Genomic connectedness between flocks – case study on Istrian sheep breed

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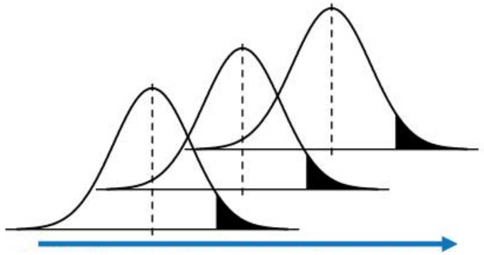
Istrian sheep

- Fancy look (Roman nose, horns, colour)
- Importance (economy, tradition & culture, tourism, gastronomy, ecology)

Istrian sheep

- Dual purpose (milk & meat)



- Selection ~ 11 flocks, 1.5K sheep
- Pedigree & phenotypic records
- Milk control (ICAR)

- BLUP_{ped}

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

Numerator relationship matrix

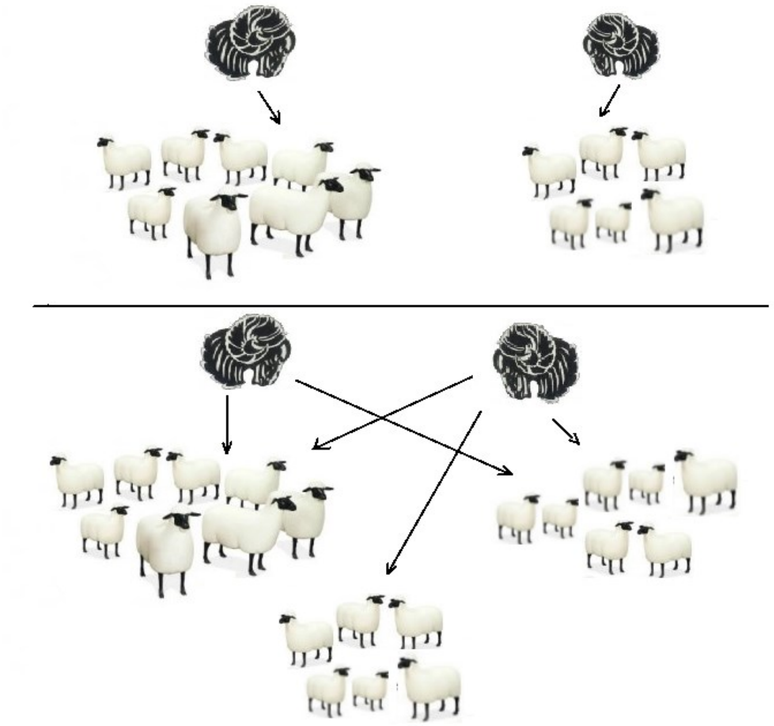
Optimum contribution selection (OCS)

- Single step Genomic BLUP
- 50K SNP array

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

BLUP is good, BLUP if funny, everybody "BLUPs" for MONEY !!

Disconnected flocks !!!!



Connected

BLUP

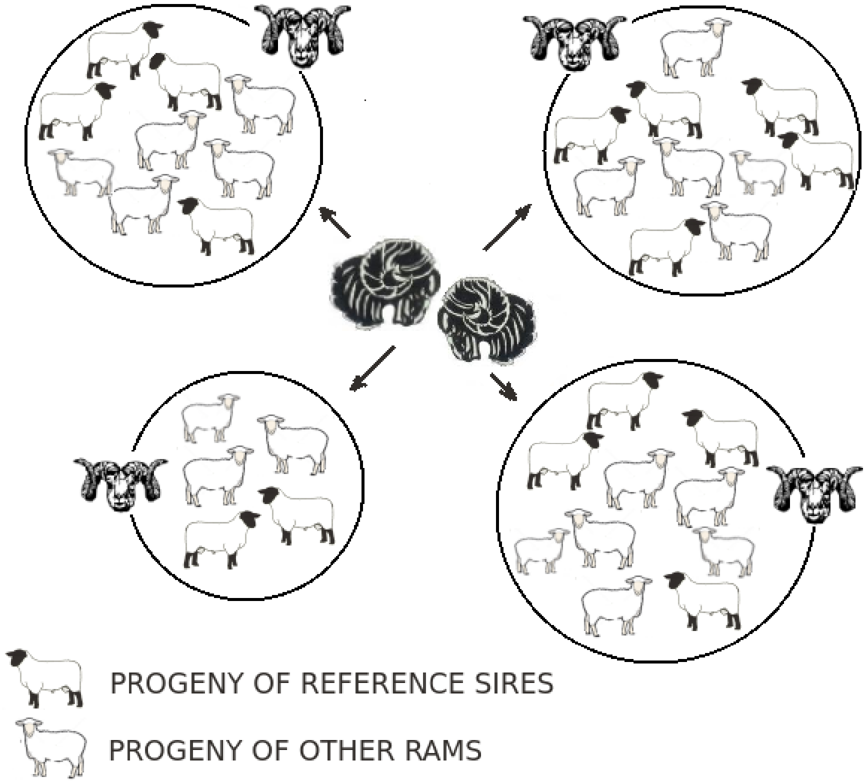
BLUP

The issue of dissconectedness:

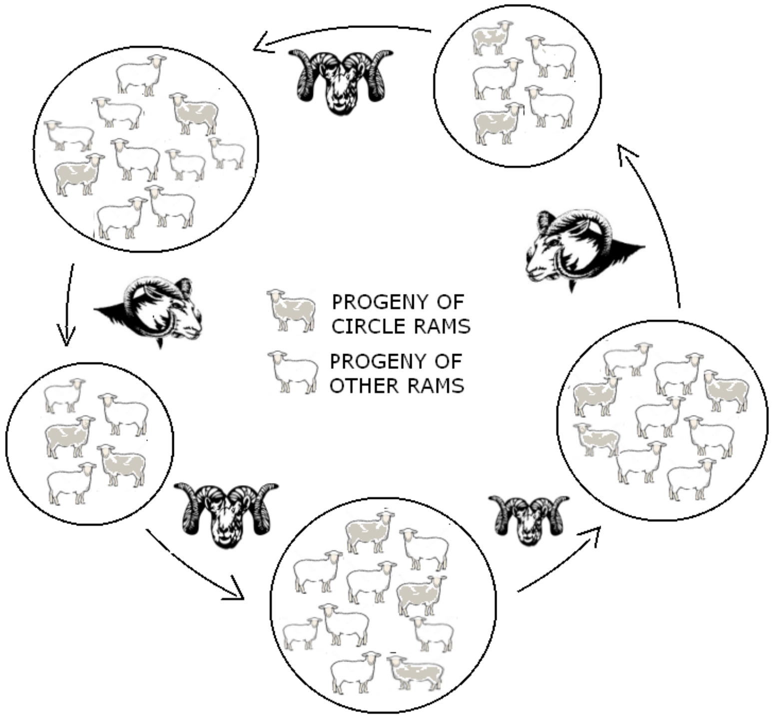
- Neglected in some breeding programs. BLUP is not MAGIC!!!
- Impossible to disentangle genetic from environmental effects
- Small ruminants and beef cattle NO/limited use of AI

Strategies for connectedness

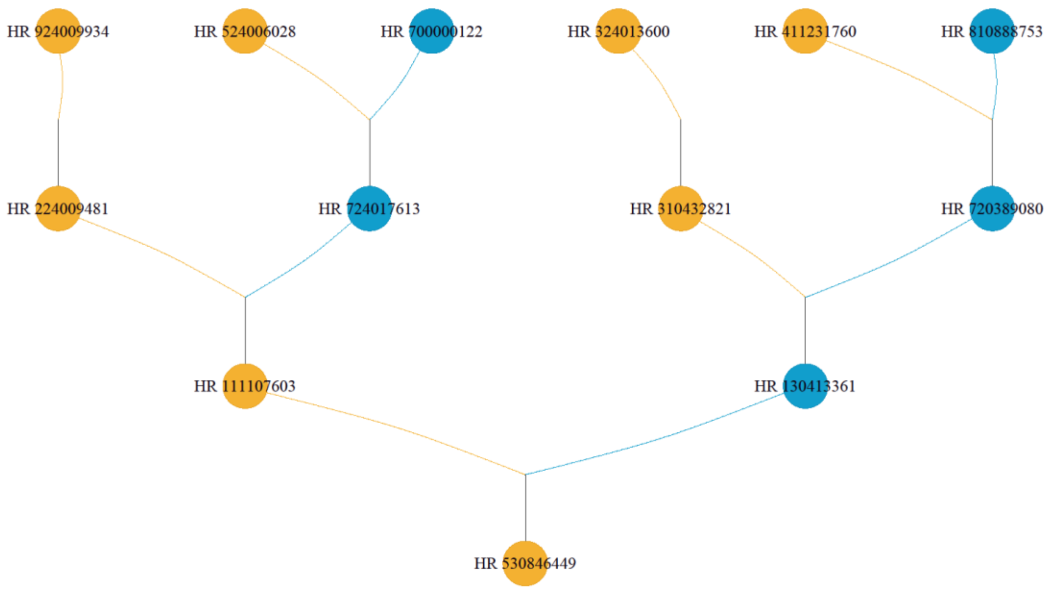
Sire referencing scheme

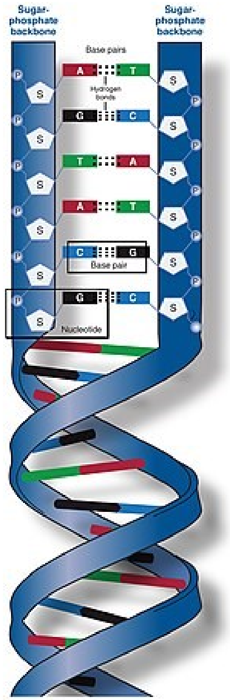


Circle rams



Can **genomic information** (SNPs) detect hidden relationships between animals in different flocks???

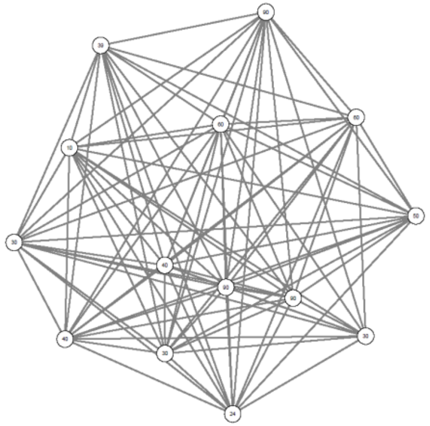




Materials and methods (n_{ped}~2000, n_{gen}=719)

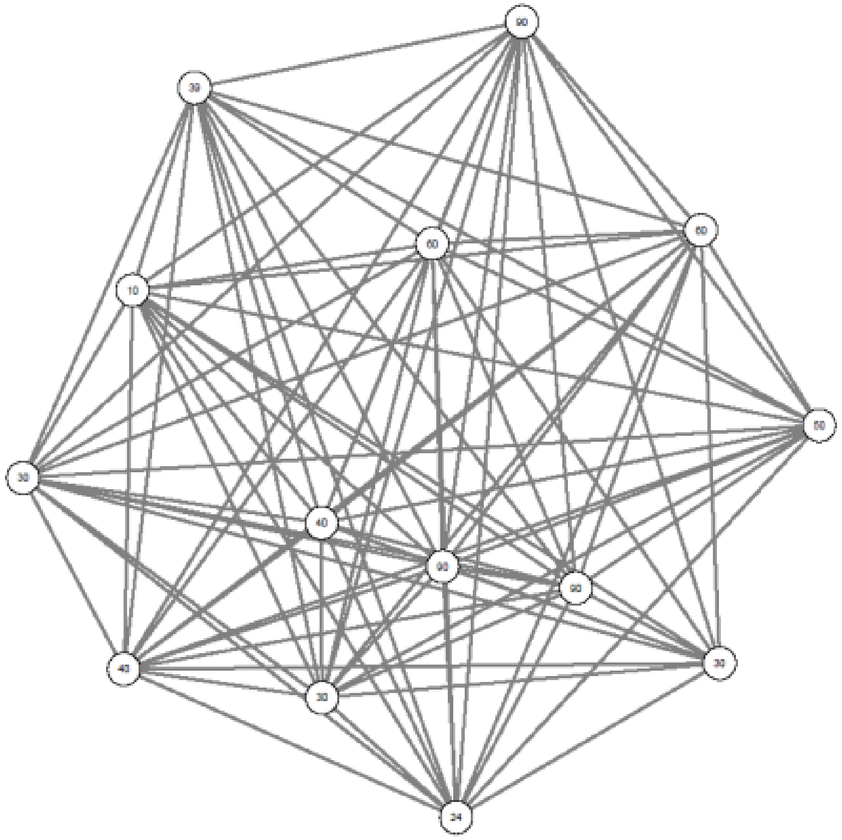
- ***PEVD*** - (Kennedy and Trus, 1993)
- $PEVD(\hat{u}_i\text{-}\hat{u}_j) = \left[PEV(\hat{u}_i) + PEV(\hat{u}_j) - 2PEC(\hat{u}_i, \hat{u}_j)\right] = \left(C_{ii}^{22} - C_{ij}^{22} - C_{ji}^{22} - C_{jj}^{22}\right) * \sigma_e^2$
- $PEVD_{i'j'} = \frac{1}{n_{i'} * n_{j'}} \sum PEVD_{i'j'}$

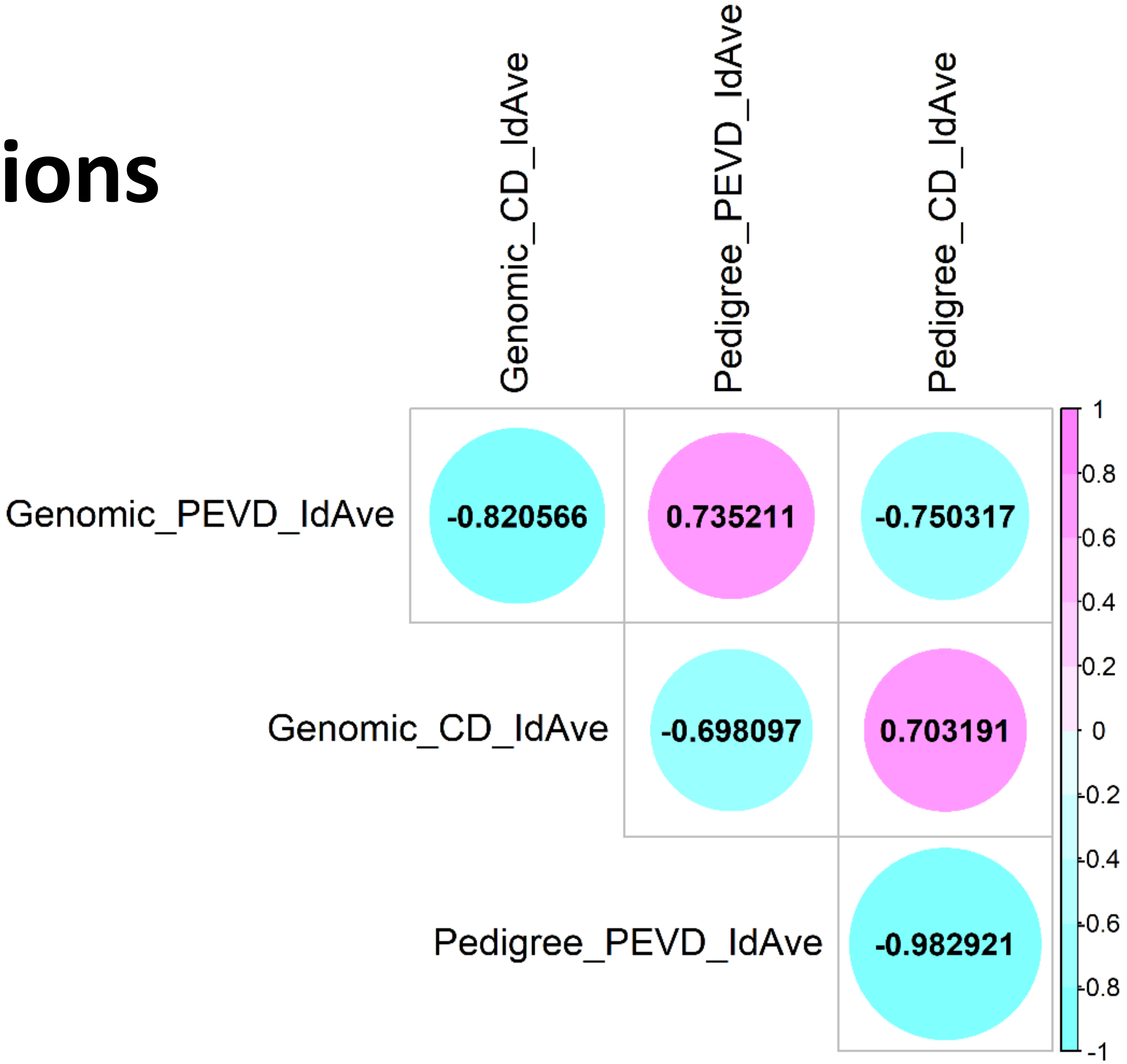
- ***CD*** - (Laloe, 1993)
- $CD_{ij} = 1 - \lambda \frac{C_{ii}^{22} + C_{jj}^{22} - 2C_{ij}^{22}}{K_{ii} + K_{jj} - 2K_{ij}}$
- $CD_{i'j'} = 1 - \lambda * \frac{\frac{1}{n_{i'} * n_{j'}} * \sum\left(C_{i'i'}^{22} + C_{j'j'}^{22} - 2C_{i'j'}^{22}\right)}{\frac{1}{n_{i'} * n_{j'}} * \sum(K_{i'i'} + K_{j'j'} - 2K_{i'j'})} = 1 - \frac{\sum PEVD_{i'j'}}{\sigma_u^2 * \sum(K_{i'i'} + K_{j'j'} - 2K_{i'j'})}$



- R package “GCA” (Yu and Morota, 2021)

Results - correlations

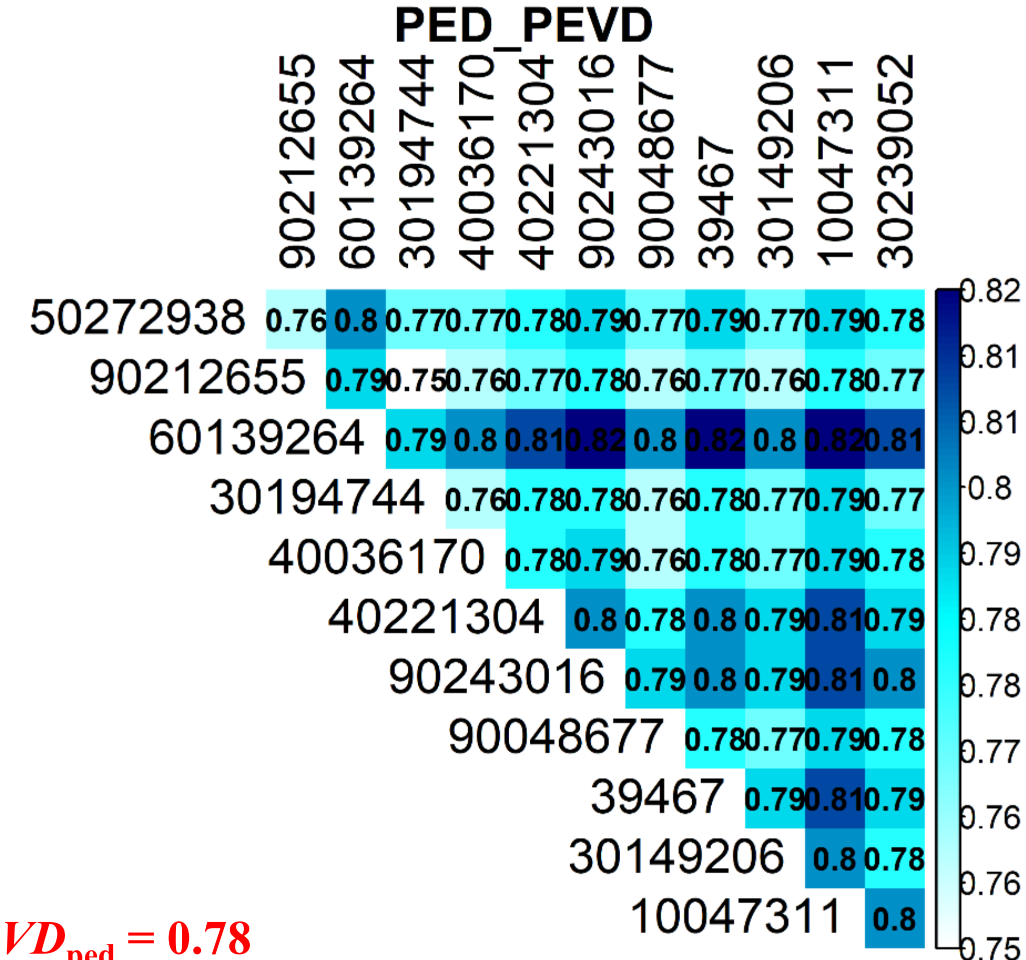




	Genomic_CD_IdAve	Pedigree_PEVD_IdAve	Pedigree_CD_IdAve
Genomic_PEVD_IdAve	-0.820566	0.735211	-0.750317
Genomic_CD_IdAve		-0.698097	0.703191
Pedigree_PEVD_IdAve			-0.982921

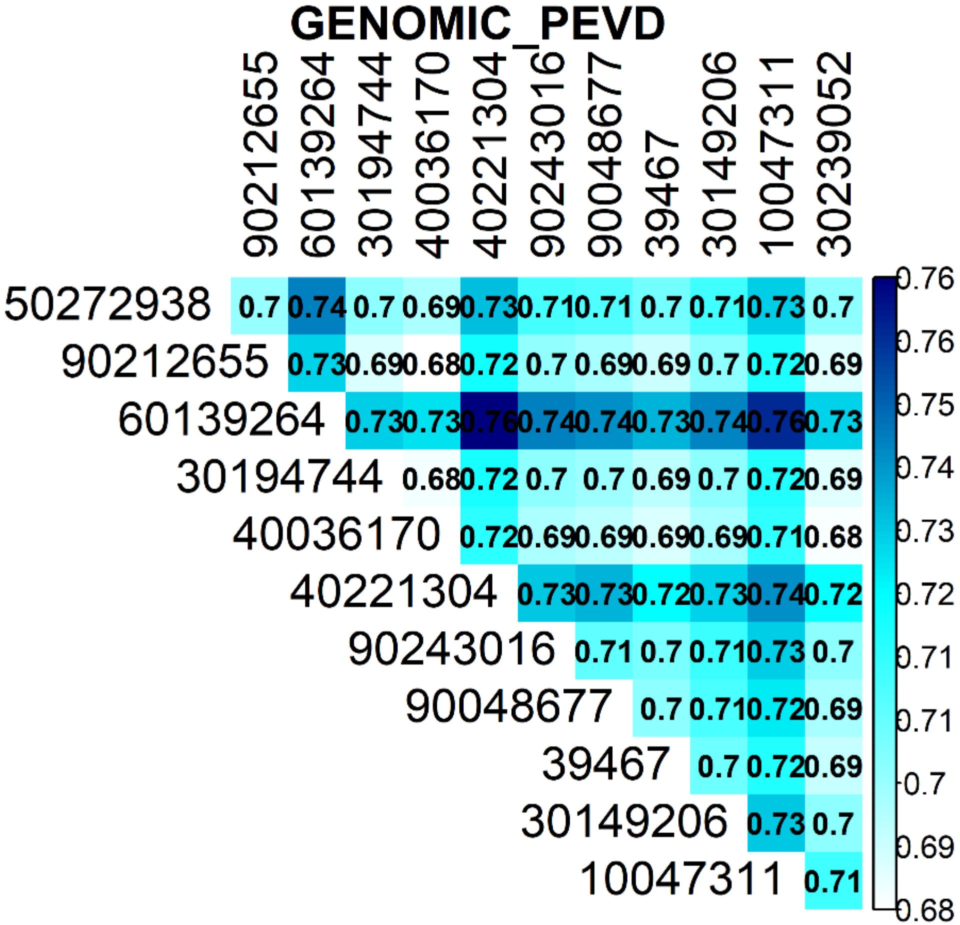
Results – PEVD → lower is better

$\Delta PEVD_{ped \rightarrow gen} = -10\%$


PED_PEVD

	90212655	60139264	30194744	40036170	40221304	90243016	90048677	39467	30149206	10047311	30239052
50272938	0.76	0.8	0.77	0.77	0.78	0.79	0.77	0.79	0.77	0.79	0.78
90212655		0.79	0.75	0.76	0.77	0.78	0.76	0.77	0.76	0.78	0.77
60139264			0.79	0.8	0.81	0.82	0.8	0.82	0.8	0.82	0.81
30194744				0.76	0.78	0.78	0.76	0.78	0.77	0.79	0.77
40036170					0.78	0.79	0.76	0.78	0.77	0.79	0.78
40221304						0.8	0.78	0.8	0.79	0.81	0.79
90243016							0.79	0.8	0.79	0.81	0.8
90048677								0.78	0.77	0.79	0.78
39467									0.79	0.81	0.79
30149206										0.8	0.78
10047311											0.8

$PEVD_{ped} = 0.78$

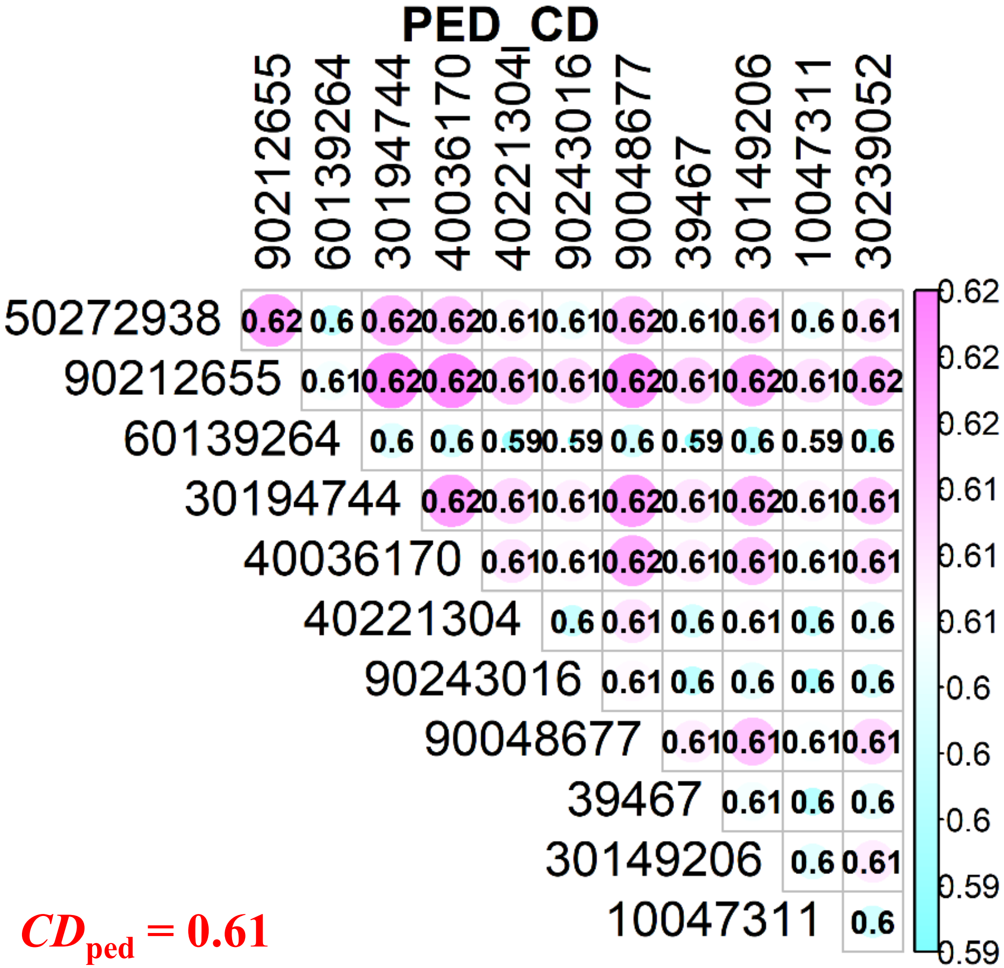

GENOMIC_PEVD

	90212655	60139264	30194744	40036170	40221304	90243016	90048677	39467	30149206	10047311	30239052
50272938	0.7	0.74	0.7	0.69	0.73	0.71	0.71	0.7	0.71	0.73	0.7
90212655		0.73	0.69	0.68	0.72	0.7	0.69	0.69	0.7	0.72	0.69
60139264			0.73	0.73	0.76	0.74	0.74	0.73	0.74	0.76	0.73
30194744				0.68	0.72	0.7	0.7	0.69	0.7	0.72	0.69
40036170					0.72	0.69	0.69	0.69	0.69	0.71	0.68
40221304						0.73	0.73	0.72	0.73	0.74	0.72
90243016							0.71	0.7	0.71	0.73	0.7
90048677								0.7	0.71	0.72	0.69
39467									0.7	0.72	0.69
30149206										0.73	0.7
10047311											0.71

$PEVD_{gen} = 0.071$

Results – CD → higher is better!!!!!

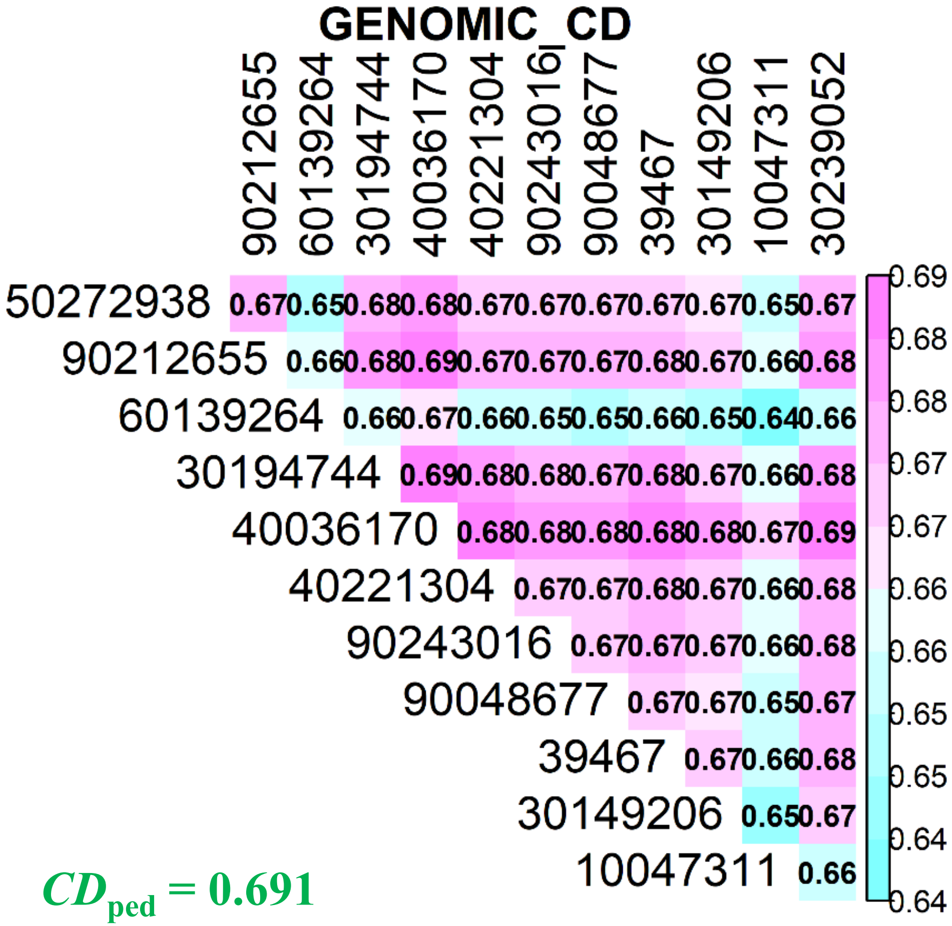
$\Delta CD_{ped \rightarrow gen} = 13\%$



PED_CD

	90212655	60139264	30194744	40036170	40221304	90243016	90048677	39467	30149206	10047311	30239052
50272938	0.62	0.6	0.62	0.62	0.61	0.61	0.62	0.61	0.61	0.6	0.61
90212655		0.61	0.62	0.62	0.61	0.61	0.62	0.61	0.62	0.61	0.62
60139264			0.6	0.6	0.59	0.59	0.6	0.59	0.6	0.59	0.6
30194744				0.62	0.61	0.61	0.62	0.61	0.62	0.61	0.61
40036170					0.61	0.61	0.62	0.61	0.61	0.61	0.61
40221304						0.6	0.61	0.6	0.61	0.6	0.6
90243016							0.61	0.6	0.6	0.6	0.6
90048677								0.61	0.61	0.61	0.61
39467									0.61	0.6	0.6
30149206										0.6	0.61
10047311											0.6

$CD_{ped} = 0.61$



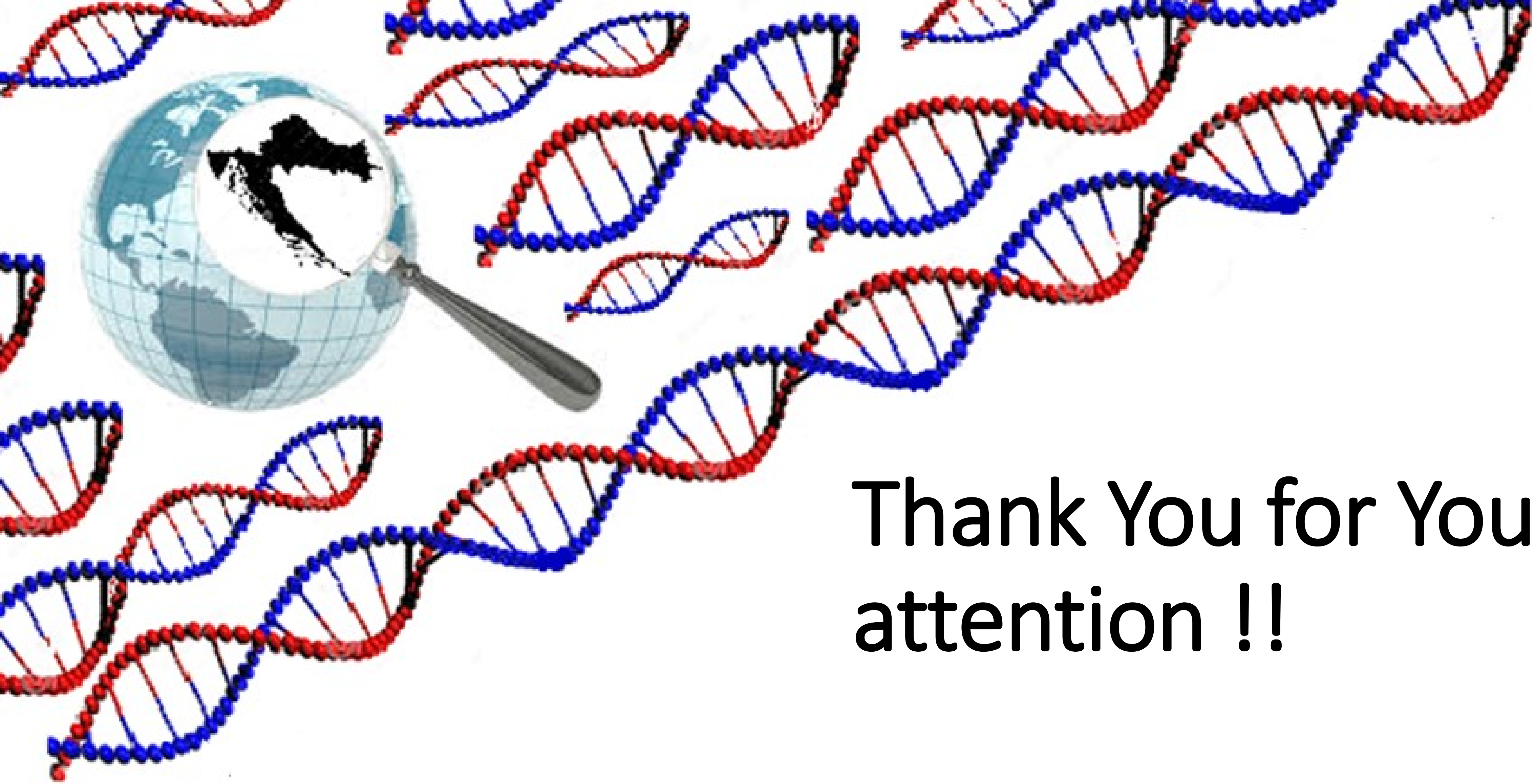
GENOMIC_CD

	90212655	60139264	30194744	40036170	40221304	90243016	90048677	39467	30149206	10047311	30239052
50272938	0.67	0.65	0.68	0.68	0.67	0.67	0.67	0.67	0.67	0.65	0.67
90212655		0.66	0.68	0.69	0.67	0.67	0.67	0.68	0.67	0.66	0.68
60139264			0.66	0.67	0.66	0.65	0.65	0.66	0.65	0.64	0.66
30194744				0.69	0.68	0.68	0.67	0.68	0.67	0.66	0.68
40036170					0.68	0.68	0.68	0.68	0.68	0.67	0.69
40221304						0.67	0.67	0.68	0.67	0.66	0.68
90243016							0.67	0.67	0.67	0.66	0.68
90048677								0.67	0.67	0.65	0.67
39467									0.67	0.66	0.68
30149206										0.65	0.67
10047311											0.66

$CD_{ped} = 0.691$

Conclusions

- Genomic information contributes to unraveling connectedness between flocks
- More accurate estimates of breeding values for genomic selection versus traditional pedigree-based selection
- Working on connectedness in population is necessary



Thank You for Your attention !!

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