Optimizing genomic breeding program designs to improve crossbred performance

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EAAP, Ghent, 27 August 2019

Acknowledgements

Financial support of

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HENDRIX GENETICS

Cobb

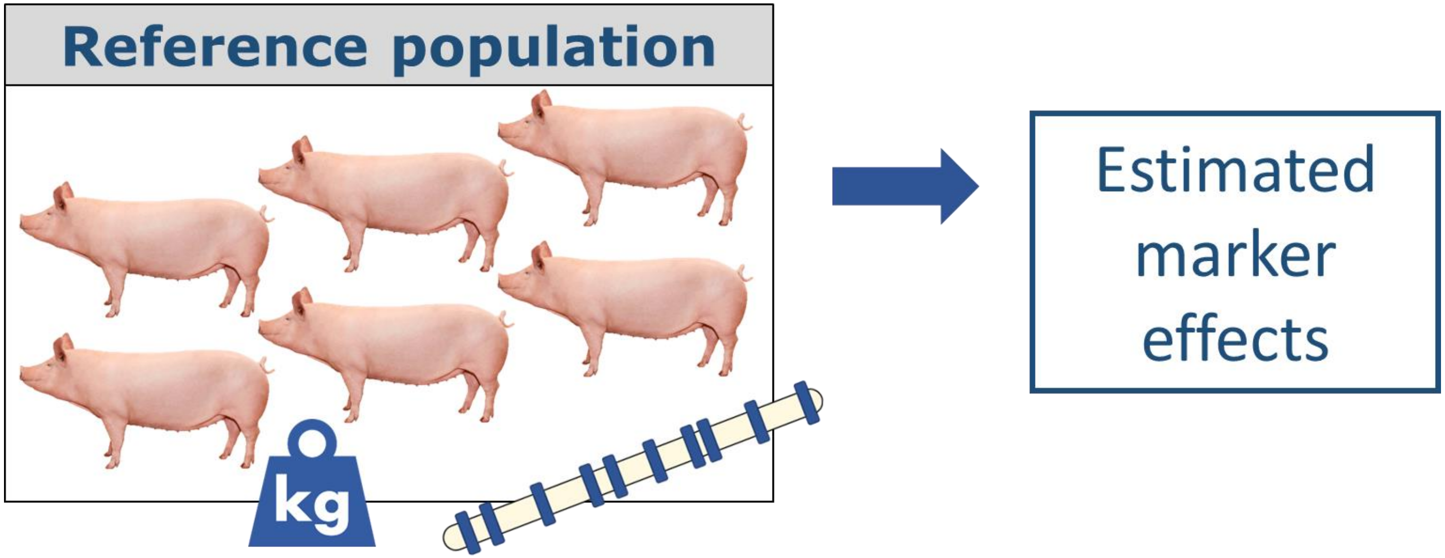
Topigs Norsvin
PROGRESS IN PIGS

CRV

WAGENINGEN
UNIVERSITY & RESEARCH

100years
1918 — 2018

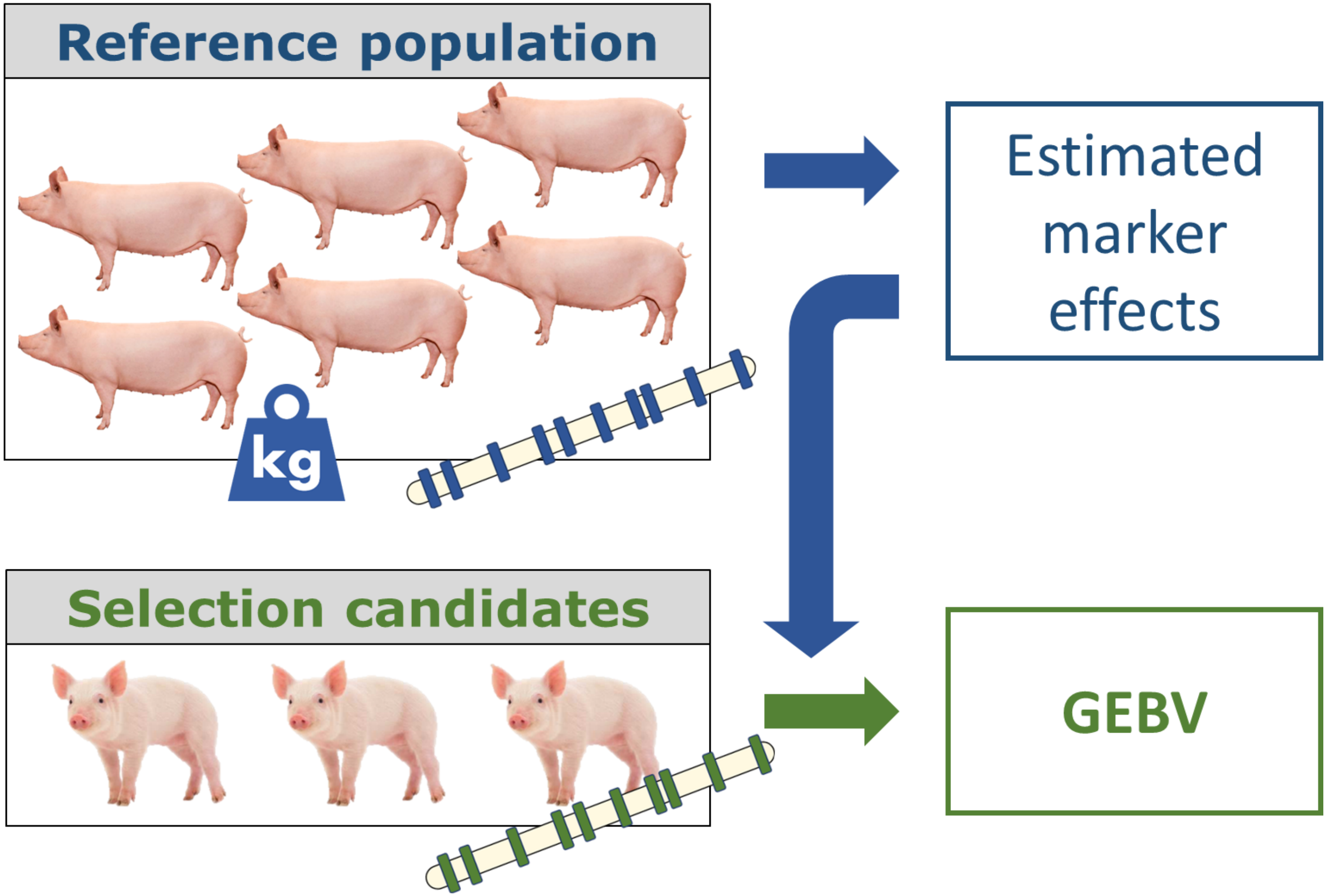
Genomic prediction



Reference population

Estimated marker effects

Genomic prediction



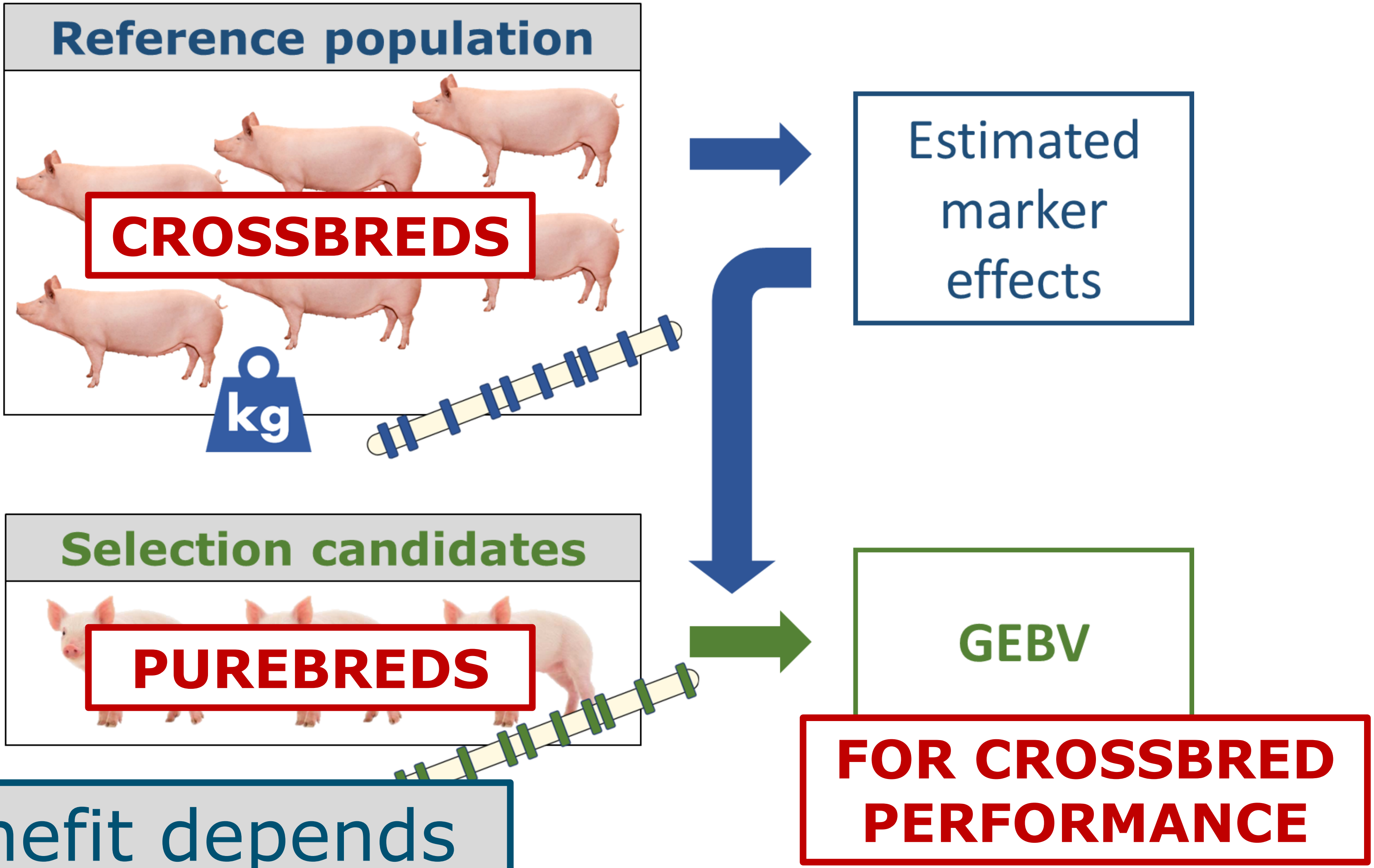
Reference population

Estimated marker effects

Selection candidates

GEBV

Genomic prediction for crossbred performance



Reference population

CROSSBREDS

Estimated marker effects

Selection candidates

PUREBREDS

GEBV

FOR CROSSBRED PERFORMANCE

Benefit depends on r_{pc}

Accuracy of genomic prediction

Depends on **relations** between reference and selection individuals

Relatedness

Accuracy

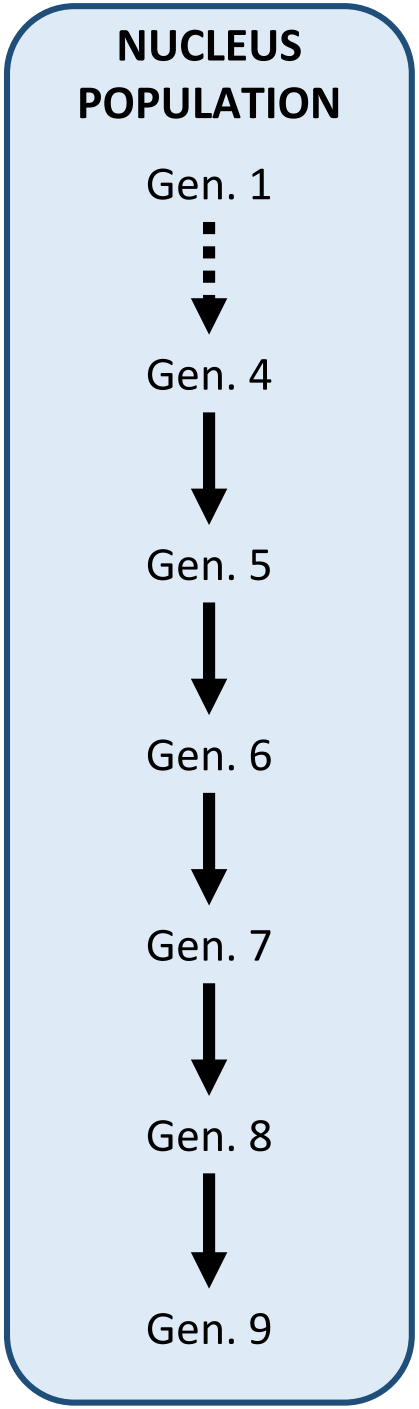
Aim of research

Investigate benefit of using a **crossbred** over a **purebred reference population** for different levels of:

- Relatedness between RP and selection candidates
- Purebred-crossbred correlation (r_{pc})
- Reference population sizes

to predict GEBV for **crossbred performance** of purebred selection candidates

Simulated breeding program



NUCLEUS POPULATION

Gen. 1

Gen. 4

Gen. 5

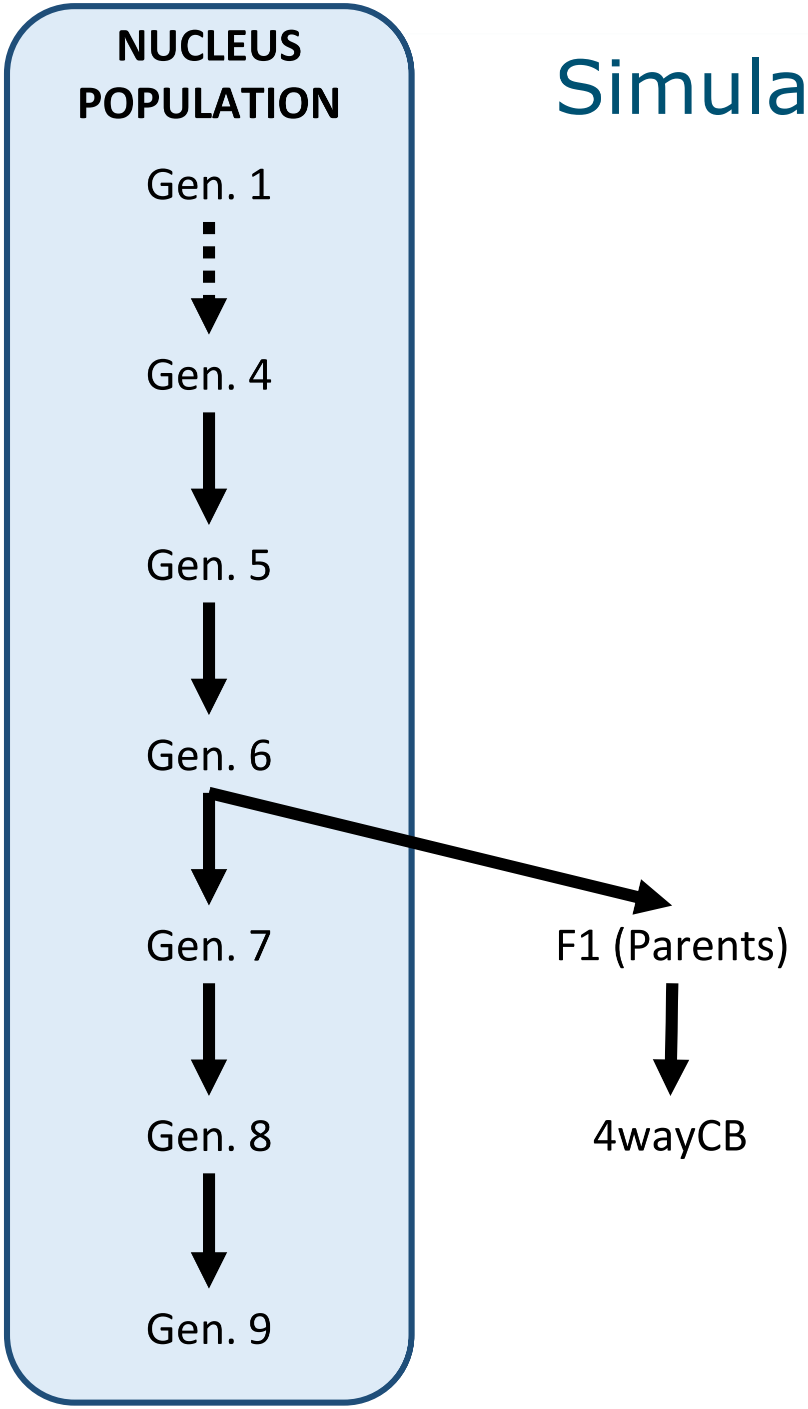
Gen. 6

Gen. 7

Gen. 8

Gen. 9

Simulated breeding program



NUCLEUS POPULATION

Gen. 1

Gen. 4

Gen. 5

Gen. 6

Gen. 7

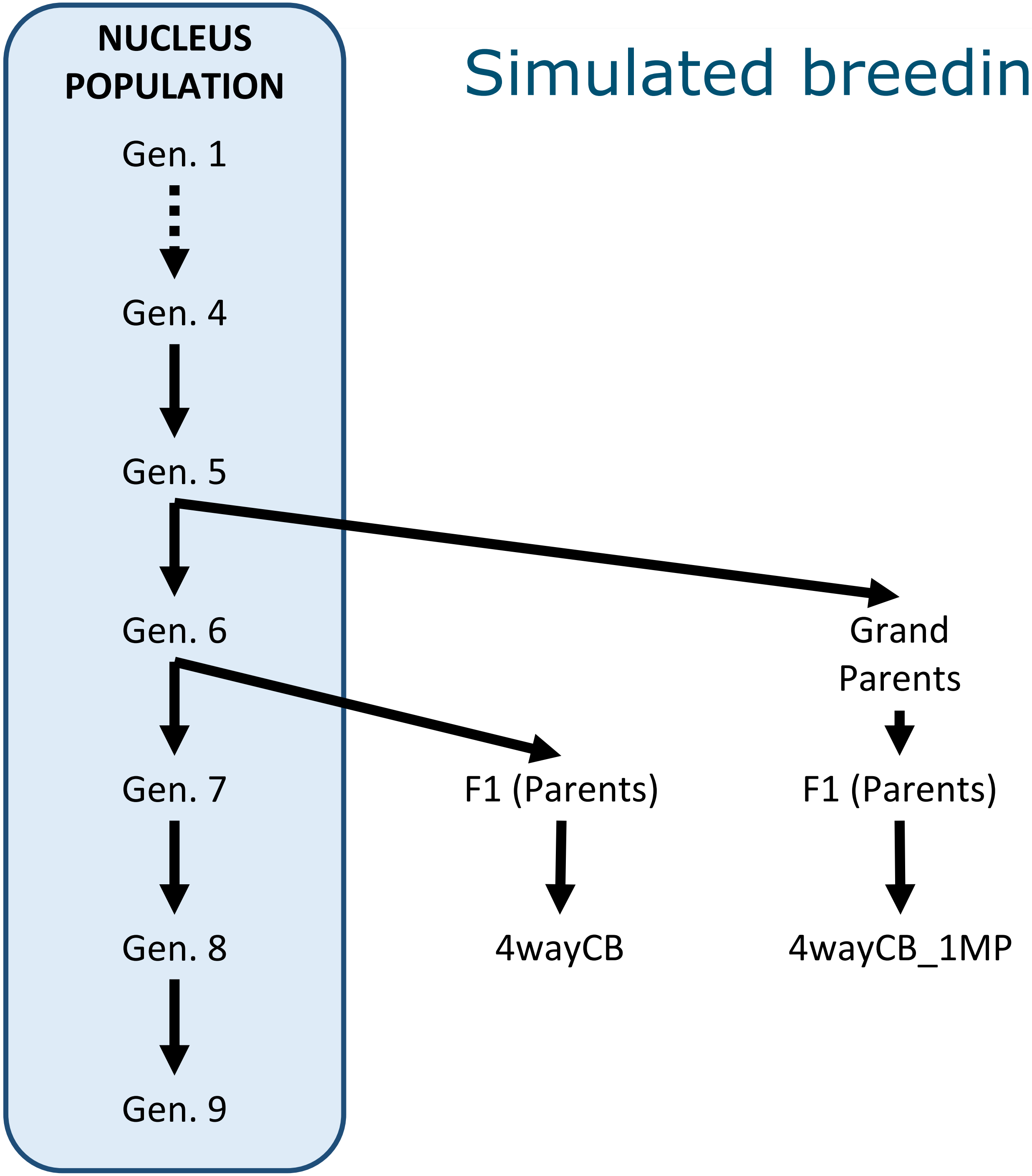
Gen. 8

Gen. 9

F1 (Parents)

4wayCB

Simulated breeding program



NUCLEUS POPULATION

Gen. 1

Gen. 4

Gen. 5

Gen. 6

Gen. 7

Gen. 8

Gen. 9

Grand Parents

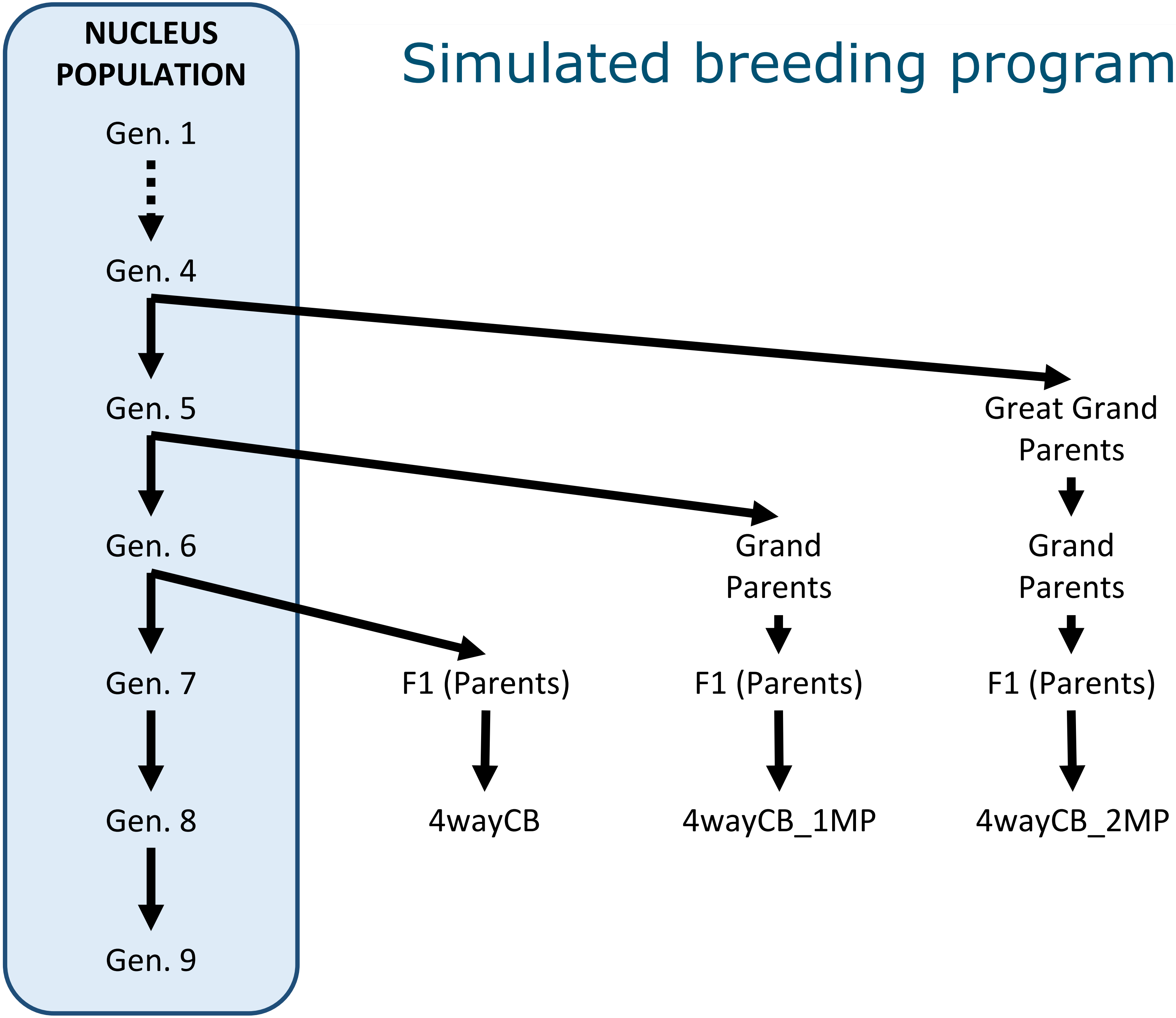
F1 (Parents)

F1 (Parents)

4wayCB

4wayCB_1MP

Simulated breeding program



NUCLEUS POPULATION

Gen. 1

Gen. 4

Gen. 5

Gen. 6

Gen. 7

Gen. 8

Gen. 9

Great Grand Parents

Grand Parents

Grand Parents

F1 (Parents)

F1 (Parents)

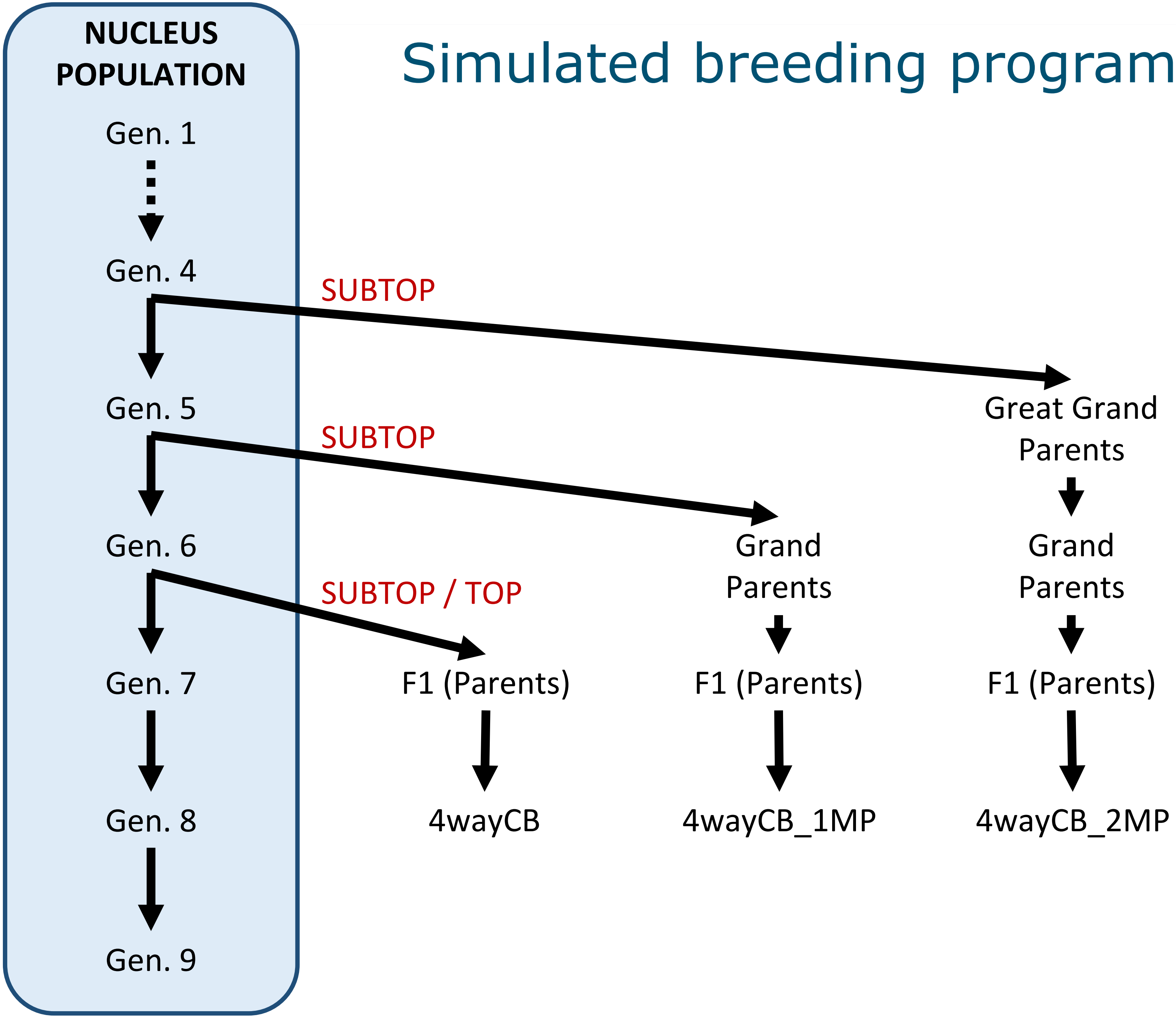
F1 (Parents)

4wayCB

4wayCB_1MP

4wayCB_2MP

Simulated breeding program



NUCLEUS POPULATION

Gen. 1

Gen. 4

SUBTOP

Gen. 5

SUBTOP

Gen. 6

SUBTOP / TOP

Gen. 7

Gen. 8

Gen. 9

Great Grand Parents

Grand Parents

Grand Parents

F1 (Parents)

F1 (Parents)

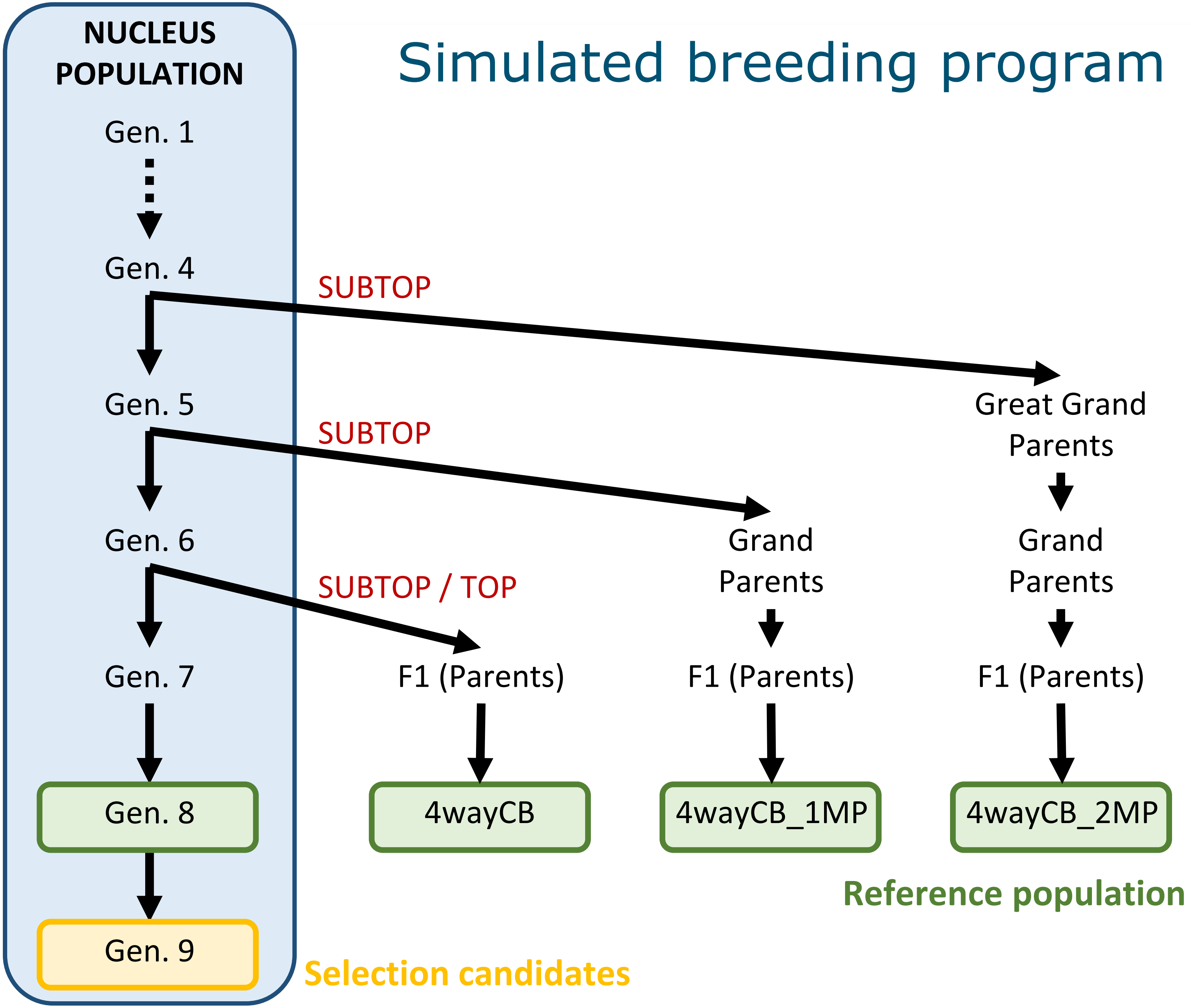
F1 (Parents)

4wayCB

4wayCB_1MP

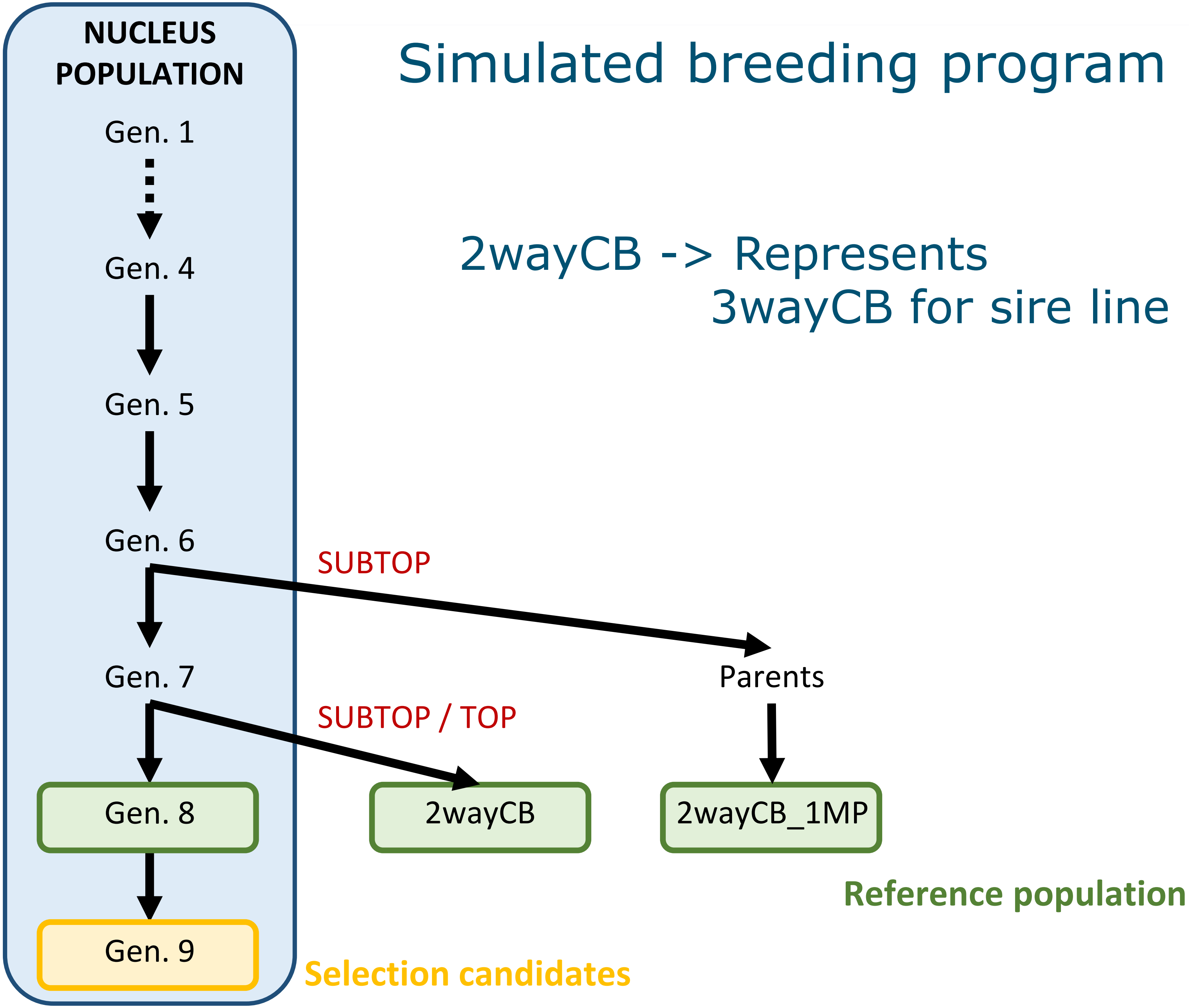
4wayCB_2MP

Simulated breeding program



Simulated breeding program

2wayCB -> Represents
3wayCB for sire line



NUCLEUS POPULATION

Gen. 1

Gen. 4

Gen. 5

Gen. 6

Gen. 7

Gen. 8

Gen. 9

SUBTOP

Parents

SUBTOP / TOP

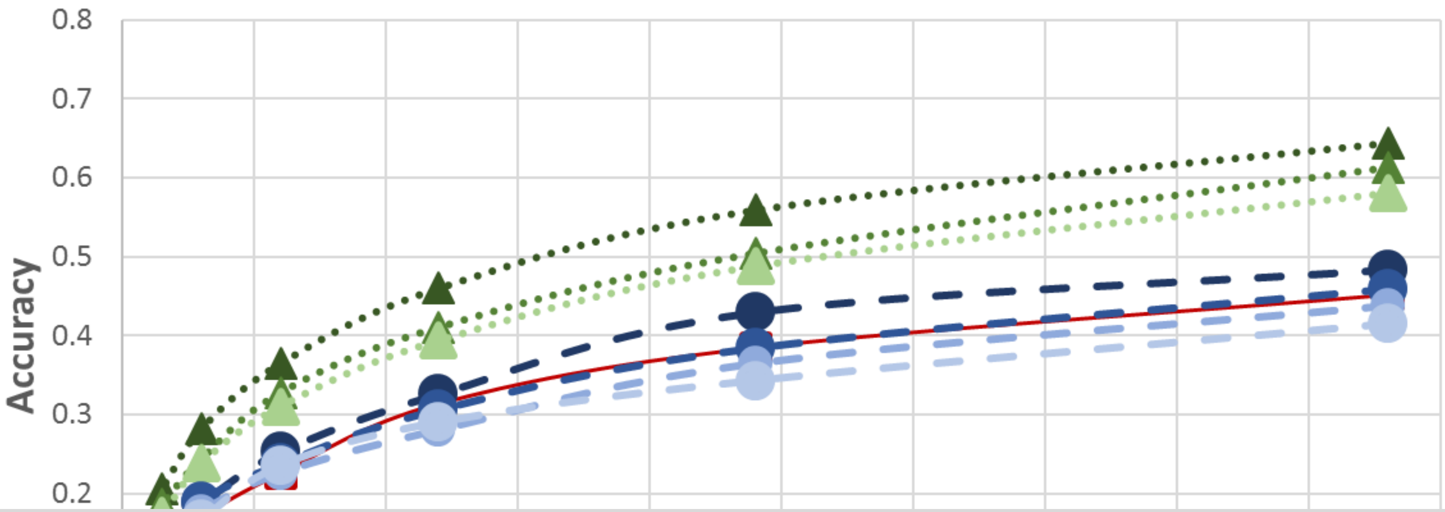
2wayCB

2wayCB_1MP

Reference population

Selection candidates

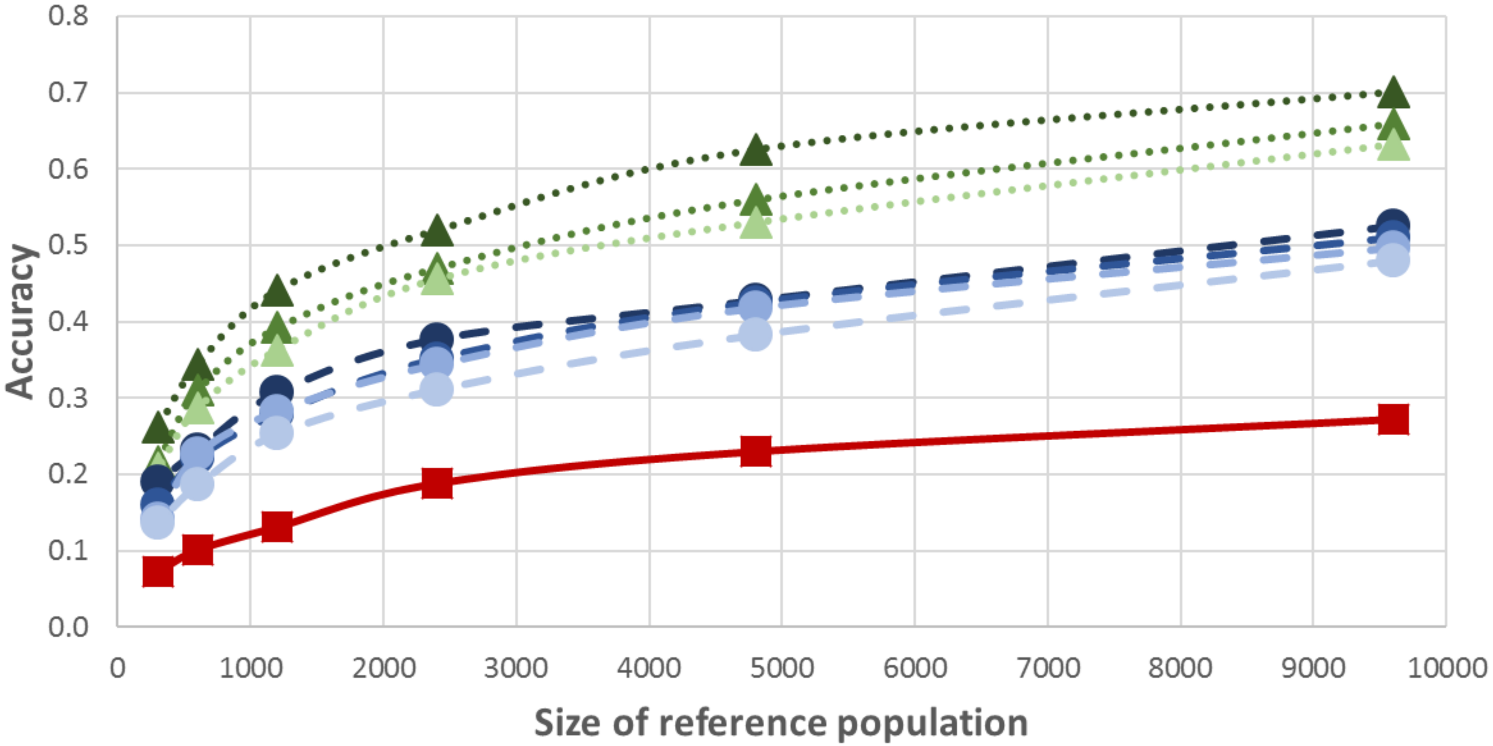
Accuracies with r_{pc} of 0.75



2wayCB > PB

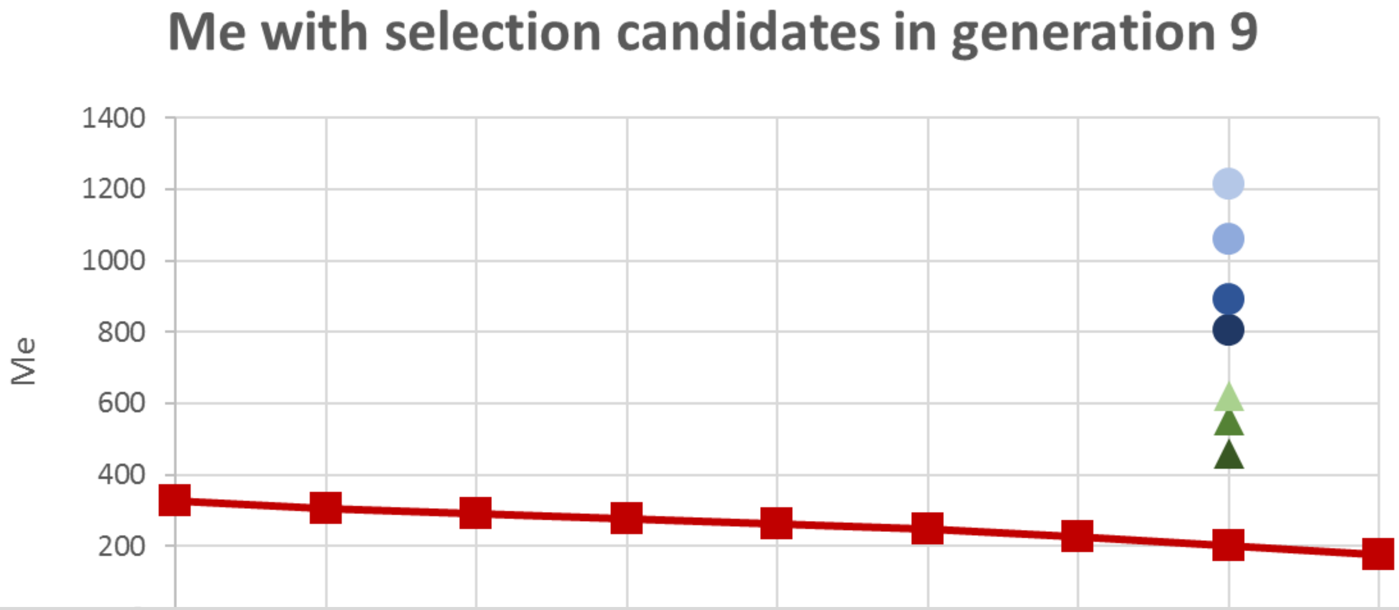
4wayCB > PB,
depending on size of RP and relatedness

Accuracies with r_{pc} of 0.5



2wayCB & 4wayCB > PB

Number of independent chromosome segments (M_e)


Me with selection candidates in generation 9

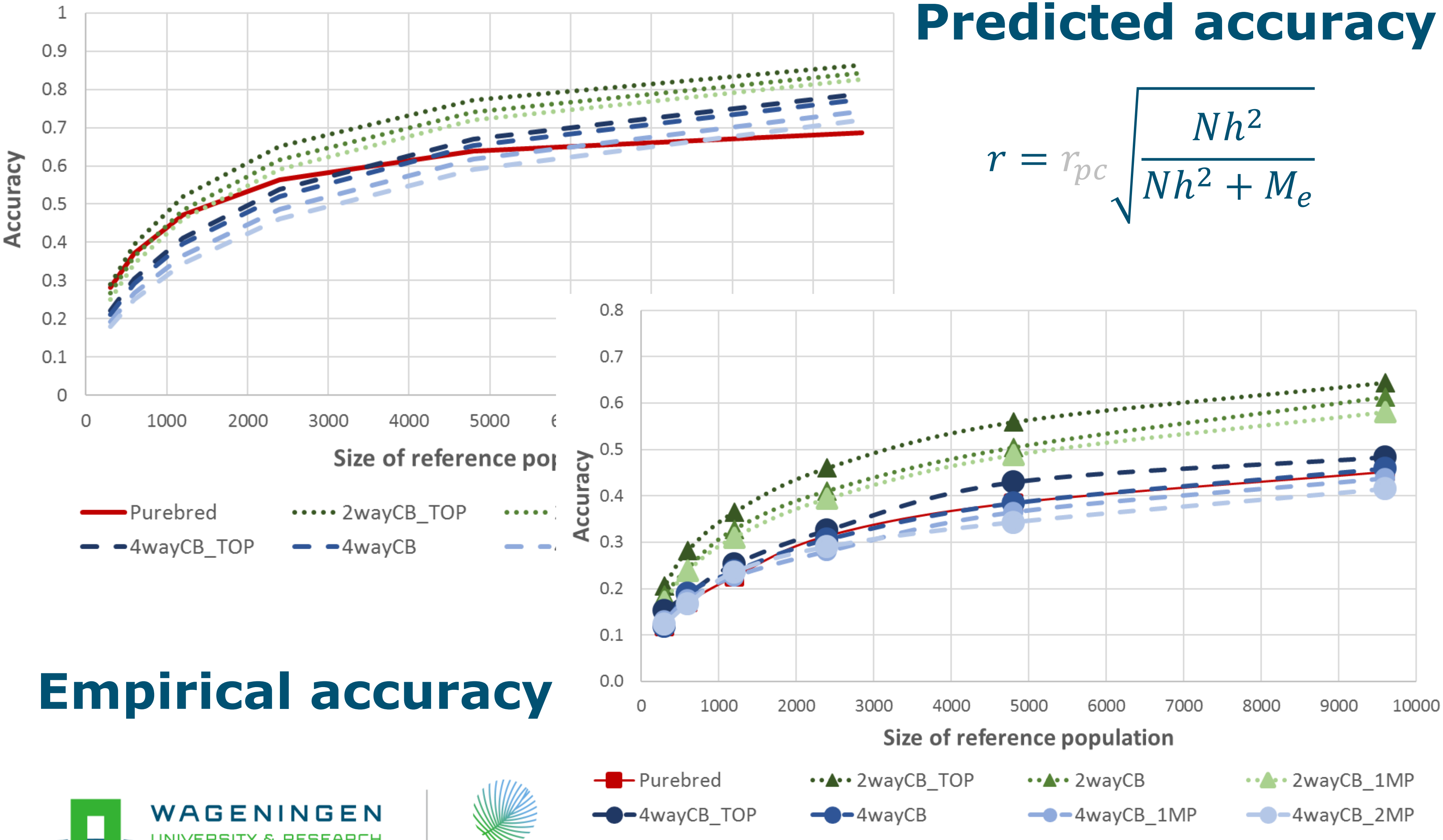
M_e 2wayCB ~ 2 M_e PB

M_e 4wayCB ~ 4 M_e PB

Predicted versus Empirical accuracy (r_{pc}=0.75)

Predicted accuracy

$$r = r_{pc}\sqrt{\frac{Nh^2}{Nh^2 + M_e}}$$



Empirical accuracy

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100years
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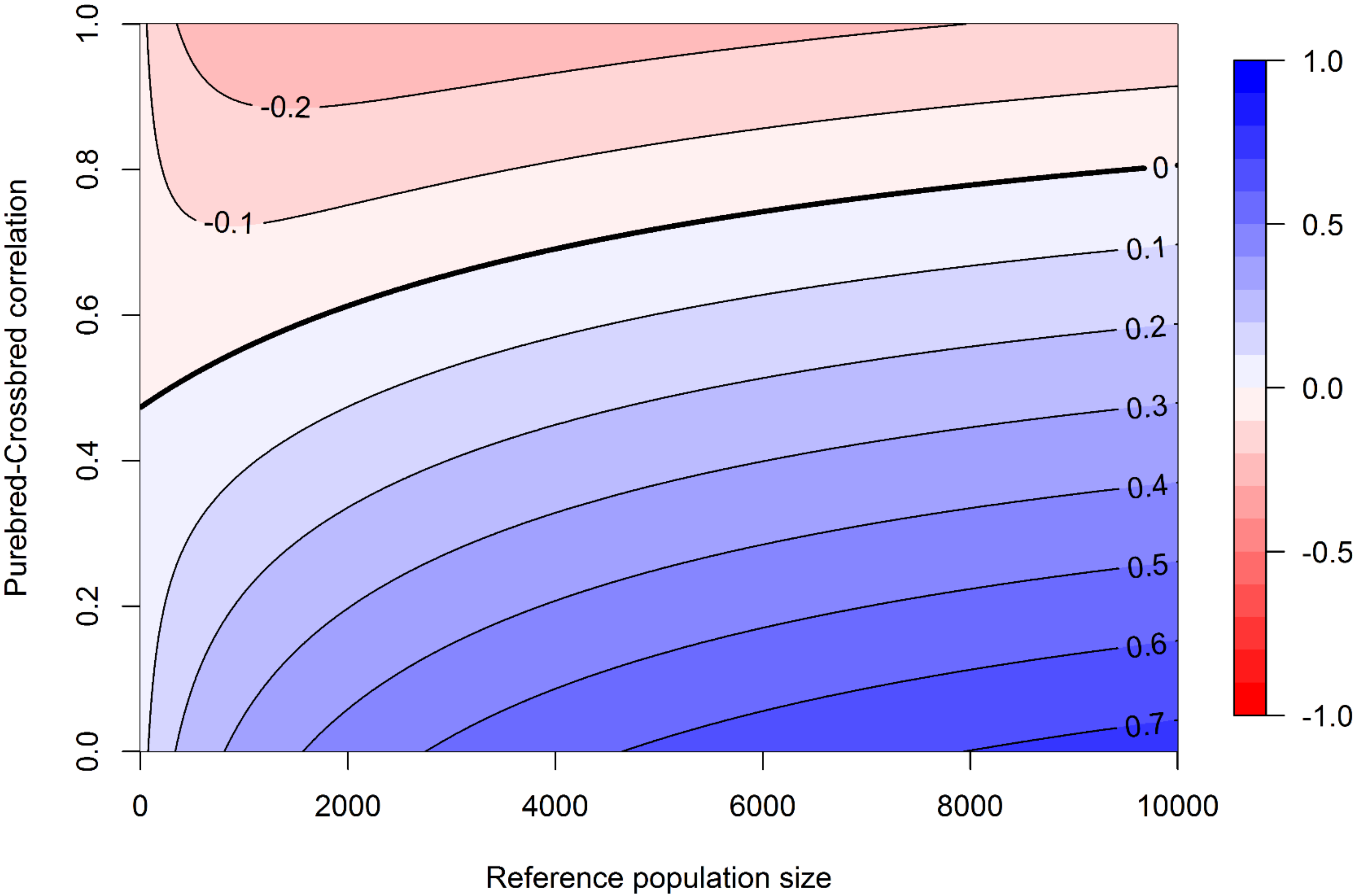
Expectations across r_{pc} and RP sizes



Conclusions breeding program design

Benefit of crossbred information depends on:

- Purebred-crossbred correlation (r_{pc})
  - Lower r_{pc}, more benefit CB

- Relatedness to the selection candidates
  - Higher relatedness (lower M_e), more benefit CB

- Size of reference population
  - Larger reference population, more benefit CB

Prediction equation can predict ranking of scenarios