

Population structure assessment using genome wide molecular information in Martina Franca donkey.

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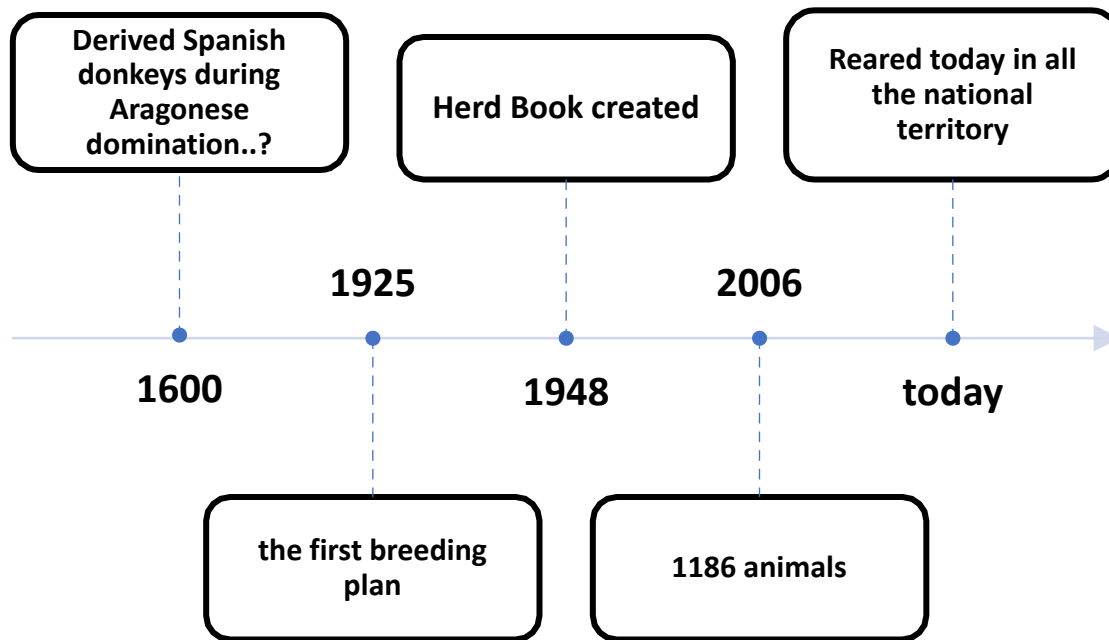
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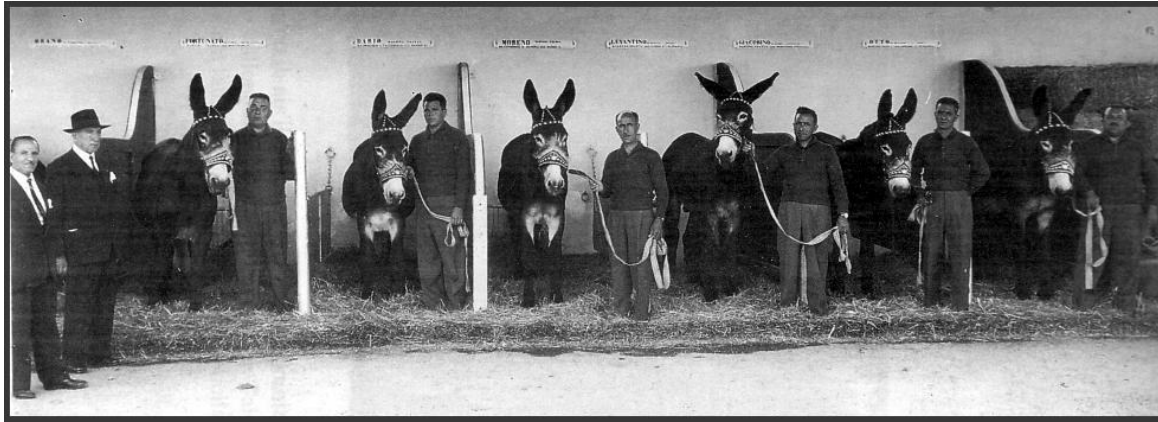
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Lyon, France - August 26th / September 1st, 2023

Martina Franca donkey...



Martina Franca donkey...



*Bari (Italy), during the XXX Fiera del Levante (picture
famiglia Pastore)*



*Donkey in typical uses in south of
Italy*





*"Alpini" corp soldiers with their mules called
"Muli Leccesi"*

Martina Franca donkey...

- Appreciated for *mule* production during the "Great War"
- *Milk* (and meat)
- *onotherapy*



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Objectives

To assess population structure

Evaluate molecular inbreeding values

Seeking divergent individuals

Check pedigree inconsistency



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Material and Methods

- *100 samples from 10 herds*
- *SNPs from DADRAGE (TGA Technology Services Srl)*
- *R software (Optisel, tidyverse etc.)*
- *Plink, Admixture, Netview, Geekparent etc.*



Material and Methods



FARM	SAMPLES
A	46
B	6
C	8
D	3
E	7
F	7
G	8
H	8
I	2
L	6

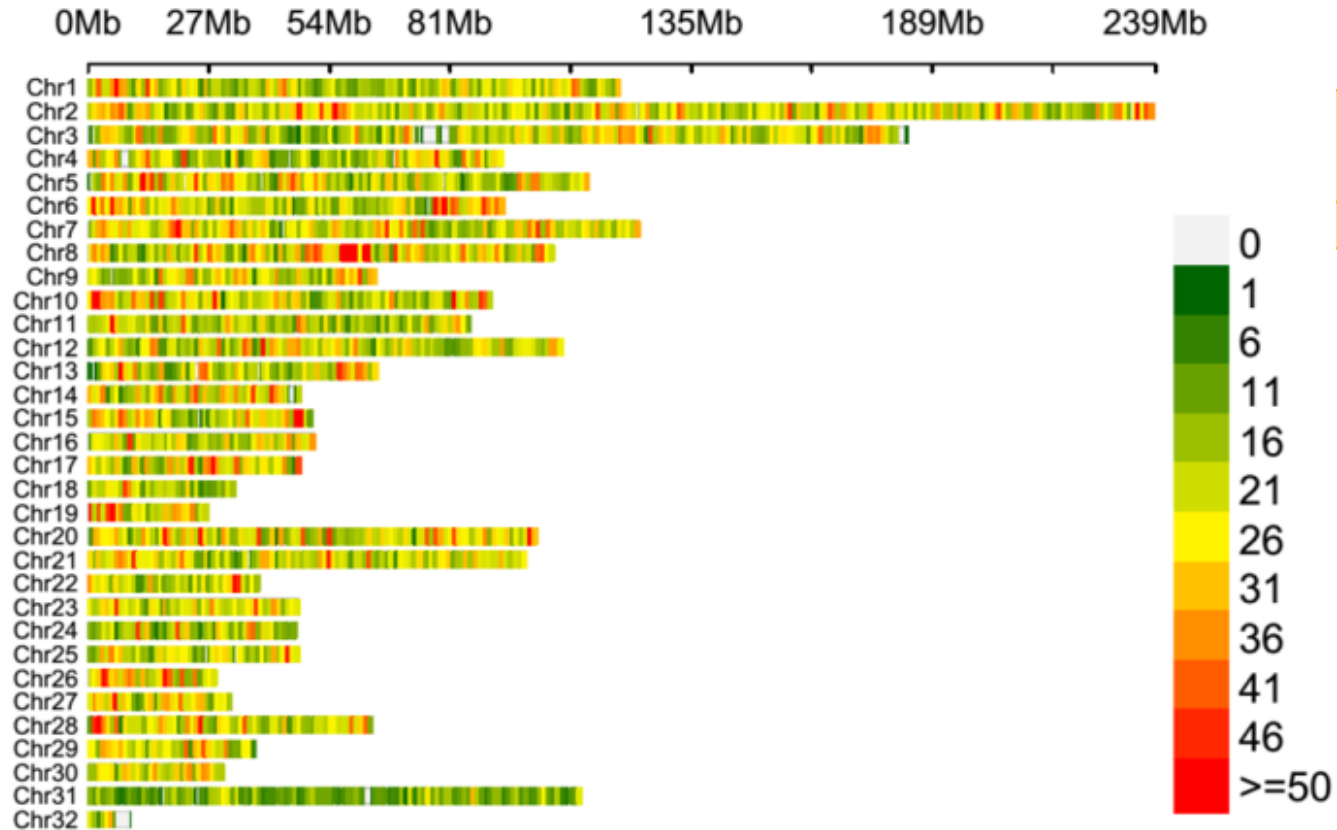
Regional conservation centre
100 female



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Results: the marker panel

The number of SNPs within 1Mb window size



	ORIGINAL	GENO 0.1	MIND 0.1	MAF 0.05	indep-pairwise 50 5 0.5
SNPs	54202	47541	47541	21280	10778

*From unpublished experiences of several colleagues...
200k or 500k Illumina iCore bead chip allow ~ 3000 polymorphic
markers*

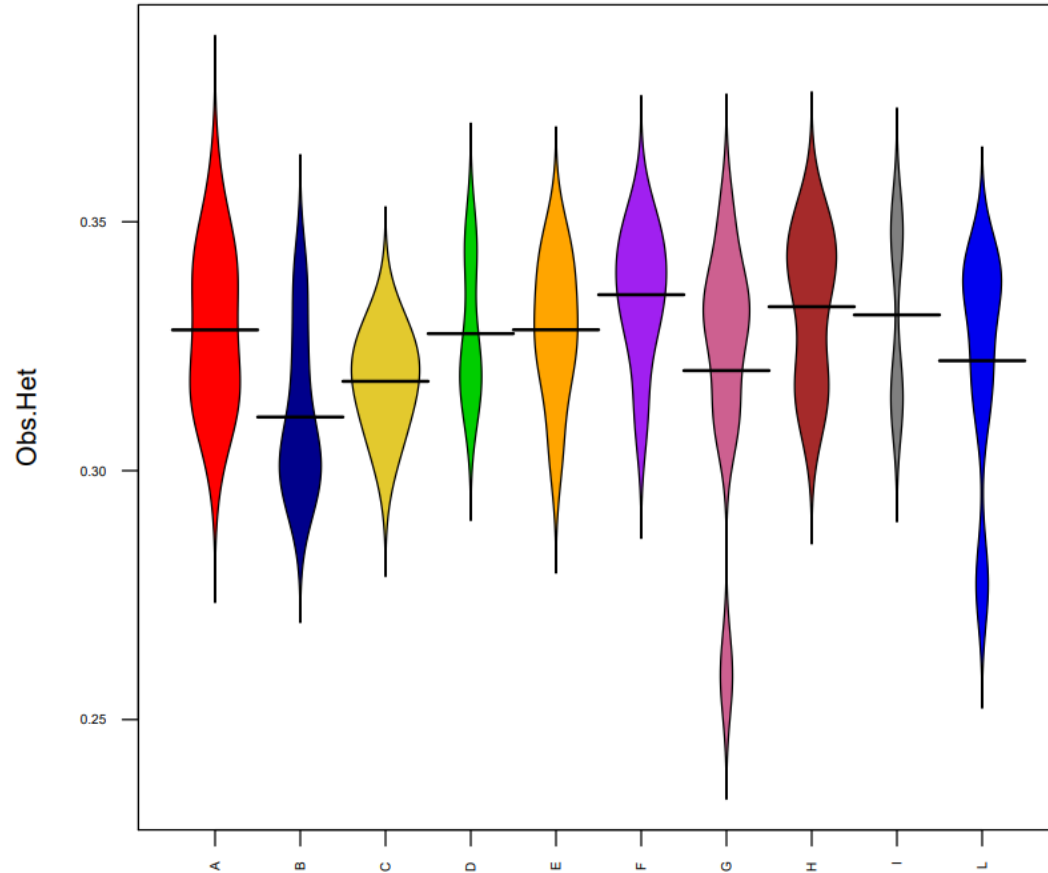


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Results: biodiversity

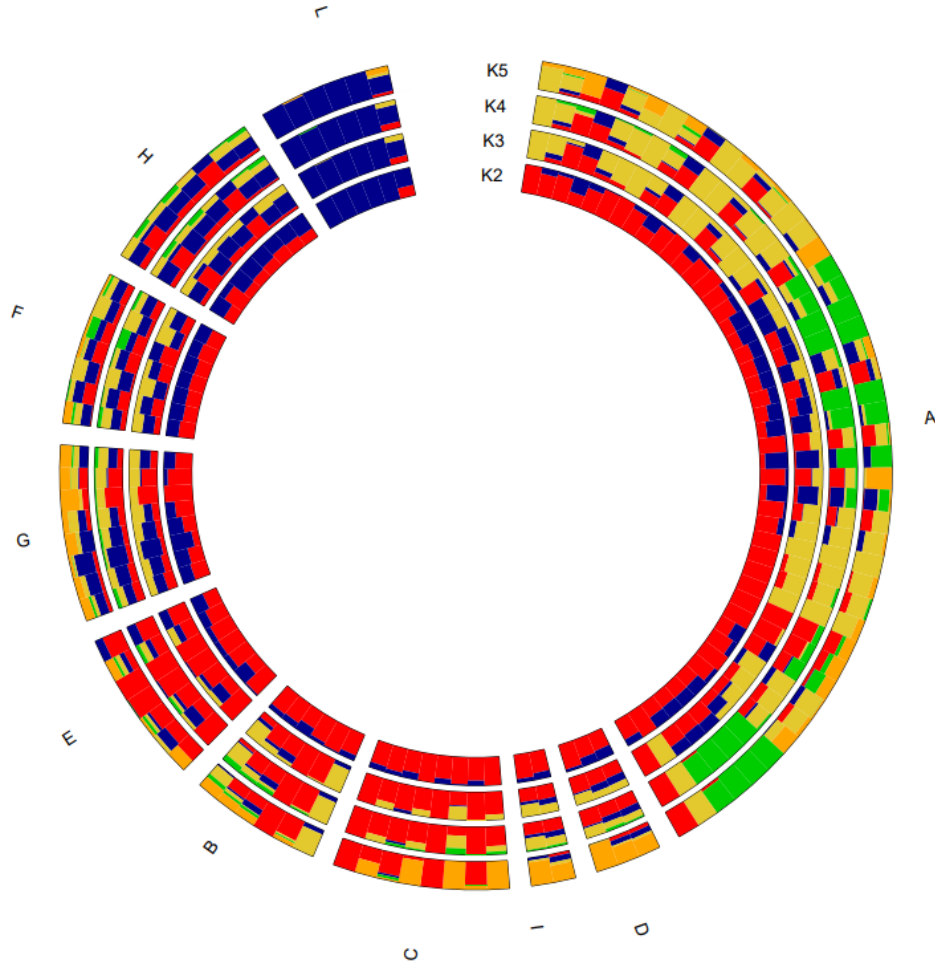
Beanplot of Observed Heterozygosity



- ✓ Median H_o around 0,32
- ✓ Higher density from 0,30 and 0,35
- ✓ High heterogeneity especially in fam **G** and **L**



Results: the admixture plot



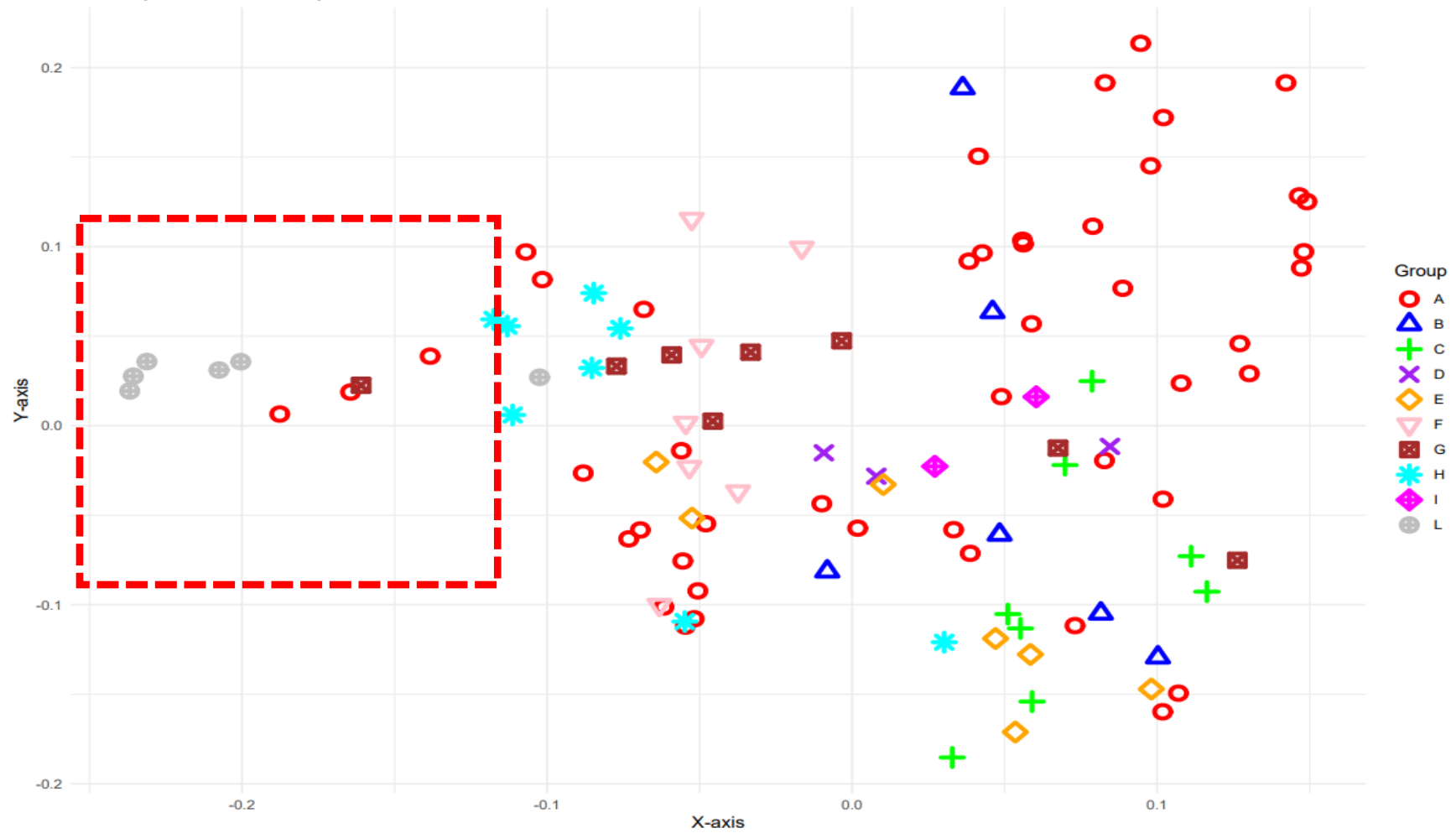
- ✓ Most likely number of $K = 5$
- ✓ Farm **A** show the highest degree of substructure
- ✓ Farm **L** is the most divergent from $k=2$
- ✓ Farm **G** and **V** diverge from $K=5$



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Results: the MDS plot

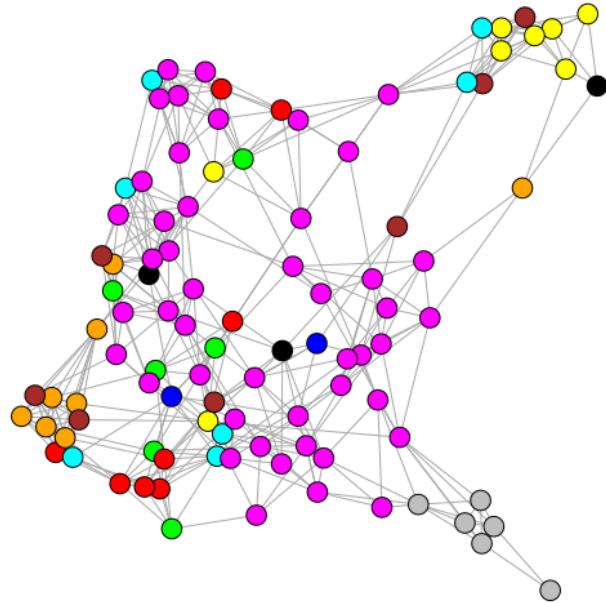


- ✓ First and second axes sum 13% of variance
- ✓ Farm A is genetically related to the whole population
- ✓ Farm L the most divergent again



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Results: the N&T&V&E&W plot



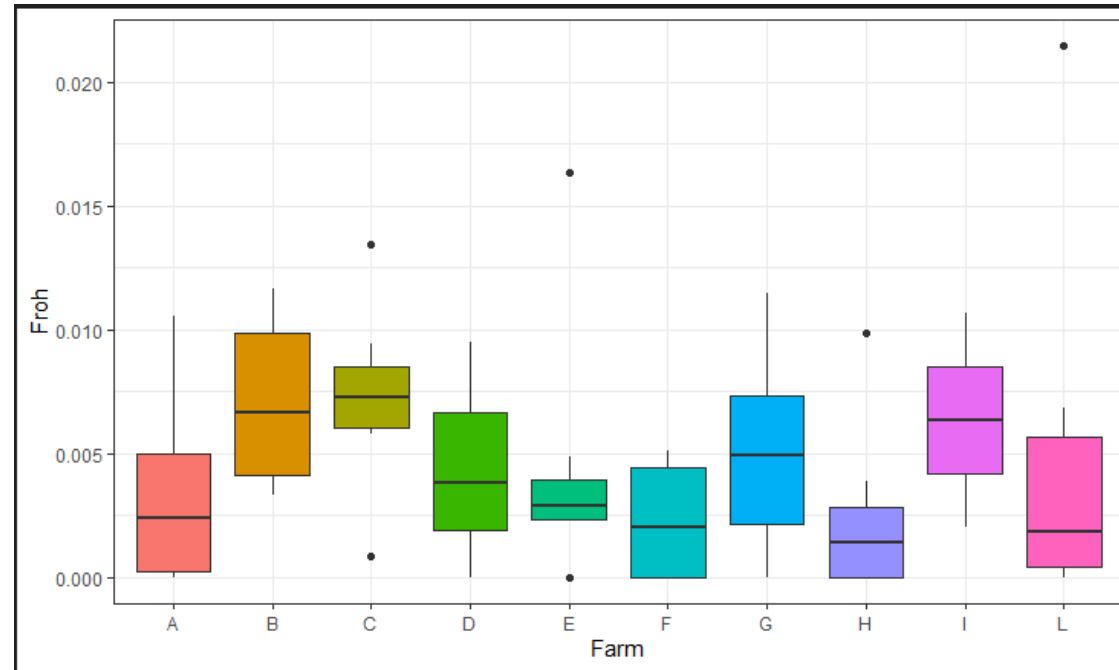
- ✓ $K=10$
- ✓ Farm **A** is genetically related to the whole population
- ✓ Farm **L** the most divergent again

FARM	COLOR
A	Magenta
B	Green
C	Orange
D	Black
E	Cyan
F	Brown
G	Yellow
H	Red
I	Blue
J	Gray



Results: the Fis and ROH

FARM	F mean
A	-0,01257
B	0,047823
C	0,014817
D	-0,01394
E	-0,01603
F	-0,03301
G	0,010093
H	-0,0218
I	-0,01071
L	0,009338



Results: the Fis and ROH

Using SeekPArentF90 whit cutoff of 2% of discordant marker on a total of 29 individual pair:

1. Total conflicts **10,3%**
2. Conflict stallion/offspring **18.2%**
3. Conflict mare/offspring **5.6%**



Conclusions

- The DDRADseq technique allows applying genomic tools even in species where there are no commercial solutions
- The results allow identifying divergent individuals that can be used for the resolution of inbreeding
- There is still a good genetic variation
- inbreeding is not very high, but some individual has very high value
- High degree of pedigree errors!





Thank for your attention!