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A green-themed graphic with a network of hexagonal nodes containing logos for NordGen, SLU, NMBU, Norsk Hestesenter, UCPH, and Faroese Horse Association. The title 'Genomic Characterization of Native Nordic Horse Breeds – "NaNo Horse"' is written in large white font. Below the title, the authors' names and affiliations are listed, followed by the master student's name and affiliation.

NordGen

NordGen
SLU
NMBU
Norsk hestesenter
NORSK HESTESENTER
UCPH
Faroese Horse Association
Føroysk

Genomic Characterization of Native Nordic Horse Breeds – "NaNo Horse"

Susanne Eriksson¹, Peer Berg², Sofia Mikko¹, Iryna Shutava¹, Cathrine Brekke², Maria Kjetså³, & Therese Selle⁴
¹Swedish University of Agricultural Sciences, ²Norwegian University of Life Sciences ³NordGen, ⁴Norsk hestesenter

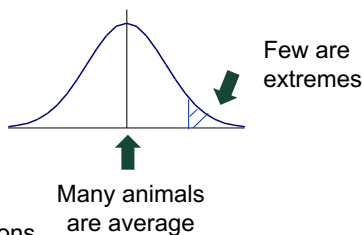
Master student: Signa Kallsøy Joensen, University of Copenhagen/Faroese Horse Association

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Small or large breeds with intensive selection

- Intensive selection result in:
 - larger genetic progress
 - faster increase in inbreeding
- BLUP is effective, but:
 - favor selection of relatives
 - may support overuse of some stallions
- Avoid quick increase in relatedness- and inbreeding
- Follow up health and function
- Watch out for hitch-hiking deleterious



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Breeds with large breeding pools and wide breeding goal

- Small risk of inbreeding on breed level
- Genetic disorders can "hide" many generations before detected
- Inbreeding can be problematic on individual level
- Report all suspected congenital disorders and fertility
- Watch out for unwanted side-effects due to intensive selection



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Small Populations of Native Horse Breeds

- Keep the number of horses to maintain the breed
- Important to keep many stallions in breeding
- Prioritize health and welfare
- Risk of genetic drift and inbreeding
- Are there any known inherited disorders?





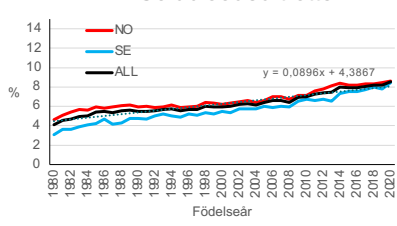
Foto: Kalle Eklund

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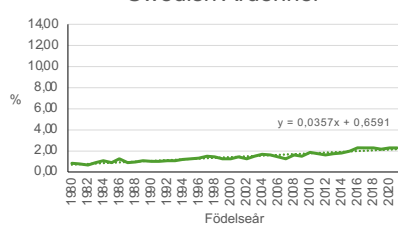


Inbreeding trends (average inbreeding coefficient %/YOB)

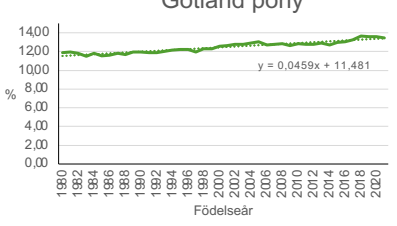
Coldblooded trotter



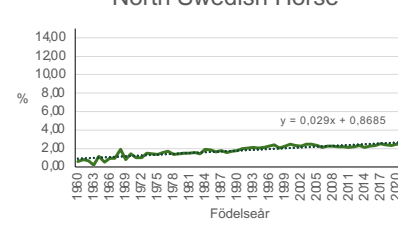
Swedish Ardenner



Gotland pony

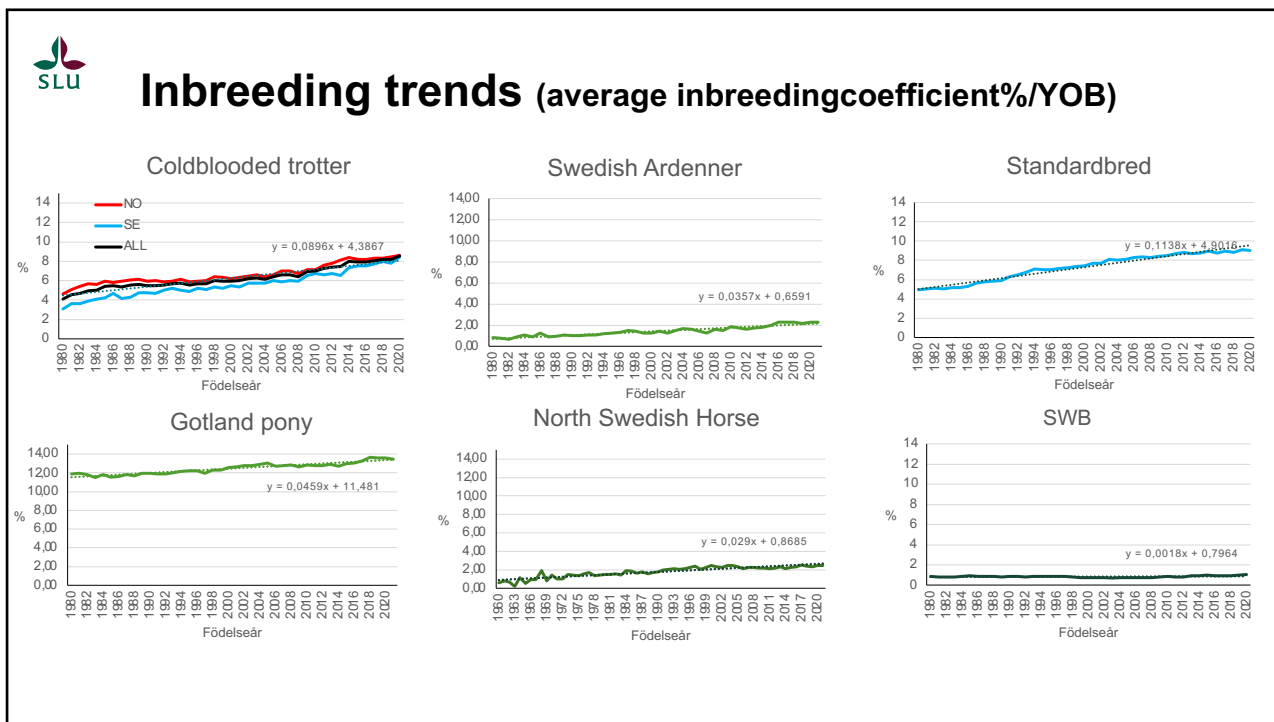


North Swedish Horse



- Estimated from SH/ST breed registry database
- The level depend on the completeness of the pedigree data
- Underestimated if information is missing.
- Very important to reduce the rate of increase

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Random events and selection will create subpopulations

- Bottleneck where genetic diversity is lost
- Founder population
- Selected group A
- Selected group B

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NaNo horse project

- Native Nordic horse breeds are at risk of extinction, except for the Finnhorse and the Icelandic Horse (Kierkegaard et al., 2020)
- The situation is more critical for some breeds than others
- Genomic information can complement pedigree information
- Swedish-Norwegian project 2022-2024, funded by SHF



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Aim of our study

- By whole genome sequencing (WGS);
 - Detect level of genomic diversity within and between native Nordic horse breeds
 - Describe structure on genomic level
 - Compare signatures of selection in the genomes of different breeds
 - Search for signs of adaptation and/or genetic load
- Focus on Norwegian and Swedish native horse breeds
- Give advice to breed organizations



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Sample collection

- Aim for 192 blood samples, 10-30/breed
 - Swedish Ardennes, Gotland pony, North Swedish horse, Dole horse, Fjord horse, Coldblooded trotter, and Faroese pony
 - Pedigree analysis to select among samples
- Majority of samples collected this year.
- Additional data from earlier project.
- Collaboration partners from other Nordic countries.



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Genetic diversity

- The study of genes and their roles in inheritance
- Species
- Breeds
- Phenotypes



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Genomic diversity

- The study of all of an individual's genes (the genome)
- Single Nucleotide Polymorphism (SNP)-chip
- Whole Genome Sequencing (WGS)



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What can population genomics tell us?

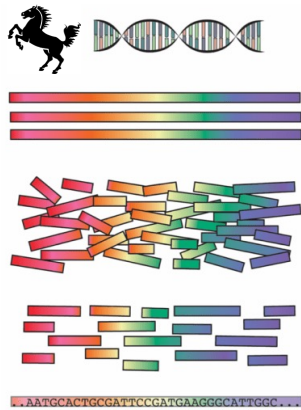
- Inbreeding at chromosome positions
- Genomic inbreeding coefficient (F or F_{ROH})
- Expected and observed heterozygosity at chromosome positions (H_{exp} & H_{obs})
- Effective population size (N_e)
- Genetic load/deleterious mutations



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Whole Genome Sequencing



Low coverage



Medium coverage

- Average coverage is a measurement of how many times each base-pair has been sequenced.
- We will sequence at quite low coverage (5-10X)

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Creation of genomic diversity

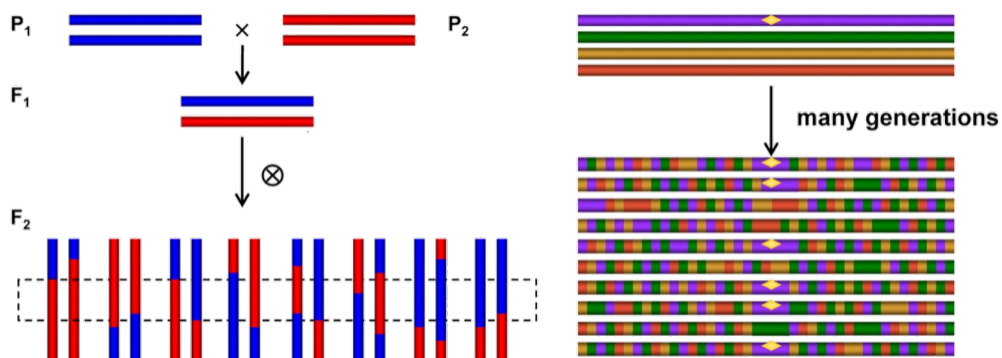
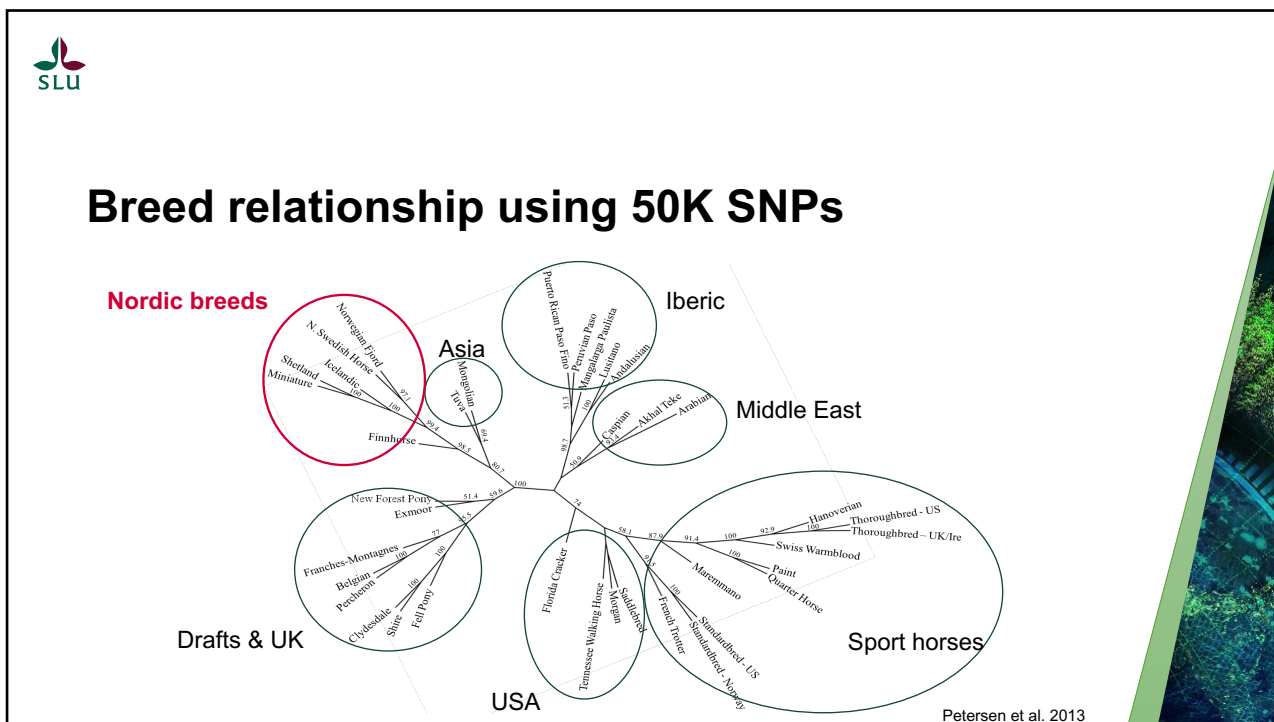


Figure from Zhu et al 2008

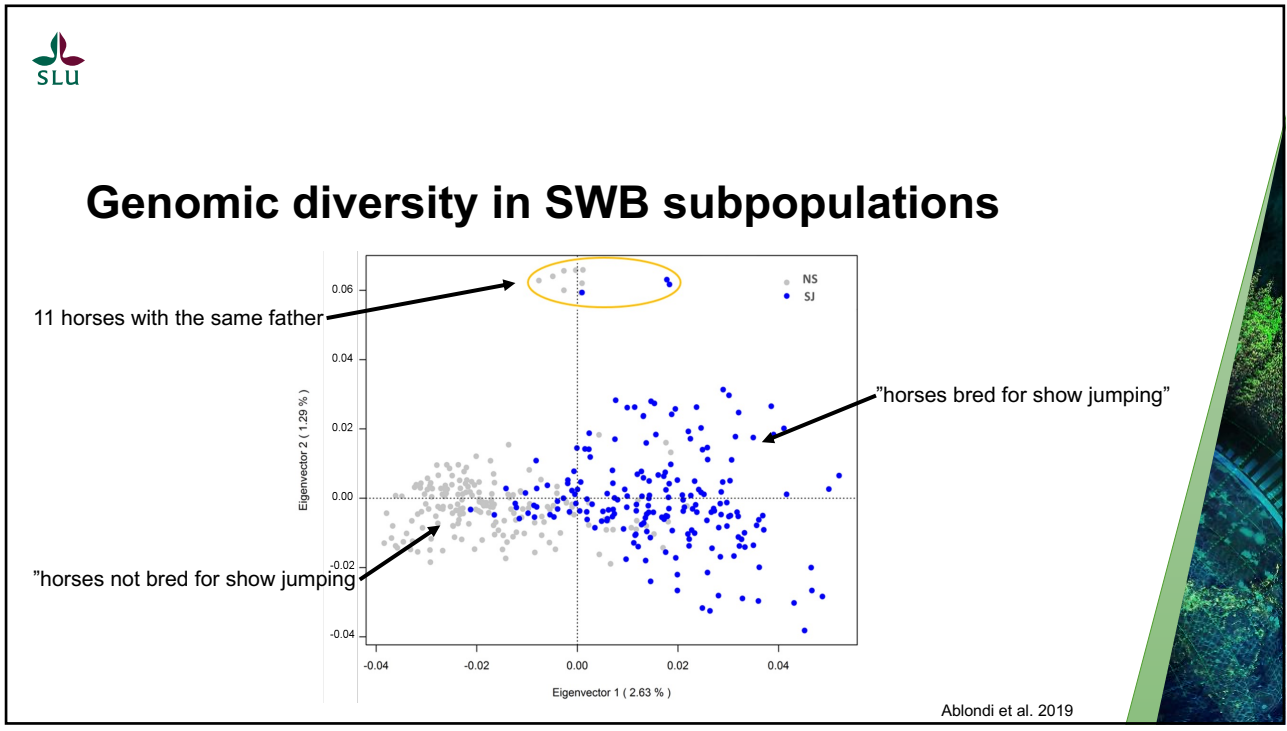
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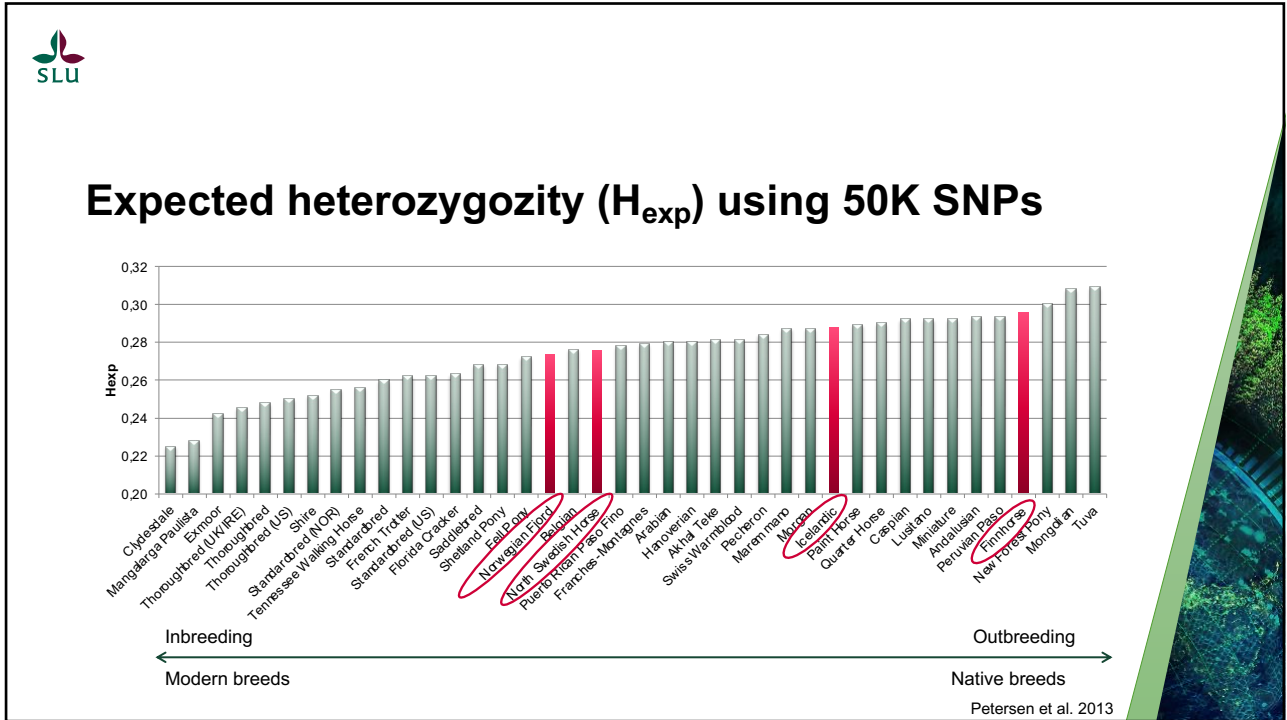
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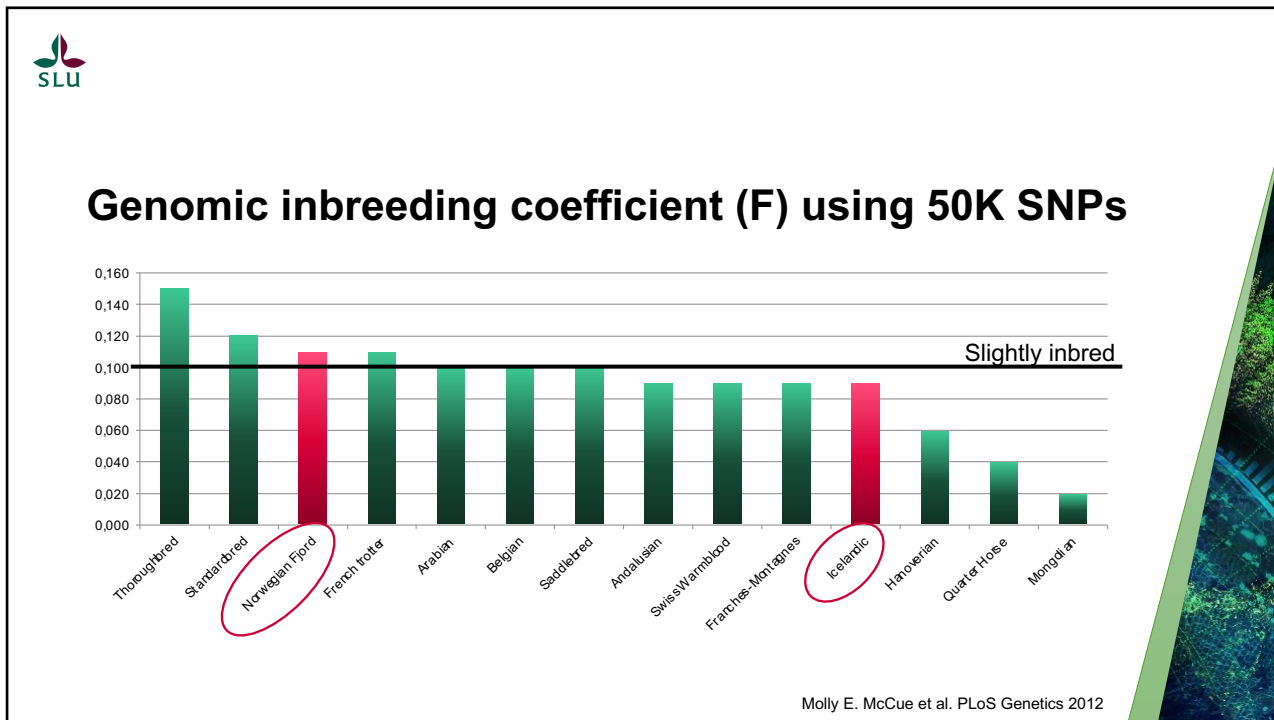
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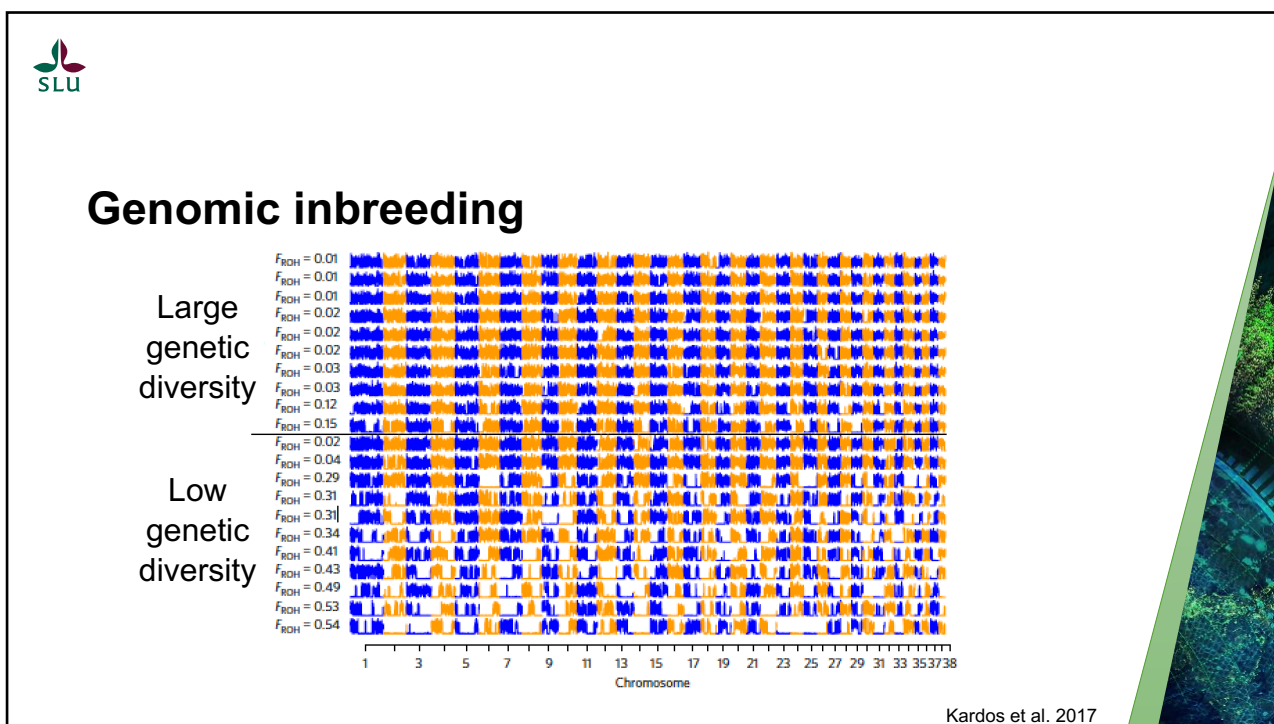
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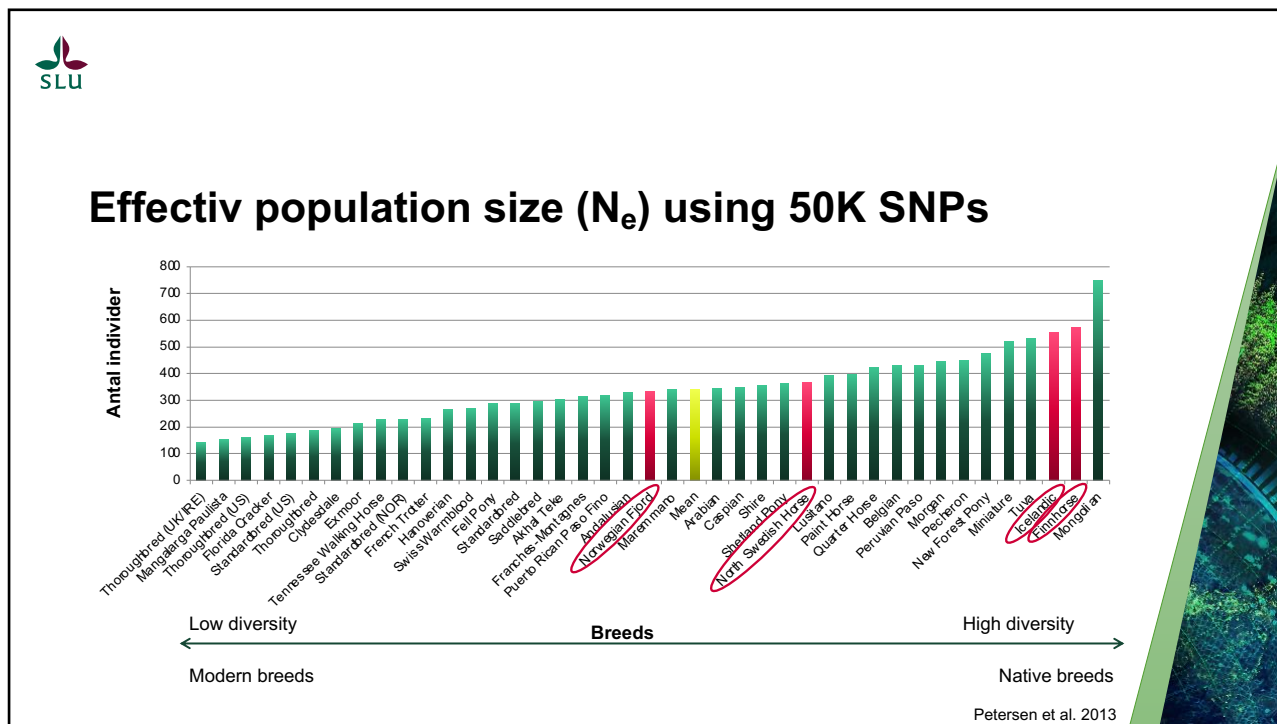
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SLU

Genetic load


- Deleterious/lethal mutations
- Masked load – heterozygotes
- Realized load – homozygotes
 - Increases for every generation of inbreeding
 - Temporary decreased after introgression
- Purging – loss of deleterious variants
- Introgression – add new variants

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Summing up

- Most samples collected
- 5-10X WGS this winter
- Characterize genomic diversity in the native nordic breeds
- Analysis primarily on population, not individual level
- Genomic inbreeding coeff, heterozygosity, N_e , genetic load
- Start-off for further studies



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NordGen



NordGen



SLU



NMBU



Norsk hestesenter



Thank You!

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