

The conservation status of Dalmatian Pramenka sheep using high-throughput molecular information

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Elena Ciani, Johannes A. Lenstra, Ino Curik, Vlatka Cubric-Curik



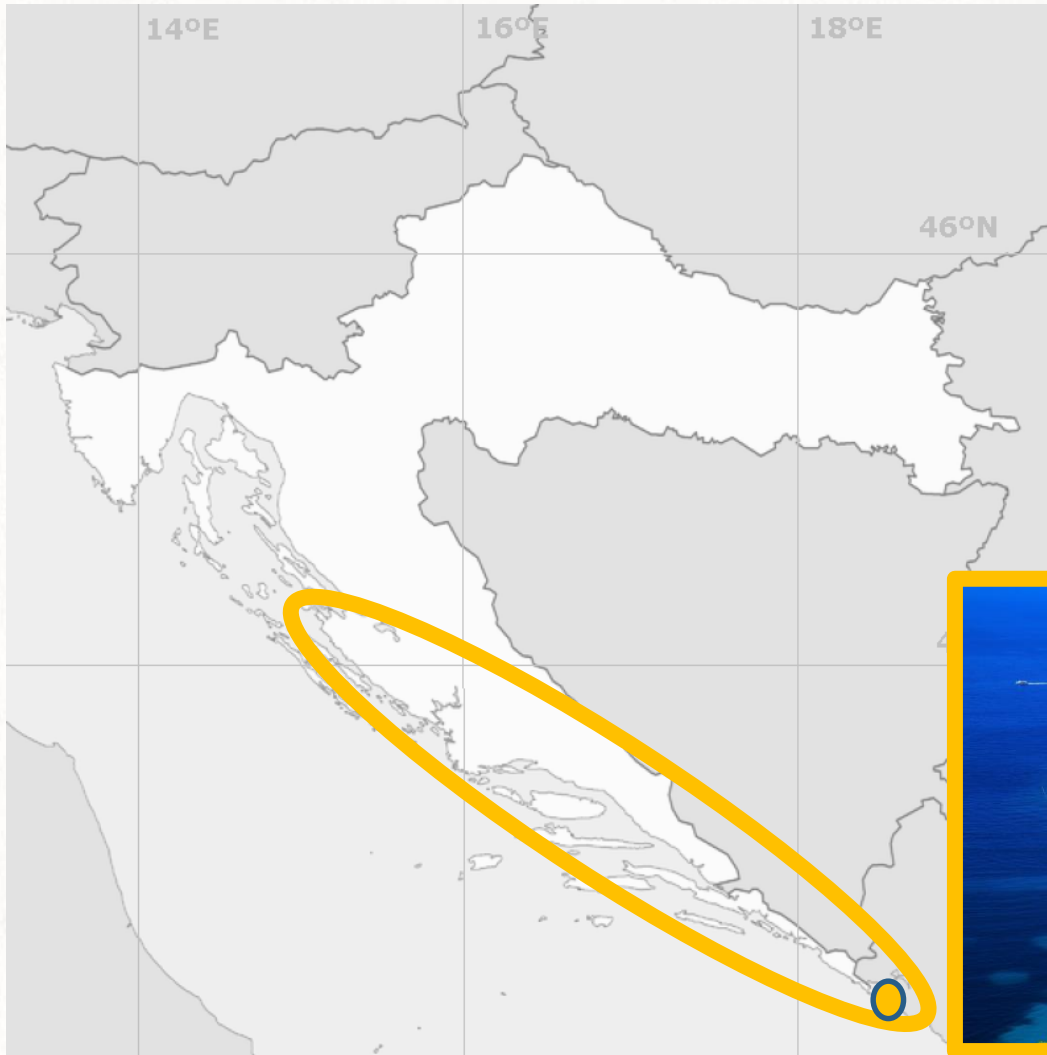
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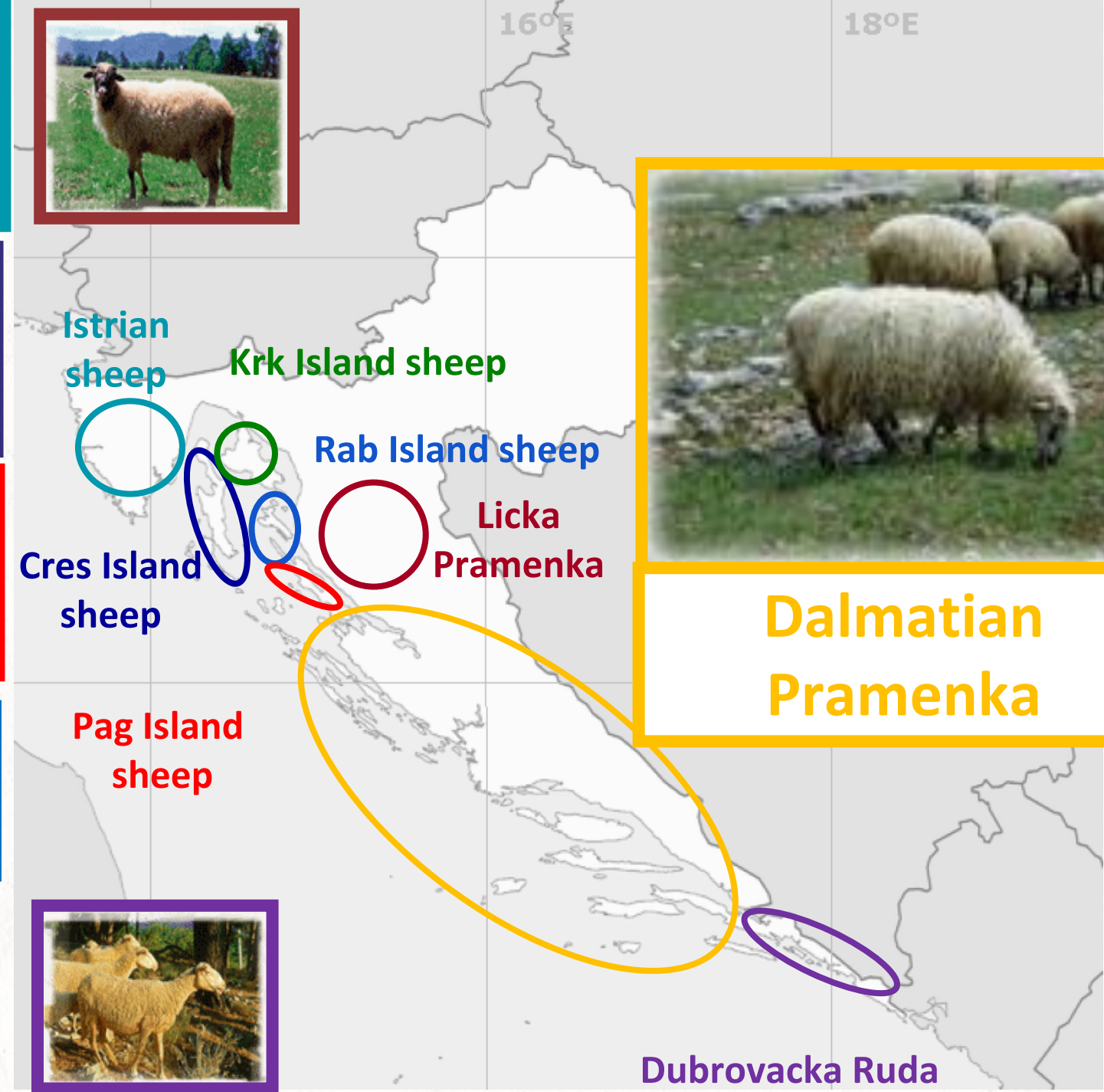
09 "Genetic diversity and Conservation"

Elafiti 1 on Monday 27 August 2018 from 14:00 – 18:00 → 17:00

The name Dalmatae → Illyrian word *delmë* → sheep in English

The **Dalmatae** or **Delmatae** were an ancient people who inhabited the core of what would then become known as **Dalmatia** after the **Roman** conquest.





Dalmatian Pramenka

Dubrovacka Ruda

Aims of the study

To assess **conservation status** of **Dalmatian Pramenka** sheep using **high-throughput genomic data**

1

To estimate genomic inbreeding (F_{ROH})

2

To estimate gametic phase disequilibrium effective population size (Ne_{GD})

3

To estimate linkage disequilibrium effective population size (Ne_{LD})

Materials & molecular methods

Data

- Our sample:
32 Dalmatian Pramenka sheep (DaP) randomly sampled over 11 farms in Dalmatia
- Public data used:
Appenninica (App), Arawapa (Ara), Australian Merino (AuM),
Churra (Chu), Finnsheep (Fin), Massese (Mas),
Sardinian White (SaW), Merinolandschaf (Mer)
Dryad digital repository: <http://dx.doi.org/10.5061/dryad.2p0qf>

Molecular analysis

- OvineSNP50 BeadChip (Illumina)

Methods: ROH genomic inbreeding level

Ferenčaković *et al. Genetics Selection Evolution* 2013, **45**:42
<http://www.gsejournal.org/content/45/1/42>



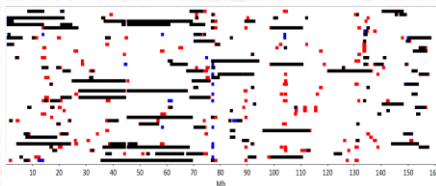
RESEARCH

Open Access

Estimating autozygosity from high-throughput information: effects of SNP density and genotyping errors

Maja Ferenčaković¹, Johann Sölkner^{2*} and Ino Curik¹

$F_{ROH>4Mb}$, $F_{ROH>16Mb}$



$$F_{ROH} = \frac{\sum_{j=1}^n L_{ROH_j}}{L_{total}}$$

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Methods: Ne_{GD} – NeEstimator v2: *Do et al., 2014*

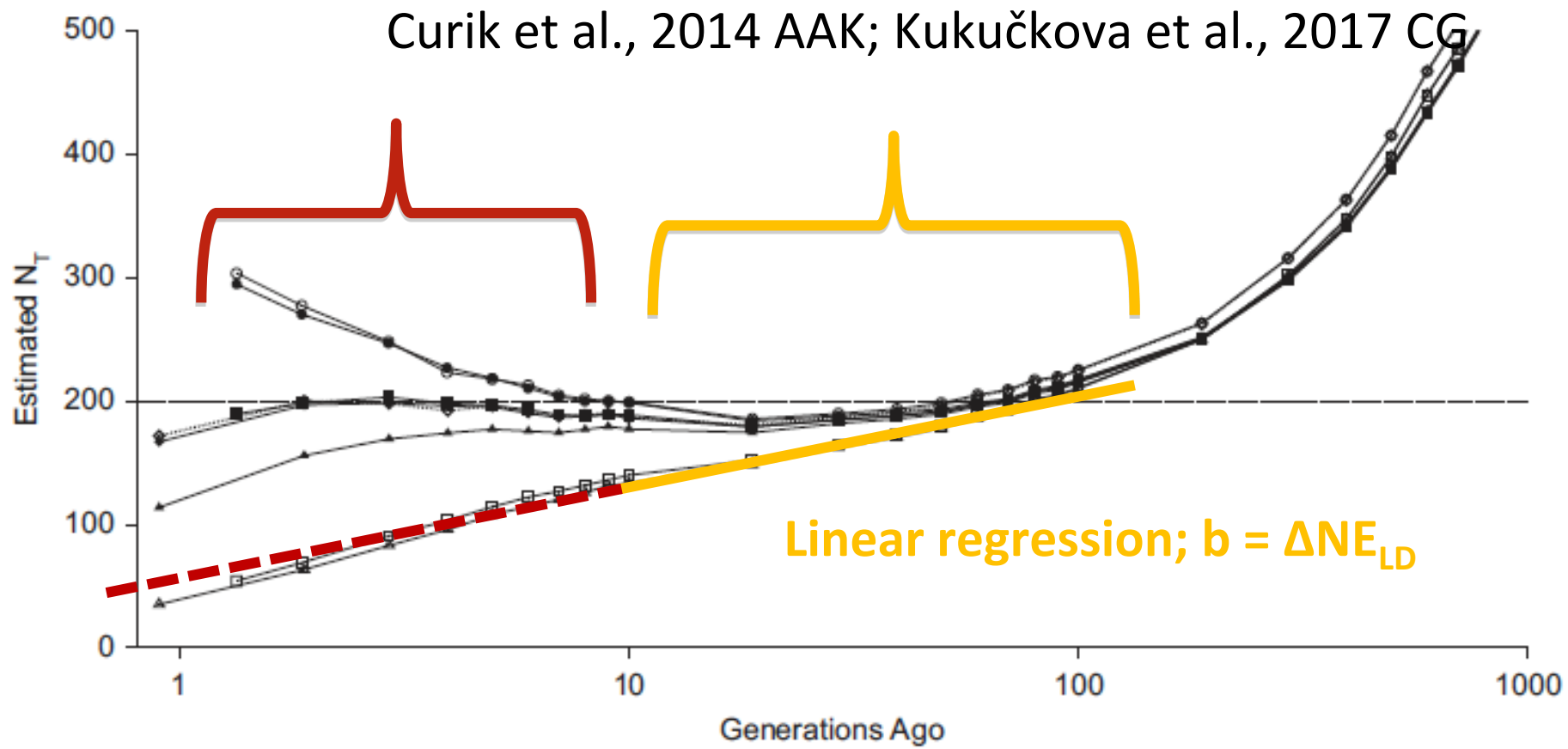
Ne_{GD} of a real population **X** is the size of a **hypothetical ideal population** (Wright-Fisher) that will result in the **same change in gametic phase disequilibrium** as in the real (actual) population considered.

Contemporary effective population size

Methods: Ne_{LD} – SNeP: *Barbato et al., 2015*

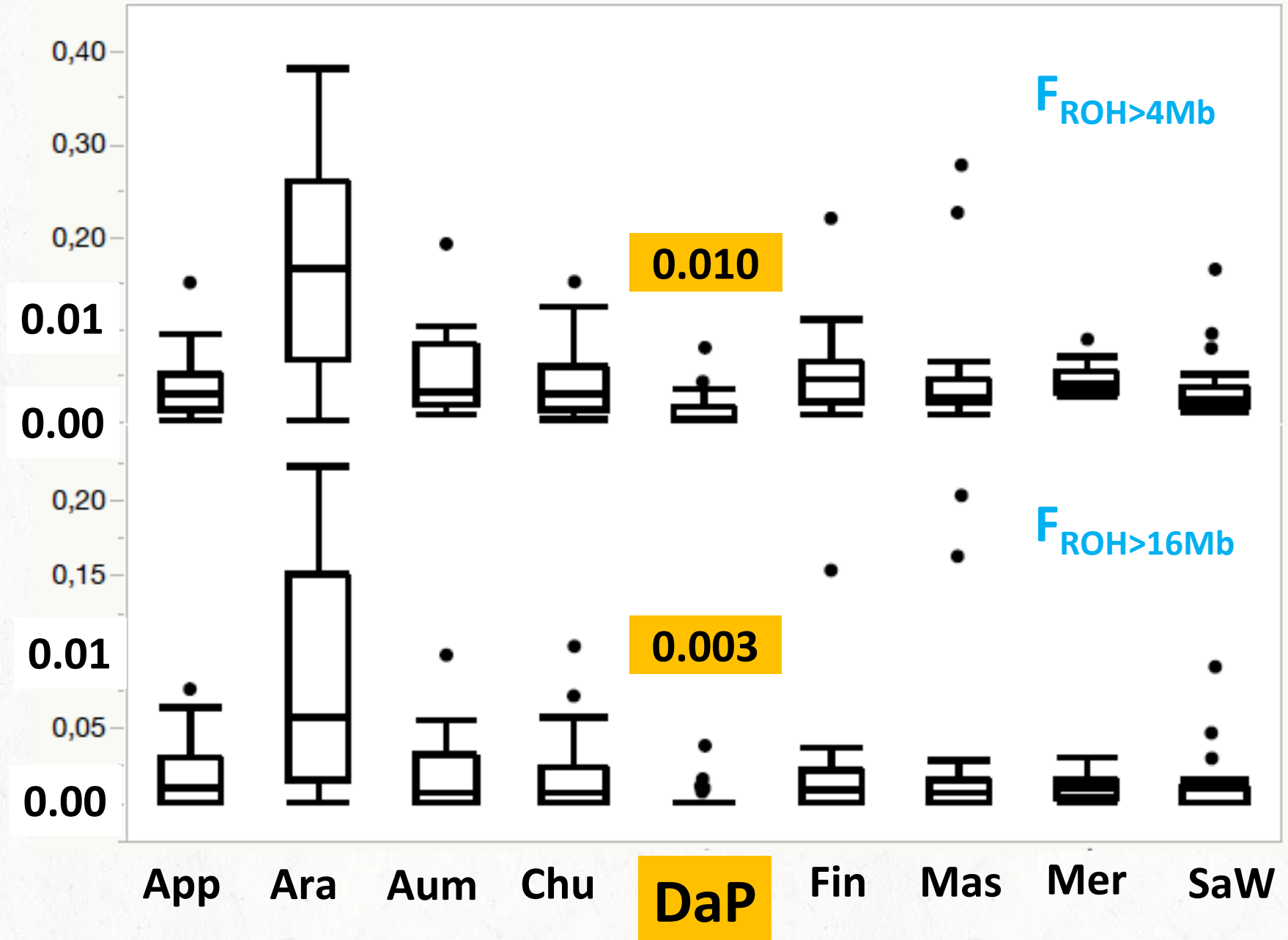
Ne_{LD} of a real population **X** is the size of a **hypothetical ideal population** (Wright-Fisher) that will result in the **same change in linkage disequilibrium** as in the real (actual) population considered.

Historical trajectories of LD effective population size



Corbin et al., 2012 JABG

Results: genomic inbreeding level



Results: Ne_{GD} – NeEstimator v2: *Do et al., 2014*

Breed	Ne_{GD}	Het_{obs}
Appenninica	120 (71 – 331)	0.369
Arawapa	11 (7-19)	0.316
Australian Merino	96 (44 – Infinity)	0.359
Churra	50 (29-135)	0.364
Dalmatian Pramenka	124 (40 – Infinity)	0.375
Finnsheep	61 (40 – 120)	0.344
Massese	34 (24 -52)	0.355
Merinolandschaf	233 (145 -568)	0.362
Sardinian White	50 (25 – 252)	0.358

Results: Ne_{LD} – SNeP: *Barbato et al., 2015*

Breed	$Ne_{LD \rightarrow 0}$	$Ne_{LD \rightarrow 20}$	$Ne_{LD \rightarrow 100}$	ΔNe_{LD}
Appenninica	18	123	540	5
Arawapa	18	79	321	3
Australian Merino	44	168	662	6
Churra	20	130	571	6
Dalmatian Pramenka	14 ?	239	1139	11
Finnsheep	36	147	589	6
Massese	30	120	479	4
Merinolandschaf	33	126	497	5
Sardinian White	29	134	553	5

Conclusion & future plans

1. Low genomic inbreeding (F_{ROH}) in Dalmatian Pramenka
2. High heterozygosity in Dalmatian Pramenka
3. Relatively high Ne_{GD} in Dalmatian Pramenka
4. Very low Ne_{LD0} and high ΔNE_{LD} , Ne_{LD20} and Ne_{LD100} values are probably caused by the large population decline followed by recent population increase
5. Good potential of high-throughput molecular information in assessing conservation status of livestock populations
6. We plan to analyze conservation status of other Croatian sheep breeds/populations

Acknowledgments



Identification of selection signals in the genome of domestic animals using high-throughput molecular information

**University of Zagreb
Scientific support projects 2015**

Thanks for your attention!



**any
questions
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