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CiBreed
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Virtuell kreuzen

Genomic characterization of native
pig breeds in Germany

Project: Oekosus

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FLI | 07.05.2025

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ÖkoSus

Project title:


Genomic characterization of endangered pig breeds as a basis for
sustainable breeding programs in organic livestock breeding

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Gefördert durch



Bundministerium
für Ernährung
und Landwirtschaft




BÖL
BUNDESMINISTERIUM
ÖKOLOGISCHER LANDBAU

Project duration: October 2024 - September 2028

aufgrund eines Beschlusses
des Deutschen Bundestages

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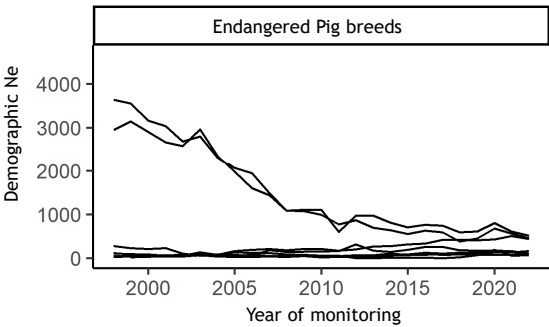
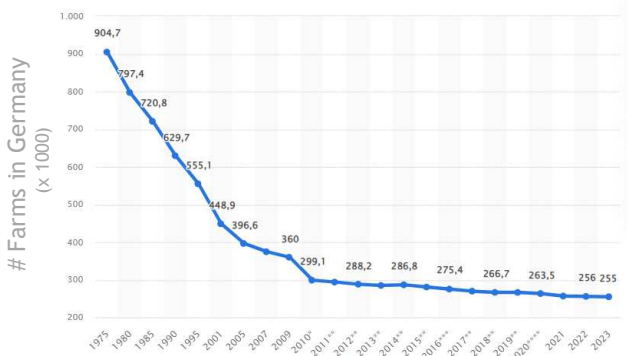
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ELGO-DIMITRA, Athens

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Background

- Declining trend of the number of farms in Germany
- associated with declining numbers of animals on livestock farms



=> To date: all indigenous purebred pig breeds in Germany are threatened

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Background

German pig breeds => included in the ÖkoSus project

Bentheim Black Pied



Leicoma



German Large White



German Saddleback



German Landrace



Breeds listed on the “Red List” of indigenous livestock breeds in Germany

- Stratified populations
- Increasing threat (diseases & Economy)
- Few genomic data available

Current challenges:

- Improvement of conservation breeding schemes
- Management of cryopreservation

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ÖkoSus aims

1. Near-complete genotyping of the herd book animals of all endangered breeds

2. Analyses of population structure and diversity

3. Targeted selection of candidate animals for cryo-conservation

4. Analyses of functional traits such as piglet survival and longevity

5. Establishment of genomically-aided conservation breeding strategies



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ÖkoSus workpackages

WP1: Comparison of array vs low-coverage sequencing

- Investigating whether genotyping using SNP arrays can be replaced by low-coverage sequencing (LC-LRS) with subsequent imputation.

Why?

Some aspects	Low Coverage Long-Read (LCLR)	SNP Genotyping
Discovery of new variants	✔ Yes (SNPs, SVs, InDels)	✘ No (predefined SNPs only)
Structural variant detection	✔ Excellent	✘ Poor
Genome coverage	✔ Nearly complete	✘ Limited to SNP markers
Ascertainment Bias	✔ Low	✘ High
SNP-level accuracy	✘ Lower (low depth, high error) => to be tested	✔ High
Bioinformatic complexity	♦ Higher => Establishing a pipeline	✔ Low



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ÖkoSus workpackages

WP1: Comparison of array vs low-coverage sequencing

↓

WP2: sample collection, sequencing and raw data preparation


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ÖkoSus Samples

Breed	Number of farms	Animals in gene bank	Estimated number of samples
Group of German Saddleback			
Angler Saddleback			
German Saddleback	49	33	665
Red Husumer			
Swabian-Hall Pig		15	800
Bentheim Black Pied		27	600
Leicoma	7	20	250
German Landrace	7		300
German Large White	8		300
Reserve			185
Total Sum			3100


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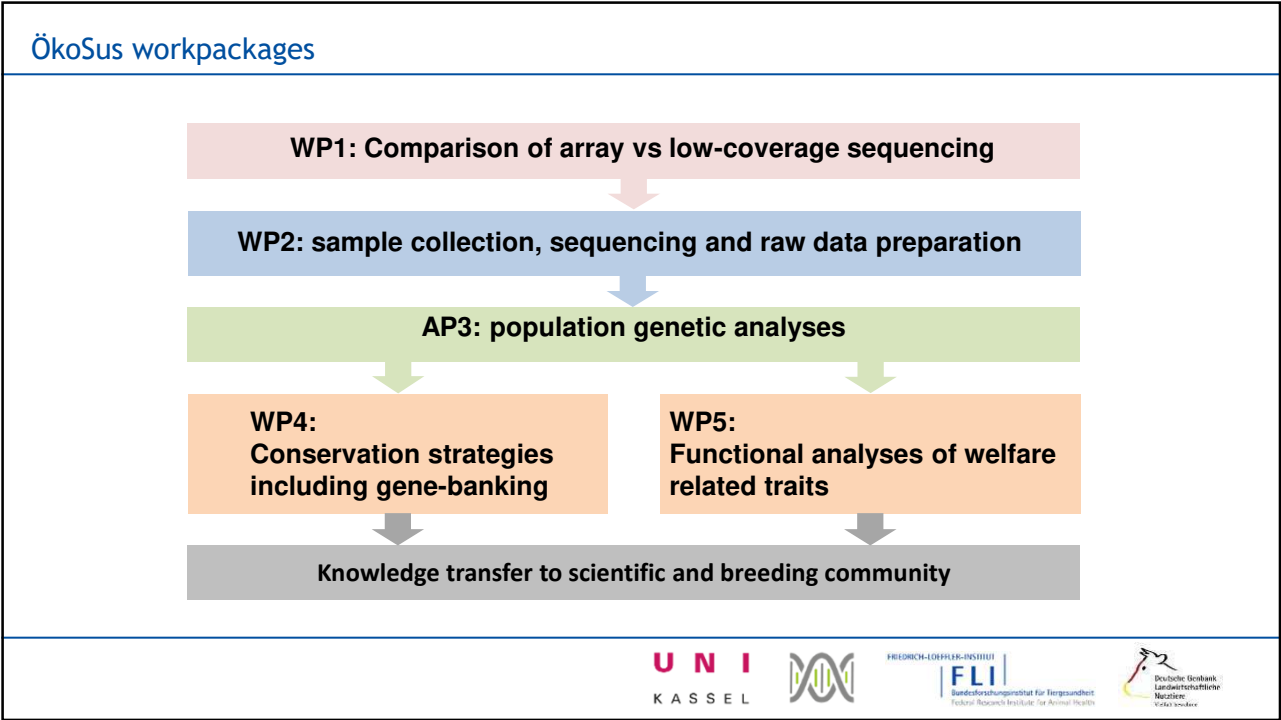
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ÖkoSus - First Results (WP1)

WP1: Comparison of array vs low-coverage sequencing




First preliminary Results

Swabian-Hall Pig (Schwäbisch-Hällisches Schwein)

- ✓ ~250 Animals
- ✓ 3 farms (affiliated with breeding association ZVHS)

Genomic characterisation

- 77k Illumina Array
- Nanopore multiplex
 - 6 animals per flowcell



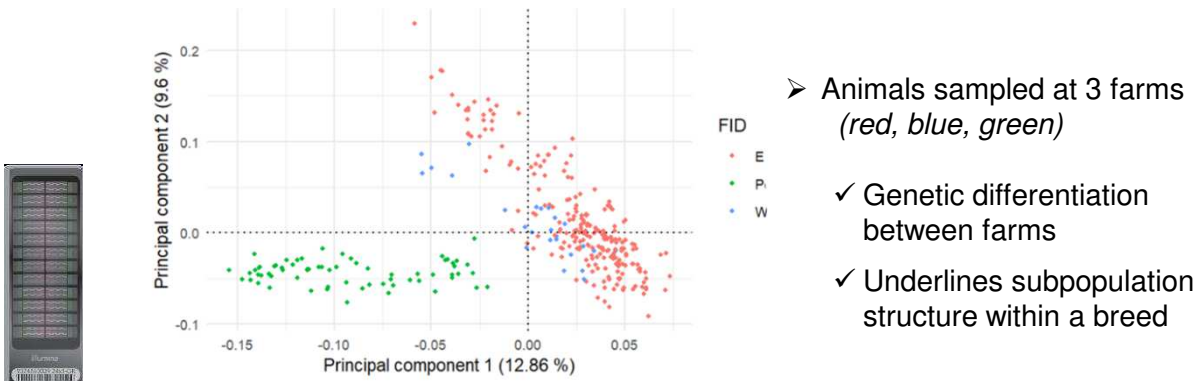
Logos: UNI KASSEL, DNA, FRIEDRICH-LOEFFLER-INSTITUT FLI Bundesforschungsanstalt für Tiergesundheit Federal Research Institute for Animal Health, Deutsche Genbank Landwirtschaftliche Nutztiere Göttingen

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ÖkoSus - First Results (WP1)

Principal Component Analysis based on SNP – Array Genotypes

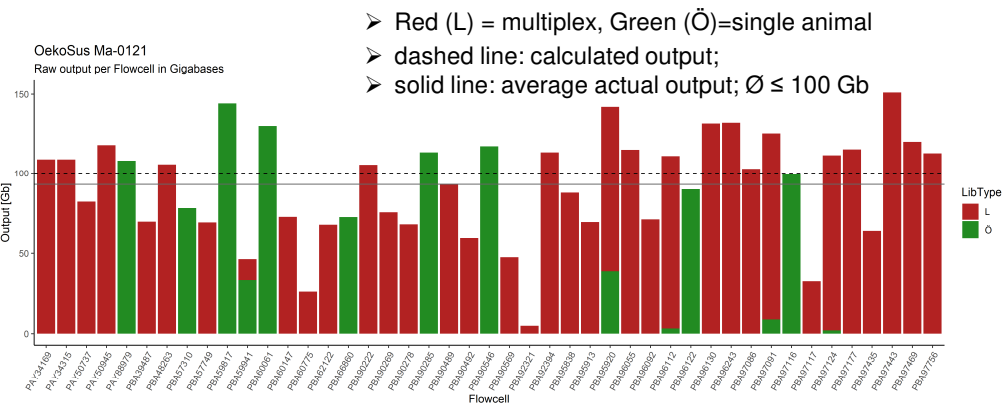
Swabian Hall Pig



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ÖkoSus - First Results (WP1)

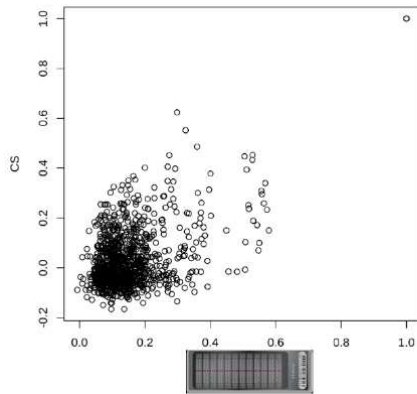
Nanopore (PromethION 2 Solo): Output per flow cell



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ÖkoSus - First Results (WP1)

Comparison between genotyping by array and by low coverage sequence



Pairwise correlations between genotyping by array (CA, X-axis) and by low coverage sequence (CS, Y-axis).

- 48 animals of Swabian Hall pig
- Pairwise correlation coefficient between genotypes

$$r = 0.8$$

- ✓ good correlation between SNP array and low coverage sequence genotypes

despite the small number of samples and the missing reference set



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Conclusion

Benefits of using low coverage sequencing for genomic characterisation:

1. Considerably more dense information compared to arrays
2. Other types of information: SVs, methylation,
3. Less ascertainment bias
4. Goal of this study is to be as cost effective as arrays
5. Integration into gene banking routines
(fast, no minimum order, one technology fits all)

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