Increasing Effective Population Size by Strengthening Genetic Connectedness Between flocks: Case Study on Pag Sheep Breed

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22.09.2022. | Zadar | Croatia

Pag sheep

- Croatian Autochthonous breed
- Population size ~ 30,000
- DAIRY orientated breed (wool)
- HARSH environment
  (“BURA” > 200 km/h)
- Forage enriched with sea salt
- Exotic Aromatic plants

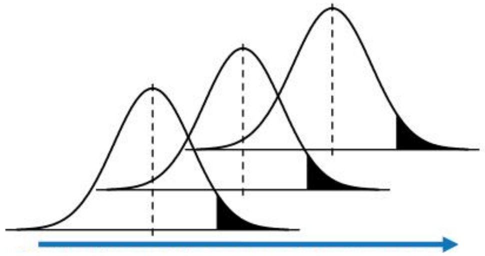
Pag sheep

- Modest milk yield ~ 0.8 Kg/day
  (120 kg in 5 months of milking)

- OUTSTANDING profitability
  fresh milk (~2 €/L) – no surpluses
  cheese (30-40 €/kg)
  curd cheese (8 €/kg)
  fresh meat (~12 €/kg)

Pag sheep

- Aim → to increase milk yield



- Selection ~ 4,500 sheep
- Pedigree records
- Milk control (ICAR)
- Pedigree BLUP → Genomic Sel.

$$\begin{bmatrix} \mathbf{b} \\ \mathbf{a} \end{bmatrix} = \begin{bmatrix} \mathbf{X'X} & \mathbf{X'Z} \\ \mathbf{Z'X} & \mathbf{Z'Z+A^{-1}\lambda} \end{bmatrix}^{-} \begin{bmatrix} \mathbf{X'y} \\ \mathbf{Z'y} \end{bmatrix}$$

Numerator relationship matrix

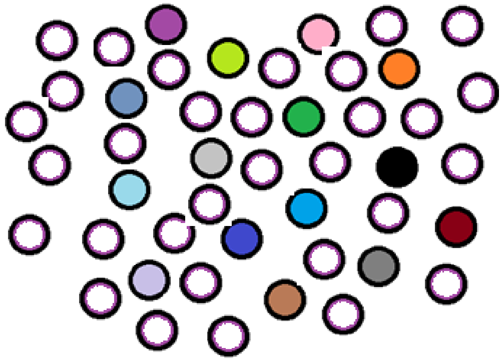
Long term goal – Genomic OCS

- Single step GBLUP (Aguilar et al., 2010.)

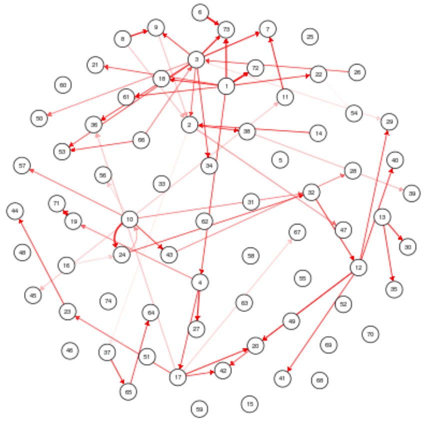
$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & G^{-1} - A_{22}^{-1} \end{bmatrix}$$

- ~1735 Genotyped animals (illumina 50K SNP ovine bead chip)

Aims of the study



1) **Effective population size (*N_e*)** → Consesrvation



2) **Connectedness** between flocks → Unbiased BLUP

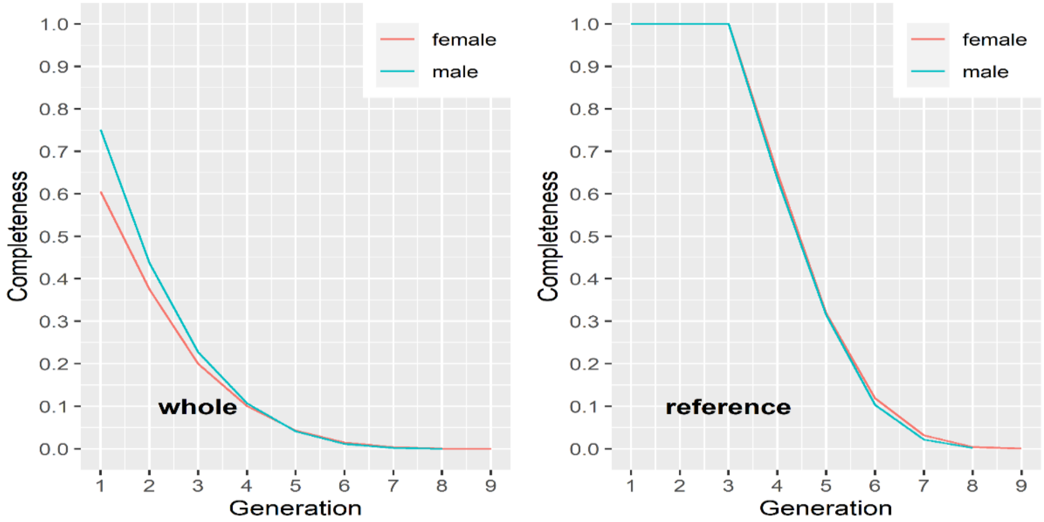
3) **Relationship** between **connectedness** and ***N_e***

Hmm!! Is there relationship between these parameters???
Can **connectedness** contribute to genetic **variability** ???

Materials and methods - pedigree

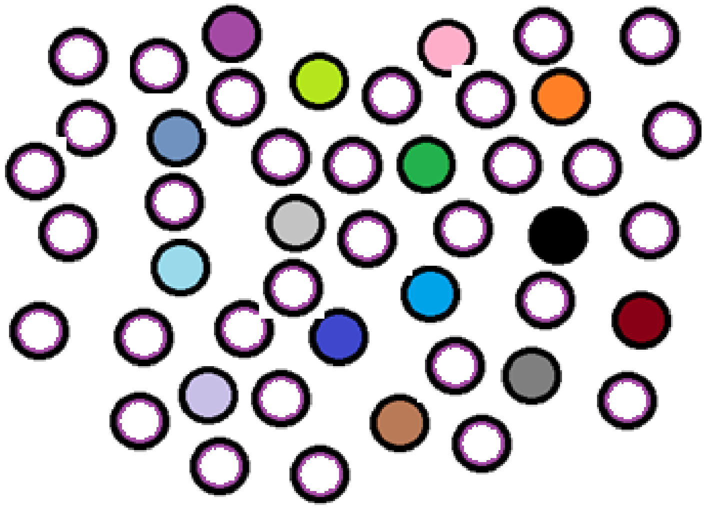
- Data (pedigree, flock) → CMA
- Pedigree → n=10451, 74 flocks (coancestry)
- Pedigree QC→ **NEG, NFG, NMG, PCI**
- **Reference population for (N_e) →**

  NFG≥3 & born 2008 – 2018



	stati.	NEG	NFG	NMG	PCI
Whole population	max	5.74	4.00	9.00	1.00
	median	1	1.00	2.00	0.25
	mean	1.36	0.89	2.26	0.29
Reference population	max	5.74	4.00	9.00	0.97
	median	4.09	3.00	6.00	0.79
	mean	4.12	3.05	6.39	0.79

Materials and methods – N_e

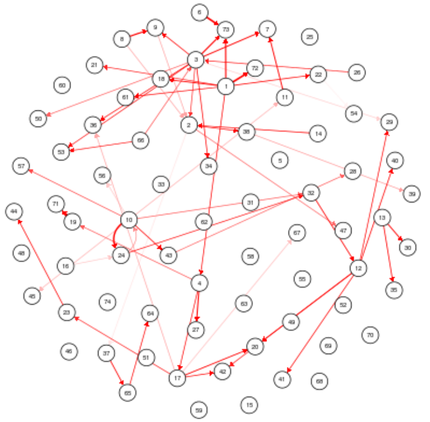


- R package “optiSel” (Wellman, 2021)
- $\boldsymbol{N_e}$ → mean rate of increase in coancestry (Cervantes et al., 2011):

$$N_e = \frac{1}{2\overline{\Delta C}} \; ; \; \Delta C_{ij} = 1 - \sqrt[\frac{g_i+g_j}{2}]{1 - C_{ij}}$$

- Sliding window approach (4 year)→
- $\boldsymbol{N_{e\,(2008-2011,\ldots,2015-2018)}} = \boldsymbol{N_{e\,(1,\ldots,8)}}$
- $\Delta \boldsymbol{N_e}$ → regression of $\boldsymbol{N_{e\,(1,\ldots,8)}}$ on $\boldsymbol{GI_{(1,\ldots,8)}}$

Materials and methods - Connectedness



- ***PEVD*** - (Kennedy and Trus, 1993)

- $PEVD(\hat{u}_i\text{-}\hat{u}_j) = \left[PEV(\hat{u}_i) + PEV\left(\hat{u}_j\right) - 2PEC\left(\hat{u}_i, \hat{u}_j\right)\right] = \left(C_{ii}^{22} - C_{ij}^{22} - C_{ji}^{22} - C_{jj}^{22}\right) * \sigma_e^2$
- $PEVD_{i'j'} = \frac{1}{n_{i'} * n_{j'}} \sum PEVD_{i'j'}$

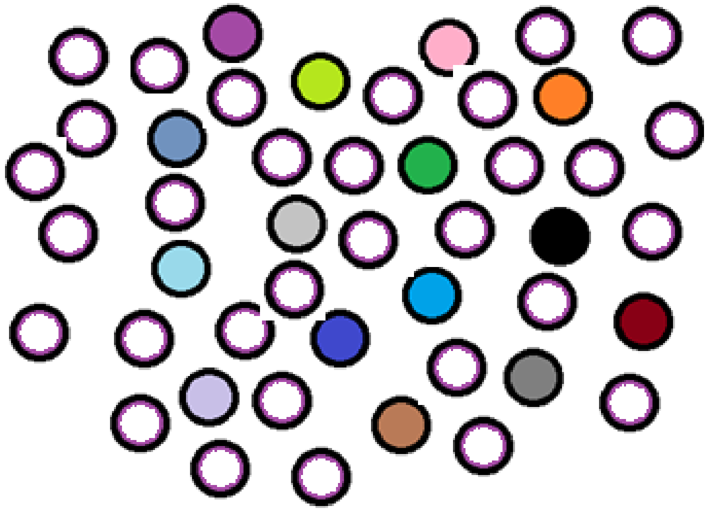
- R package "GCA" (Yu and Morota, 2021)

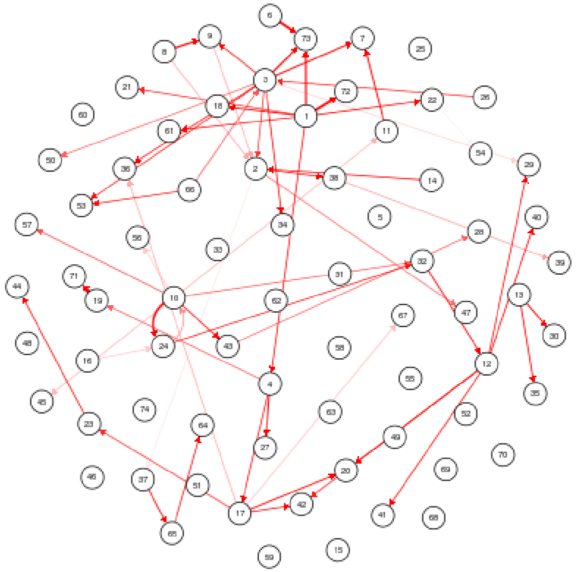
- The sliding window→ $\overline{\boldsymbol{PEVD}_{\boldsymbol{i',j'}\ \mathbf{(2008-2011,\ldots,2015-2018)}}}$ = $\overline{\boldsymbol{PEVD}_{\boldsymbol{i',j'}\ \mathbf{(1,\ldots,8)}}}$

- $\overline{\boldsymbol{\Delta PEVD}_{\boldsymbol{i',j'}}}$ → Regression of $\boldsymbol{PEVD}_{\boldsymbol{i',j'}\ \mathbf{(1,\ldots,8)}}$ on $\boldsymbol{GI}_{\mathbf{(1,\ldots,8)}}$

Materials and methods: Connectedness ←→$\boldsymbol{N_e}$

- Regression of $\boldsymbol{N_{e\,(1,\ldots,8)}}$ on $\boldsymbol{PEVD_{i',j'\,(1,\ldots,8)}}$



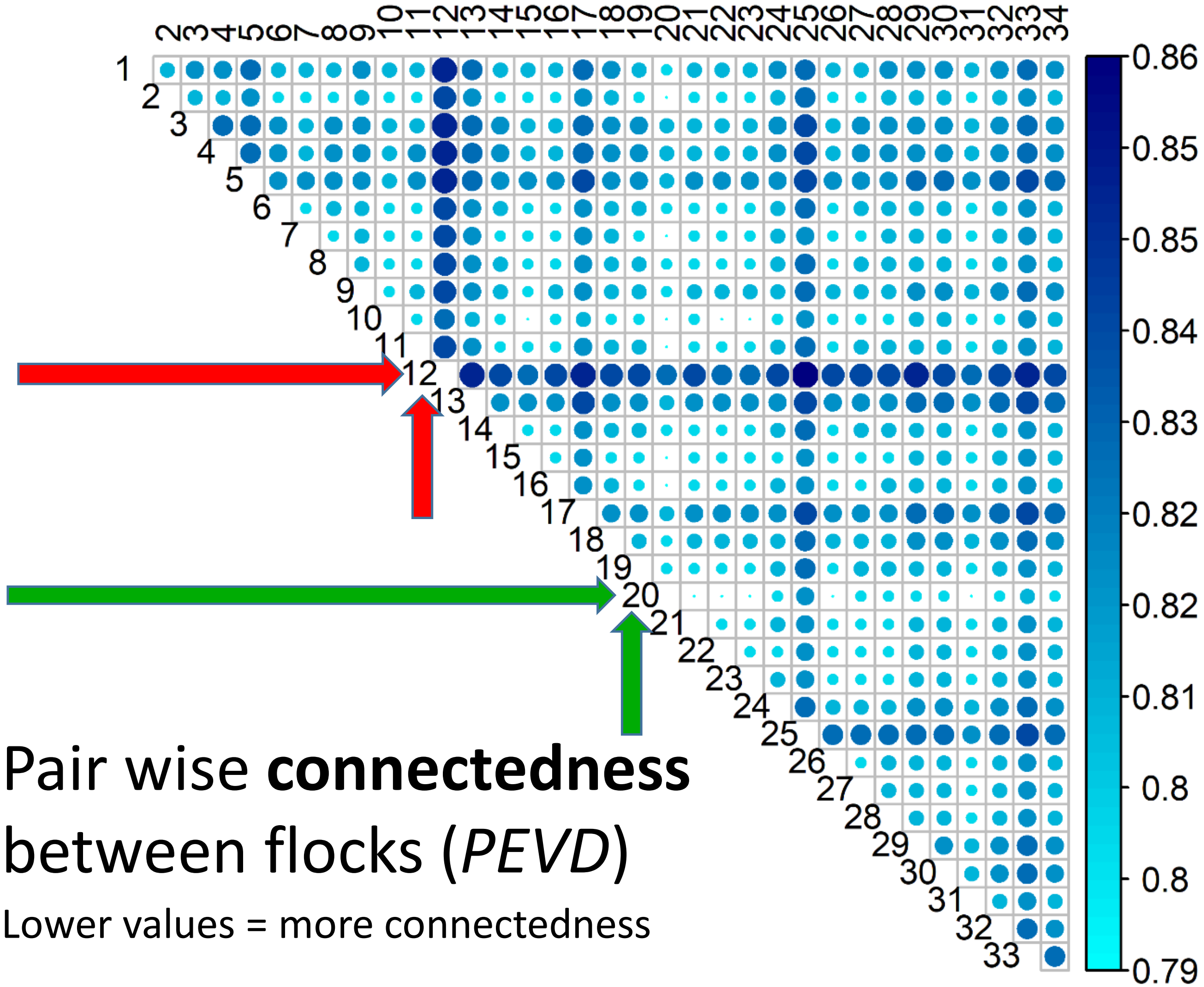


Results (1): *Effective population size (N_e)*

GI (Years)	N_{ref}	$\overline{\Delta C}$	N_e	N_e/N_{ref}
8 (2008-2011)	1833	0.0096	52	0.03
7 (2009-2012)	1703	0.0083	60	0.04
6 (2010-2013)	1721	0.0069	73	0.04
5 (2011-2014)	1700	0.0066	76	0.04
4 (2012-2015)	1719	0.0058	86	0.05
3 (2013-2016)	1740	0.0050	100	0.06
2 (2014-2017)	1715	0.0043	117	0.07
1 (2015-2018)	1457	0.0039	127	0.09

ΔN_e~11 animals

Results (2) - *Connectedness (PEVD)*



Pair wise **connectedness** between flocks (*PEVD*)

Lower values = more connectedness

$PEVD_{i\prime,j\prime(min)}$ = 0.77

$PEVD_{i\prime,j\prime(max)}$ = 0.86

$\overline{PEVD_{i\prime,j\prime}}$ = 0.81

$\overline{PEVD_{20,j\prime}}$ = 0.80

$\overline{PEVD_{12,j\prime}}$ = 0.84

Result (3): *Connectedness (PEVD)* ←→ $\boldsymbol{N_e}$

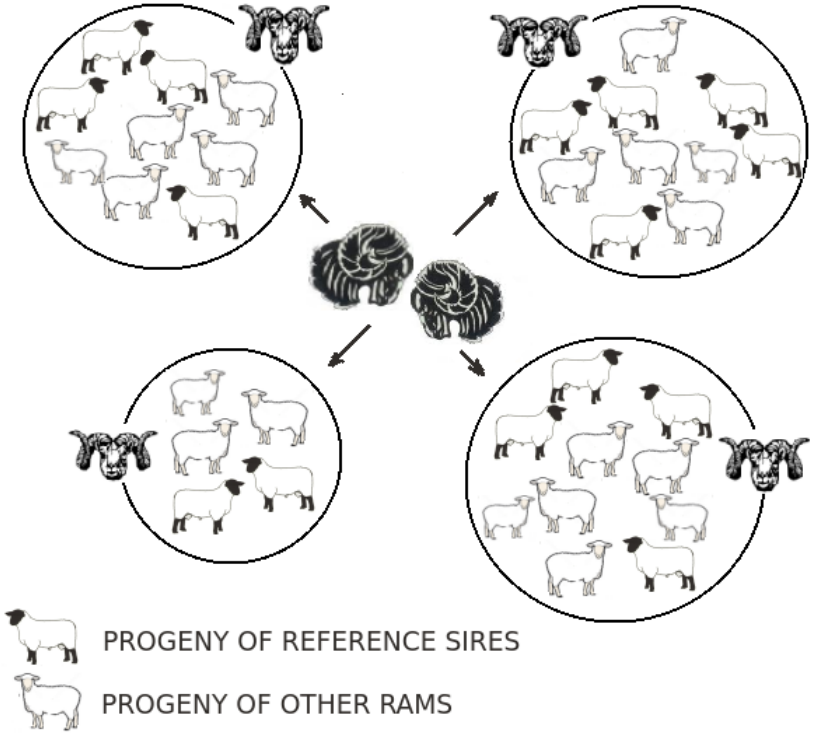
- Regression of $\boldsymbol{N_{e\,(1,\ldots,8)}}$ on $\boldsymbol{PEVD_{i',j'\,(1,\ldots,8)}}$ →

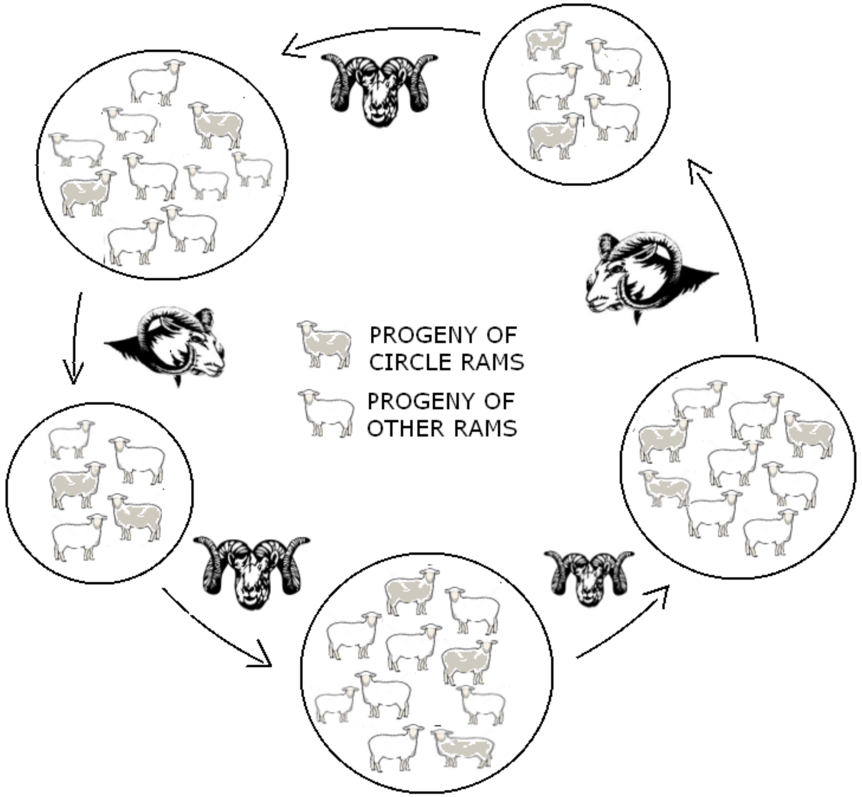
$\overline{\Delta PEVD_{i',j'}}$ - 0.01 = ΔN_e + 5.5 animals (*P*=0.054)

- **CONNECTEDNESS** ←⊕→ $\boldsymbol{N_e}$ in Pag sheep population

Discussion

- Positive ΔN_e→ surprising !!! Breeders avoid inbreeding → OCS
- **Connectedness** → insufficient for many flocks (BIAS)→ SRS, RR





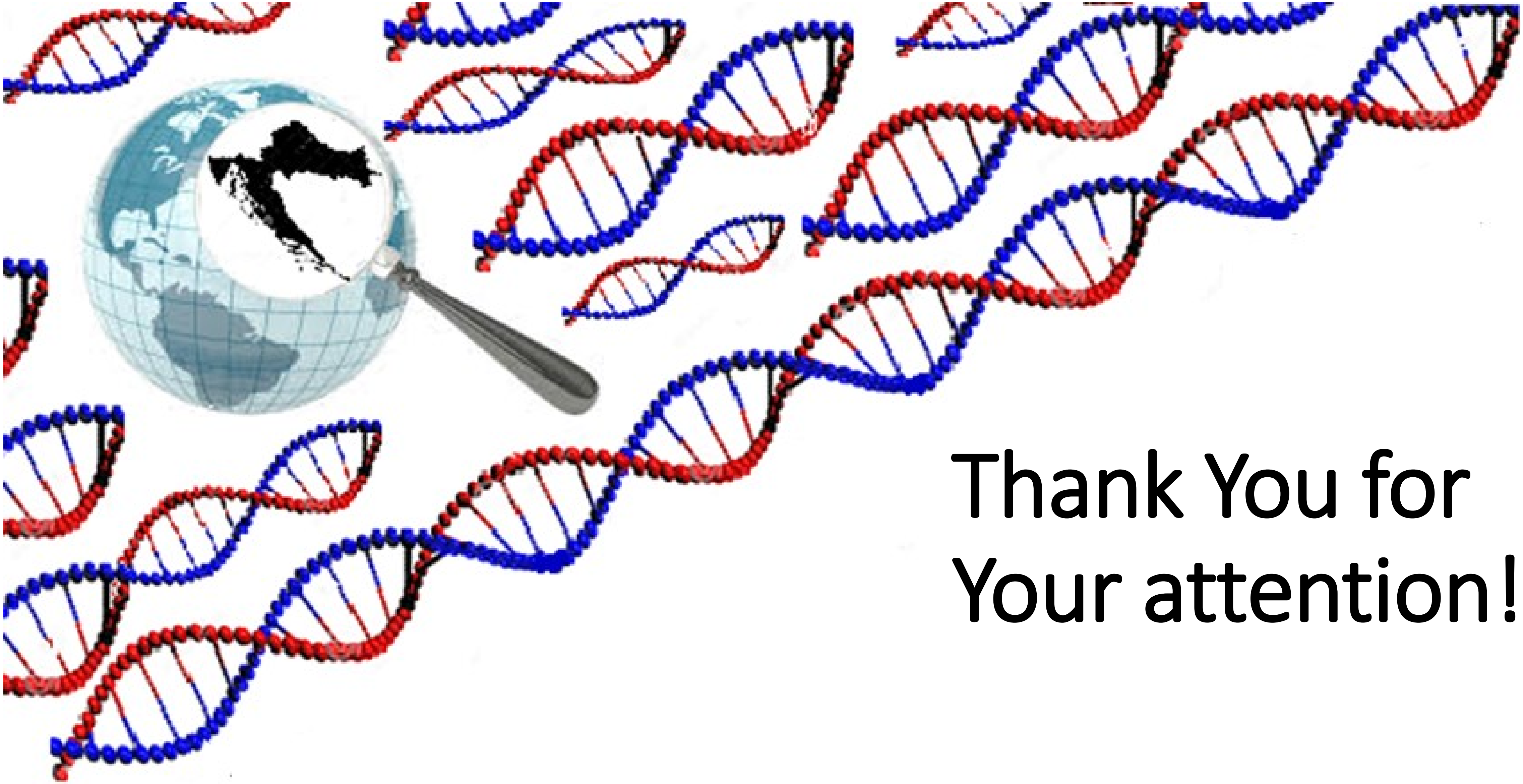
Discussion

- **First** insight into relationship between rate of **connectedness** and $\boldsymbol{N_e}$
- Discrepancy in number of animals used in estimation of partial **connectedness** and $\boldsymbol{N_e}$→ **inconclusive** relationship
- The result is **logical** (the more exchange of animals between flocks, the more “shuffling” of the genome in the population)

Conclusions

- The “**candidate**” relationship between connectedness and effective population size should be additionally investigated, preferably under the framework of genomics.

- The Pag sheep breed has Good perspective for implementation of **OCS**, but in order to exploit all the available genetic pool of the breed, more efforts should be made to provide connectedness.



Thank You for Your attention!

Acknowledgements: To Croatian Science Foundation for funding this research (project OPTI-SHEEP, grant number IP-2019-04-3559).