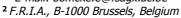
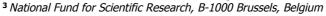
# First approaches for a combined use of microsatellites and pedigree data to estimate relationships

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# The message

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### Estimating relationships to measure and manage intra-breed genetic variability

Traditional estimation based on: **Pedigree** (often incomplete or limited in depth, very informative for close relations) **Genotypes** (very informative, expensive)

→ Combined use of pedigree and DNA information avoid losing information

# **Objective**

Estimating relationships in the Skyros pony breed by combination of DNA and pedigree information

## Methods

s Estimation of the relationships thanks to:

Lynch & Ritland (L&R) estimator

• Combined estimator  $\longrightarrow$   $Cr_{XY} = 0.5*[\underline{\omega}*r_{XY}+(2-\omega)*PIC_m*r_{XY,mol}]$ 

Weighting: depends on generation equivalent

DNA coefficient:

depends on total

allelic relationship

• Correlations (Pedigree vs. Estimation)

Principal Component Analysis (space representation of the results)

#### Reference data

Skyros pony breed

- Indigenous local breed
- 3 sub-populations
- I Preliminary studbook of the breed
- og DNA analysis of 99 hair samples





#### Results High correlation No correlation between pedigree between pedigree 0.5 coefficients and 0.4 coefficients and combined 0.3 L&R estimated 0.2 coefficients coefficients. high percentage of negative value -1.0 0.0 Lynch & Ritland relationship Combined relationship (>75%)Combined estimator L&R estimator Distinction between the 3 No real sub-populations distinction between the Few exceptions three sub-✓ Animals with descendants populations only in another sub-population of horse ✓ Animals with no descendant and parents from another sub-Green = Skyros Blue = Thessaloniki population Red = Corfu

#### **Conclusions**

 Classical DNA-based estimators assume zero relatedness between sampled individuals → often not the case in small and/or captive populations → negative values

sampled animals → reflects better the reality for small population