

Persistence of genomic evaluations over time in pigs and broilers

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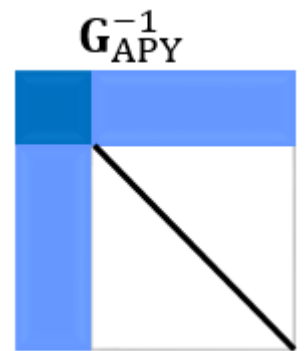
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Persistence of genomic evaluation

- Farm populations – small effective population size N_e
- Inheritance in form of independent chromosome segments
 - About 15k in cattle, about 5k in pigs and chickens (Pocrnic et al, 2016)
 - Genomic selection predicts 5k-15k segments
- High accuracy and persistence if:
 - Most QTLs explaining most variance located and well estimated, or
 - All chromosome segments well estimated

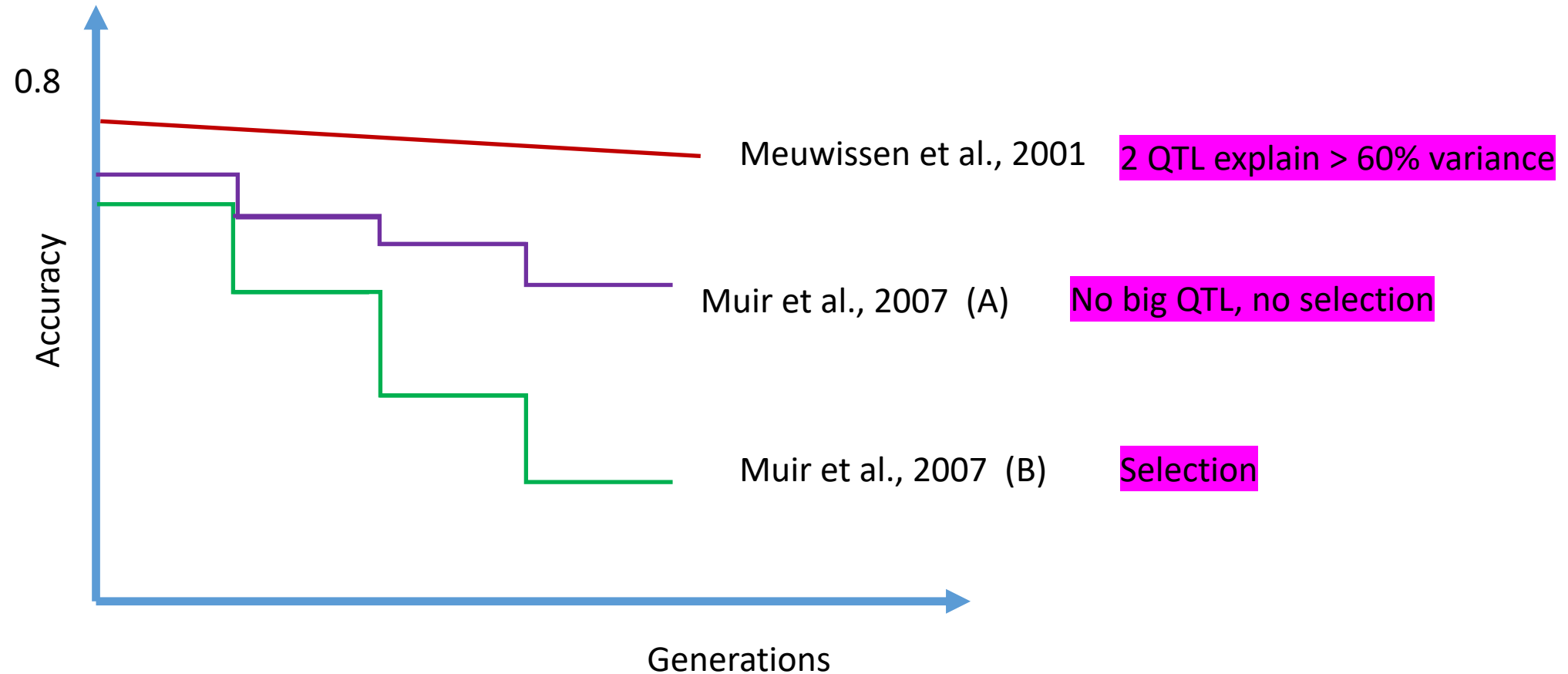
$$r = \sqrt{\frac{Nh^2}{Nh^2 + M_e}}$$

Accuracy formula
Daetwyler et al., 2008



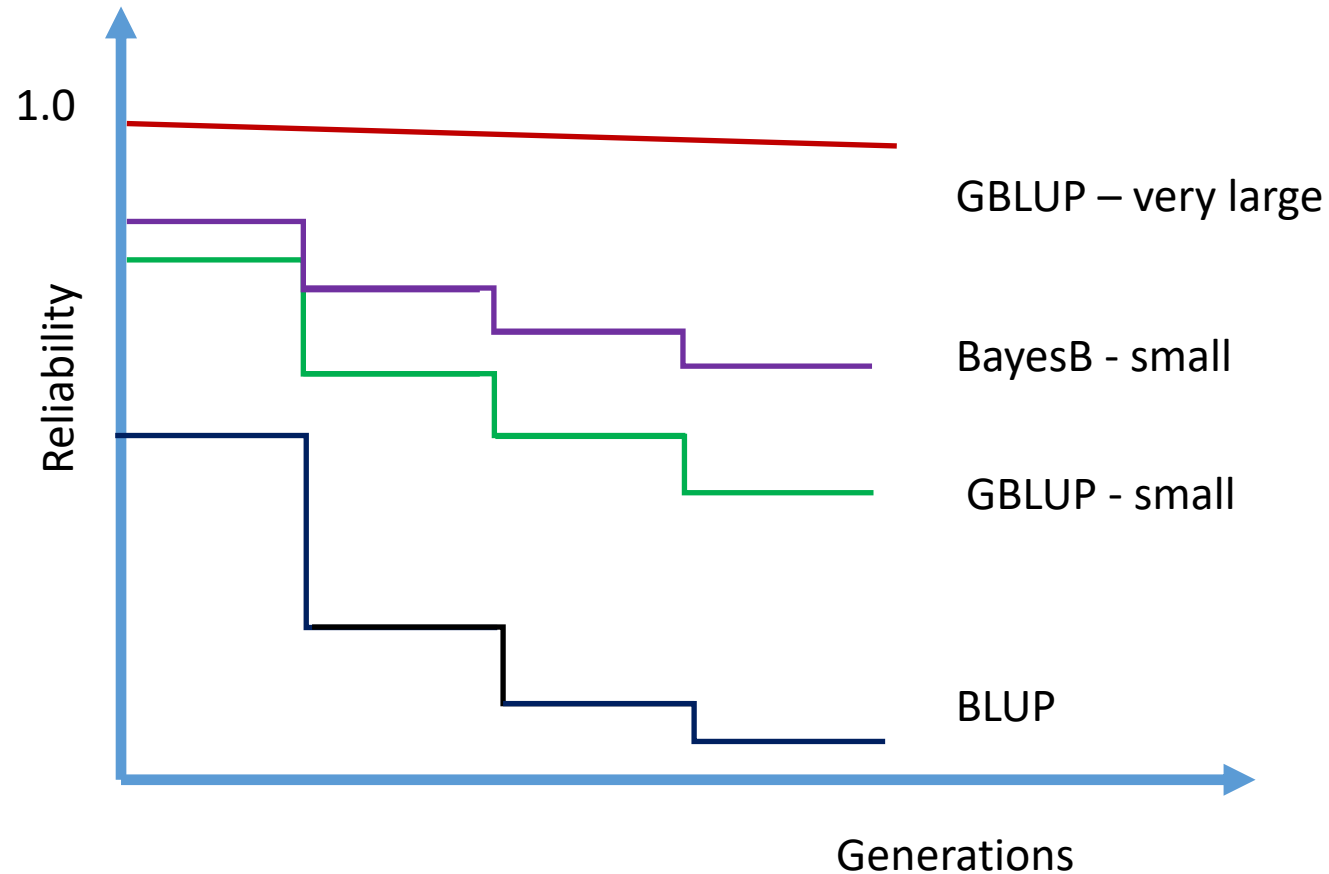
APY inverse of GRM
Misztal et al., 2014

Persistence in literature – small data



Small data – selection on most popular clusters of chromosome segments (Pocrnic et al., 2018)

Hypothetical persistence over generations with different sizes of reference populations



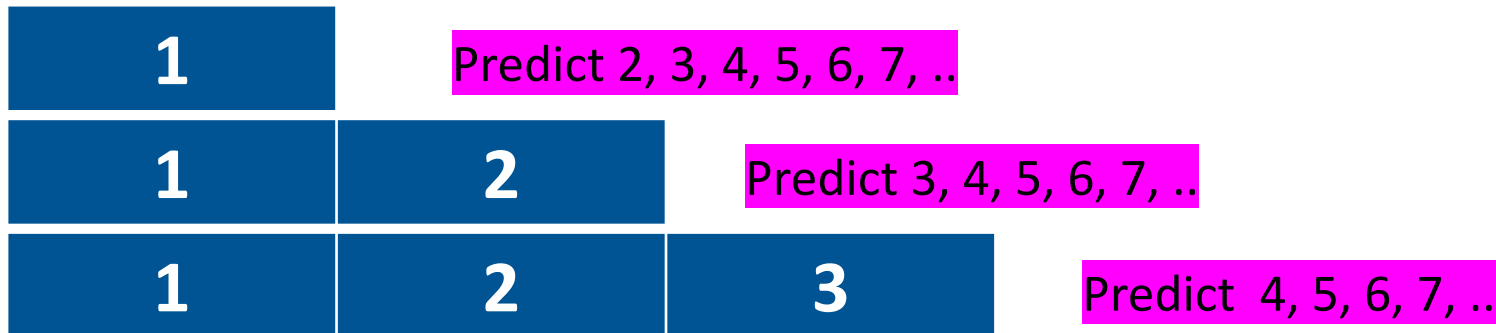
High accuracy by GBLUP if all chromosome segments well estimated

Persistence and real life

- Large phenotypic data in pigs and chickens, smallest N_e
- Many generations
- Is persistence high with large data?
- Do we need to keep on phenotyping?

Methods

- ssGBLUP
- Accuracies by method LR
- Based on reference population 1:n, predict accuracy for generations n+1, n+2,..



Pig data set

150k records on growth ($h^2=0.21$)

25k records on fitness ($h^2=0.05$)

53k genotyped animals

9 generations

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

For genotyped animals only

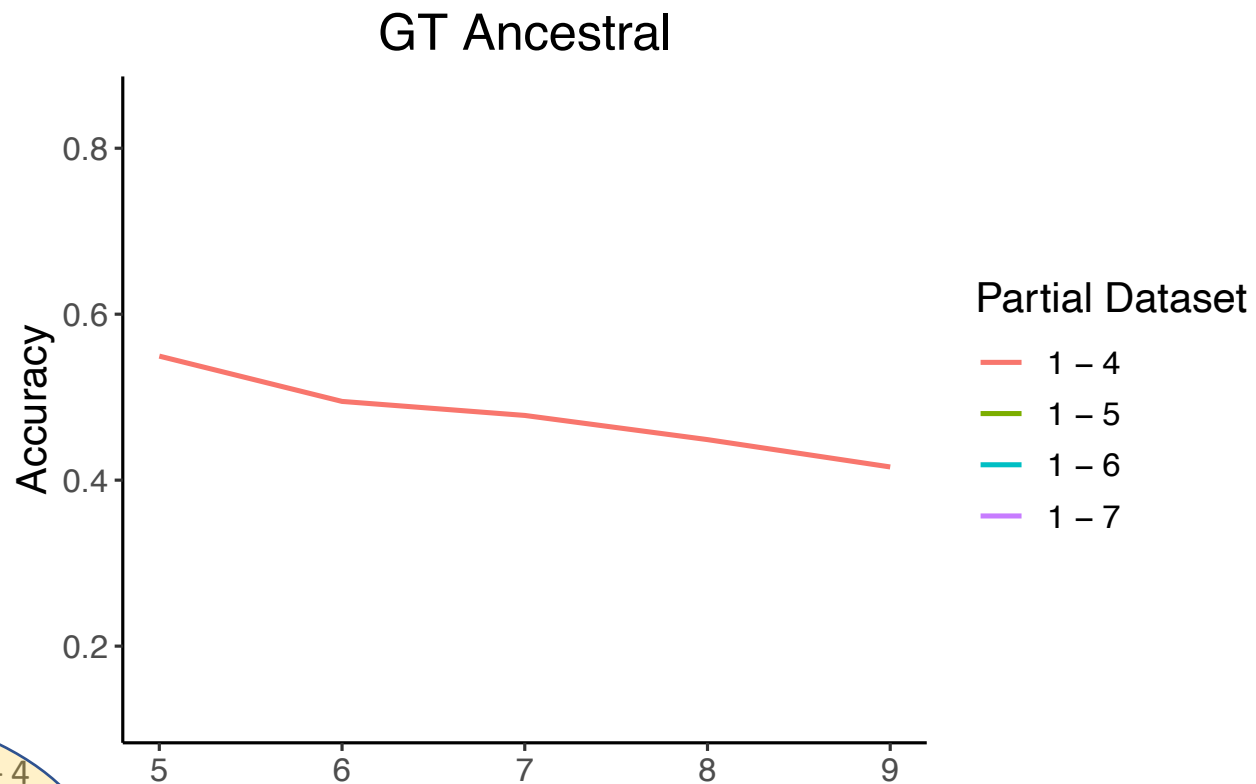
$$\text{growth} \sqrt{\frac{53k * 0.21}{53k * 0.21 + 5k}} = 0.83$$

$$\text{fitness} \sqrt{\frac{25k * 0.05}{25k * 0.05 + 5k}} = 0.44$$



Persistence for pigs based on different reference populations

Growth trait



Phenotypes 30k
Genotypes 3k

1 - 4

5

23k

3k

6

26k

6k

7

28k

10k

8

25k

11k

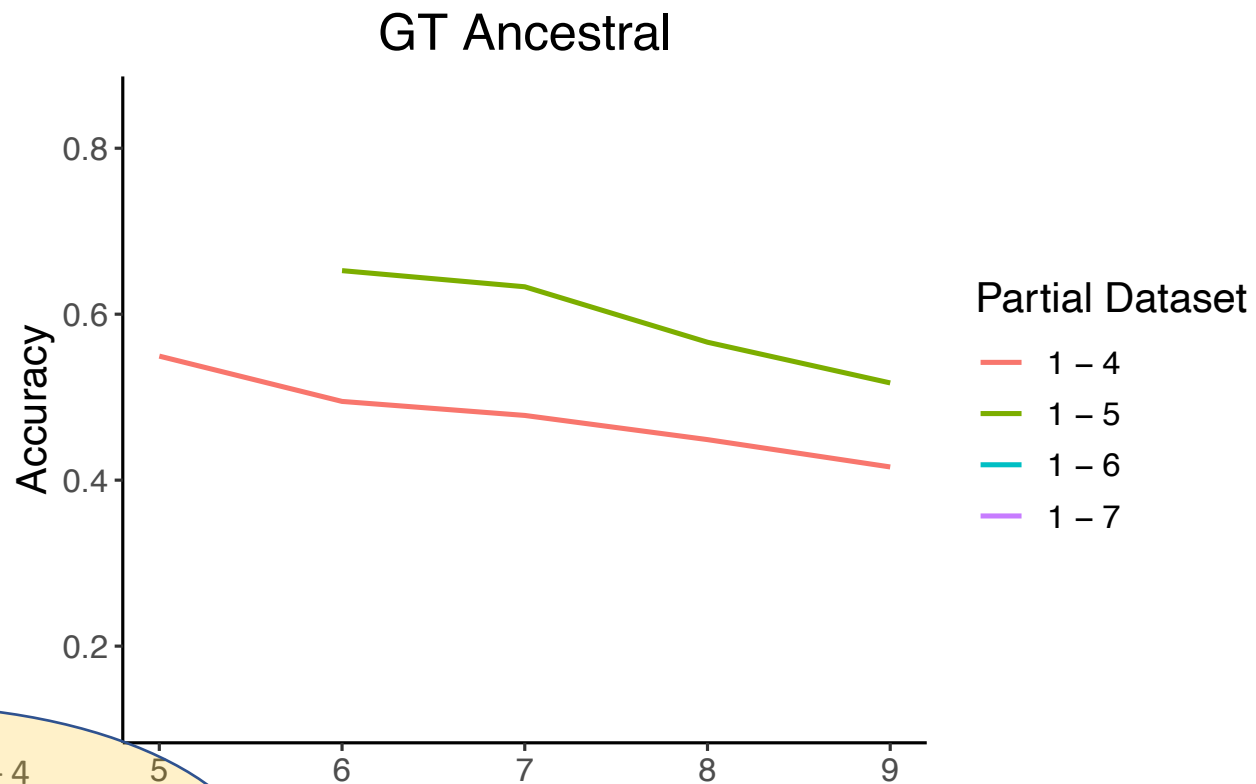
9

17k

8k

Persistence for pigs based on different reference populations

Growth trait



	1 - 4	5
Phenotypes	30k	23k
Genotypes	3k	3k

26k

28k

25k

17k

6k

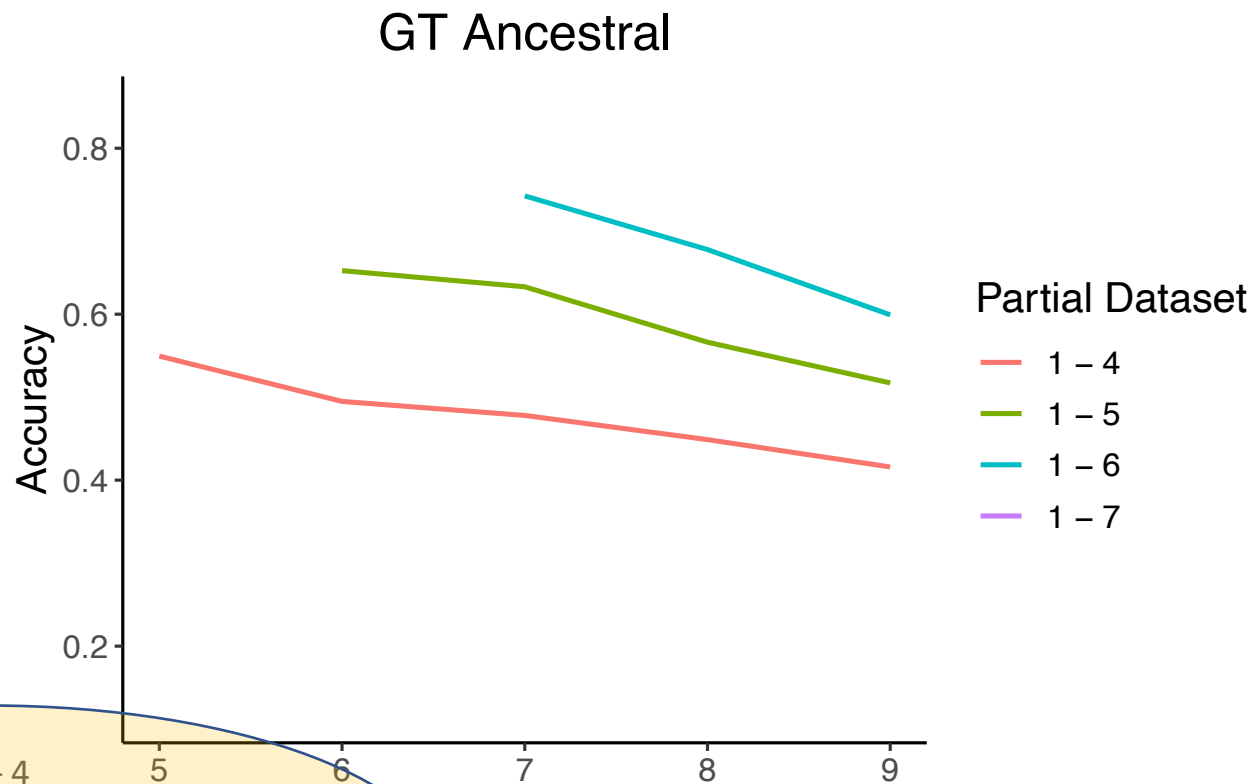
10k

11k

8k

Persistence for pigs based on different reference populations

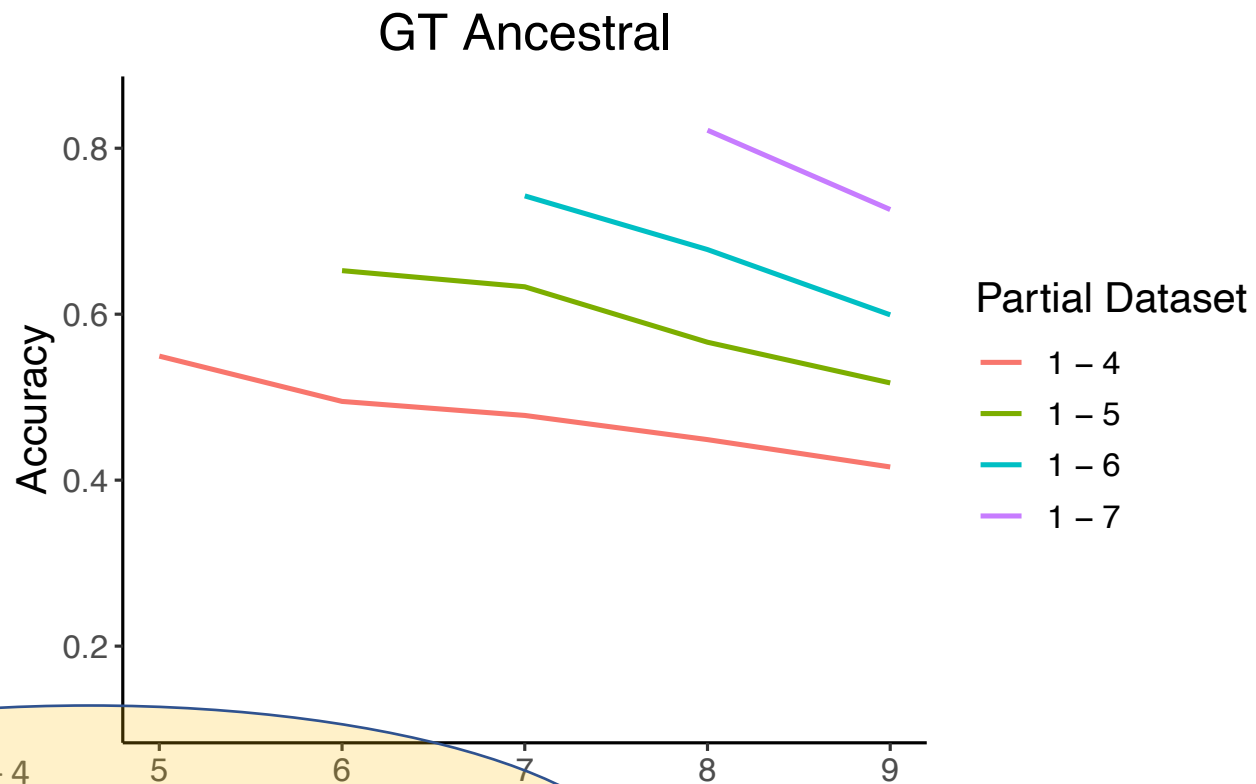
Growth trait



	1 - 4	5	6	7	8	9
Phenotypes	30k	23k	26k	28k	25k	17k
Genotypes	3k	3k	6k	10k	11k	8k

Persistence for pigs based on different reference populations

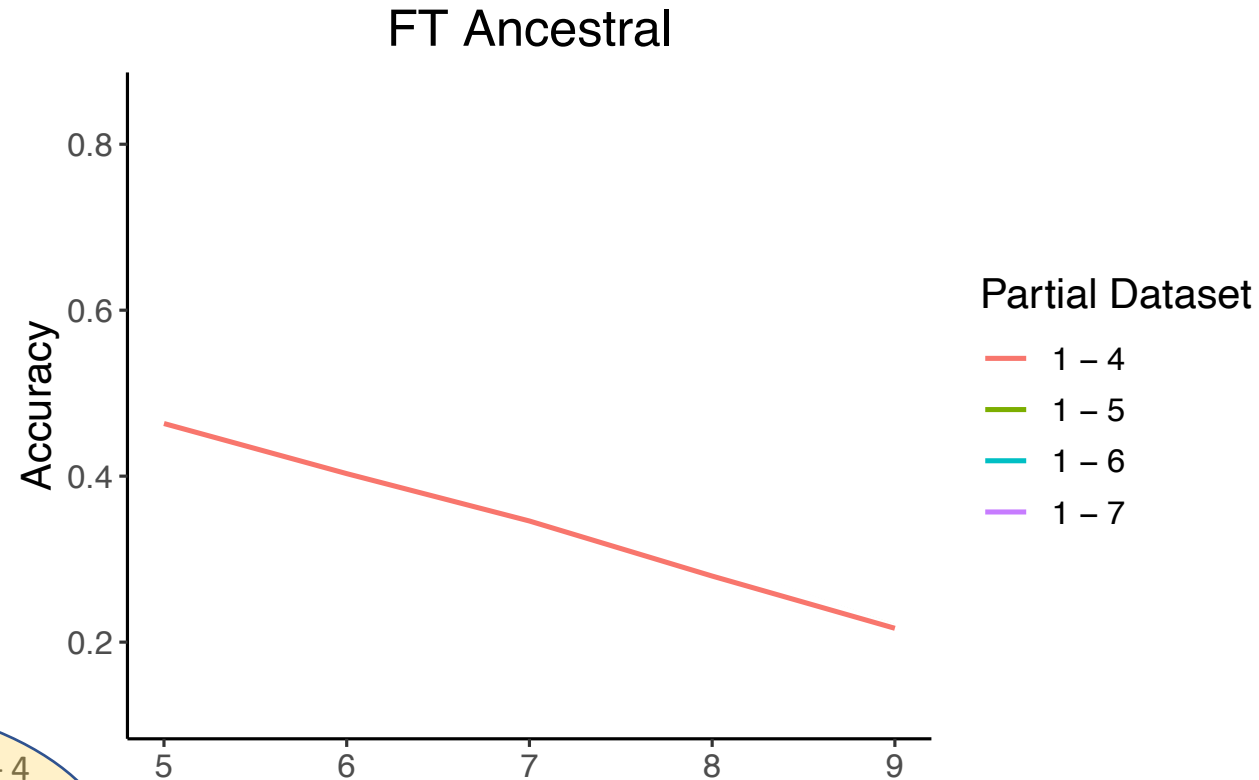
Growth trait



	1 - 4	5	6	7	8	9
Phenotypes	30k	23k	26k	28k	25k	17k
Genotypes	3k	3k	6k	10k	11k	8k

Persistence for pigs based on different reference populations

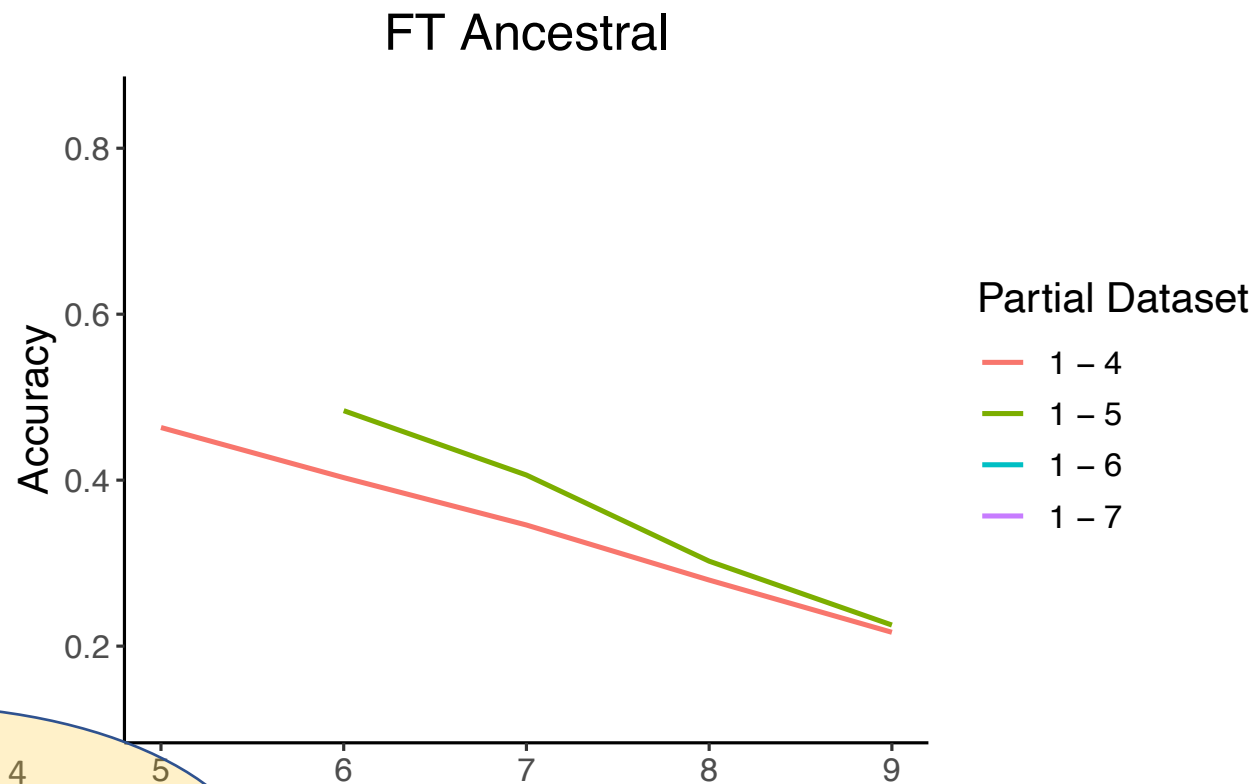
Fitness trait



	1 - 4	5	6	7	8	9
Phenotypes	11k	4k	4k	3k	2k	1k
Genotypes	3k	3k	6k	10k	11k	8k

Persistence for pigs based on different reference populations

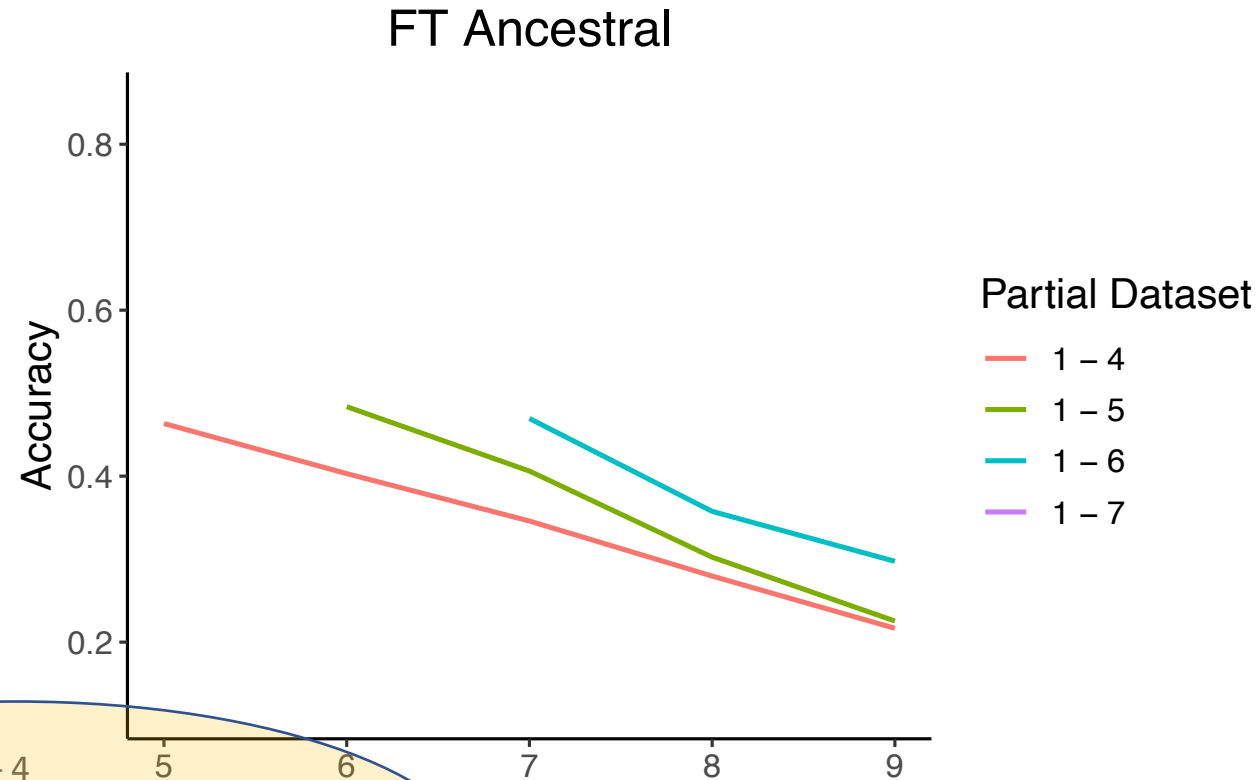
Fitness trait



	1 - 4	5	6	7	8	9
Phenotypes	11k	4k	4k	3k	2k	1k
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Persistence for pigs based on different reference populations

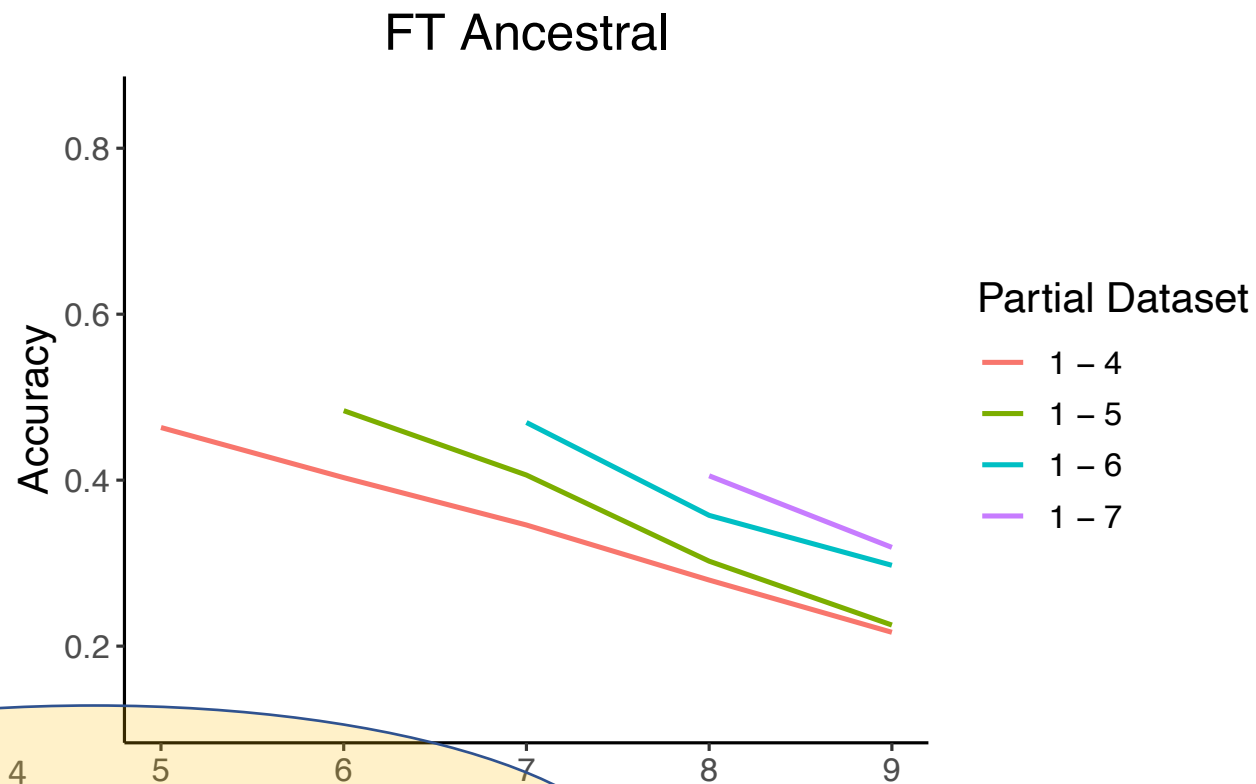
Fitness trait



	1 - 4	5	6	7	8	9
Phenotypes	11k	4k	4k	3k	2k	1k
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Persistence for pigs based on different reference populations

Fitness trait



	1 - 4	5	6	7	8	9
Phenotypes	11k	4k	4k	3k	2k	1k
Genotypes	3k	3k	6k	10k	11k	8k

Broiler chicken data set

820k phenotypes for growth

$$h^2=0.3$$

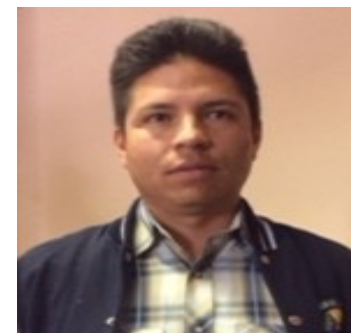
150k genotyped

7 years

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

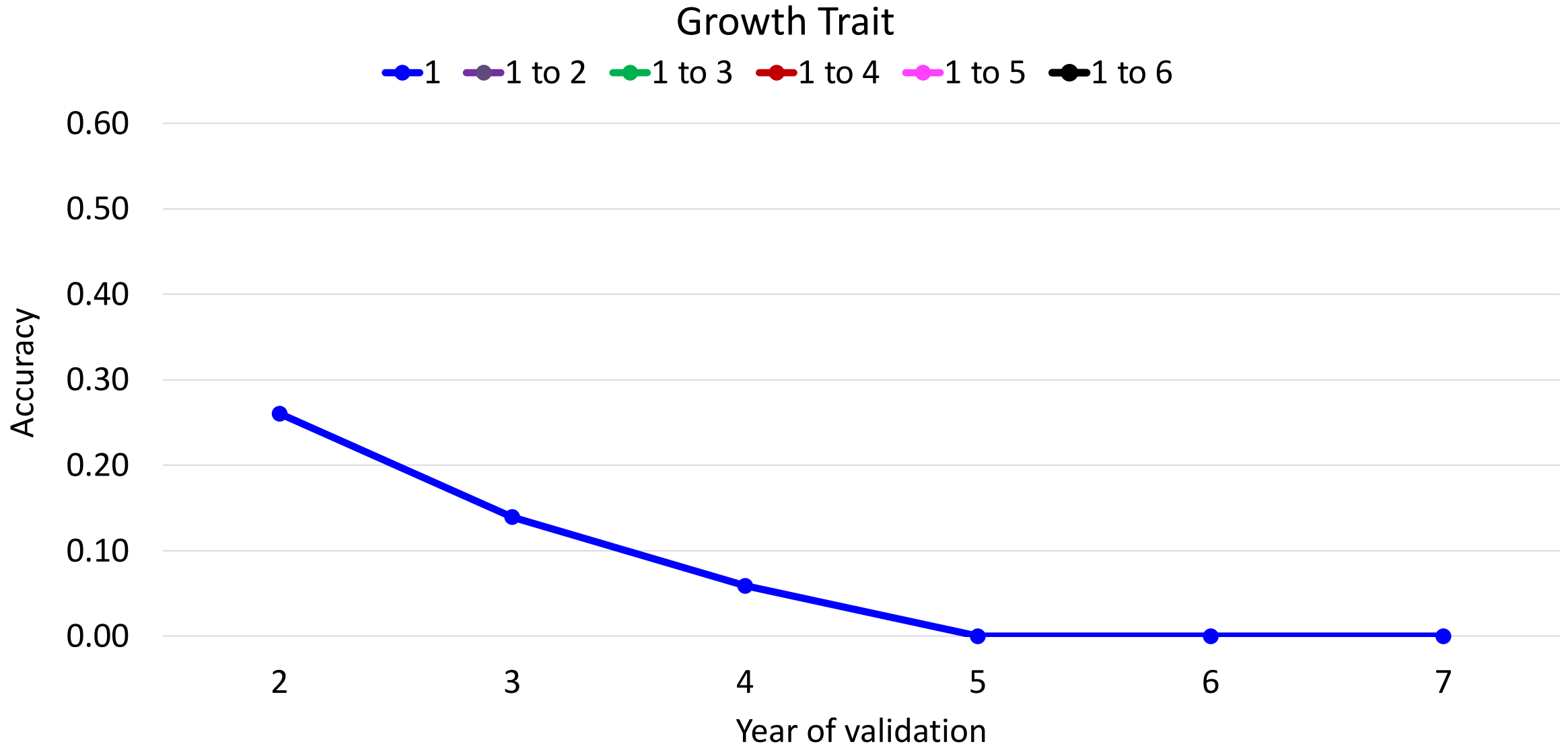
For genotyped animals only

$$\sqrt{\frac{150k * 0.3}{150k * 0.3 + 5k}} = 0.94$$



Hidalgo et al., 2021

Persistence for chicken based on different reference populations

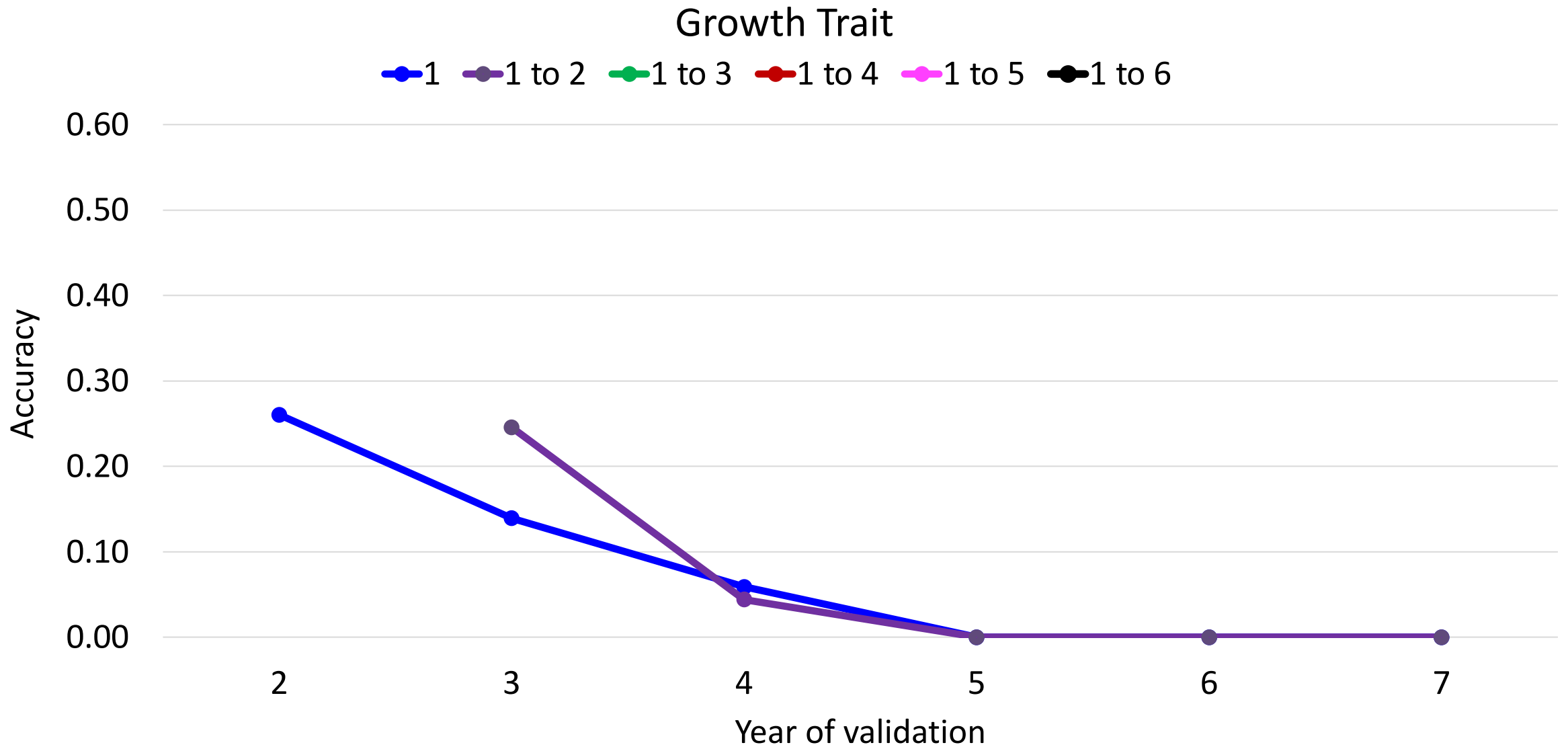


100k phenotypes / year

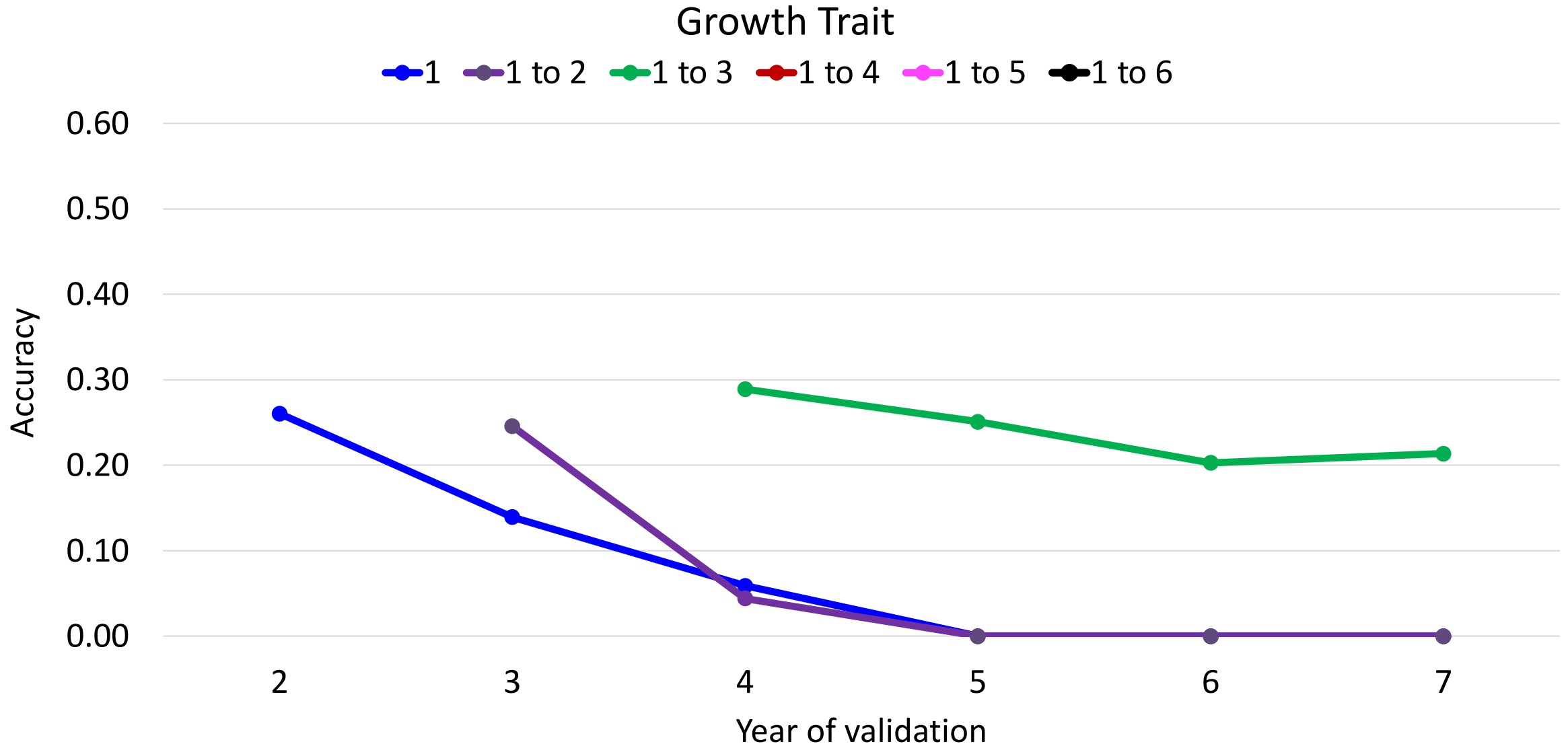
Genotypes from gen 4

~ 40k/year

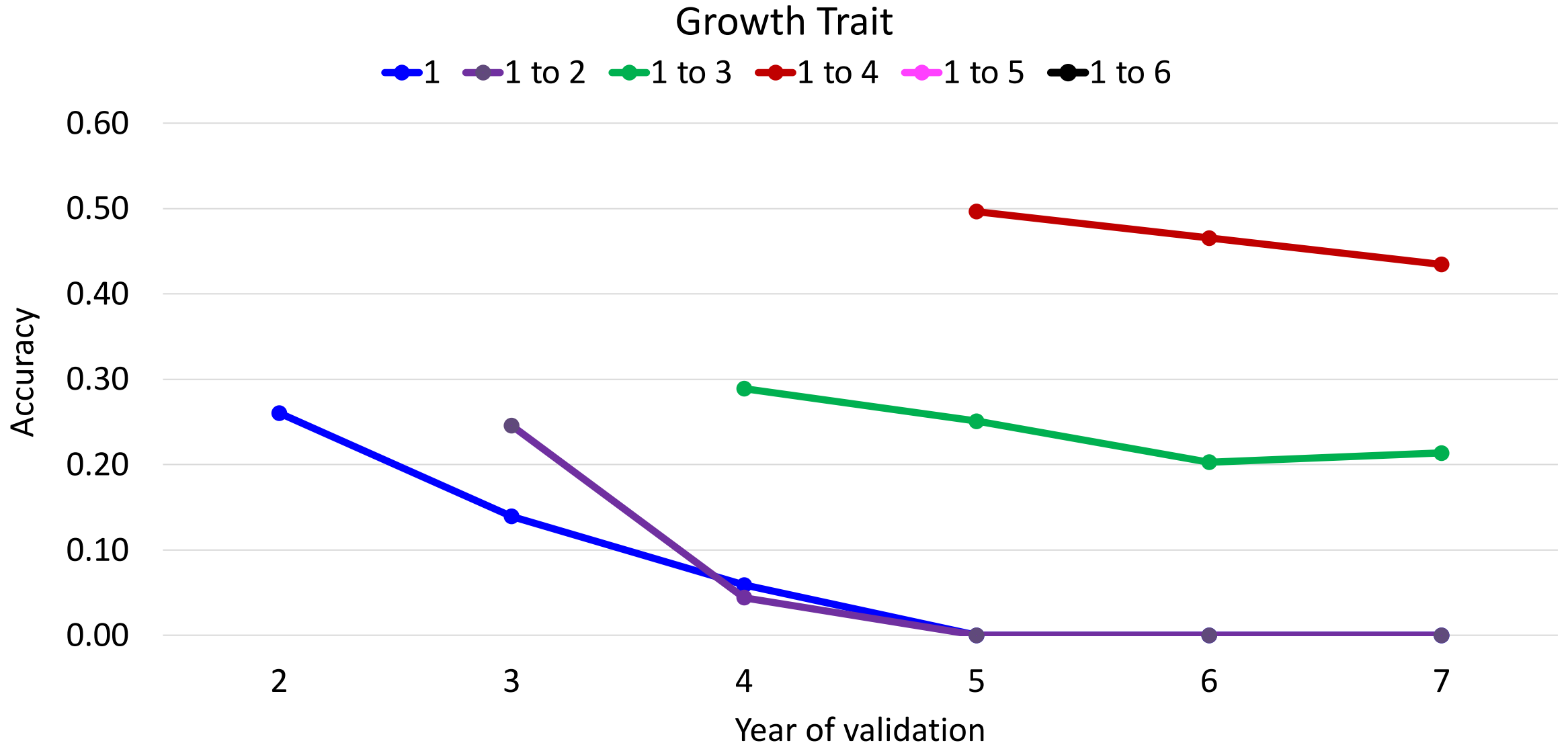
Persistence for chicken based on different reference populations



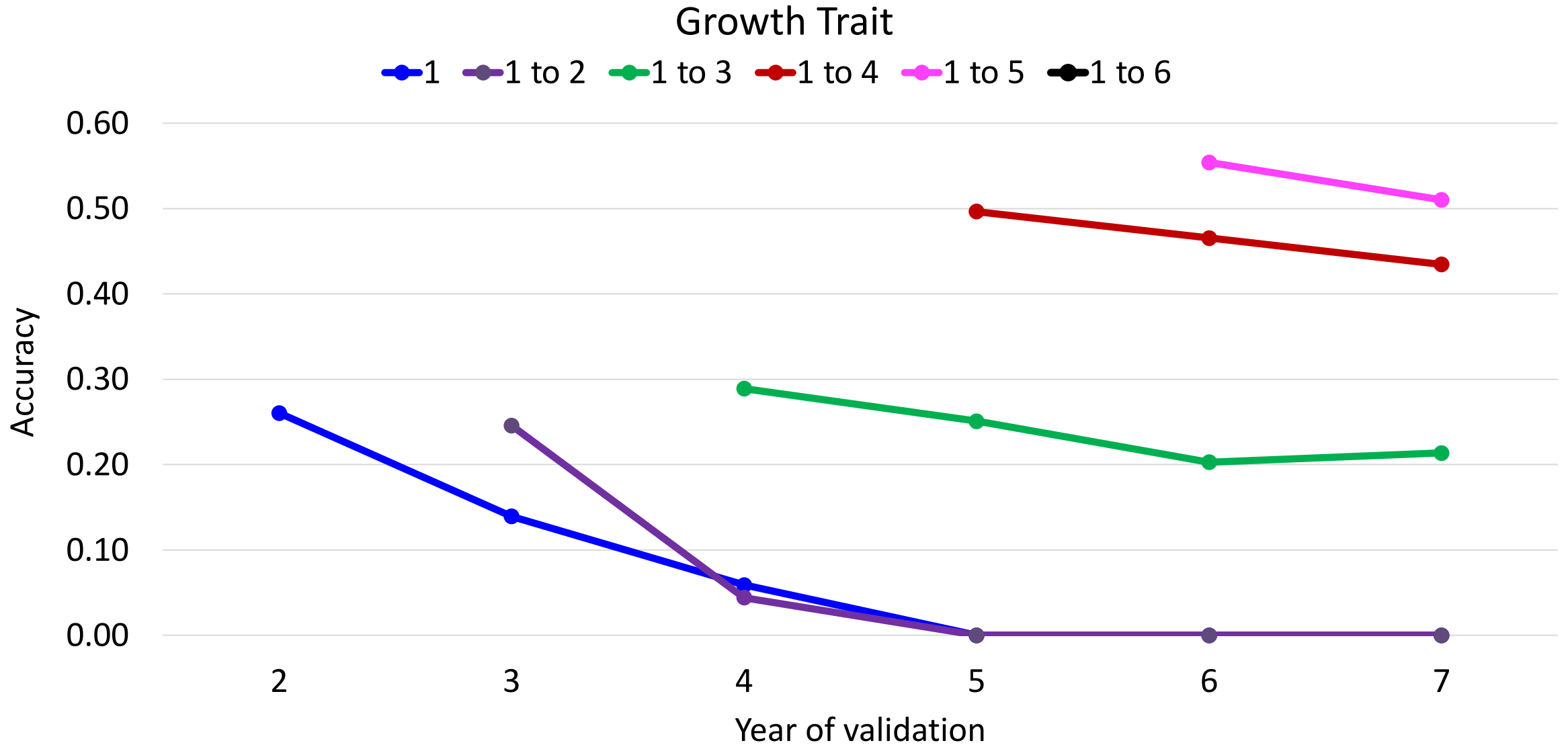
Persistence for chicken based on different reference populations



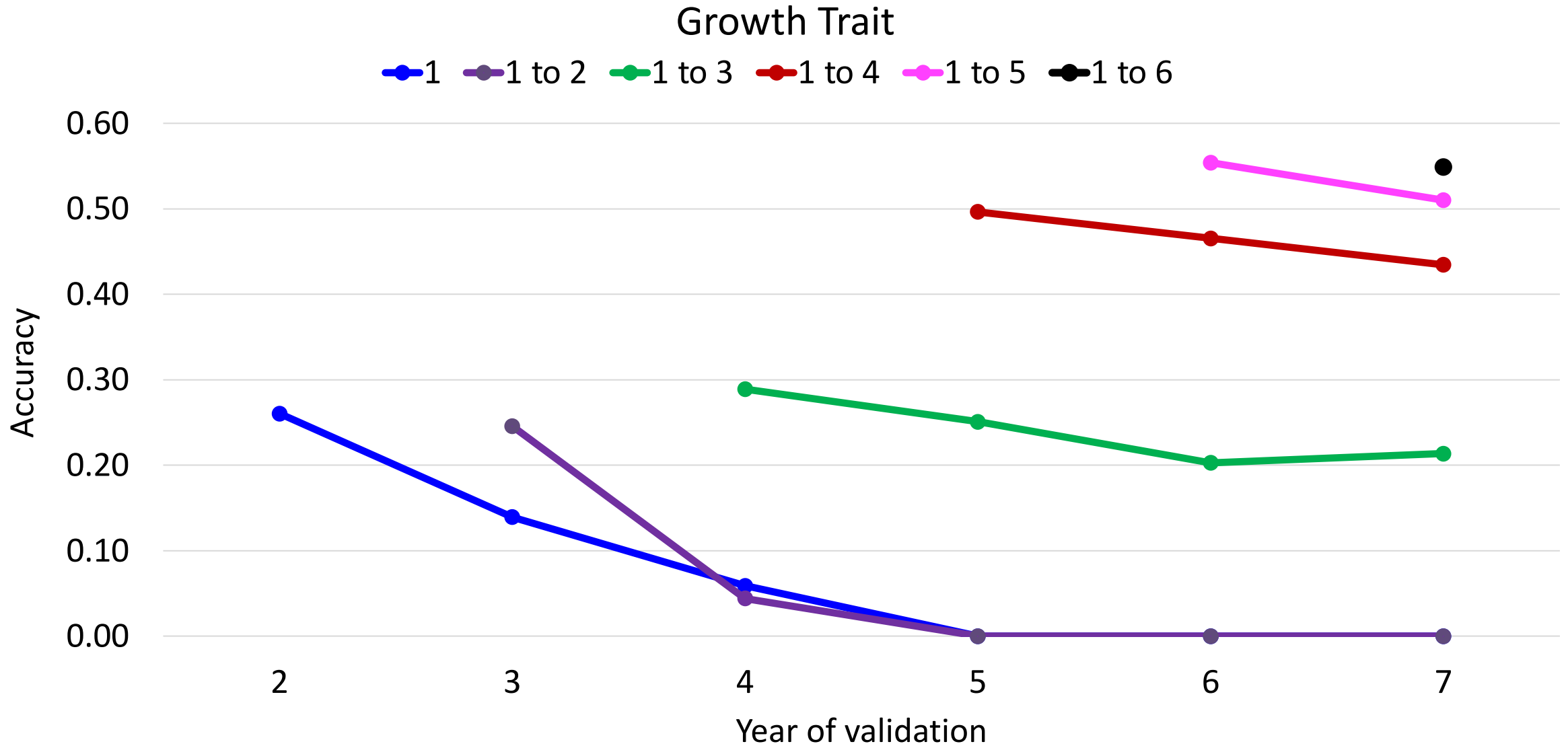
Persistence for chicken based on different reference populations



Persistence for chicken based on different reference populations



Persistence for chicken based on different reference populations



Why lower accuracy for chickens despite more data?

Method LR

Legarra and Reverter, 2018

$$\widehat{acc}_{LR} = \sqrt{\frac{cov(\hat{u}_w, \hat{u}_p)}{(1 - \bar{F})\sigma_a^2}}$$

\hat{u}_w = breeding values estimated using whole data

\hat{u}_p = breeding values estimated using partial data

\bar{F} = average inbreeding in validation animals

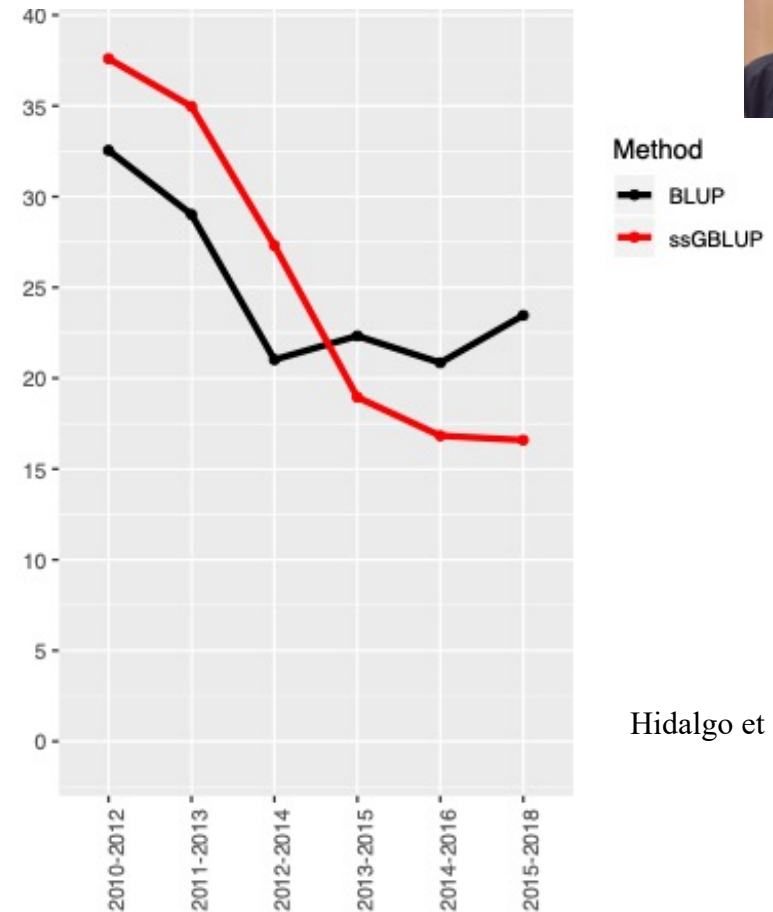
σ_a^2 = additive genetic variance

If variance 100% → 50%

acc 0.60 → 0.84

Special breeding scheme – selective genotyping for best growers, etc.

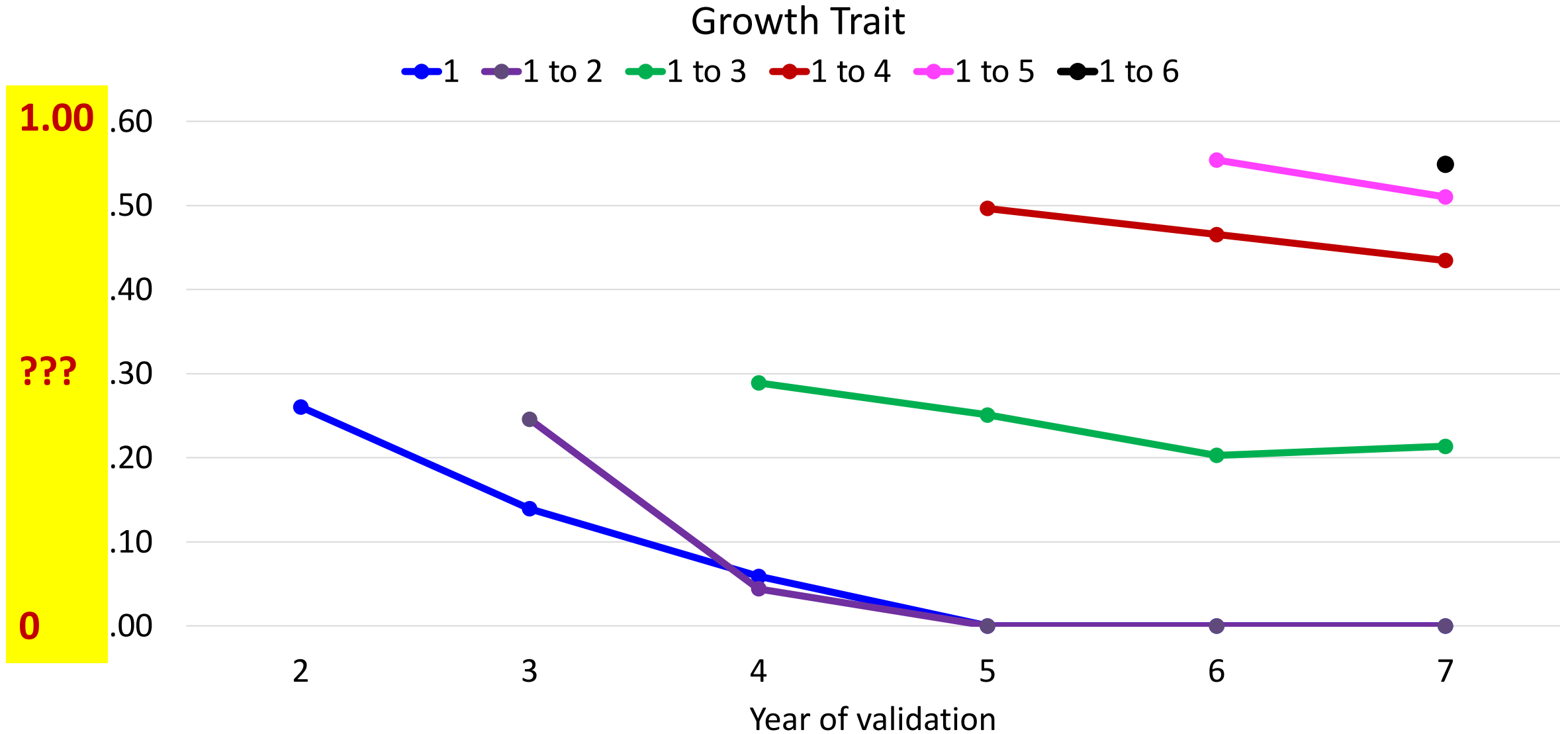
Heritability for growth



Hidalgo et al. (2019)



Persistence for chicken based on different reference populations



Conclusions

- With more data, higher accuracy and more persistence
- Low accuracy and persistence in low h^2 traits
- Calculated accuracies with field data affected by:
 - Decreasing additive variance
 - Complex breeding structure

Acknowledgements




Smithfield®

zoetis

PIC



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