

# Calculate relationships using pedigree and marker information - What to combine into a single estimator?

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**Why?** Implementing conservation strategies need the knowledge of **relationships** within the concerned population, for example to measure and manage *intra-breed* genetic variability



## Objective

Develop a **new method to estimate relationship** by **combining molecular with pedigree data** into a single estimator for situations, where neither pedigree nor molecular data are complete.

## Methods

### What to combine?

→ Regressions between:

- Additive relationship coefficient ( $a_{xy}$ ) and total allelic relationship ( $ta_{xy}$ )
- Wright relationship coefficient ( $r_{ped,xy}$ ) and transformed  $ta_{xy}$  ( $r_{mol,xy}$ )
- Objective: determine the influence of:
  - Inbreeding
  - Markers quality (measured by PIC)

### How to combine?

→ use of partial least square regression (SAS)

For more information: presentation 11, Session 28

How?



## Conclusions

### Inbreeding

- Has an influence on:
  - ✓ regression parameters
  - ✓ correlation value
- Use of Wright relationship coefficient did not allow to minimize this influence but decreased the SD of residuals

### Quality of marker

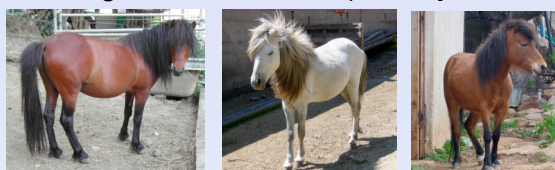
- Choose markers according to PIC is useless
  - ✓ For all parameters, no significant differences were observed when only the most informative markers were used



## Data simulation

### Parameters

- Pedigree: 20 to 25 founders born before 1907, 100 years of simulation with reproducing and living parameters close to the one of the Skyros pony (an endangered Greek breed) - **5 repetitions**



- Genotypes: 25 microsatellites with equal allele frequencies in founder population - **10 repetitions**

### Results

- Simulated pedigree:
  - ✓ 750 to 1134 animals in pedigree
  - 182 to 277 living animals in 2007
- Mean inbreeding: from 13.58 to 33.08 %  
Maximum inbreeding: from 28.03 to 45.99 %
- Simulated genotypes:
  - ✓ Mean PIC /pedigree: from 0.53 (most inbred pedigree) to 0.71 (less inbred pedigree)
  - ✓ Per marker: Minimum = 0.06 / Maximum = 0.85

## Results

### Regressions

- Equation:  $ped\_coeff = a * mol\_coeff + b$ 
  - ✓ a between 0.09 and 0.38
  - ✓ b between 0.15 and 0.22
- No significant differences between the value obtained with  $a_{xy} / ta_{xy}$  and with  $r_{ped,xy} / r_{mol,xy}$
- Significant differences between pedigree linked to differences in inbreeding level

### Correlations

- Mean correlation coefficients between pedigree and marker -based coefficient from 0.34 to 0.54
- In pedigree: Min = 0.28 / Max = 0.58
- Again, no significant differences between the value obtained between  $a_{xy} / ta_{xy}$  and between  $r_{ped,xy} / r_{mol,xy}$  and significant differences between pedigree linked to inbreeding level

### Residuals

- SD between 0.032 and 0.059
- Significant differences between the value obtained with  $a_{xy} / ta_{xy}$  and with  $r_{ped,xy} / r_{mol,xy}$  and between pedigree but not linked to inbreeding level