



## Assessing inbreeding and genetic diversity in South American Brown Swiss cattle: The Ecuadorian experience



Luis F. Cartuche-Macas<sup>1</sup>, Edilberto Chacón<sup>2</sup>, Miguel M. Gutiérrez-Reinoso<sup>2</sup>, Manuel García-Herreros<sup>3,4</sup>

<sup>1</sup>Asociación Holstein Friesian del Ecuador, Ecuador

<sup>2</sup>Medicina Veterinaria, Universidad Técnica de Cotopaxi, Ecuador

<sup>3</sup>Instituto Nacional de Investigación Agrária e Veterinária (INIAV), Portugal

<sup>4</sup>CIISA-AL4AnimalS, Faculty of Veterinary Medicine, University of Lisbon, Portugal



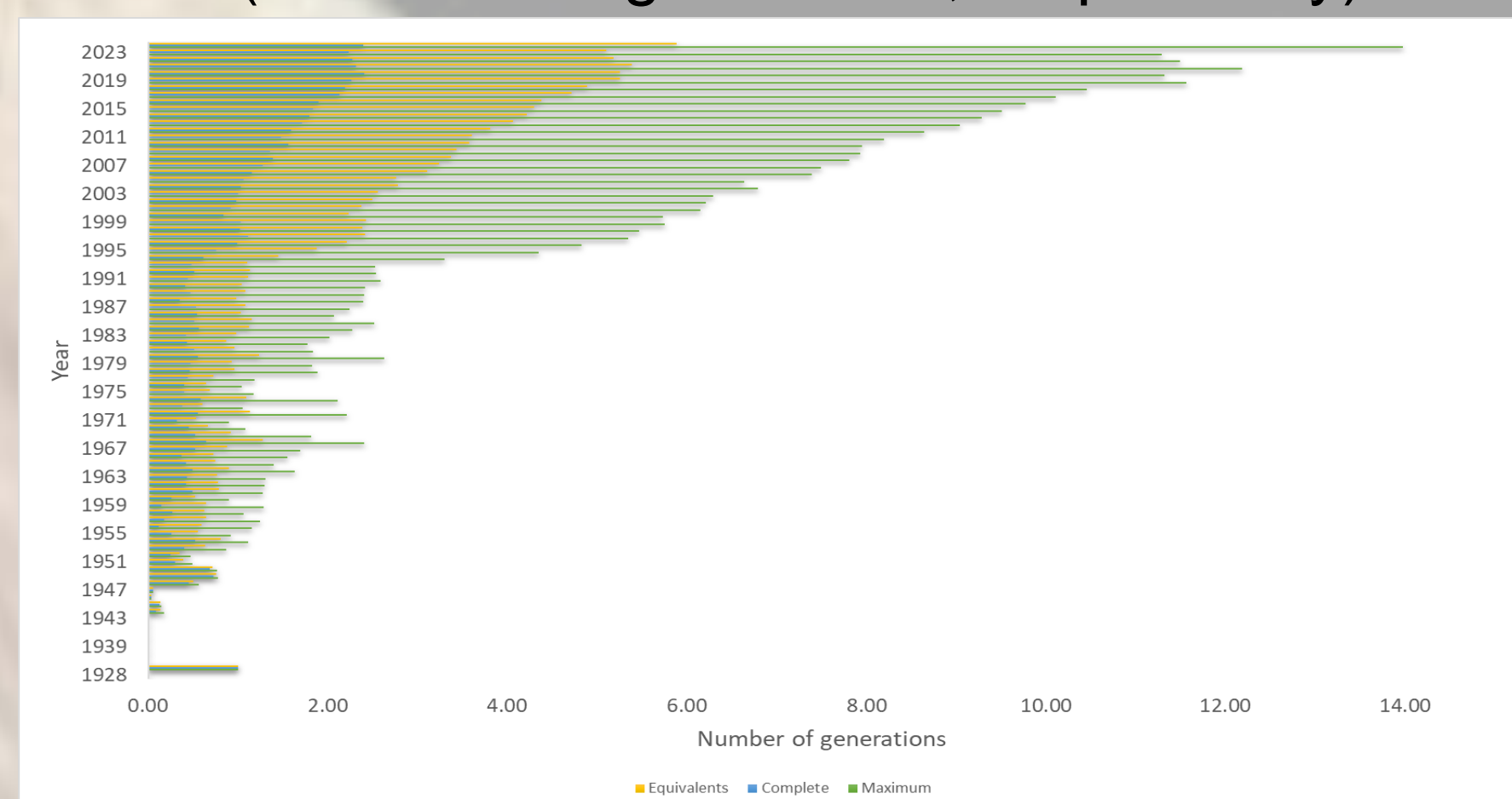
### INTRODUCTION & AIM

Brown Swiss cattle is the second most important dairy breed in Ecuador. Genetic improvement programs require monitoring population structure and genetic diversity (GD) over time. The objective of this study was to analyze the current structure and GD of the Brown Swiss breed in Ecuador.

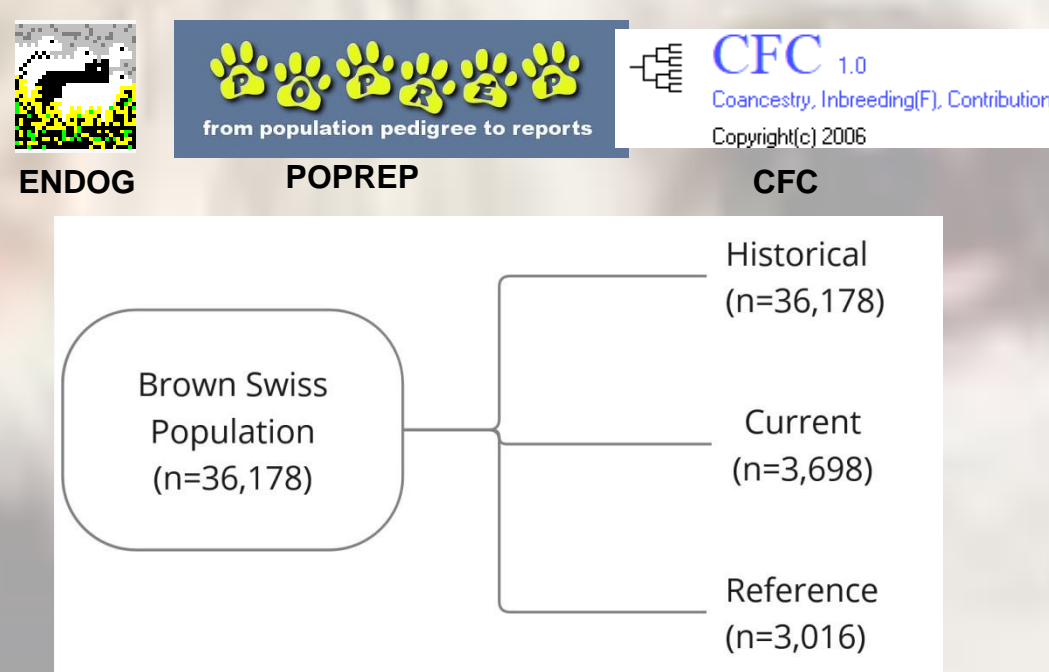
### RESULTS & DISCUSSION

#### Population structure

PCI in the historical population ranged between 68.0 and 16.3% and between 81.7 and 63.9% in the current population (first to sixth generation, respectively).



### MATERIAL & METHODS



#### Ecuadorian Highlands/Lowlands

500-3,400 m.a.s.l.

**Population structure:** pedigree completeness index (PCI), number of equivalent (GEq), complete (GCom) and maximum (GMax) generations and generation interval (GI).

**Genetic diversity:** inbreeding (F), inbreeding increment ( $\Delta F$ ), average relatedness (AR), co-ancestry (C), Non-random mating ( $\alpha$ ), effective population size ( $N_e$ ) and genetic conservation index (GCI).

**Gene origin probability:** number of founders (f), effective number of founders (fe) and ancestors (fa), number of equivalent genomes (fg), fe/fa and fg/fa ratio and DG losses.

GEq in the current population was 2.61, while the GI decreased from 6.85 to 5.70 years in the historical (n=10,655) and current (n=1,582) population, respectively.

#### Inbreeding, coancestry, average relatedness and genetic conservation index

Population	F (%)	C (%)	AR (%)	$\Delta F$ (%)	GCI
Current	2.35	1.12	2.23	0.41	10.41
Historical	0.62	0.49	0.98	0.16	3.67

The  $N_e = 120$  (2015-2020) values were observed.

#### Gene origin probability

Gene origin probability in the reference population was  $f=1,384$ ,  $fa=40$ ,  $fe=157.60$ ,  $fg=24.86$ ,  $fg/fe=0.16$  showing an important GD loss (2.01%) due to an unequal contribution of founders (0.32%) and bottleneck and genetic drift (2.01%).

Parameter	Value
Genetic diversity (GD)	97.99
Genetic diversity loss (GDL)	2.01
GDL due to unequal founder contributions (%)	0.32
GDL due to bottlenecks and genetic drift since founders (GL) (%)	2.01

### CONCLUSION

The slight reduction in GI and low F,  $\Delta F$ ,  $N_e$  and AR values, an important GD loss showed the urgent need for optimal management of mating schemes when using closely related individuals.