GENOMIC SELECTION OF AGRONOMIC IMPORTANT TRAITS IN SPRING BARELY

AHMED JAHOOR

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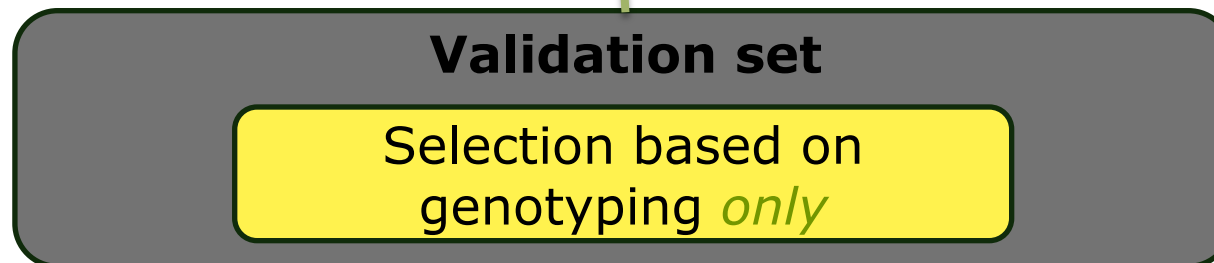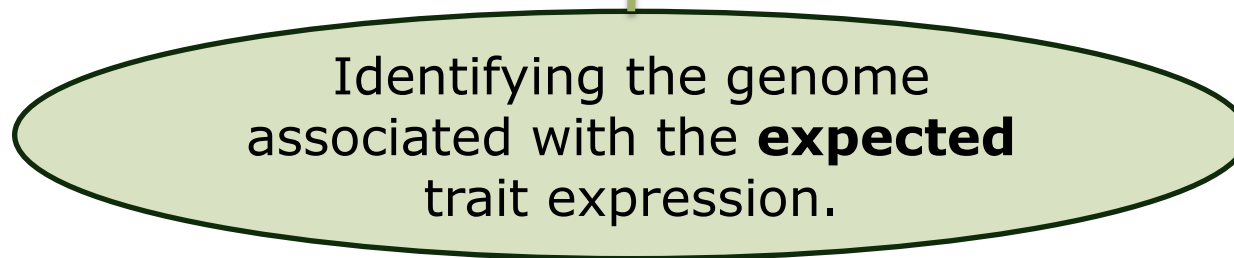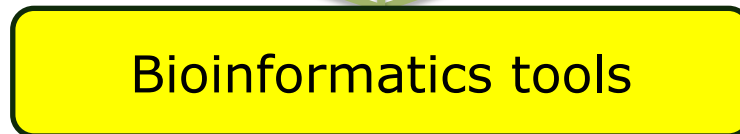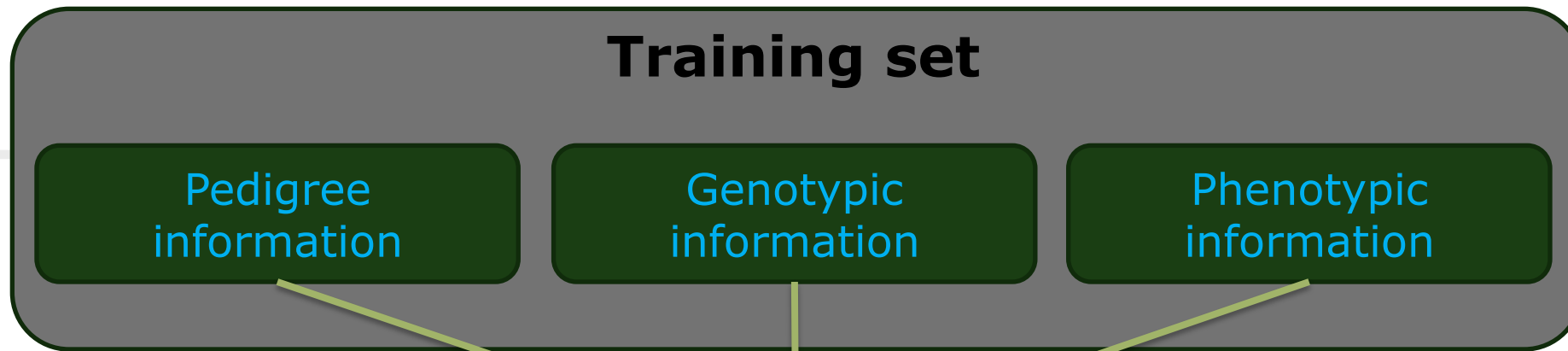
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Genomic selection

- The idea of "genomic selection, (GS)" was proposed by Meuwissen et al. (2001)

  - Omit significance testing and to use estimates of genetic marker effects.

  - GS is developed to accurately predict the genomic breeding value of lines by using genome-wide markers data.

  - Dense marker coverage is needed to maximize LD between markers and QTLs related to the trait of interest.

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GS advantage

- In GS, the underlying genetic control and biological function is not known (the cost of obtaining that knowledge is not needed)

- Most important advantages are reductions in the length of the selection cycle and phenotyping cost resulting in greater genetic gain per year.

- Genomic information may not be as accurate as real phenotypes, but it may be cheaper and faster

- One maker-genotyping can predict many traits

- Improvement of complex traits

- Better protection against copying by competitors (improvement is based on many makers)

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Training set

Pedigree information	Genotypic information	Phenotypic information

Bioinformatics tools

Identifying the genome associated with the **expected** trait expression.

Validation set

Selection based on genotyping *only*

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MODELS

- Yield and moisture (several locations and reps)

  pheno = LYT + idg + id + lyid + lyx + e

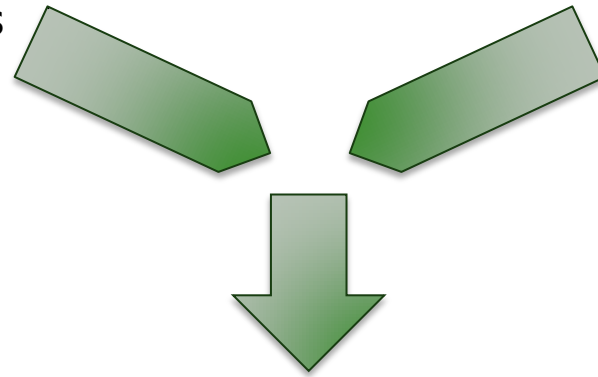 **y is year*

- Heading and height (one location no reps)

  pheno = LYT + idg + lyid + e

- Single line cross-validation

Genomic selection: blending markers and phenotypic selection

Classical MAS:
- One or a few genetic markers
- Quick breeding cycles (Backcrosses) to move positive alleles from one variety to another
- Traits affected by few gene, e.g. disease resistance genes

Phenotypic selection:
- Only use phenotypes
- Need large numbers of test crosses in large field trials
- Long and multi-stage breeding cycle
- Traits affected by many genes, e.g. yield

Genomic selection:
- Join many markers and phenotypes
- Combine quick breeding cycles and less field trials
- Target traits affected by few or many genes

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Genomic Selection in plant breeding
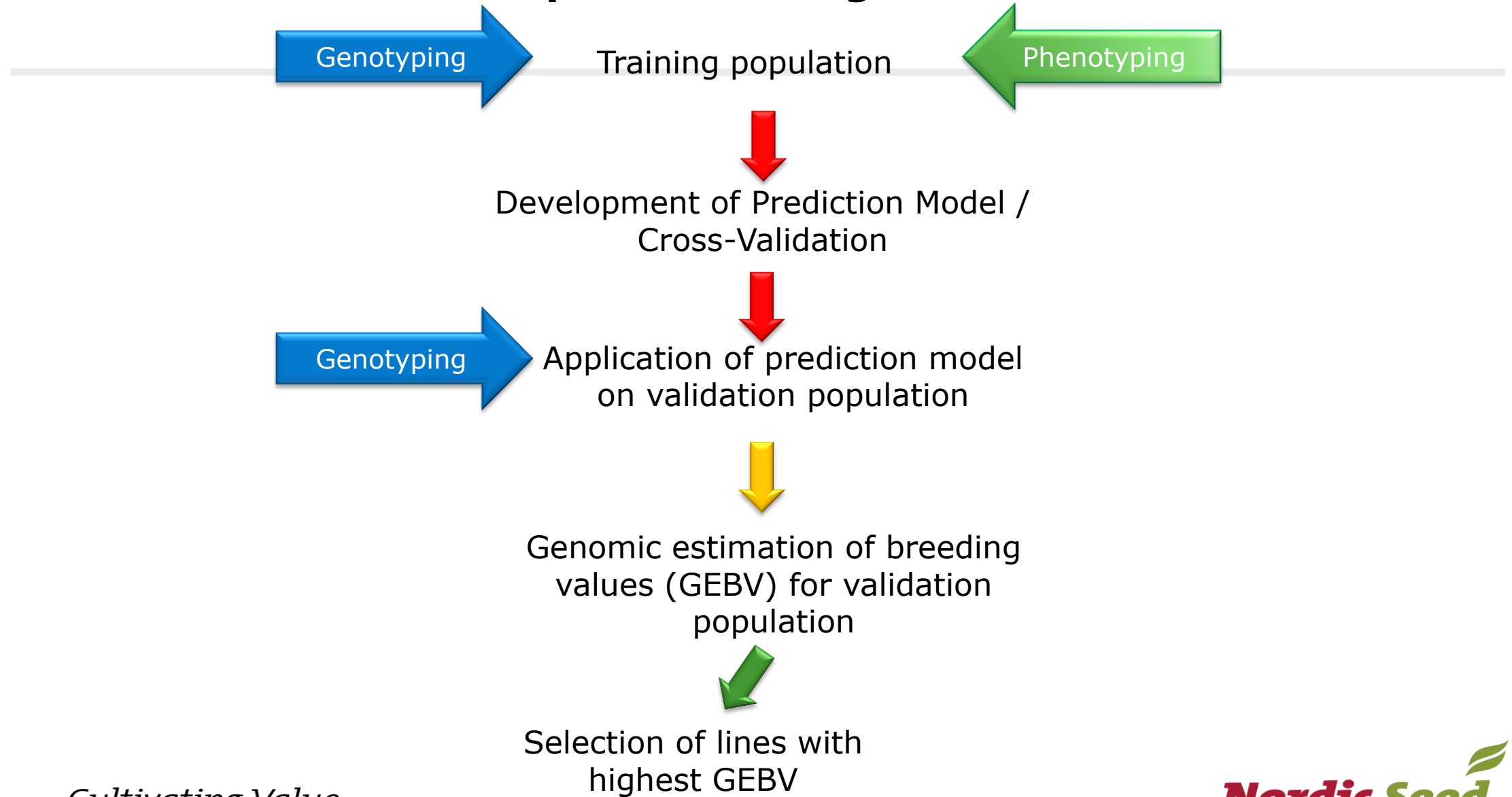
GS advantage

- Most important advantages are reductions in the selection cycle length and phenotyping cost at the same time increasing genetic gain per year.

- In GS, the underlying genetic control and biological function is not known (the cost of obtaining that knowledge is not needed).

- Genomic information may not be as accurate as real phenotypes, but it is cheaper and faster.

- Genomic selection can improve the complex and costly traits.

- Better protection against copying by competitors (improvement is based on many makers)

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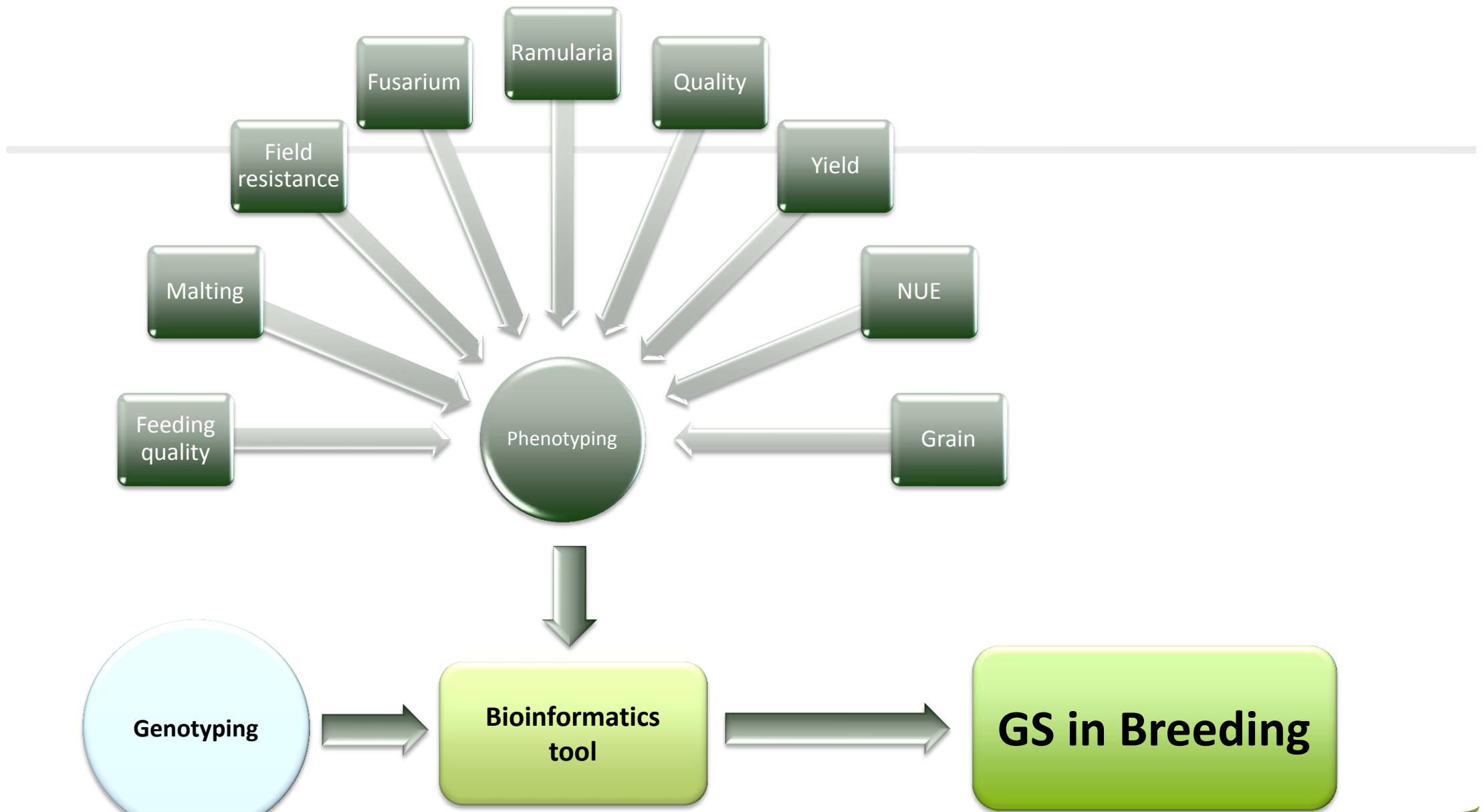
Phenotypic data

Year: 2013-2016, Locations : Abildgaard, Dyngby, Holeby

Grain quality   (3 Loc, 1 rep)

– 2.8   2.5   2.2   >2.5   >2.2   <2.2mm   Protein %   SW (kg/hl)

Malting quality   (3 Loc, 1 rep)

– Extract yield   Filtering speed   Wort color ß-Glucan Viscosity   Wort clearness

Disease   (1 Loc, 1 rep)

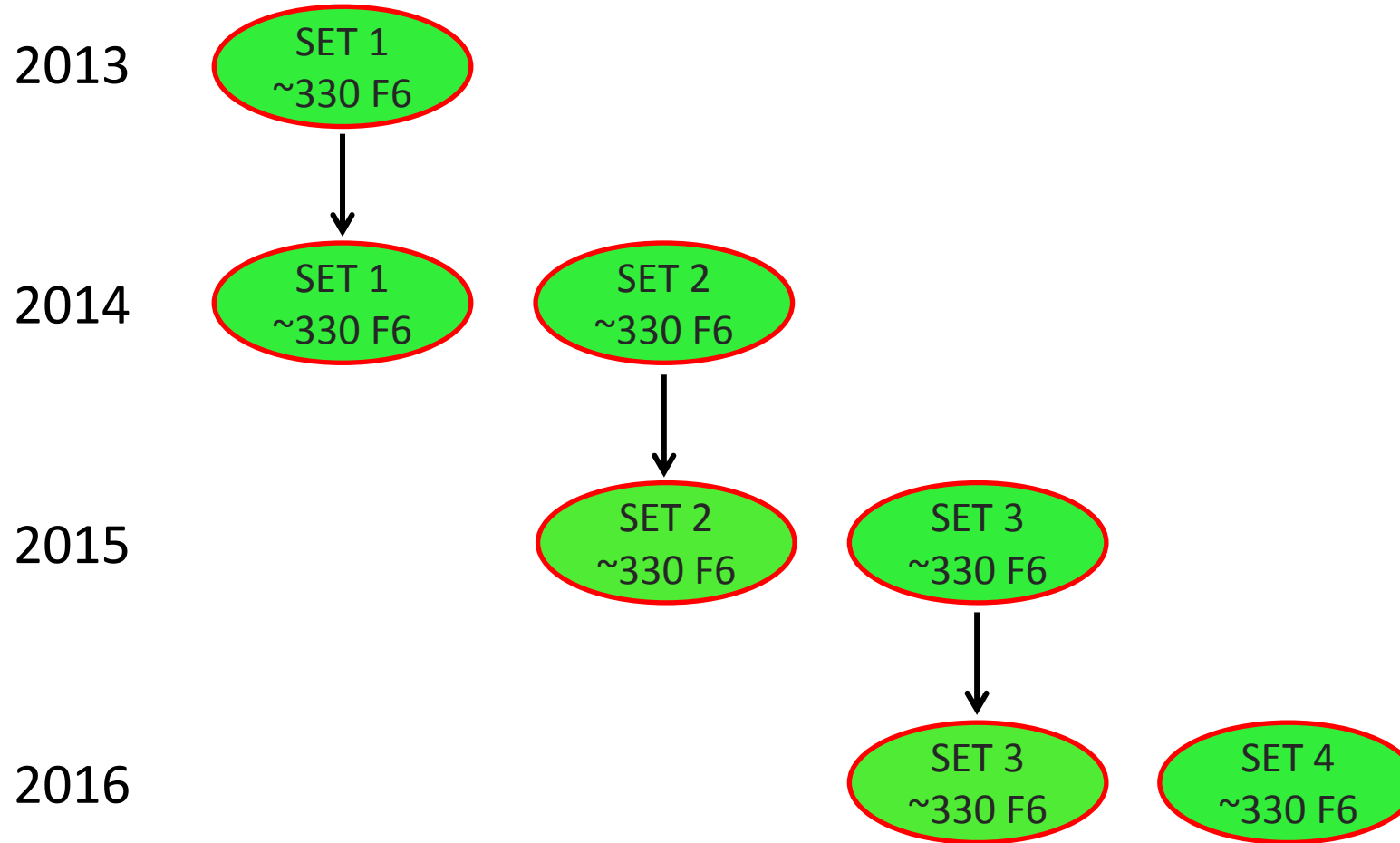– Mildew   Net Blotch   Rust   Rhynchosporium

Yield and moisture   (3 Loc, 3 rep)

Straw breaking   (1 Loc, 3 rep)

Necking   (2 Loc, 1 rep)

Heading and height (1 Loc, 1 rep)

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Data collection

2013

SET 1
~330 F6

2014

SET 1
~330 F6

SET 2
~330 F6

2015

SET 2
~330 F6

SET 3
~330 F6

2016

SET 3
~330 F6

SET 4
~330 F6

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Summary

- Theory of genomic selection sounds good

- The model of genomic selection in plants are mostly on place

- Applicability of genomic selection has to be proofed

- Future breeding based on genomic selection needs more results

- Saving resources and shortening of breeding cycle

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Research and development group at Nordic Seed

- **Ahmed Jahoor**, Head of breeding and research

- **Jihad Orabi,** Head of molecular breeding

- **Jens Due Jensen,** Barley breeder

- **Vahid Edriss,** Post Doc. quantitative genetics / GS

- **Nanna Hellum Nielsen,** Post Doc. Malt quality/ GS

- **Hanne Svenstrup,** Laboratory technician

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THANK YOU FOR LISTENING

Genomic selection of agronomic important traits in Spring barely

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