Improvement Institute (NAGII)

Introduction

- Verify and assign parents using genotype information helps to:
 - Fill gap in the national database and hasten the genetic gains
 - Evaluate performance of AI bulls and taking breeding decision
- Therefore, the analysis was done to identify close relatives and proposing parentage re-assignments and estimate inbreeding coefficient



Methodology

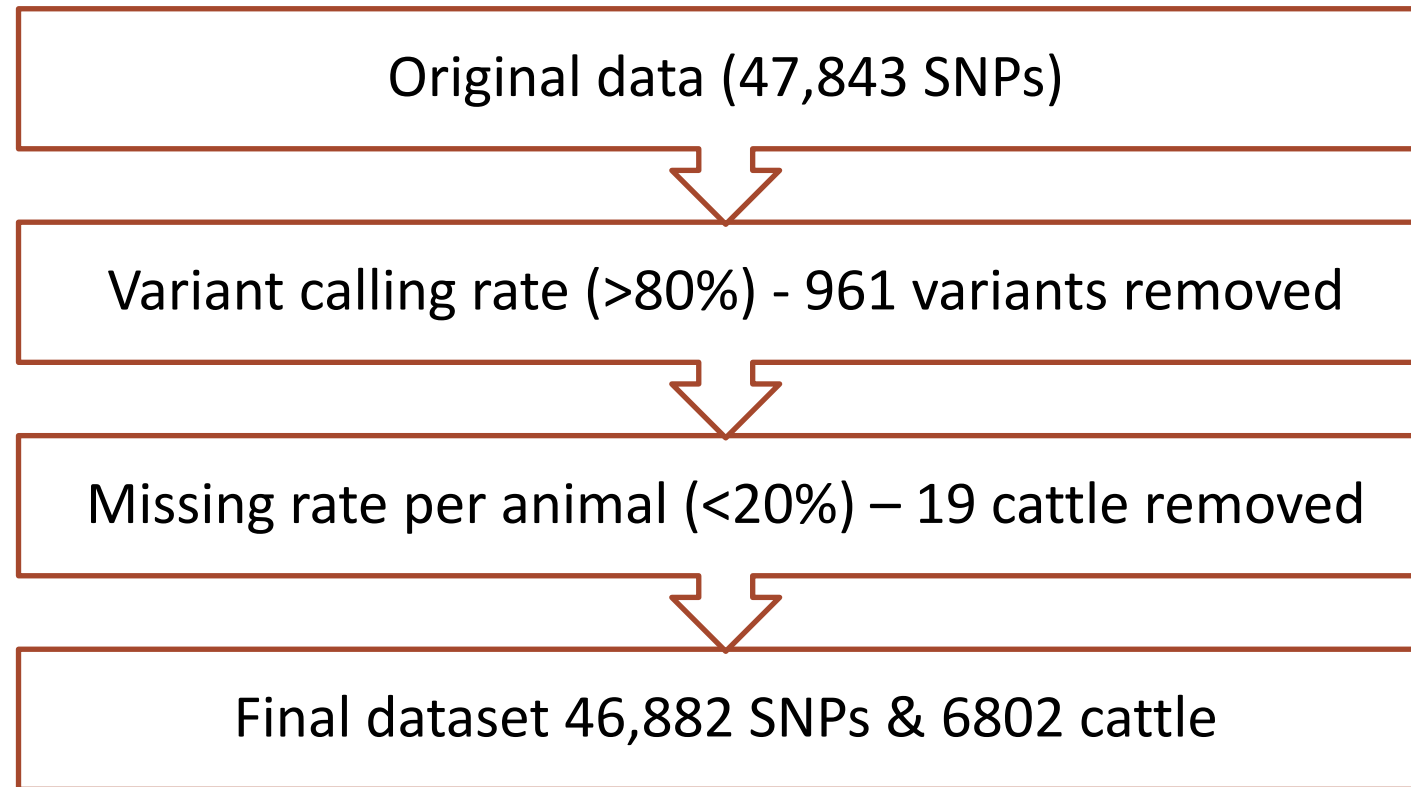
DNA extraction and genotype

- ADGG project in collaboration with NAGII has collected hair samples from selected herds.
- Number of animals = 6,821 animals from Oromia, Amhara, SNNP, Tigray, and Sidama region, and Addis Ababa in Ethiopia.
- DNA is extracted from hair sample
- Genotyped using the Illumina BovineSNP50 BeadChip, which consists of 54,609 (Version 2) - Neogen Genomics company.



Methodology

Quality control pipeline – PLINK (version 1.9)



Methodology

Approaches - KING (version 2.2.7):

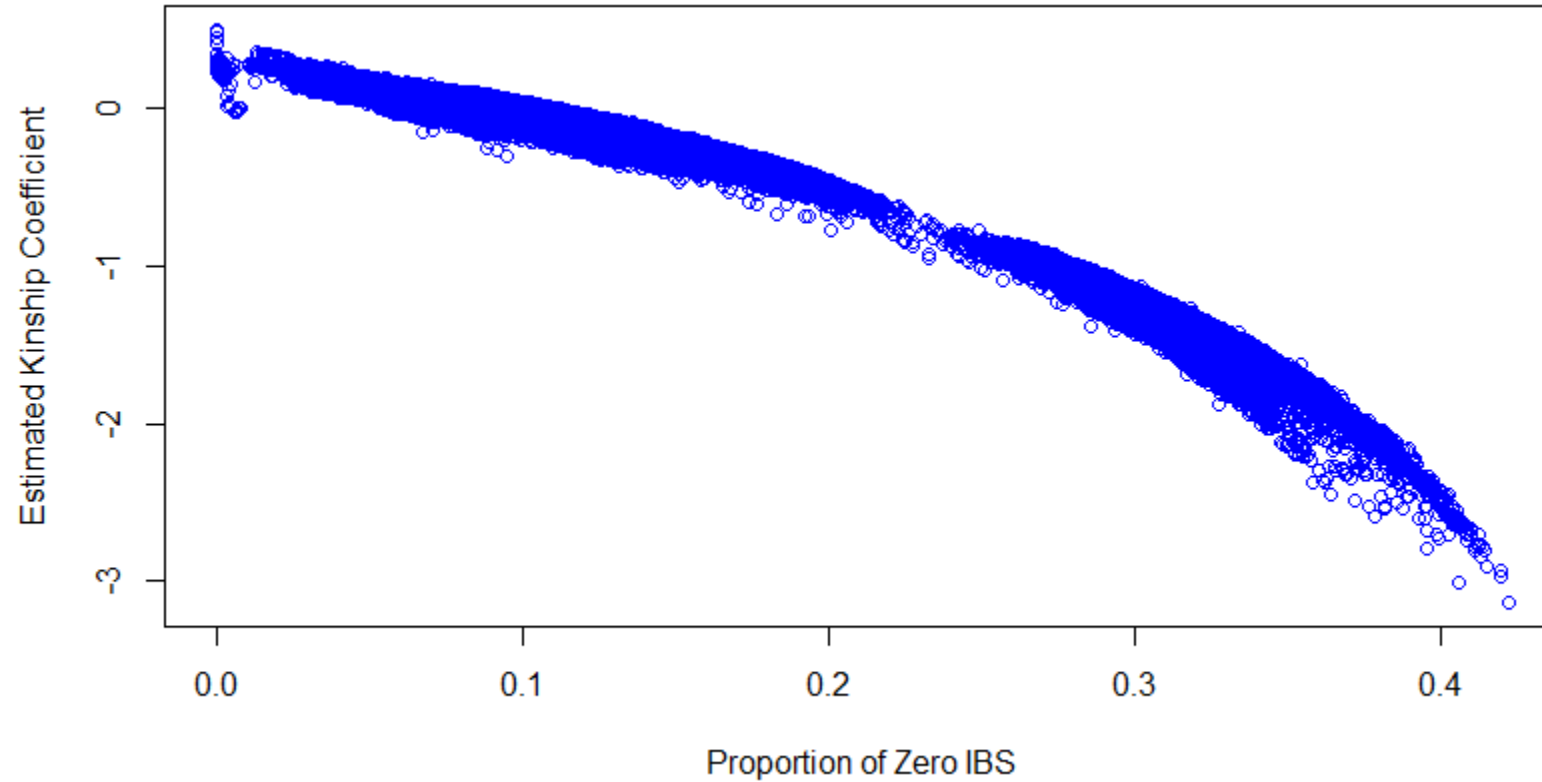
1. **Kinship**: Estimated kinship coefficient (ϕ) from the SNP data
 - $\phi > 0.354$ = MZ twin /duplicate
 - ϕ between 0.177 and 0.354 = 1st degree relationship
 - ϕ between 0.0884 and 0.177 = 2nd degree relationship
 - ϕ between 0.0442 and 0.0884 = 3rd degree relationship
2. **PropIBD**: Proportion of genomes shared identical-by-descent
 - The proportion of a locus, at which a pair of individuals shared 0 allele IBD
 - Used to classify the relationships between parent-offspring (PO) and full sibling (FS).

Methodology

- The inbreeding coefficient calculated
 - Observed versus expected number of homozygous genotypes in PLINK 1.9 program.
- Run of homozygosity (ROH) performed in KING program
 - All individuals with proportion of their genomes being ROH > 4.4%
 - Corresponds to being offspring of parents that are 2nd-degree or closer

Results

Total number of pairs compared: 23,130,202.



Results

- MZ/duplicate
 - King – inferred 75 pairs were identified

The result looks potential duplicates.

Human error:

- Same hair sample placed in different envelop, labeled with wrong animal ID
- Laboratory error – mixing up sample

Example

ET000027164 – BD 28th Aug 2014 – Amhara

ET000012873 - BD 9th May 2017 – Addis Ababa



Results

- 2,133 pairs of parent-offspring
 - Parentage assignment or re-assignment is possible
 - Can be updated on the main national DB

Example

Bull_ID	No_Offspring	EBV_Reliability
ET000001787	34	0.85

Results

- 689 pairs of full-sibs relationship
- Whilst 125,929 pairs are sorted under second degree relationship,
 - Contributed about 0.5% of the total pairs 23,130,202.
- 783,530 pairs – categorized third degree relationship
 - 3.39% out of the total pairwise comparison
- Understanding the relationship:
 - Ensure to minimize risk of inbreeding



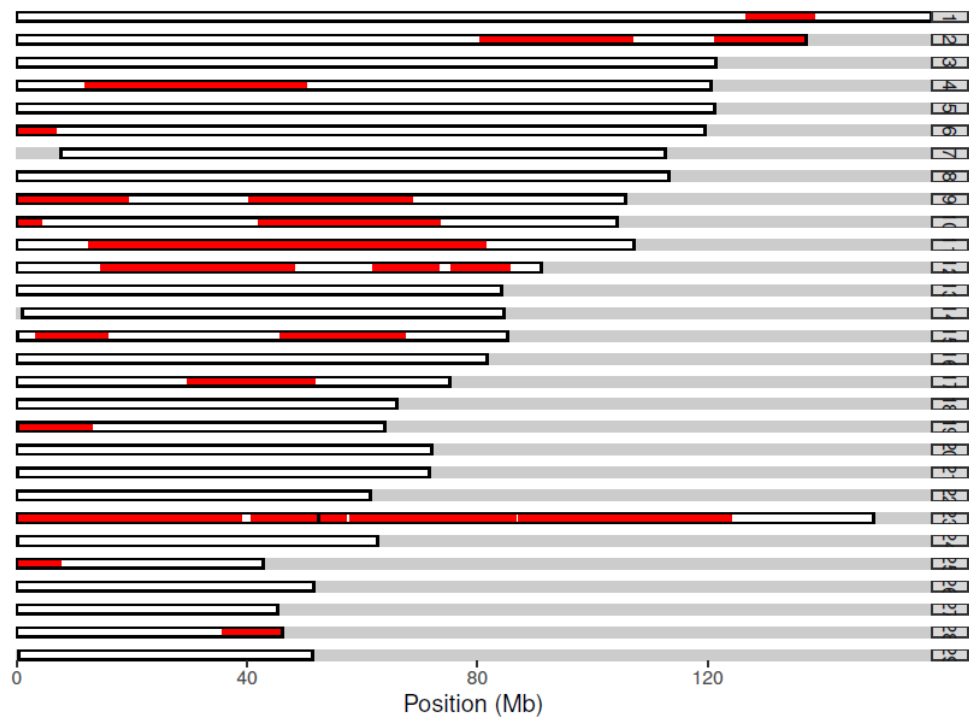
Results

Inbreeding

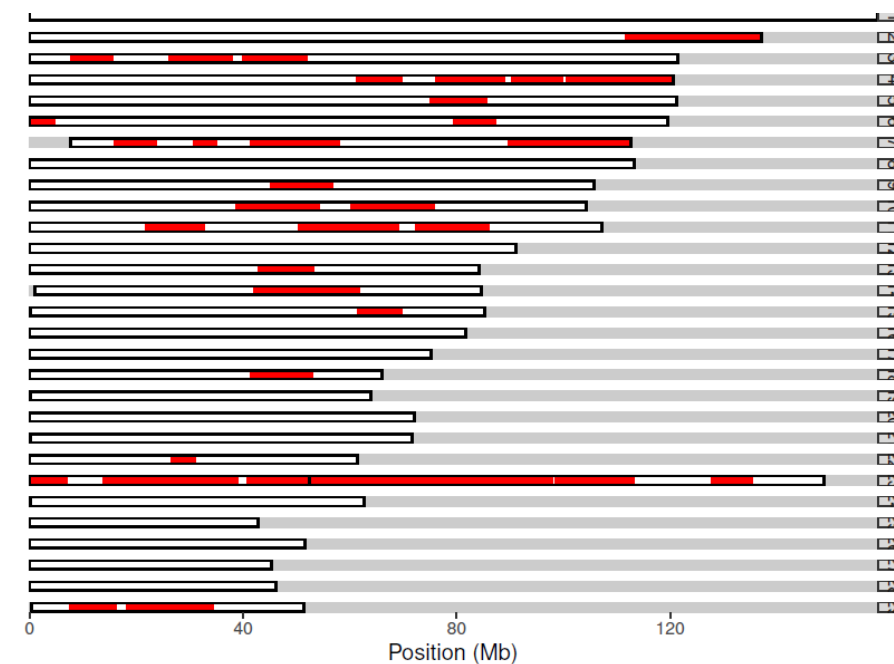
- Population average inbreeding coefficient was 0.02
- Nearly one tenth of the population had above 10 % inbreeding coefficient
- 622 animals having - FROH > 4.4%
 - Nearly 9% of the population

Results

ET000038162 $F_{ROH} = 0.16$



ET000009759 $F_{ROH} = 0.14$



Conclusion

- In conclusion, drawing relationship inference for close relatives in the crossbred cattle population provides **complementary information for:**
 - **Genetic evaluation** to estimate **highly reliable breeding value**
 - **Breeding decision at a farm and country level**
- Additionally, the status of the inbreeding coefficient reported requires attention in the national breeding plan to ensure sustainable genetic improvement program.
 - **Keeping herds in safe zone**

Thank you እናመሰግናለን



NAGRC & DB



Centre for Tropical Livestock Genetics and Health



BILL & MELINDA GATES foundation



National/regional Institutions/govts.

Dairy Farmers & Farmer organizations