1st EAAP Companion Animals workshop

Analysis of genomic diversity in the Slovak Cuvac dog

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https://db.slovensky-cuvac.cz/

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History of Slovak Cuvac

Country of origin - Slovakia (Czechoslovakia): 15th to 17th century arrival with the Wallachians

Group of white mountain dogs - Pyrenean Mountain dog, Tatra Mountain Sheepdog or Kuvacz

Kuvacz (HU)

Slovak Cuvac (CZ/SK)

Tatra Mountain Sheepdog (PL)

History of Slovak Cuvac

The breed faced existential problems **during the rabies epidemic** in the early **20th century**, when it was blamed for causing the disease along with the Kuvasz and **culled**

Regeneration proces based on four individuals

Initially, only inbreeding was used, externally similar individuals.

Breeders' Club founded in 1933

The breed standard has not changed since its recognition in 1965

Aims of the study

Analysis of analyse the genomic diversity in Slovak Cuvac dog using **high-throughput genomic data**.

1. **estimated by genomic inbreeding**
2. **current and historical effective population size**

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3. **comparison of genomic data analysis with genealogical data analysis**

Data

Genomic data

- **40 most important individuals**
- **After QC 250k authosomal SNP**

Pedigree data

- **collected since 1925 (breed was founded)**
- **information about 17 thousand animals**

Methods: ROH genomic inbreeding level

- **Consecutive aproach – implemented in detectRUNS** (Biscarini et al., 2019)

  $F_{ROH\ 2\text{-}4Mb}$, $F_{ROH\ 4\text{-}8Mb}$, $F_{ROH\ 8\text{-}16Mb}$

- **The hidden Markov model – implemented in RZooRoh** (Bertrand et al., 2019)

  Generations: 0 - 6; 6 – 12, 12 - 24

Methods: Current and historical effective population size

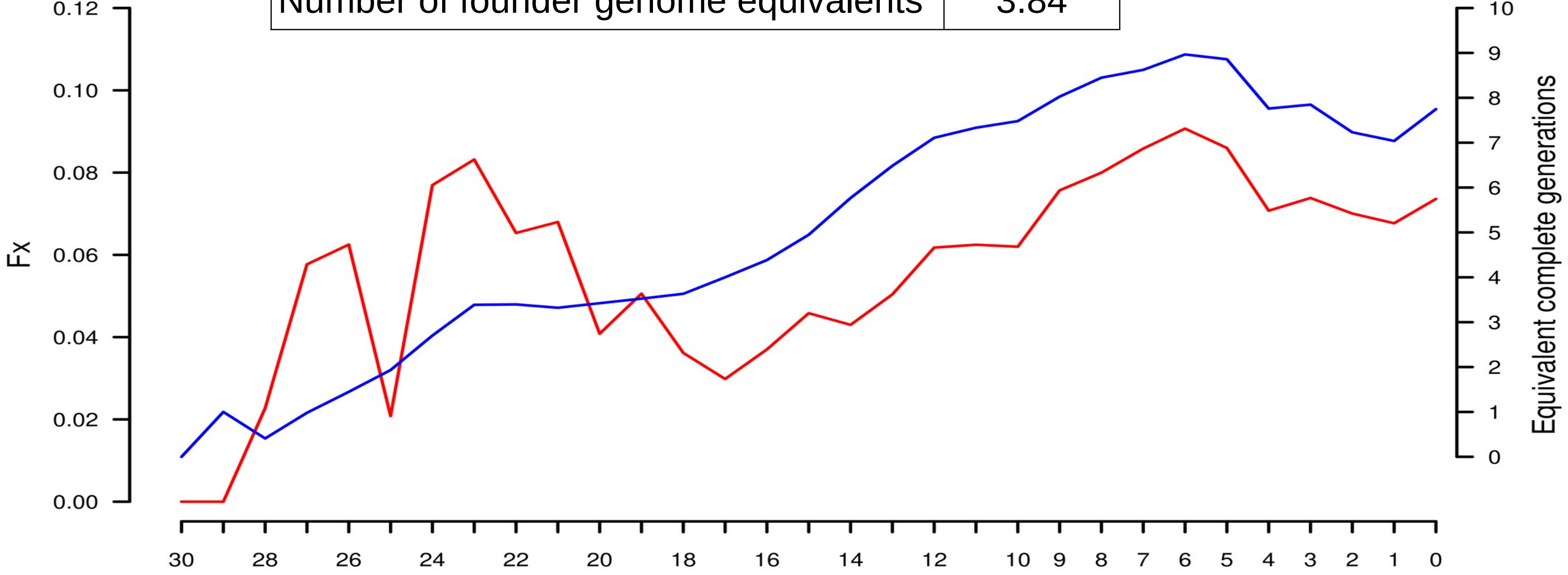
- **Linkage disequilibrium, GONE -> software** (Santiago et al., 2021)

Methods: Genealogical data

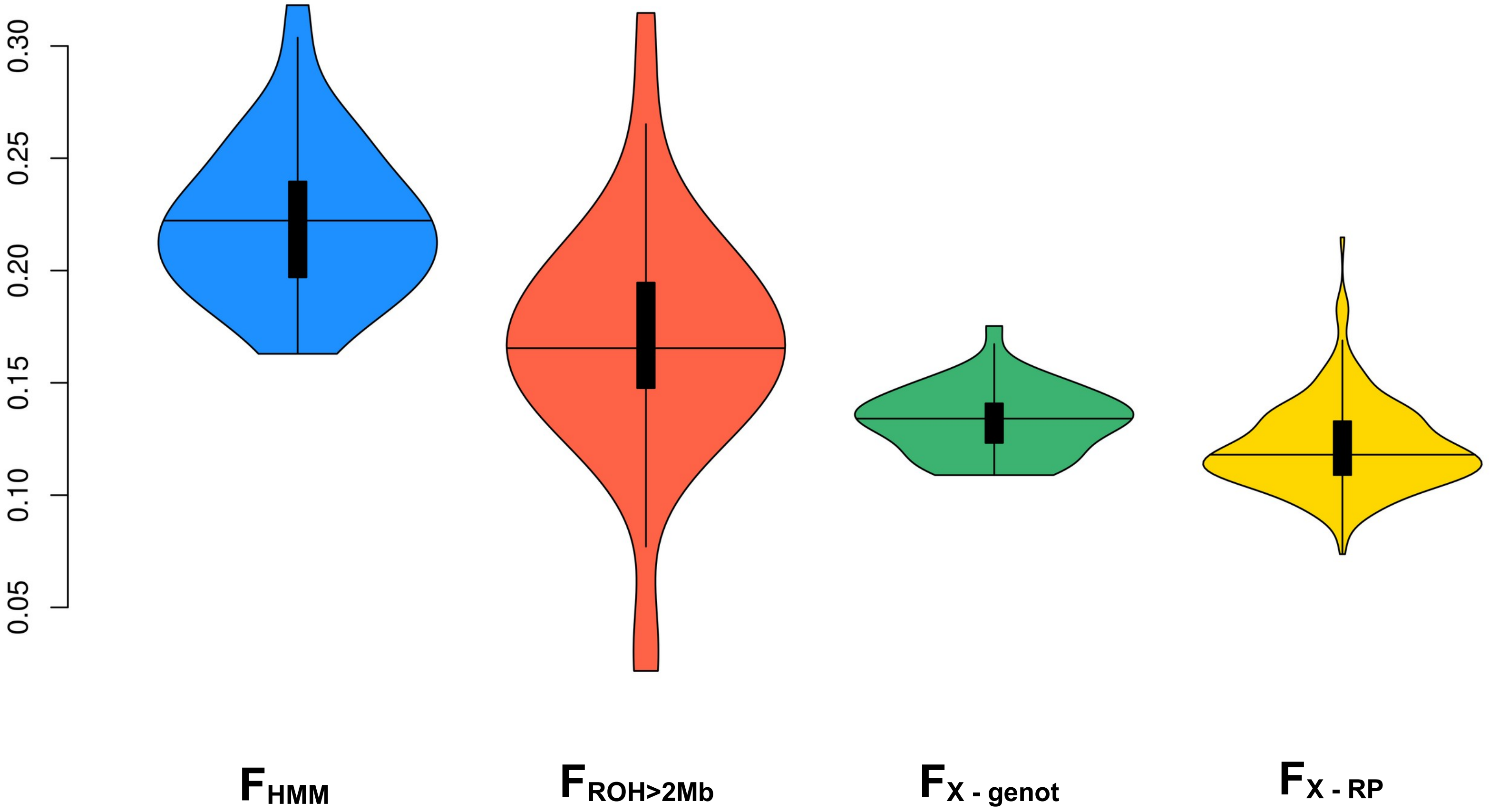
- **Loss of genetic diversity based on genealogical data - typical analyses**
  - **Current generation (generation 0) vs. reference population**
    - Inbreeding coefficient
    - Effective population size **(Gutiérrez et al., 2008)**
    - Parameters based on gene origin

Results: Pedigree data - RP

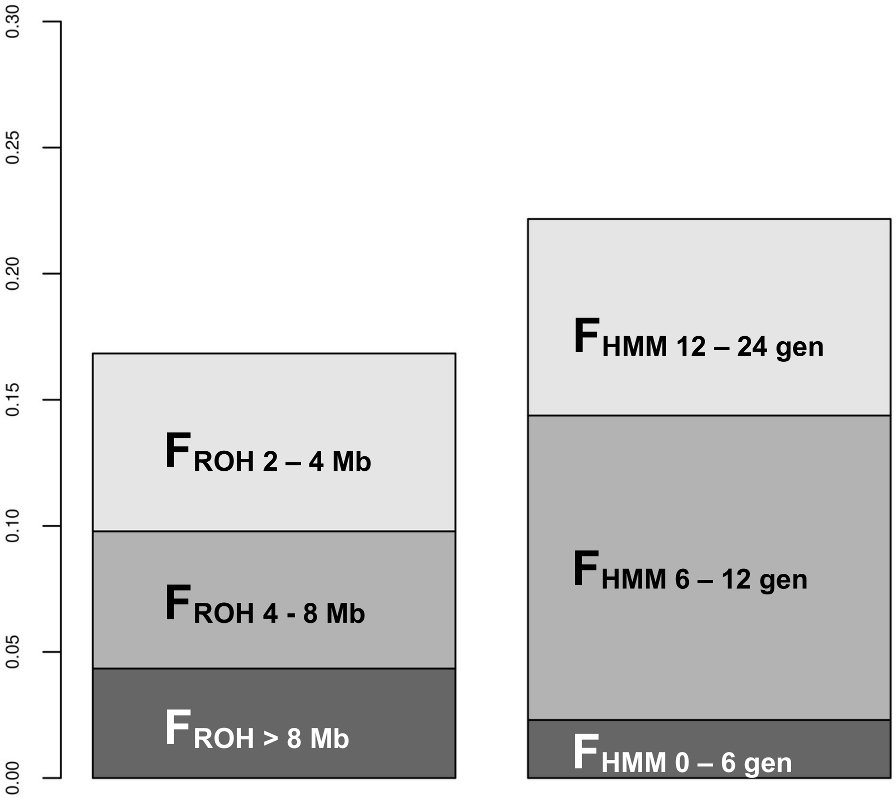
Total number of founders	41
Effective number of founders	16.59
Total number of ancestors	942
Effective number of ancestors	14
Number of founder genome equivalents	3.84



Inbreeding: genomic vs. genealogical



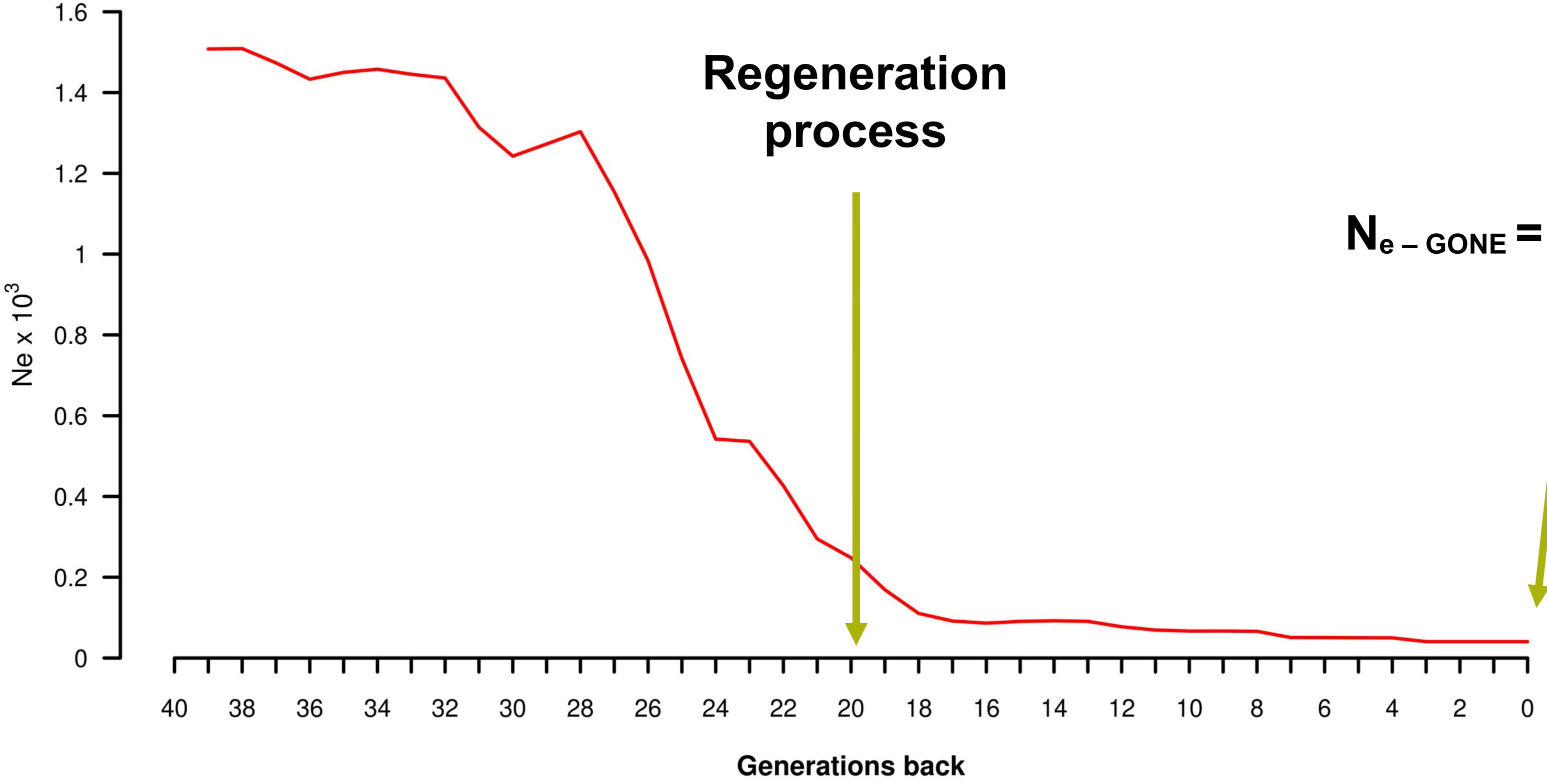
Genomic inbreeding - separations



Effective population size

$N_{e-RP} = 47$ (45 - 49)

Gutiérrez et al. (2008)



Regeneration process

$N_{e-GONE} = 41$ (37-45)

Conclusions

- ✓ Genomic inbreeding reached higher values than genealogical inbreeding
- ✓ The hidden Markov model framework showed higher values than the consecutive method
- ✓ N_e showed lower values than the recommended by FAO (2018; $N_e = 50$)
- ✓ Historical values of effective population size confirmed by bottleneck effect at the beginning of the 20th century
- ✓ High quality pedigree records show comparable values of populations parameters as genomic data

Acknowledgments

any
Questions ?

Thanks for
your
attention!

https://www.ecanis.cz/clanky/cuvac-je-velmi-oddanym-veselym-a-skvelym-partakem-_2760.html?klic=871