Mating strategies using genomic information reduce rates of inbreeding in animal-breeding schemes

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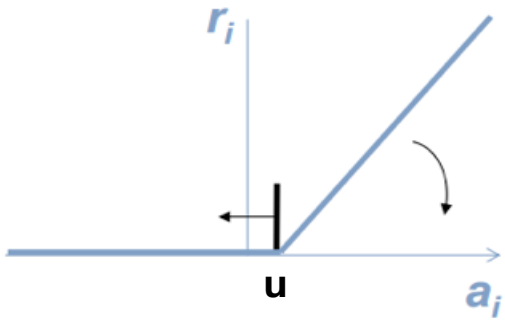
Mating strategies

- Optimize combinations of genetic materials
- Improve family structure
- May generate lower rates of inbreeding and/or higher genetic gain

Genetic contribution theory

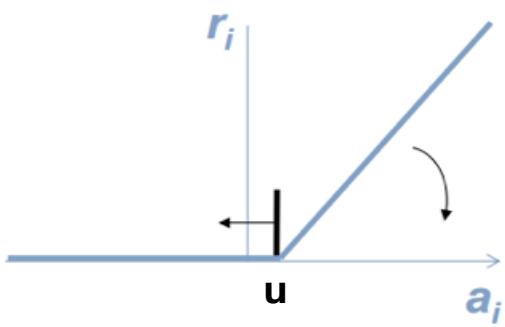
Long-term contribution

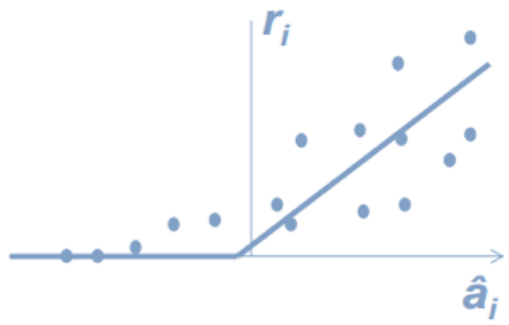


Mendelian sampling terms

Genetic contribution theory

Long-term contribution





Mendelian sampling terms

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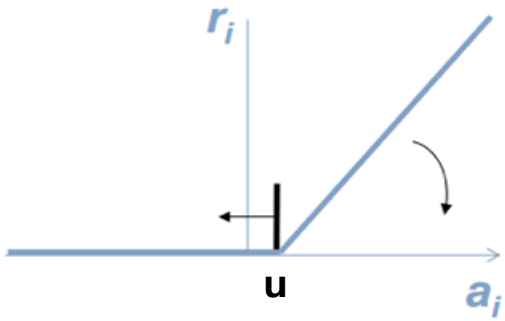
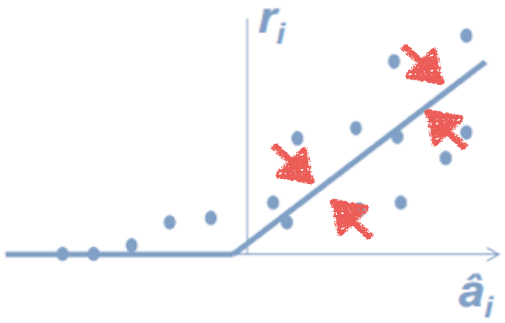


Mendelian sampling terms

Non-random mating strategies



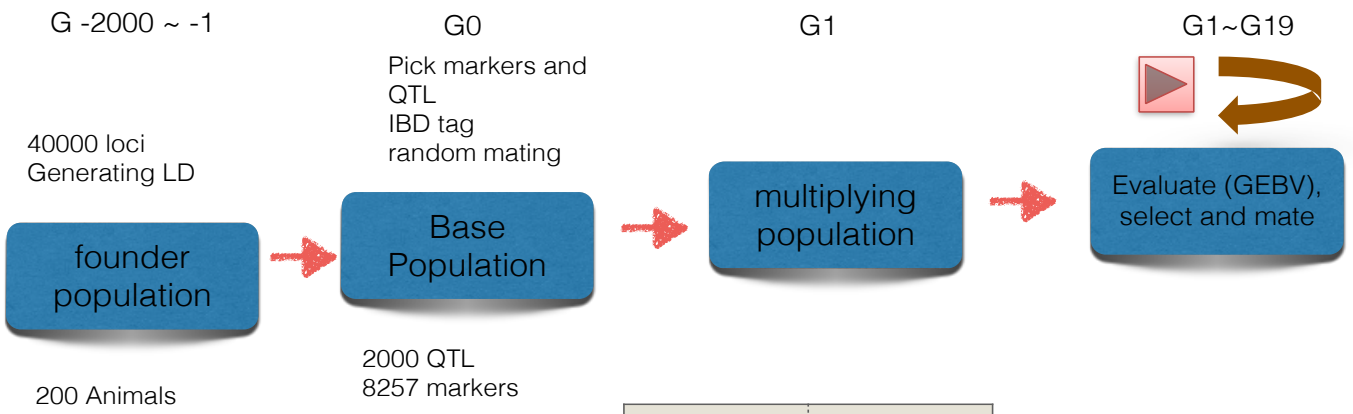
Mating strategies with genomic information?

- provide additional information on Mendelian inheritance
- increase independency
- closer alignment $\rightarrow$ lower inbreeding

Hypothesis

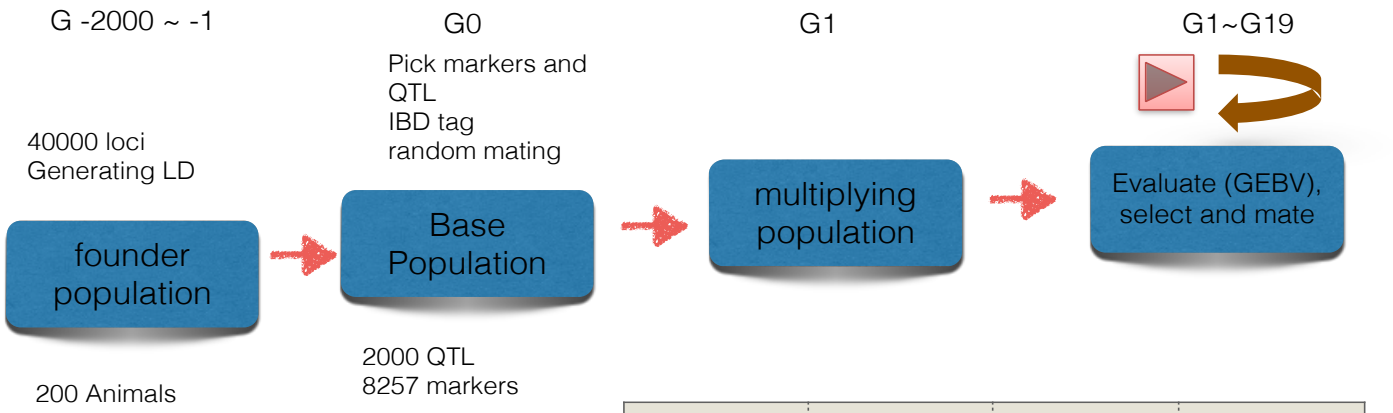
- The mating strategies using genomic information realizes lower rates of inbreeding without decreasing the genetic gain than using pedigree information

Experimental design



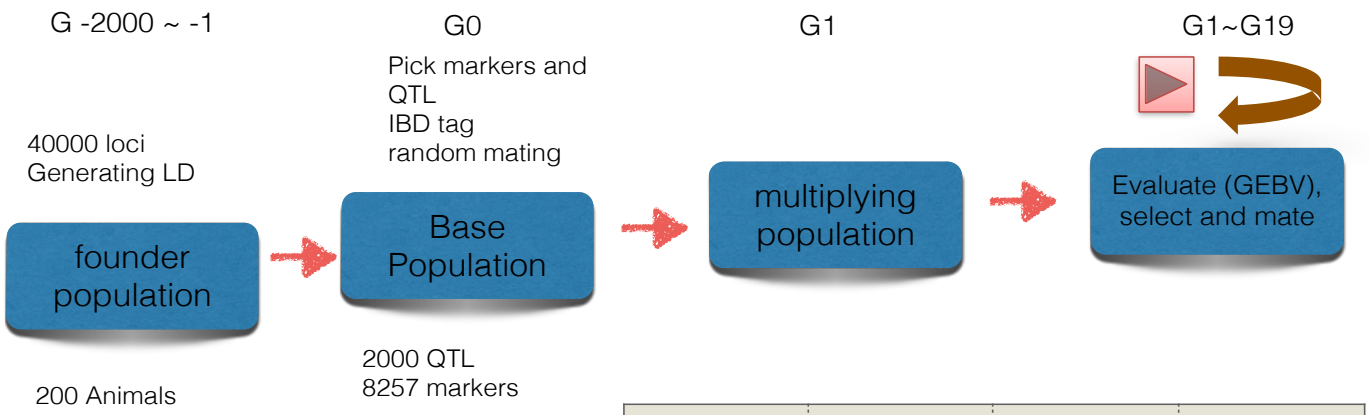
Breeding scheme	population size
1	1200
2	1200
3	400
4	400
5	400

Experimental design



Breeding scheme	population size	number of sires	number of dams
1	1200	20	120
2	1200	20	20
3	400	20	20
4	400	20	40
5	400	20	40

Experimental design



full-sib families

Breeding scheme	population size	number of sires	number of dams
1	1200	20	120
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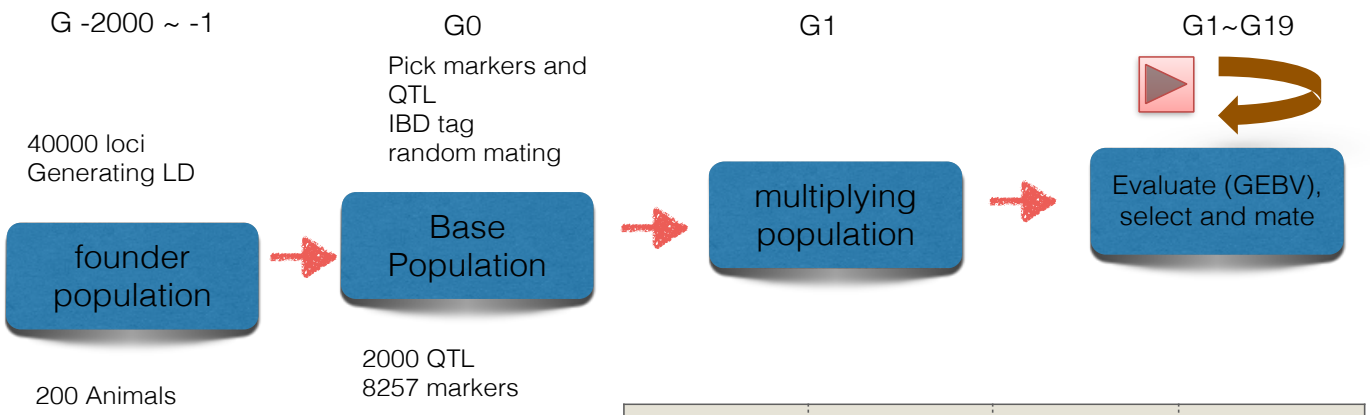
Experimental design



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h^2=0.1

h^2=0.4

Mating strategies

- MC:minimum-coancestry mating
- MCAC:mating by minimising the covariance between ancestral contributions

	MC	**MCAC**
Pedigree	MC_Ped	MCAC_Ped
Genomic	MC_Mrk	MCAC_Mrk

- MC_Ped and MCAC_Ped $\rightarrow$ computing additive numeritor relationship **A** or genetic contribution **C**
- MC_Mrk and MCAC_Mrk $\rightarrow$ computing genomic relationship **G** or genomic contribution $\mathbf{C}_{\mathbf{\_Gen}}$ by LDL' decomposing **G**w
- random mating as the reference point

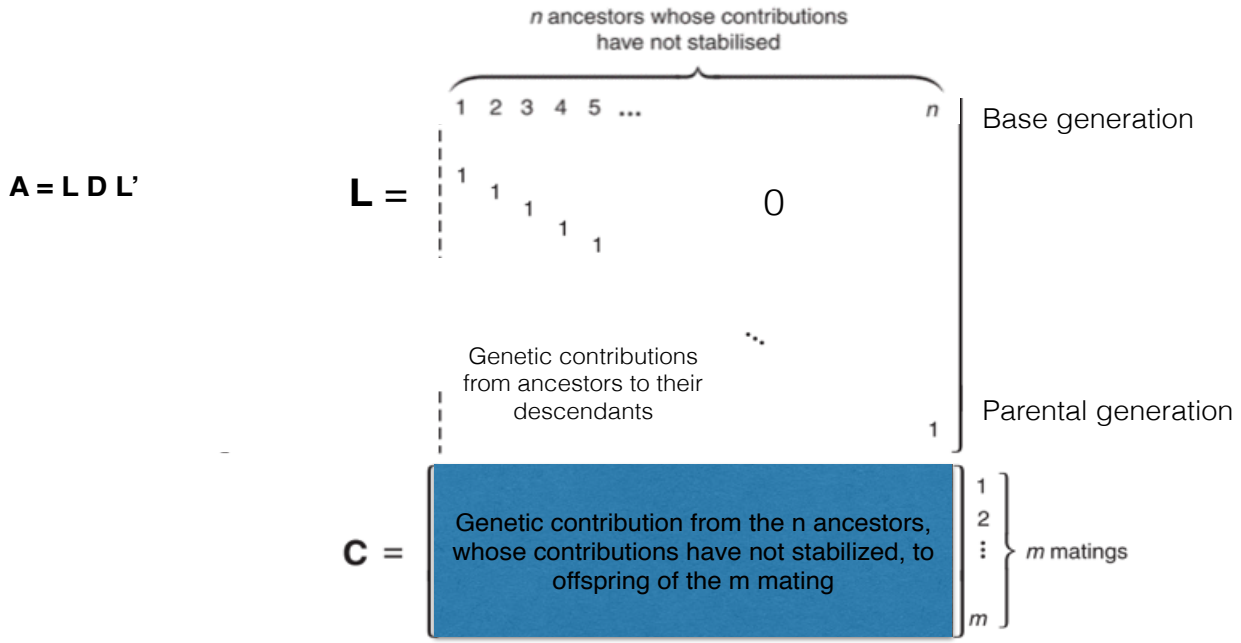
genomic contribution

A=LDL'

L is a lower triangular matrix and traces the flow of genes from one generation to the other.

It accounts only for direct (parent-offspring) relationships

genomic contribution



(Henryon et al. 2009)

genomic contribution

A=LDL'

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It accounts only for direct (parent-offspring) relationships

Gw=0.8***G**+0.2***A**, to keep it positive definite

Gw= **LDL'**

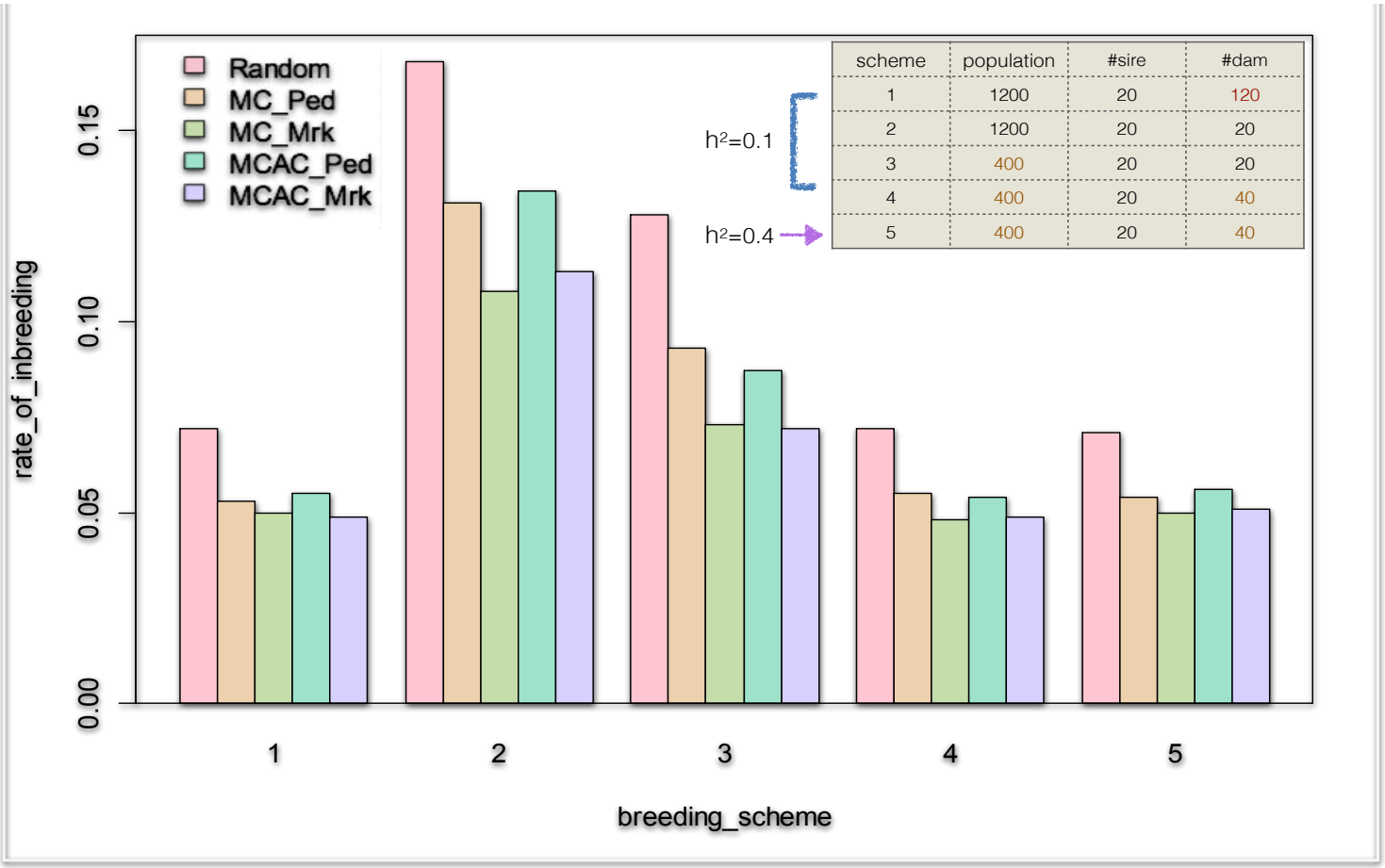
$\mathbf{C}_{\mathbf{-Gen}}$ is directly derived from **L**

Comparison criteria

- Main comparison
  - Rates of inbreeding (ΔF)
    - The proportion of genome being IBD (true inbreeding)
  - Rates of long_term genetic gain (ΔG)

- Supporting analysis
  - Number of ancestors making genetic contributions to the offspring in generation 20

Rates of inbreeding (ΔF)



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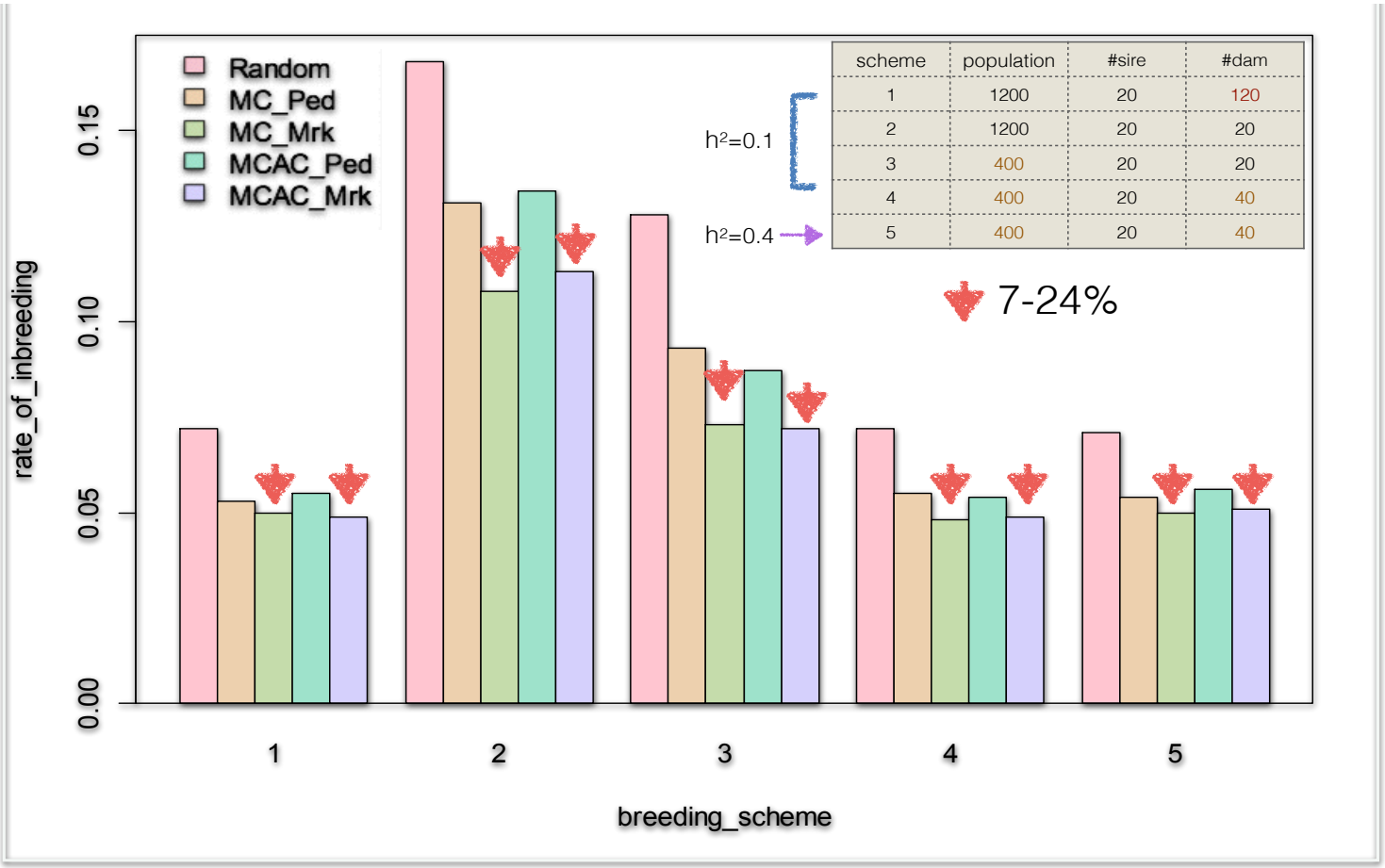

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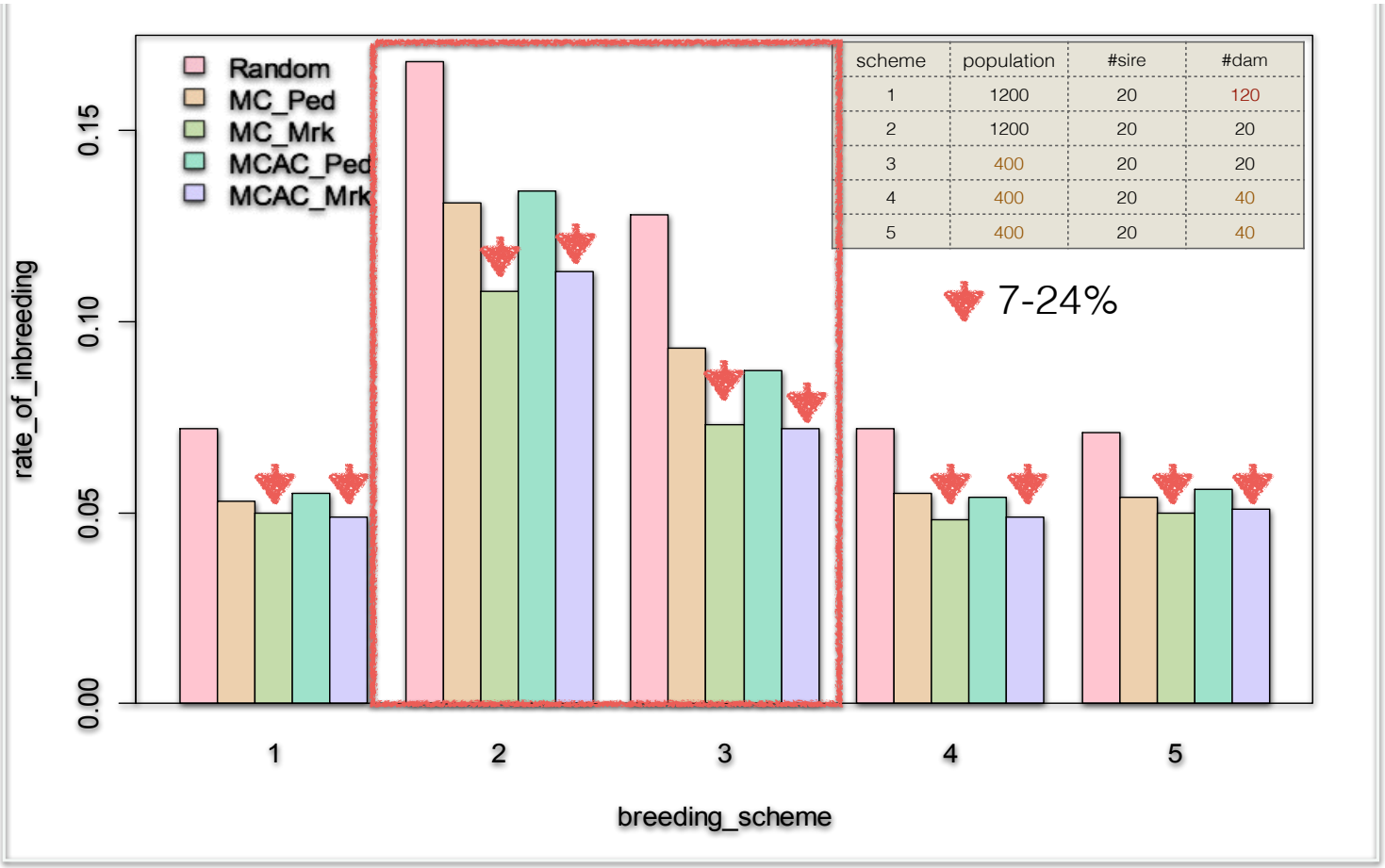

scheme	population	#sire	#dam
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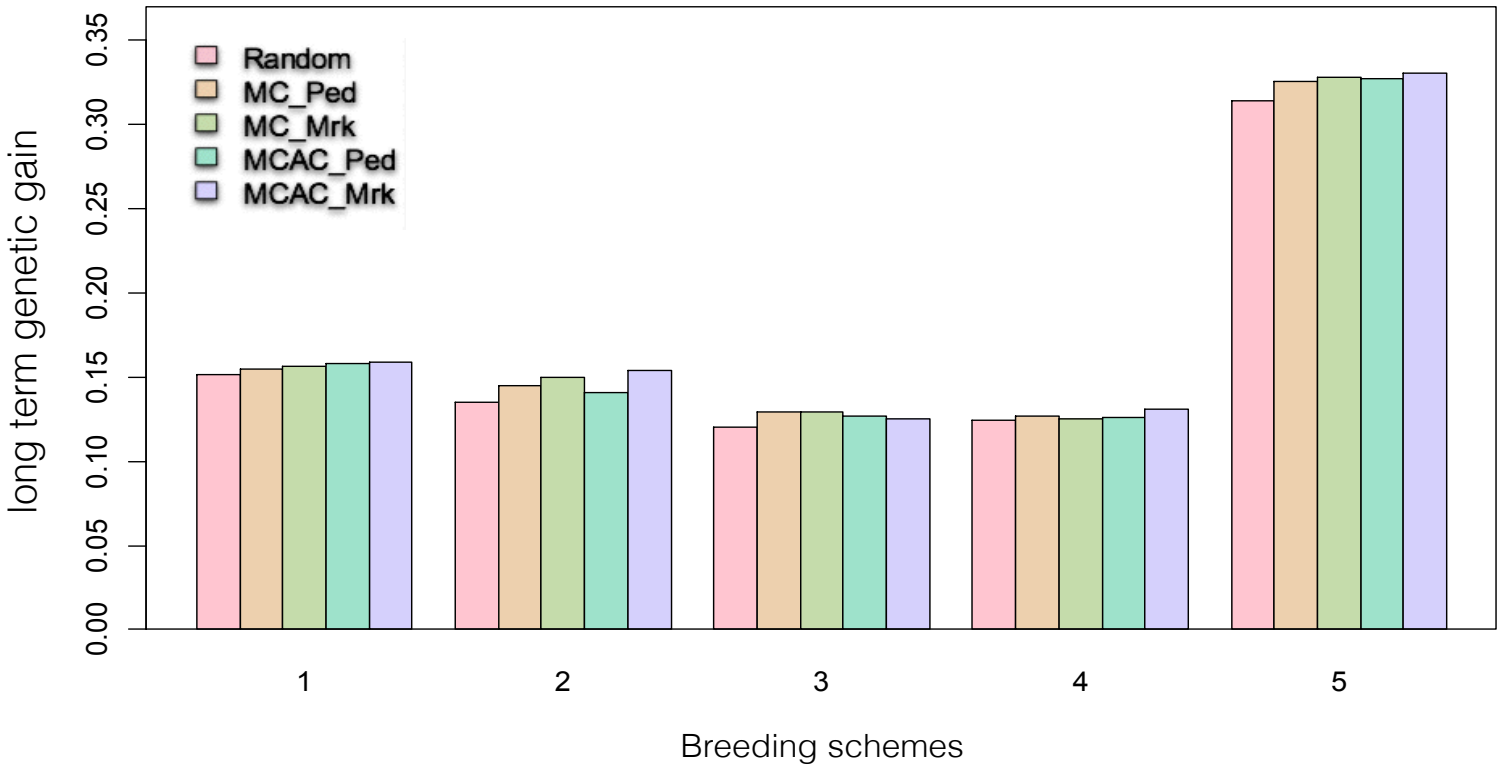
Rates of gain (ΔG)



Number of ancestors making genetic contributions

Scheme	RAND	MC_Ped	MCAC_Ped	MC_Mrk	MCAC_Mrk
1	**41.24**	*43.69*	*43.64*	*46.56*	*46.06*
2	**7.93**	*9.76*	*9.77*	*10.58*	*10.49*
3	**10.41**	*12.03*	*12.07*	*12.88*	*13.06*
4	**19.24**	*21.75*	*21.71*	*22.72*	*22.30*
5	**21.31**	*23.23*	*23.11*	*23.72*	*23.70*

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Conclusions

- Using genomic information source in MC or MCAC mating strategies can significantly reduce rate of inbreeding without compromising genetic gain
- It can be achieved without burdening breeding schemes with extra costs.

  $\rightarrow$ Genomic data should be applied to more than just genomic prediction.
- These mating strategies can be beneficial especially with full-sib families.
- Next step: investigate the optimal way to compute co-ancestry and genetic contributions using genomic information.

Thank you very much!

Table S1. The average of variance of genetic contributions per offspring and the average of the sum of covariance of ancestral contributions over all of the offspring based on 20 replicates.

	RAND	MC_Ped	MCAC_Ped	MC_Mrk	MCAC_Mrk
VAR	***0.0117***	***0.0062***	***0.0076***	***0.0054***	***0.0055***
COV	***0.0437***	***0.0350***	***0.0326***	***0.0311***	***0.0308***