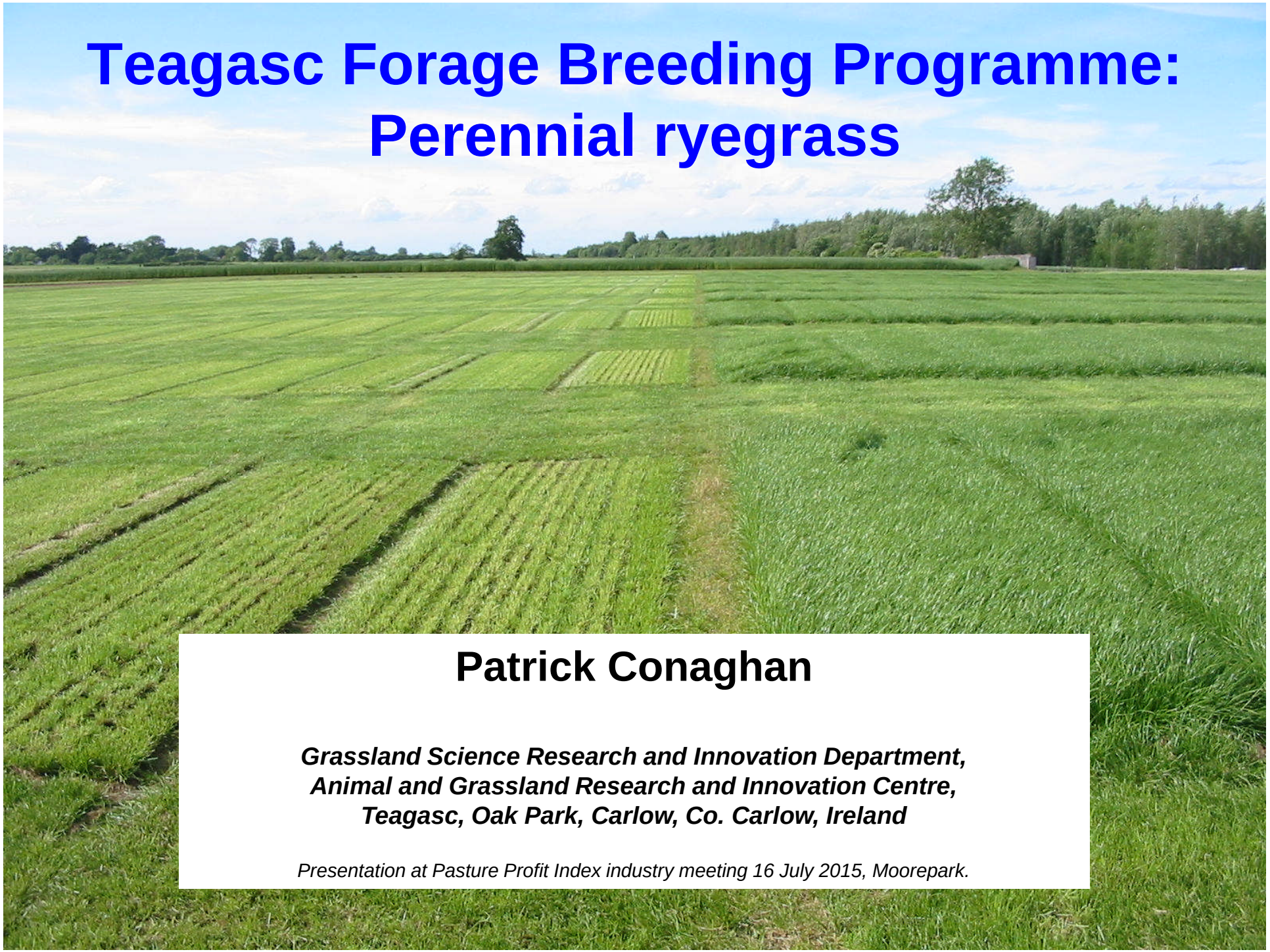
Teagasc Forage Breeding Programme: Perennial ryegrass



Patrick Conaghan

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Teagasc, Oak Park, Carlow, Co. Carlow, Ireland

Presentation at Pasture Profit Index industry meeting 16 July 2015, Moorepark.

Variety improvement

Stage 1

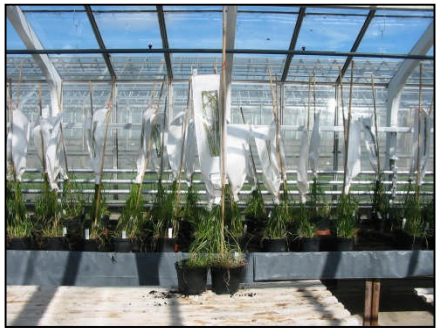
Breeding
(Variety development)
7 to 10 years

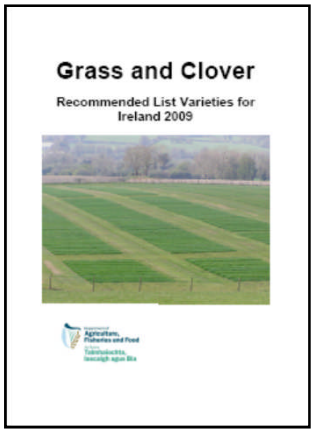
Stage 2

Independent
variety testing
(DAFM)
5 years

Stage 3

Commercialisation
(Seed release)
≥ 2 years





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What is grass breeding?

Breeding is man directed evolution

Evolution: The genetic change in a species over time

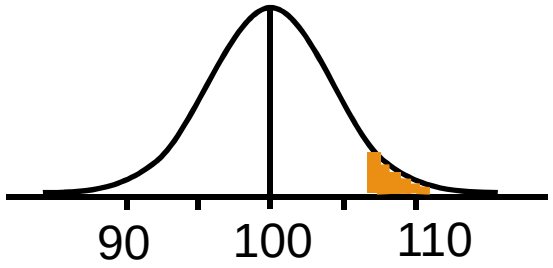
- Natural and ongoing process
- Slow
- Direction of evolution favoured by man & nature may be different

Breeding is necessary:

- To speed up the process of evolution
- To ensure evolution proceeds in a direction favourable to man's needs

Breeding process

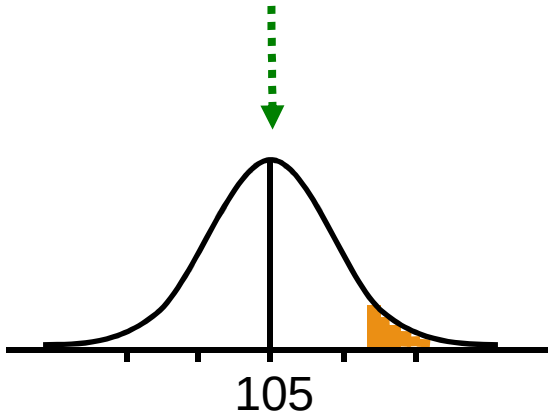
Yield



(1) Evaluation

(2) Selection

(3) Recombination



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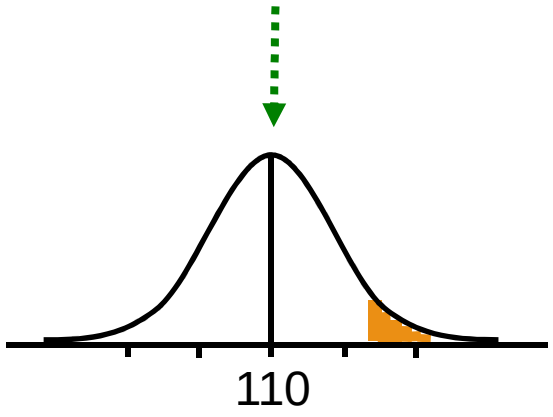

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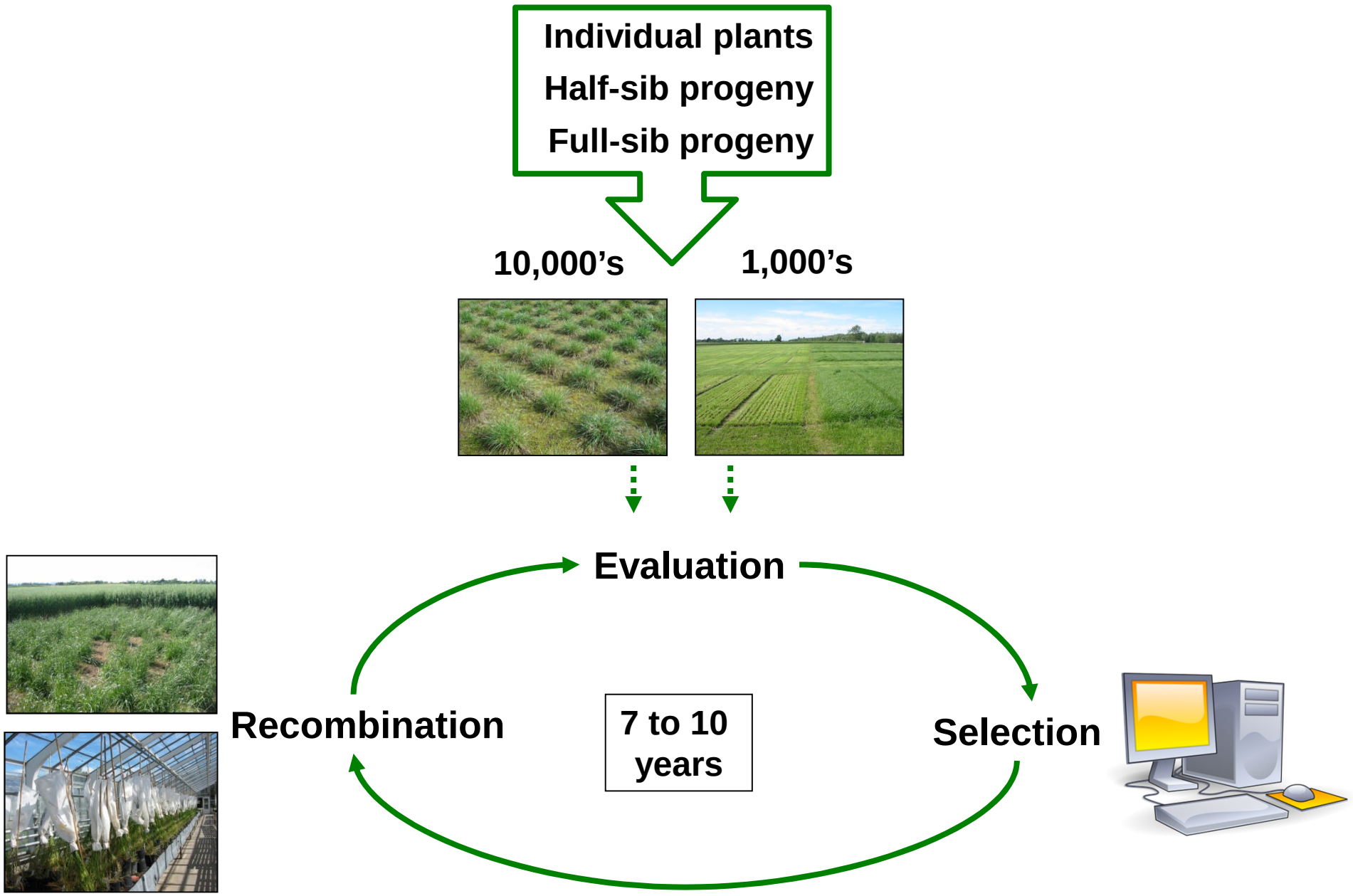
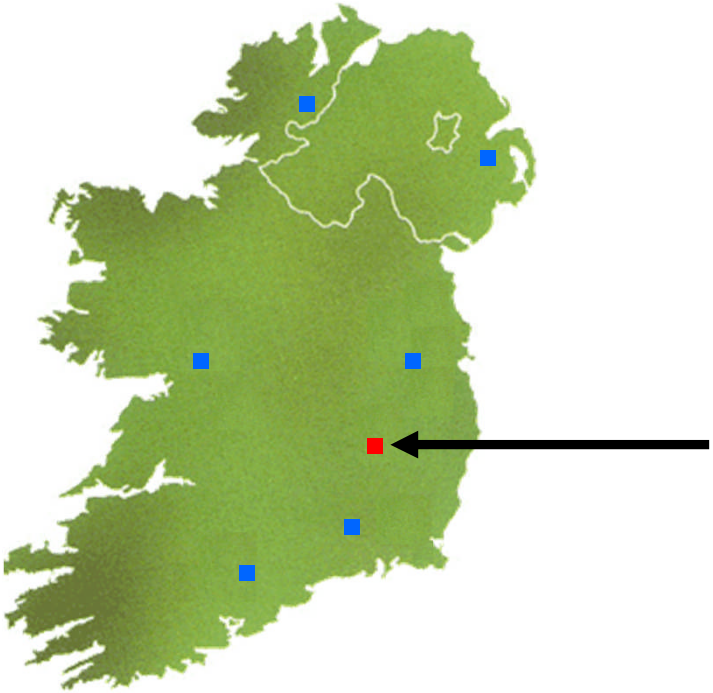
Breeding process



Teagasc breeding station



Animal & Grassland Research & Innovation Centre, Teagasc, Oak Park, Carlow

40 ha for forage breeding

Breeding traits: now & future

More traits = more time, slower gain

Rule no. 1: Select the minimum number of only the most important traits

Improvement traits:

- Persistency (change in yield over time)
- Grazing yield (spring, autumn + annual)
- Quality (digestibility, leafiness)
- Ground cover
- Disease resistance (crown rust)

Maintenance traits:

- Silage yield

Future:

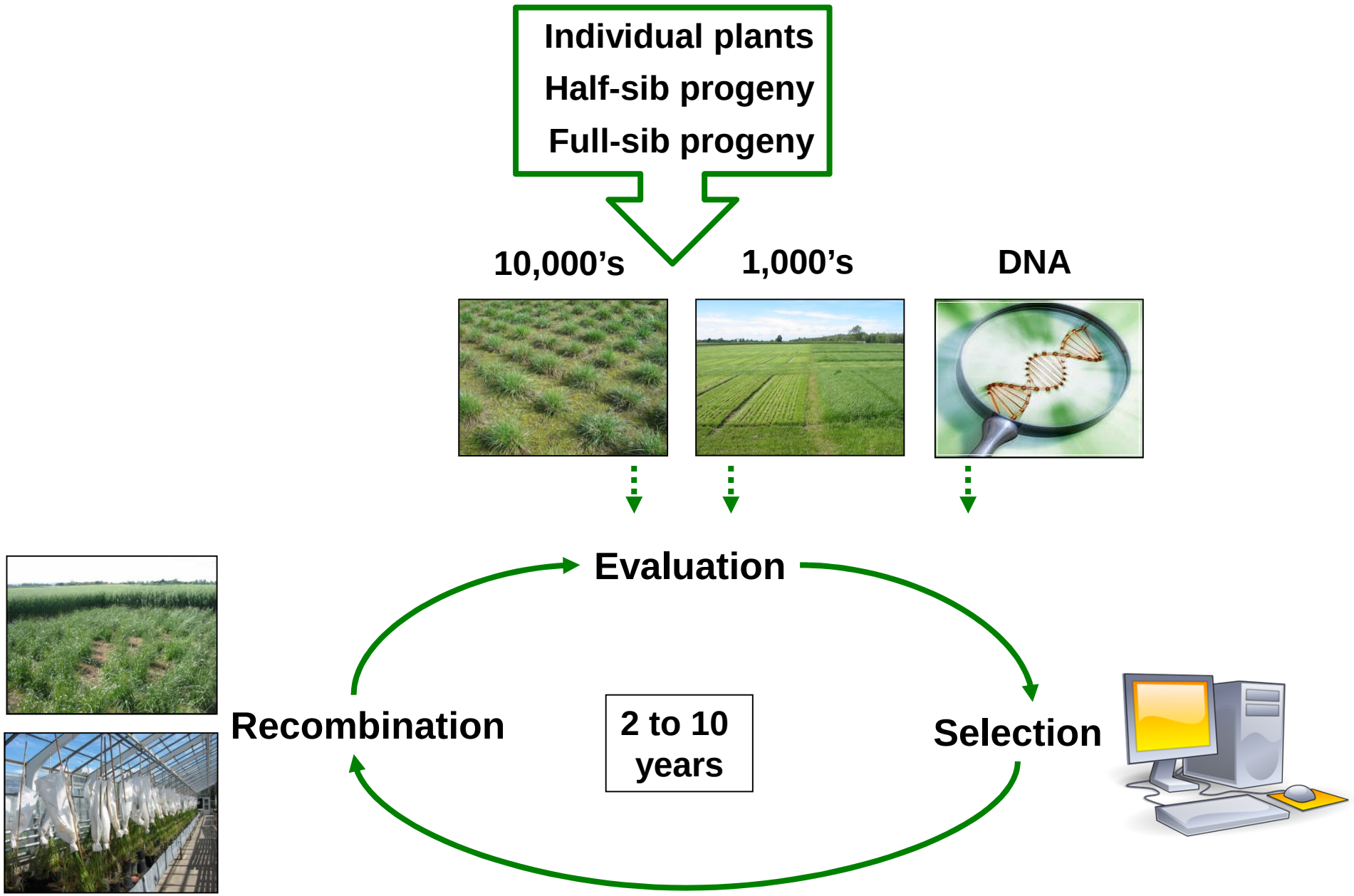
- Current traits remain foundation
- May be change in classification from improvement to maintenance trait
- New traits introduced depending on research, agricultural laws, farming practices etc.

Future breeding methods

Genomic selection: Selection based on DNA analyses

Advantages:
- Speed (3 cycles GS vs. 1 cycle conventional breeding)
- Cost

Breeding process



Genomic selection

Underway

Part 1: Genotyping

DNA analysis

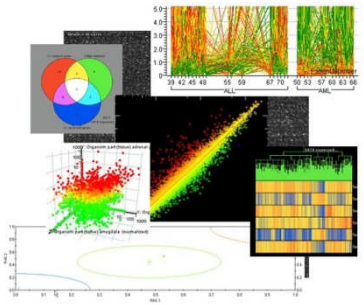
Underway

Part 2: Phenotyping

Plant evaluation

Part 3: Statistical analyses

Applying genomic selection values



Genomic selection in 2018

Acknowledgements

Supported by:

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