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Assessing Among Flocks Genetic Diversity in Istrian Sheep to Define a Framework for Optimum Contribution Selection

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Applications of genetic diversity studies

- Preserve genetic resources
- Determine genes involved in domestication
- Selection of parents for a breeding program
- Establish effective breeding methods

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The research supported by Croatian Science Foundation. Project: *Genomic characterization, preservation, and optimum contribution selection of Croatian dairy sheep (OPTI-SHEEP). Grant number IP-2019-04-3559.*

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Measures of genetic diversity

- Observed heterozygosity (H_o)
- Expected heterozygosity (H_e)
- Wright's *F* statistic (F_{ST})
- Linkage disequilibrium (LD)
- Runs of homozygosity (ROH)
- Effective population size (N_e)
- …

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Objective

- To analyse genetic diversity between and within flocks of Istrian sheep

- Implementation of optimum contribution selection

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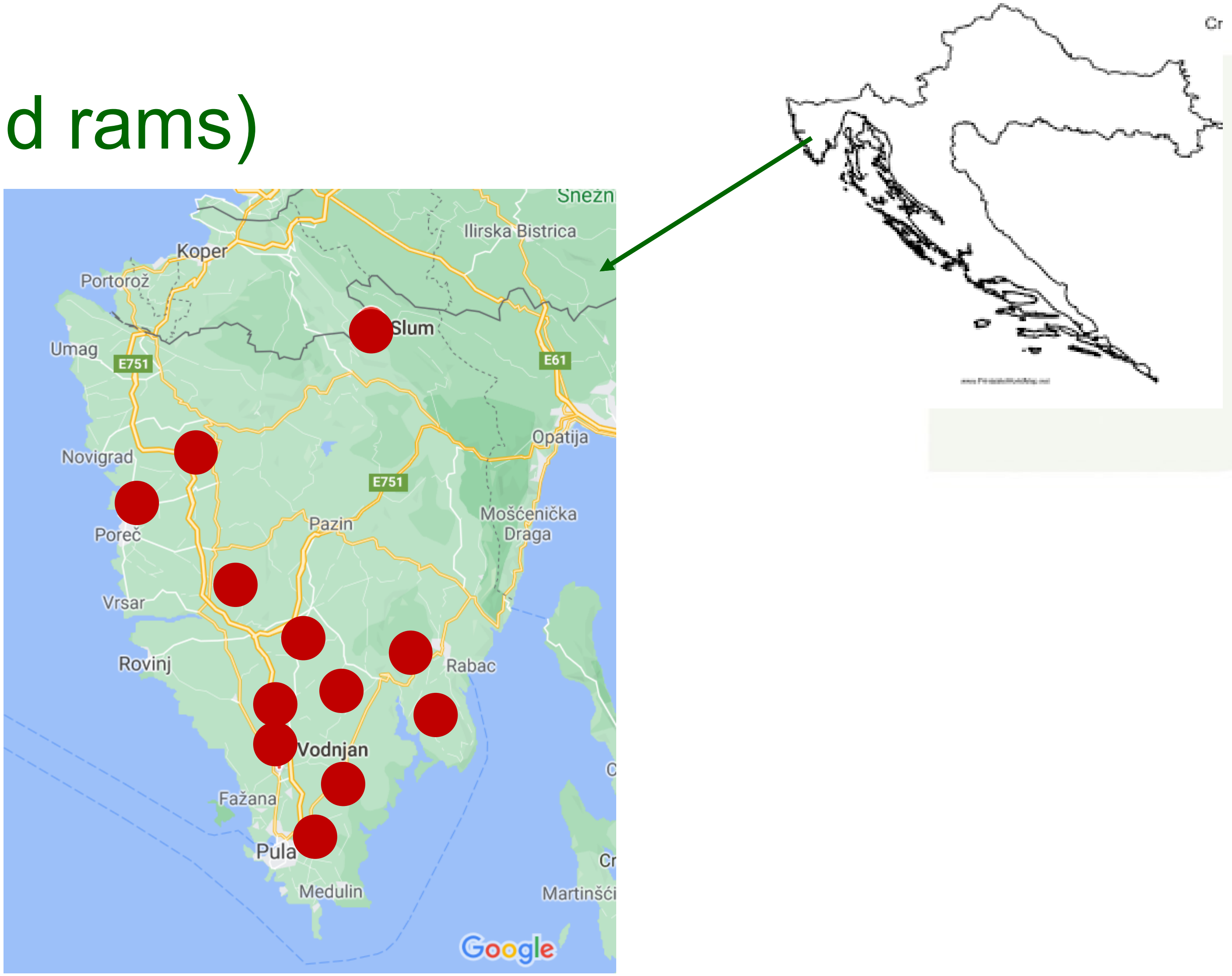
Material

- 719 animals (ewes and rams)
  - Milk recording (ICAR)
  - Pedigree BLUP
  - From 12 flocks



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Material cont.

- Illumina OvineSNP50K BeadChip® v.2 (52,152 SNPs)
- Quality control
  - autosomal SNPs only
  - SNP and individual genotype call rate > 0.90
  - **47,793 SNPs**

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Method

- Calculation of genomic population parameters
  - snpReady

- Post hoc statistical analysis
  - ggplot

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Results

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Genetic diversity parameters

- Expected heterozygosity (H_E) → 0.357
- Observed heterozygosity (H_O) → 0.332
- Inbreeding coefficient (F) → 0.07

Italian Journal of Animal Science

ISSN: (Print) (Online) Journal homepage: https://www.tandfonline.com/loi/tjas20

Estimation of genetic parameters and the effect of inbreeding on dairy traits in Istrian sheep

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To cite this article: Marija Špehar, Jelena Ramljak & Ante Kasap (2022) Estimation of genetic parameters and the effect of inbreeding on dairy traits in Istrian sheep, Italian Journal of Animal Science, 21:1, 331-342, DOI: 10.1080/1828051X.2022.2031320

To link to this article: https://doi.org/10.1080/1828051X.2022.2031320

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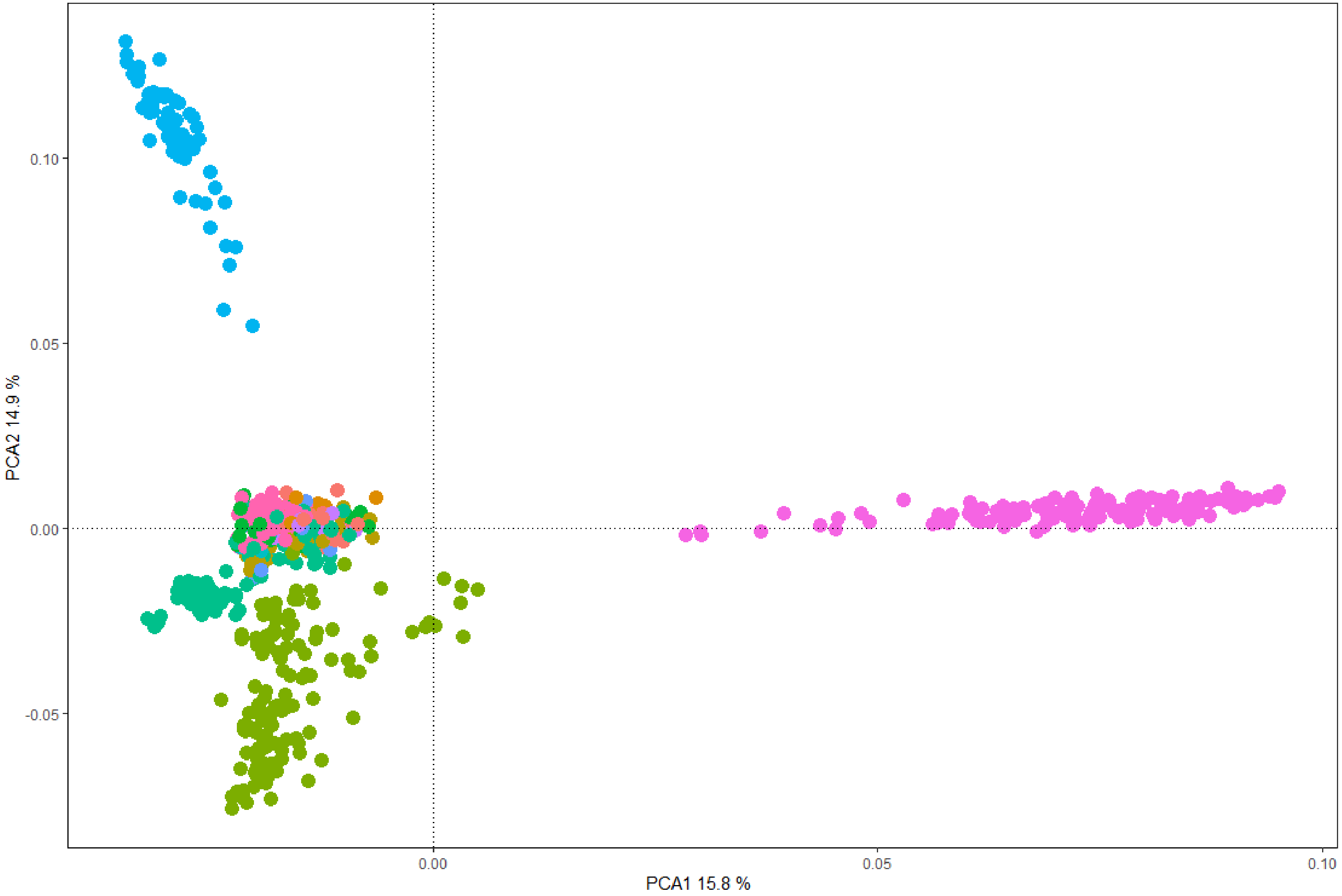
Pair-wise genetic differentiation among flocks

	IST2	IST3	IST4	IST5	IST6	IST7	IST8	IST9	IST10	IST11	IST12
IST1	0.088	0.081	0.33	0.046	0.087	0.077	0.058	0.104	0.129	0.138	0.219
IST2		0.102	**0.413**	0.028	0.096	0.117	0.055	0.189	0.189	0.16	0.283
IST3			0.366	0.04	0.09	0.085	0.057	0.124	0.149	0.147	0.245
IST4				0.342	0.282	0.405	0.307	0.405	0.372	0.29	0.369
IST5					0.069	**0.016**	0.027	0.059	0.106	0.129	0.218
IST6						0.09	0.073	0.105	0.12	0.131	0.19
IST7							0.047	0.154	0.172	0.155	0.274
IST8								0.072	0.103	0.124	0.197
IST9									0.195	0.163	0.28
IST10										0.167	0.262
IST11											0.214

Average pair-wise genetic differentiation (F_{ST}) among flocks = **0.194**

Principal component analysis



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Conclusions

- Preserved substantial amount of genetic diversity
- Moderate level of inbreeding
- Separation of three flocks / overlaping of the rest
- Contribution to design appropriate and successful genomic selection program

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Future work

- Ongoing genotyping
- Estimation of signals of selection for dairy traits
- Genetic profile and relationship with another breeds
- SS GBLUP (developed on basic level but not implemented in routine genetic evaluation)
- GWAS for dairy traits

Thank You For Listening

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