# Partition of genetic trend for milk yield by gender and flock in Pag sheep

#### **Ante Kasap**<sup>1</sup>, Leonarda Božulić<sup>1</sup>, Ramljak Jelena<sup>1</sup>, Mioč Boro<sup>1</sup>, Marija Špehar<sup>2</sup>

<sup>1</sup>University of Zagreb, Faculty of Agriculture, Svetošimunska 25, 10000 Zagreb, Croatia; <sup>2</sup>Croatian Agency for Agriculture and Food, Svetošimunska 25, 10000 Zagreb, Croatia









22.06.2022. | Vodice | Croatia

# Pag sheep

- Autochthonous dairy orientated breed
- HARSH ENVIRONMENT
- OUTSTANDING profitability milk (~2 €/L) cheese (~30 €/kg)

suckling lamb meat (12 €/kg)





# Pag sheep

- Breeders seek to permanently increase milk yields in their "flocks"
- Recording system (phenotypes-daily milk yield, fat and protein content and pedigree)
- BLUP genetic evaluation system
- ESTIMATED BREEDING VALUES (EBVs)





Aim -> to validate success of breeding and selection in Pag sheep -> to find main contributors to milk related genetics between flocks and genders



#### How?? Via analysis of genetic trends for milk yield

### How to decompose genetic trend on contributors??

- Calculation of selection differentials for the different paths (Van Tassell and Van Vleck, 1990) -> not a trivial task (overlapping pedigrees)
- The more sophisticated method, proposed by Garcia-Cortes et al. (2008) relies on a direct transformation of EBVs by pedigree

### AlphaPart 0.8.1. (Gorjanc et al., 2021) →

- cattle (Gorjanc et al., 2011; Gorjanc et al., 2012; Špehar et al., 2011)
- pigs (Škorput et al., 2015)
- sheep (Špehar et al., 2021)



## Materials and methods

• Test-day records → AT (ICAR) n=113,075 collected on 9,629 ewes in 21 flocks



• Covariance components & EBVs  $\rightarrow$ 

multi-trait repeatability test-day animal model (Špehar et al., 2020)

- FIXED CLASS → Parity, litter size, season of lambing, and flock
- FIXED CONTINUOUS  $\rightarrow$  days in milk and age at lambing
- RANDOM → Flock-test-day, permanent environmental effect within lactations, and direct additive genetic effect

### Material and methods

#### **Estimation of genetic trends**

• obtained as the average of  $\hat{a}$  (BVs) by birth year of animals (2010 to 2018)

#### **Decomposition of genetic trends**

•  $\hat{a}$  was partitioned by the gender and flock in R (R Core Team, 2020) with the package AlphaPart 0.8.1. (Gorjanc et al., 2021).

• 
$$\widehat{a} = TP_1T^{-1}\widehat{a} + TP_2T^{-1}\widehat{a} + \dots + TP_kT^{-1}\widehat{a}$$



### Results – decomposition of $\hat{a}$ by gender



- DMY gain = 0.0087 kg (cumulative lactation gain per year was ~1 kg)
- Females have been main contributors to overall genetic trend for DMY

### Results – decomposition of $\hat{a}$ by flock



- relative importance to the overall genetic gain was inconsistent
- non-systematic selection with changeable success between years

## Conclusions

- The estimates are a credible reflection of the true genetic change and the main contributors of genetic gain in this population
- Results implicate that females in this population have been exposed to higher selection pressure than males (**paradox**)
- Flocks included in the national genetic evaluation system had non-uniform contribution to the overall selection gain
- The results of the study should serve to:
  - 1) improve selection practices (selection of replacements on EBVs)
  - 2) demonstrate the way of monitoring trait-related genetic changes in this and similarly structured breeding programs (populations under selection)

# Thank You for Your attention

This research was funded by the Croatian Science Foundation (Genomic characterization, preservation, and optimum contribution selection of Croatian dairy sheep, OPTI-SHEEP), under grant number IP-2019-04-3559.

