



U N I K A S S E L
V E R S I T Ä T

Selection for beef meat quality using ultrasound or genomic information

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Motivation

- Current situation (e.g., in Germany):

Weight at 200 days



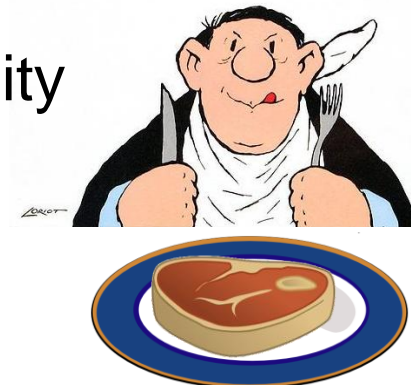
Weight at 400 days



Muscling score



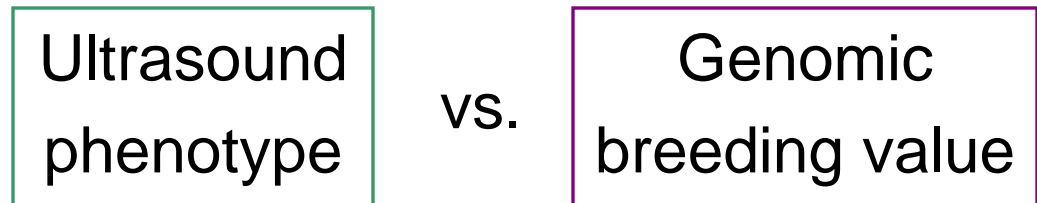
- Extending it to select for meat quality





Objective

- Compare different breeding strategies that make use of alternative information sources for improving meat quality.





Methods

- Selection Index Theory
 - accuracy of the index
 - expected genetic gain per generation
- Breeding goal: **W200**, **W400**, **MUSC** and **MARB**
- Relative economic weights:
 - same on all traits;
 - doubled on **MARB**;
 - tripled on **MARB**



Methods

- Breeding scenarios:

Scenario	Traits in the selection index
1	W200 + W400 + MUSC
2	W200 + W400 + MUSC + UIMF
3	W200 + W400 + MUSC + gMARB
4	W200 + W400 + MUSC + UIMF + gMARB
5	gW200 + gW400 + gMUSC
6	gW200 + gW400 + gMUSC + gMARB



Methods

- Selection Index Theory

- Conventional → [Hazel \(1943\)](#)

$$\mathbf{b} = \mathbf{P}^{-1}\mathbf{G}\mathbf{w} \quad \begin{matrix} \sigma_I^2 = \mathbf{b}'\mathbf{P}\mathbf{b} \\ \sigma_H^2 = \mathbf{w}'\mathbf{C}\mathbf{w} \end{matrix} \quad R_{IH} = \frac{\sigma_I}{\sigma_H} \quad \Delta G = (i)R_{IH}\sigma_H$$

- **b** → selection index coefficients;
 - **w** → economic weights;
 - **P** → (co)variances between components of the index;
 - **C** → genetic (co)variances between traits in the goal;
 - **G** → covariances between components of the index and additive genetic values of traits in the goal.



Methods

- Selection Index Theory
 - Genomic → [Dekkers \(2007\)](#)

$$\text{Cov}(P_i, \text{GEBV}_j) = r_{MG_j}^2 \rho_{G_{ij}} \sigma_{G_i} \sigma_{G_j}$$

$$\text{Cov}(P_i, \text{GEBV}_i) = r_{MG_i}^2 \sigma_{G_i}^2$$

$$\text{Cov}(\text{GEBV}_i, \text{GEBV}_j) = r_{MG_i}^2 r_{MG_j}^2 \rho_{G_{ij}} \sigma_{G_i} \sigma_{G_j}$$

r_{MG} → accuracy of GEBV as a predictor of the true breeding value
(varied from 0.1 to 0.9 in steps of 0.1)



Methods

- Assumed parameters:

Trait	W200	W400	MUSC	UIMF	MARB
W200	0.24	0.78	0.31	-0.06	-0.17
W400	0.72	0.33	0.14	-0.15	-0.37
MUSC	0.10	0.12	0.64	-0.12	-0.18
UIMF	-0.01	-0.03	-0.06	0.38	0.66
MARB	-0.04	0.14	-0.09	0.62	0.45
σ_P^2	625	1444	2.02	0.94	0.61



Methods

- Number of animals to achieve a given r_{MG} :

[Daetwyler et al. \(2010\)](#)

$$N_P = \frac{r_{MG}^2 \hat{M}_e}{h^2 (1 - r_{MG}^2)}$$

[Goddard \(2009\)](#)

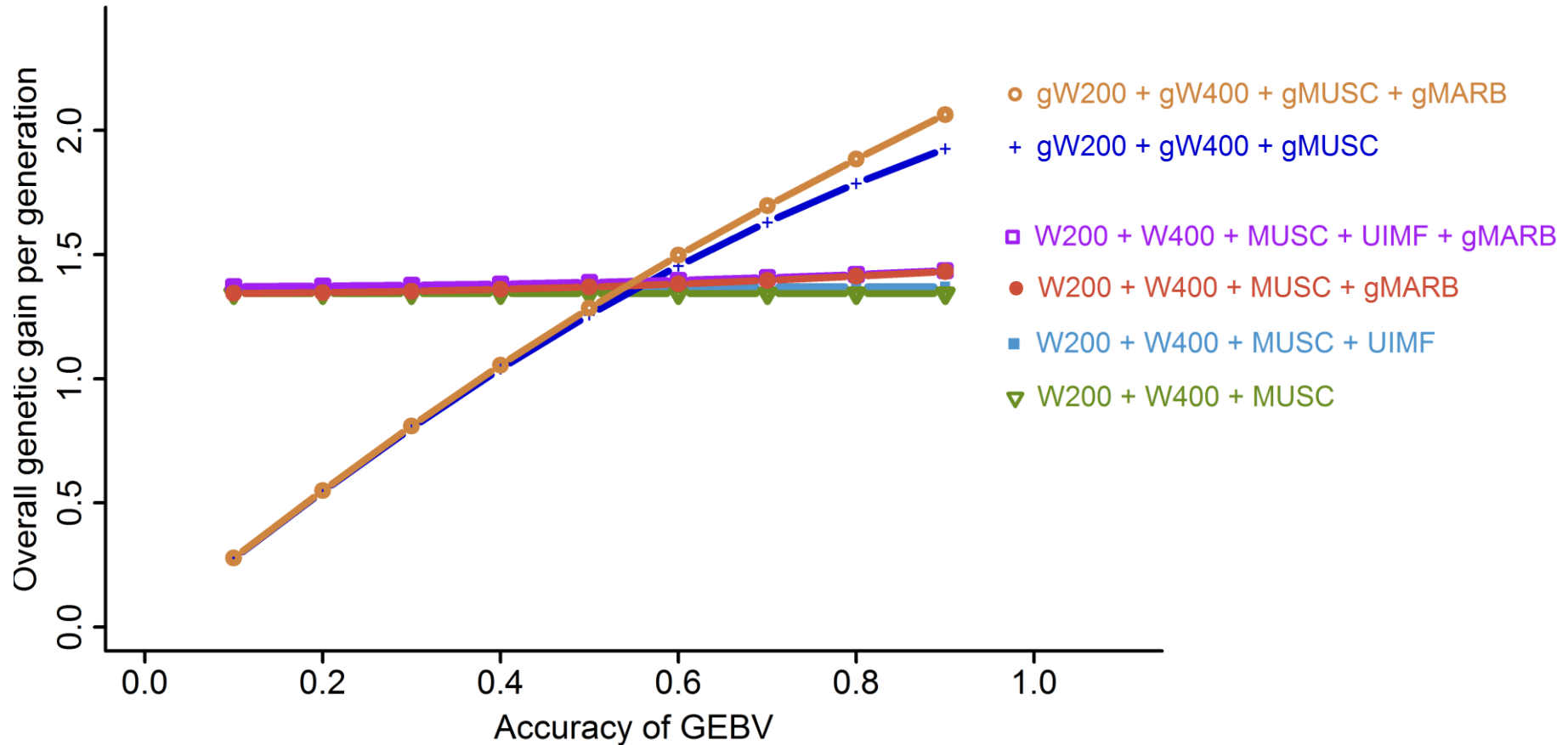
$$\hat{M}_e = \frac{2N_e L}{\log(4N_e L)}$$

- M_e → number of independent chromosome segments;
- L → genome length (30 M);
- N_e → effective population size (100).



Results

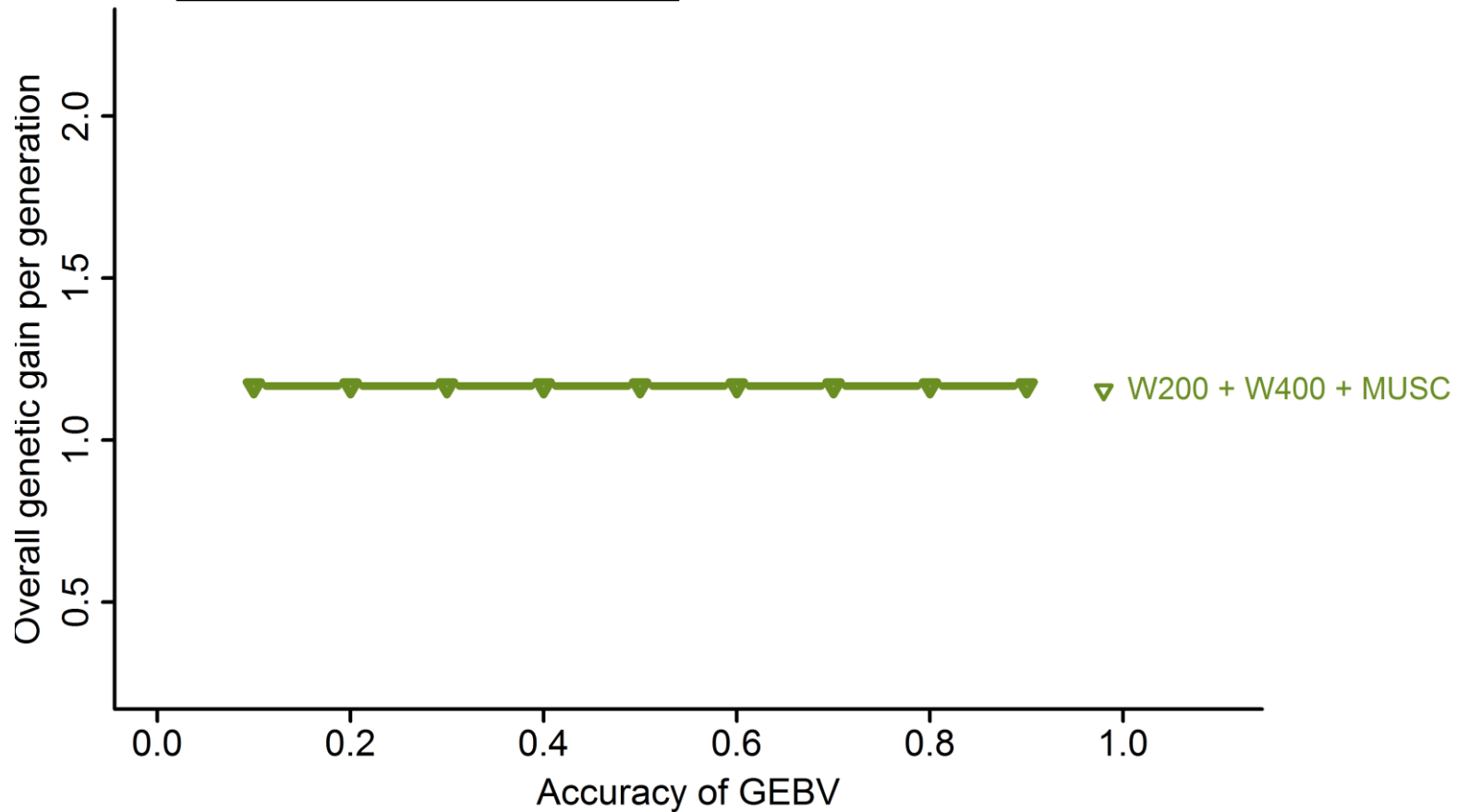
Same weight on all traits





Results

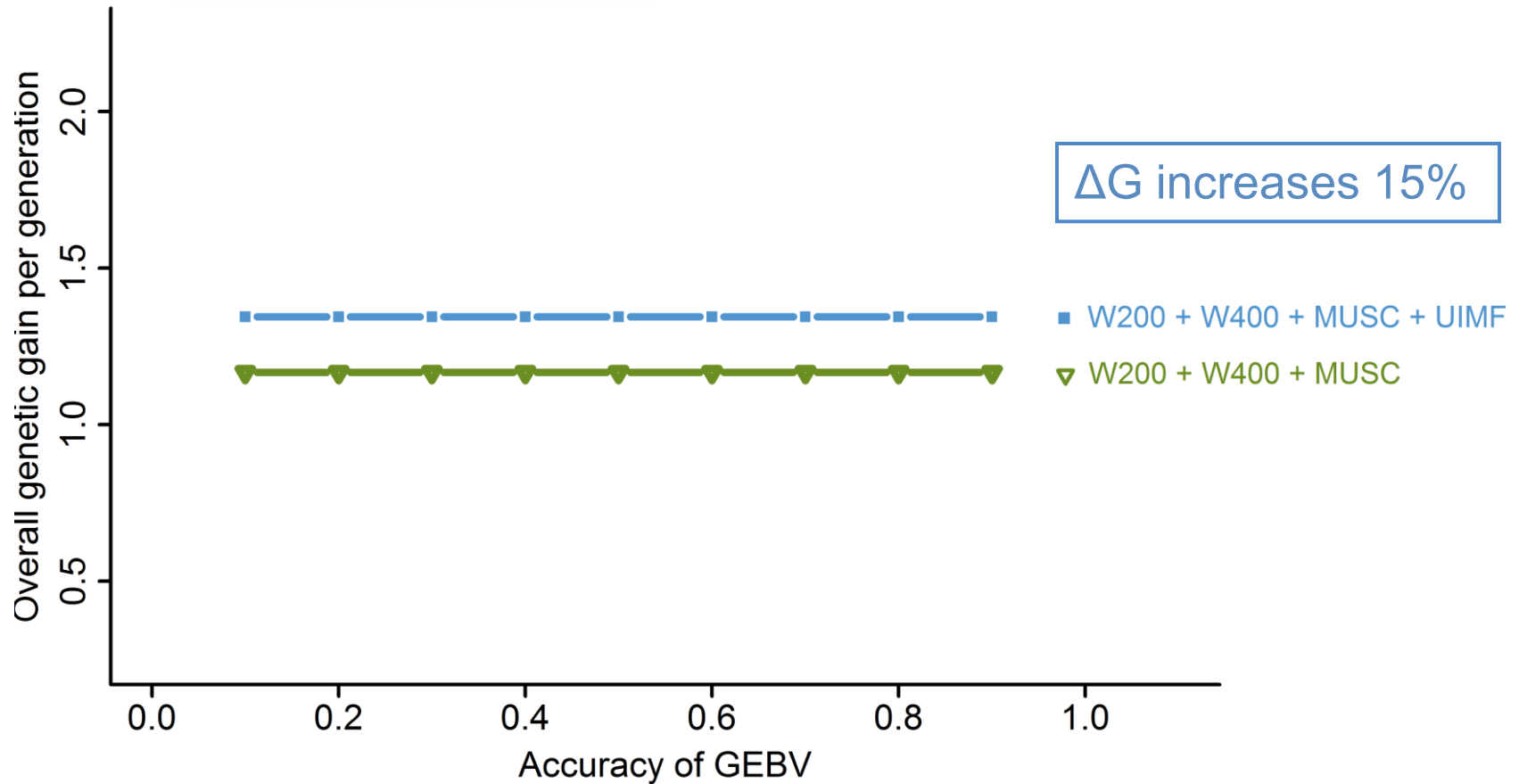
Weight on MARB is doubled





Results

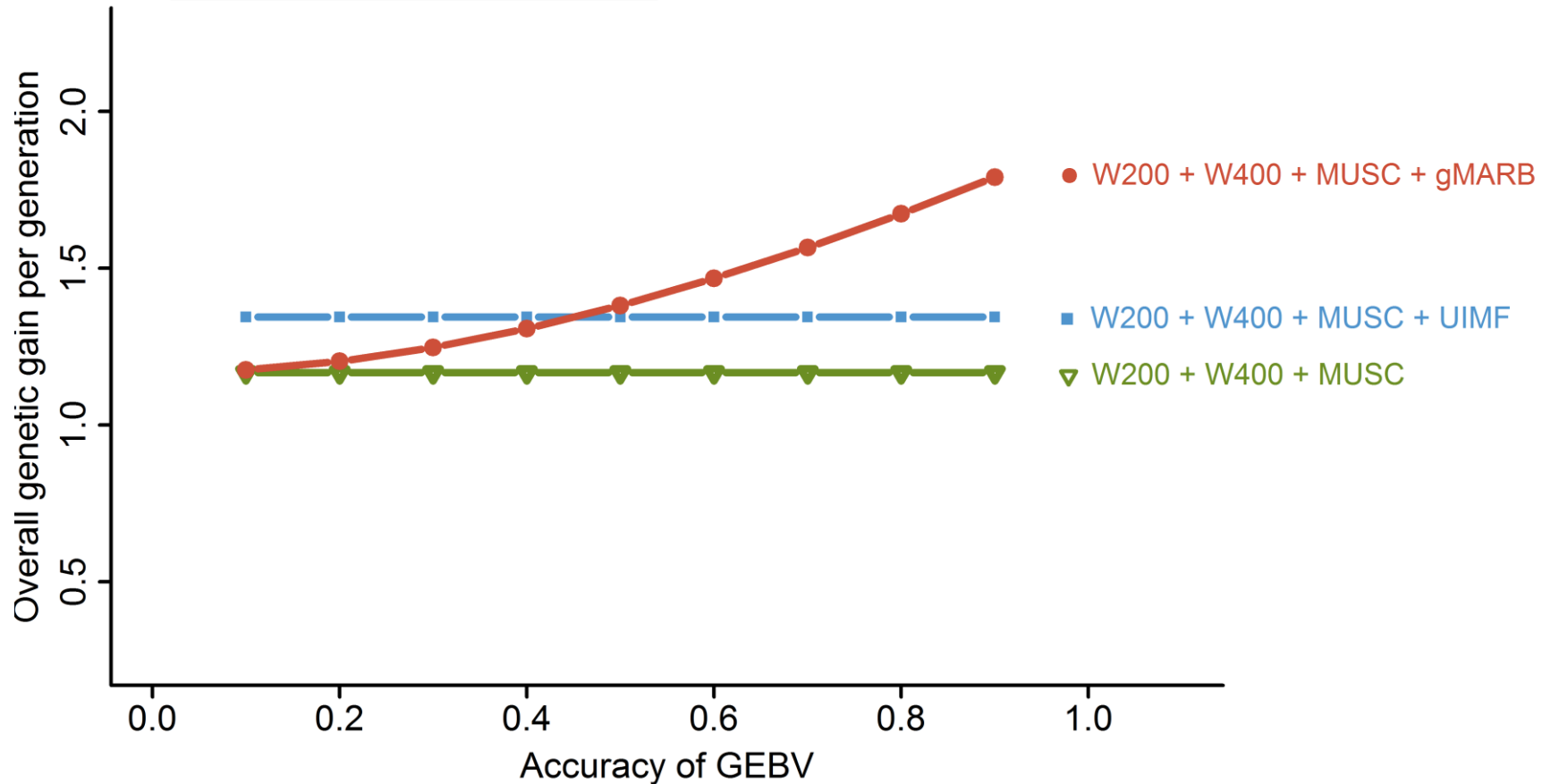
Weight on MARB is doubled





Results

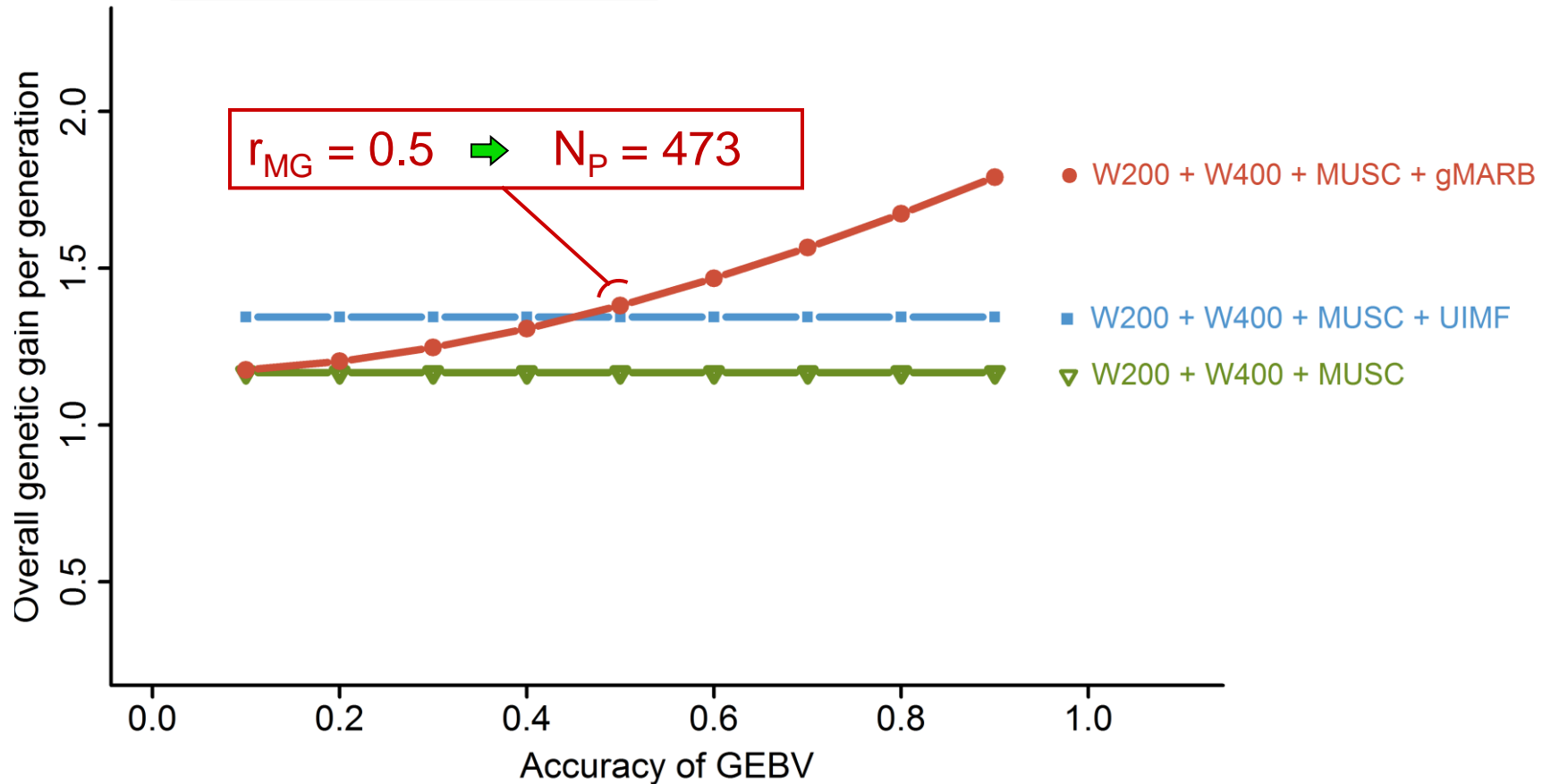
Weight on MARB is doubled





Results

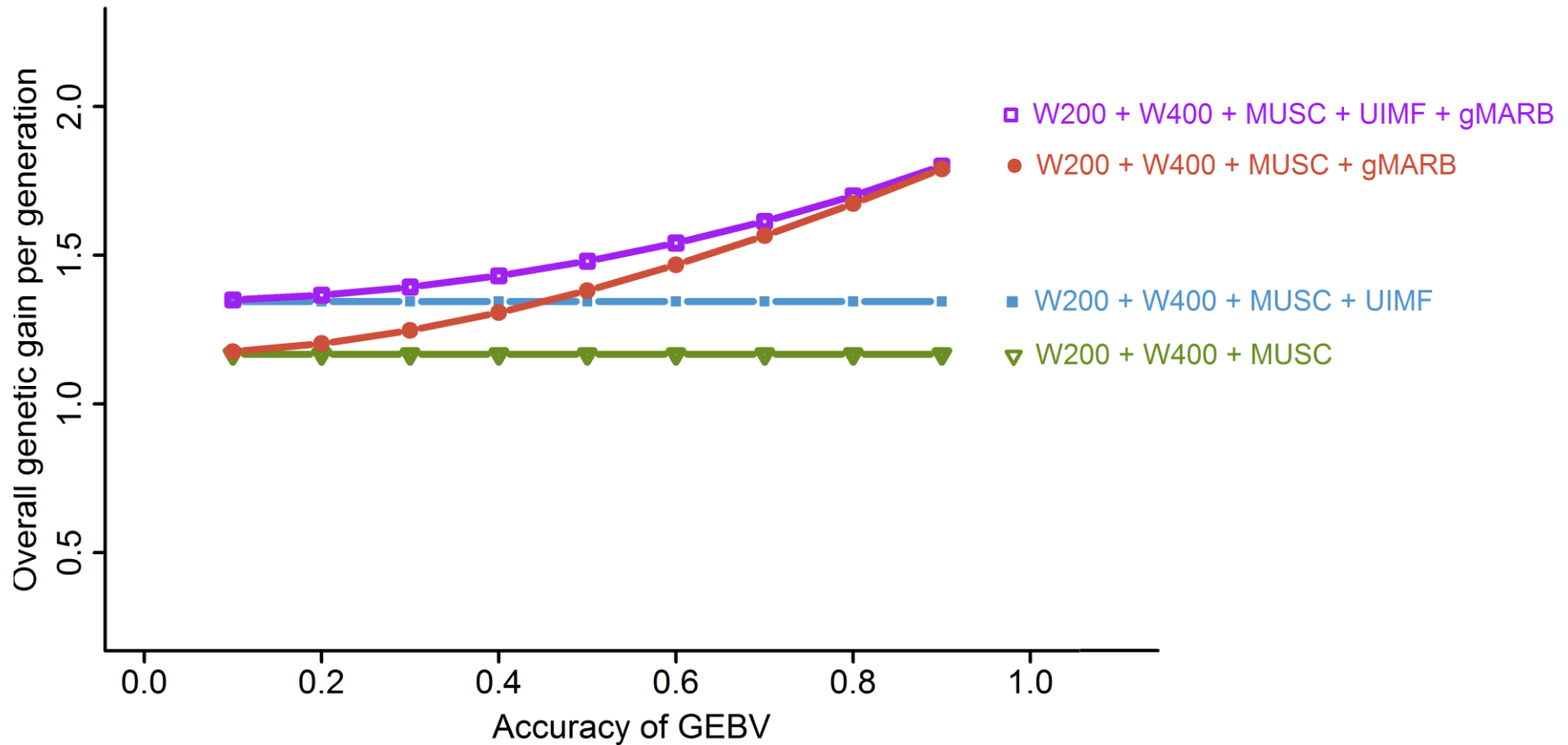
Weight on MARB is doubled





Results

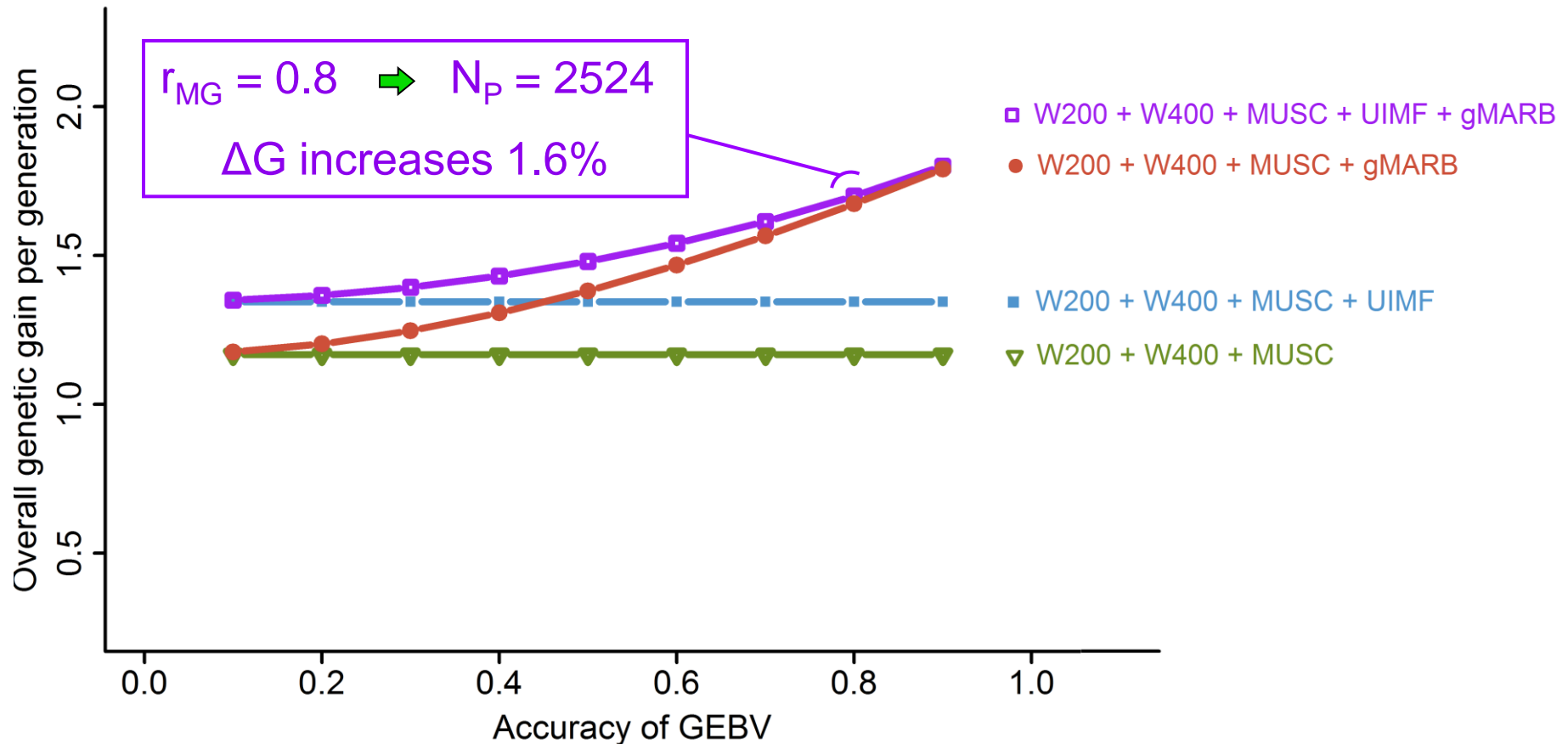
Weight on MARB is doubled





Results

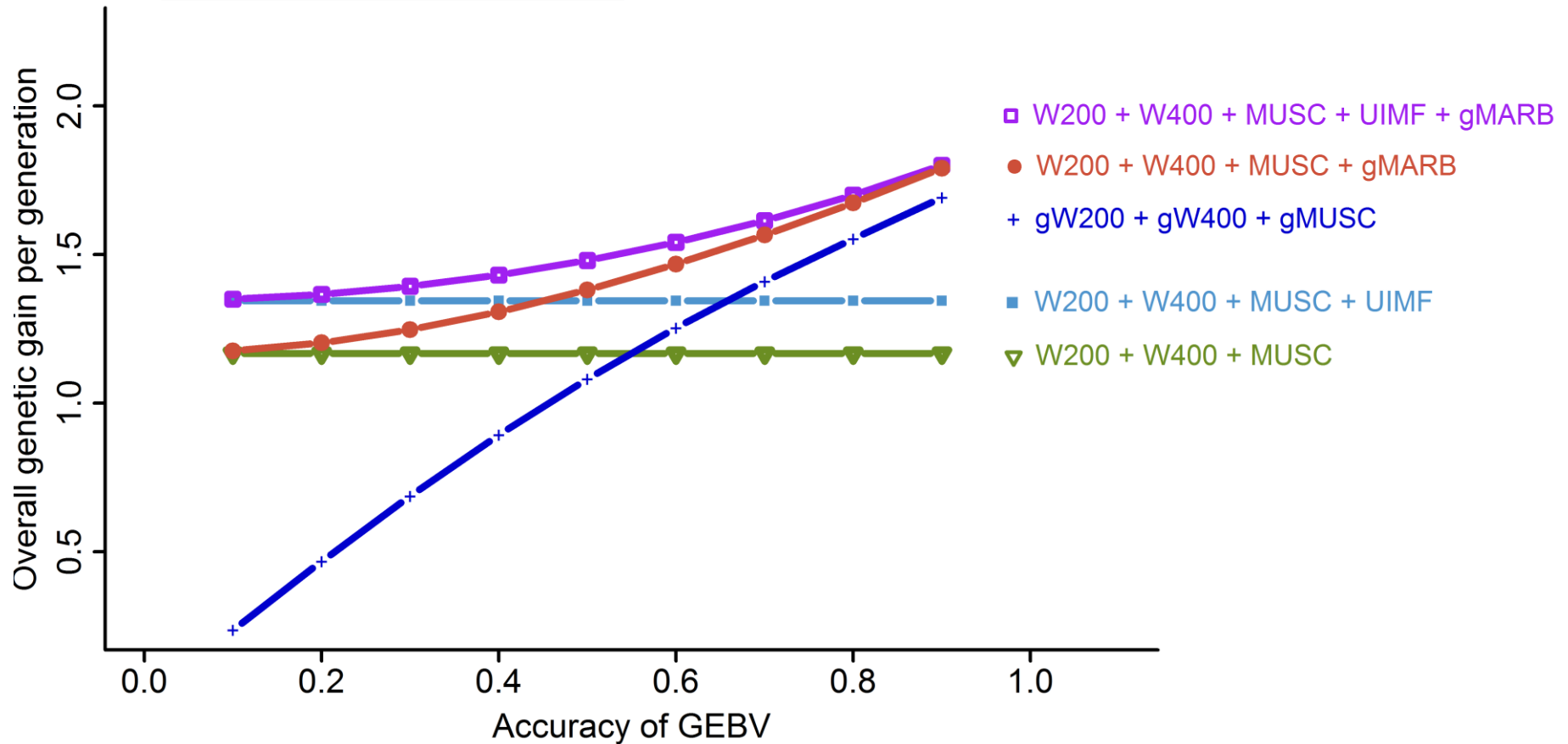
Weight on MARB is doubled





Results

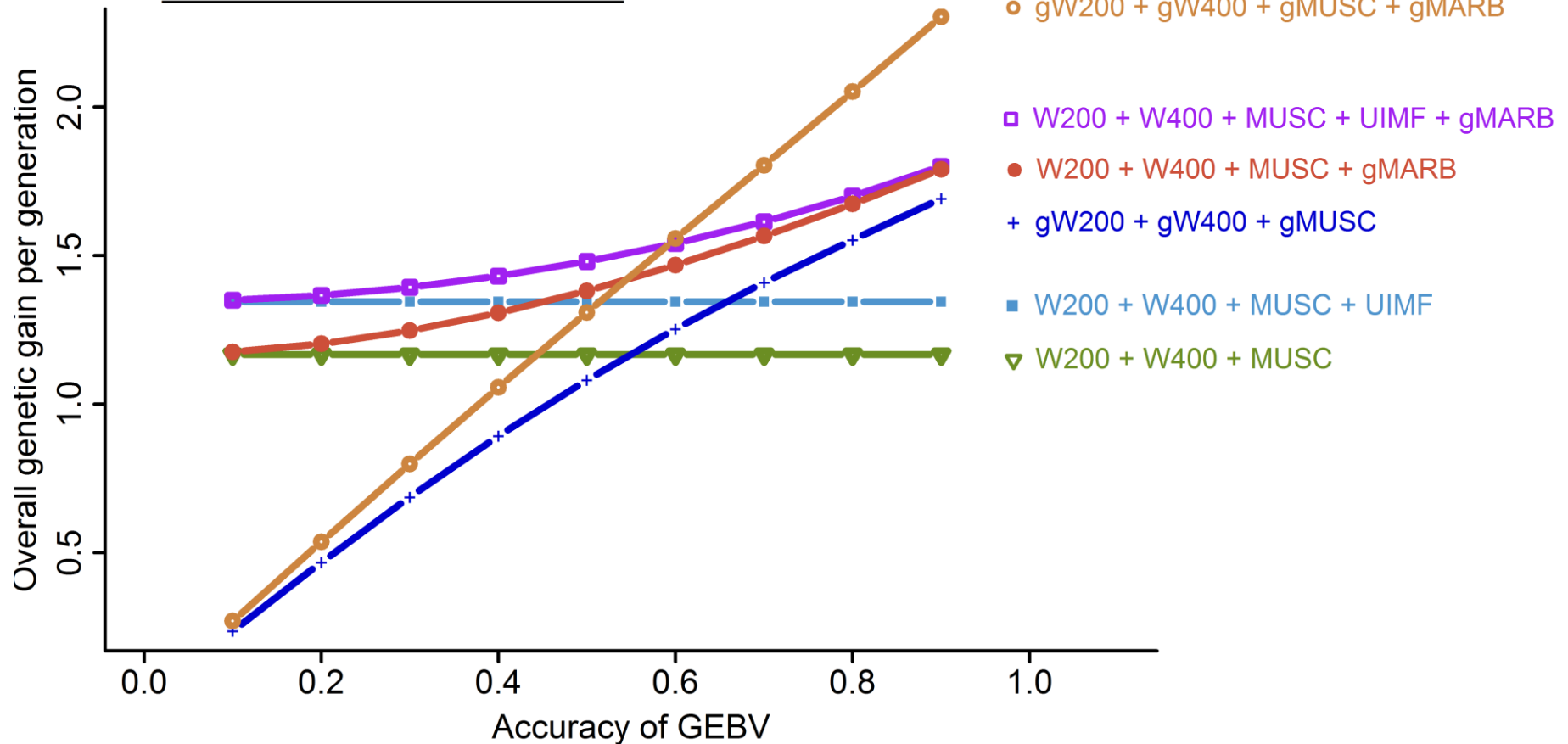
Weight on MARB is doubled





Results

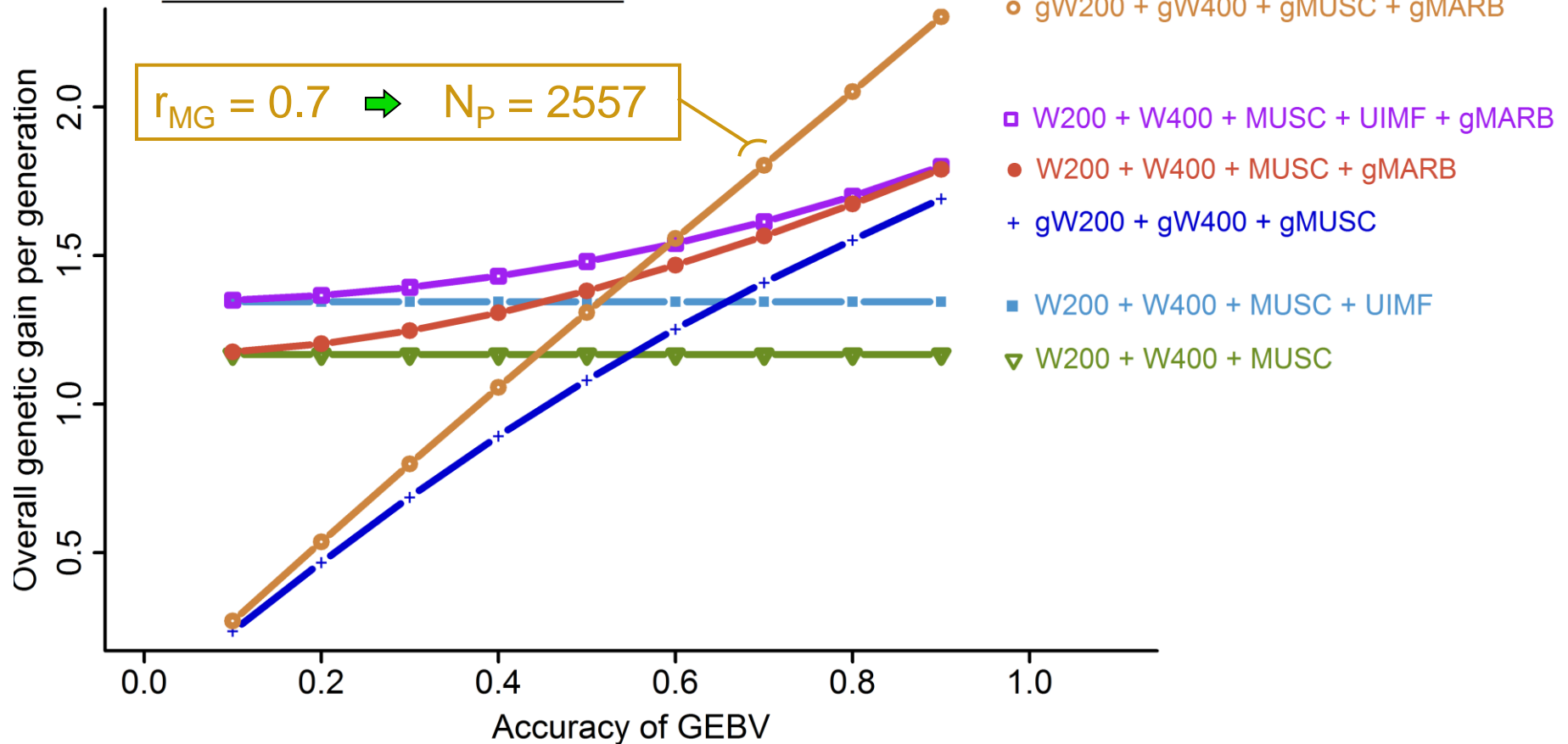
Weight on MARB is doubled





Results

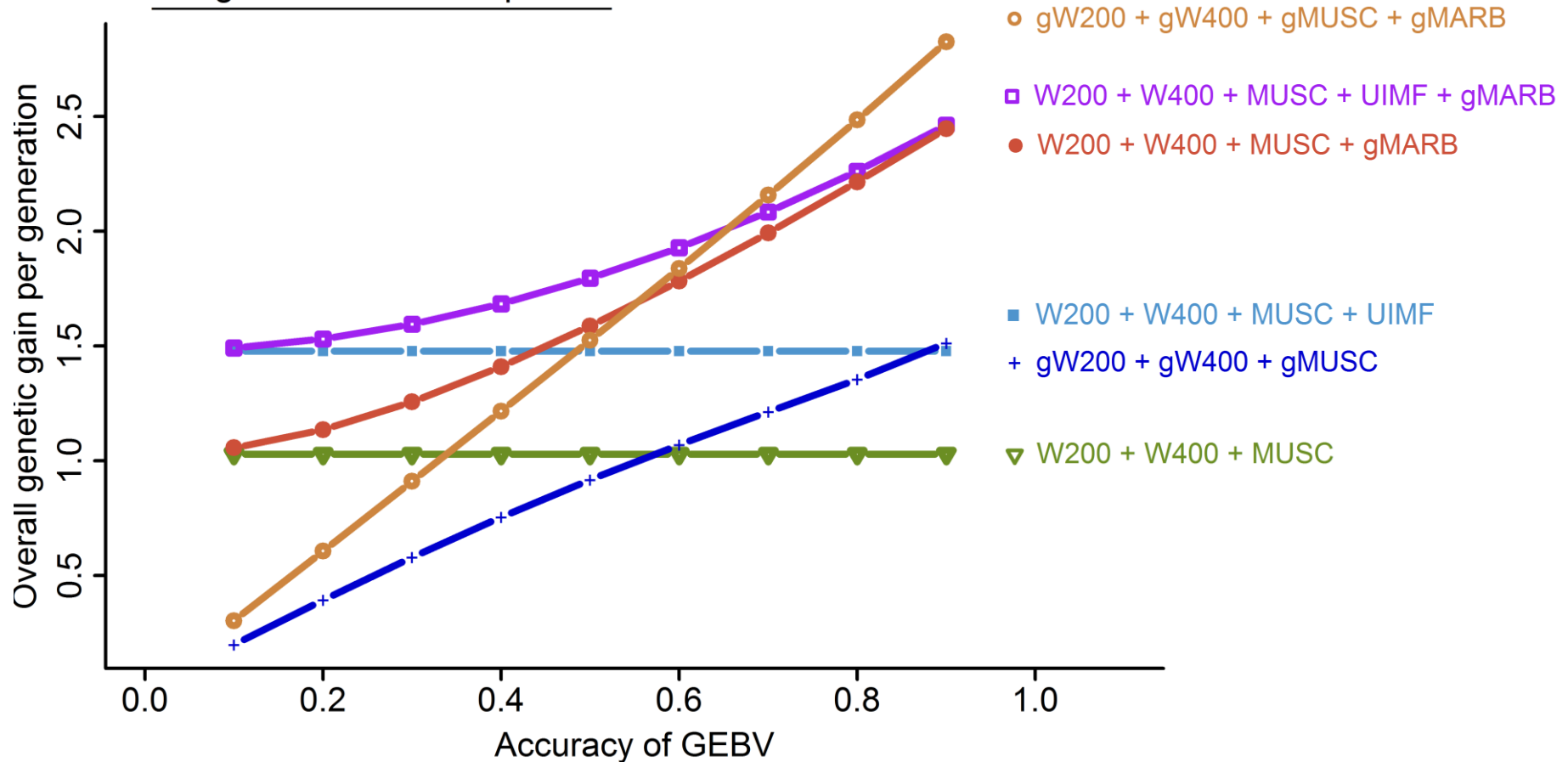
Weight on MARB is doubled





Results

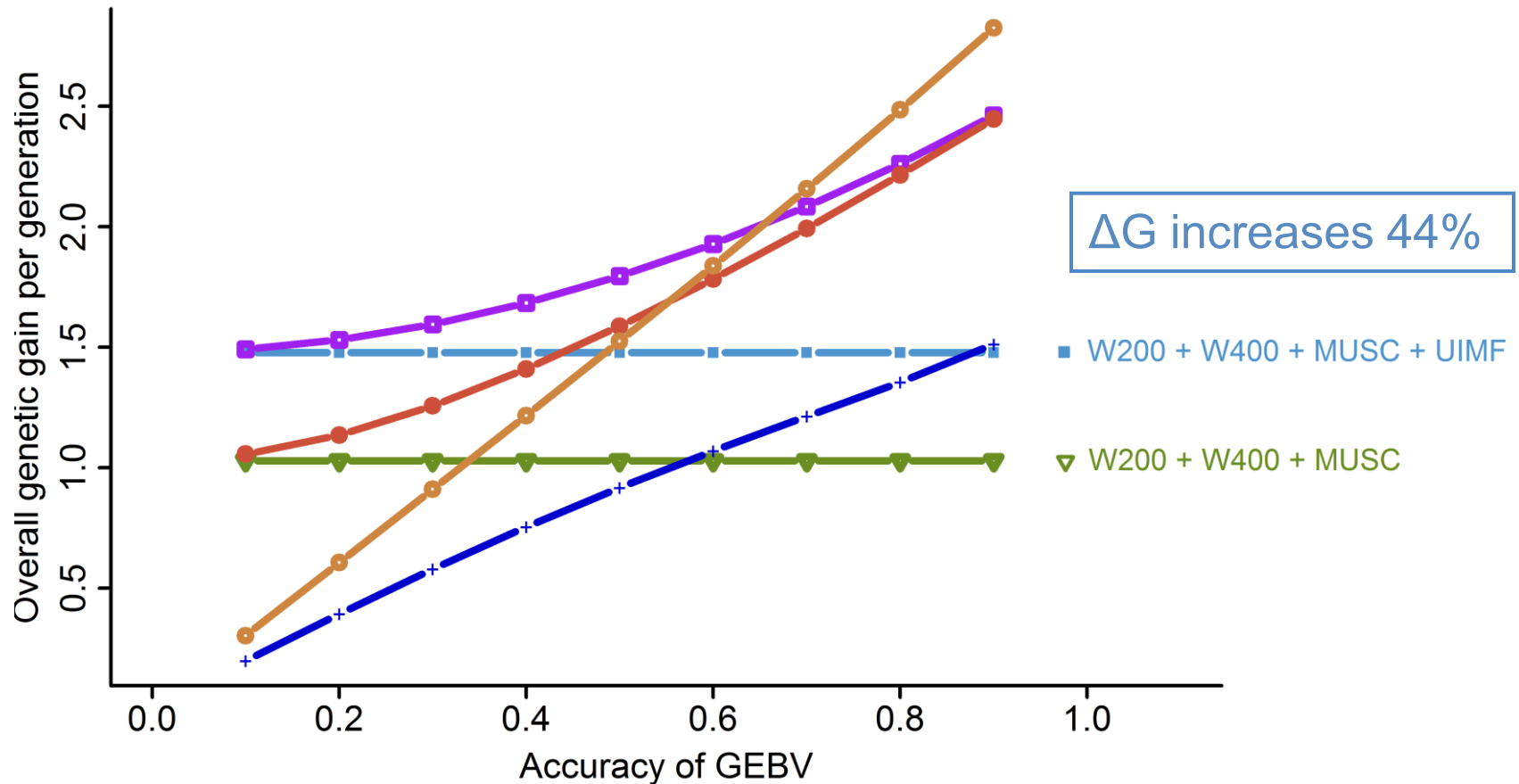
Weight on MARB is tripled





Results

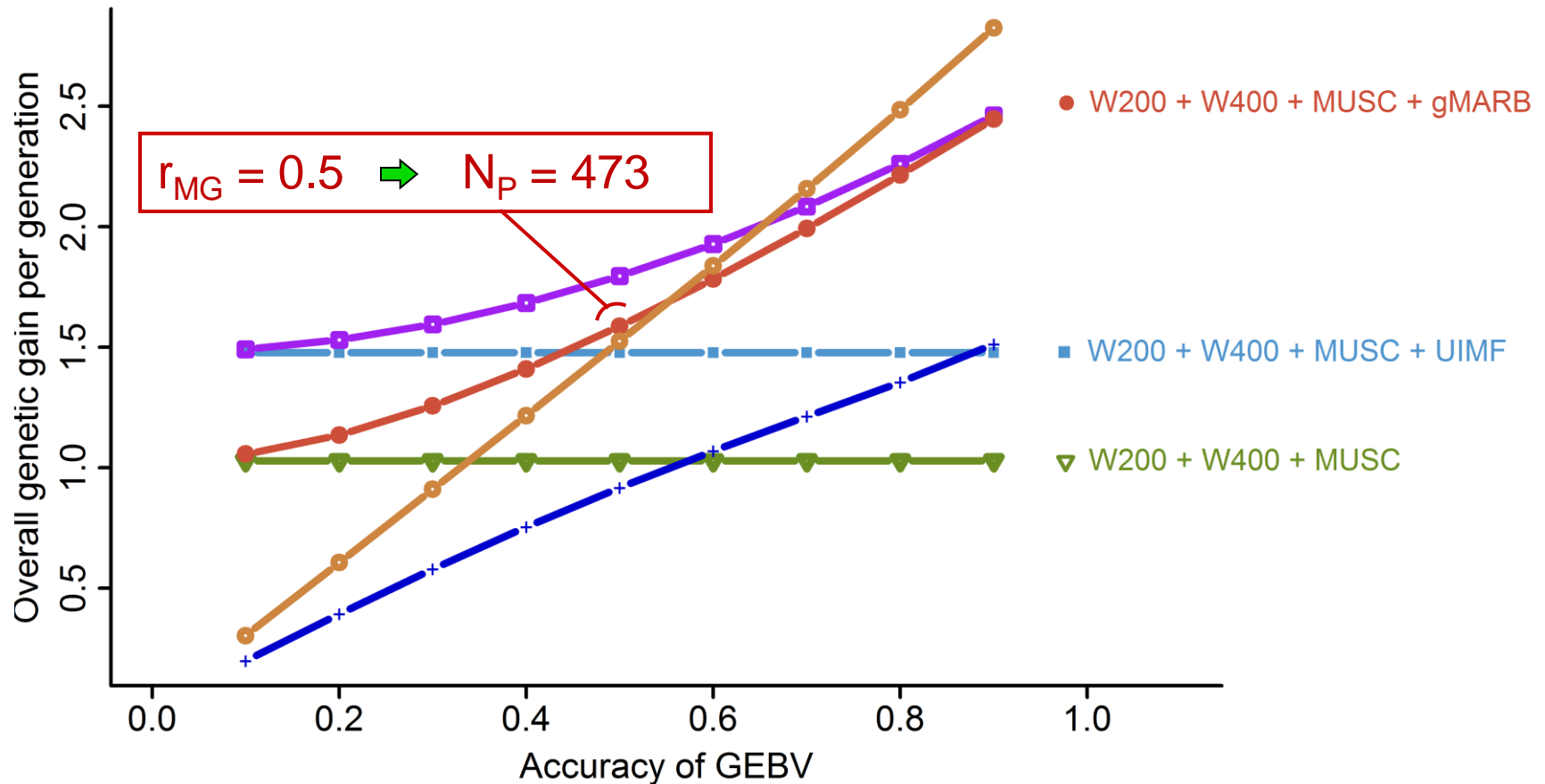
Weight on MARB is tripled





Results

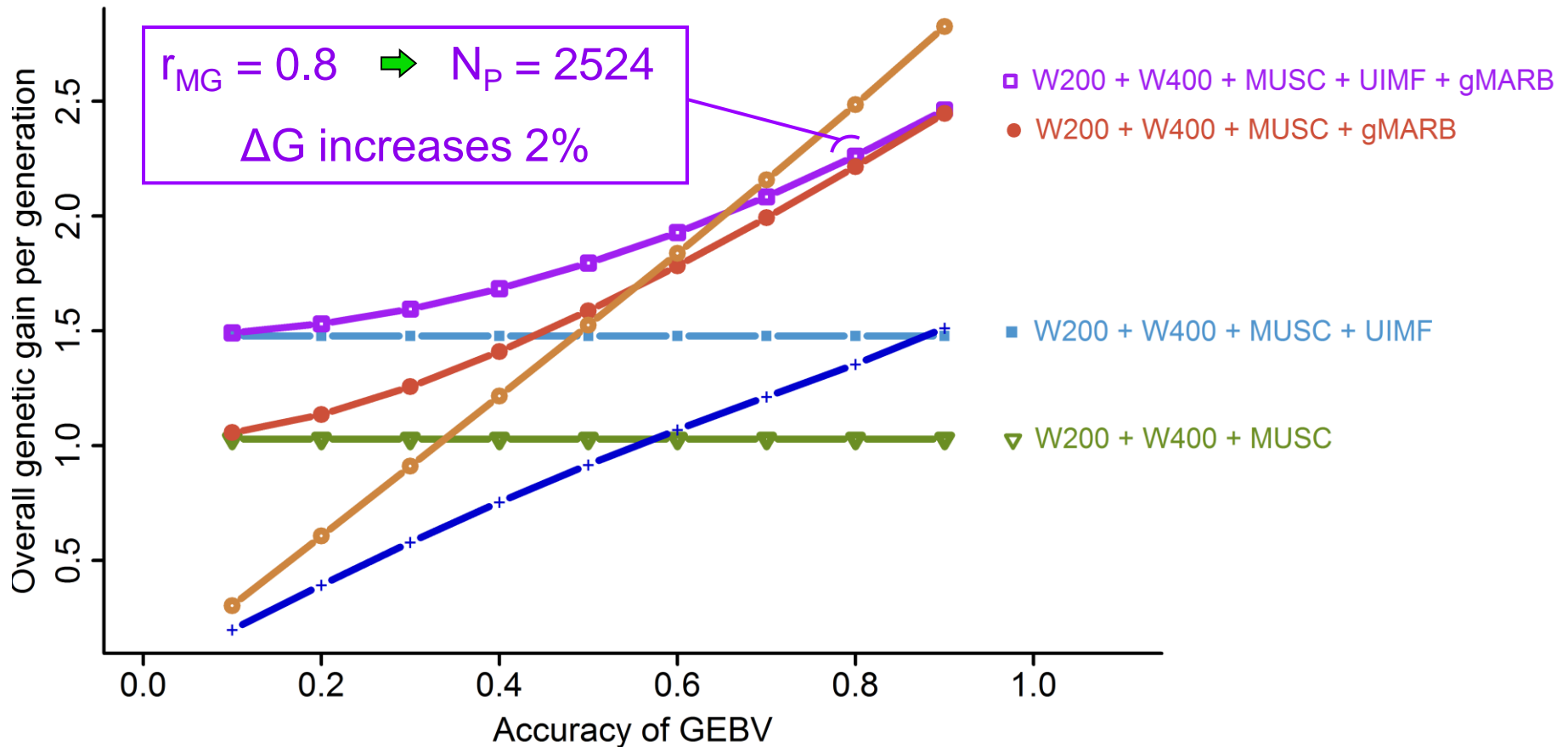
Weight on MARB is tripled





Results

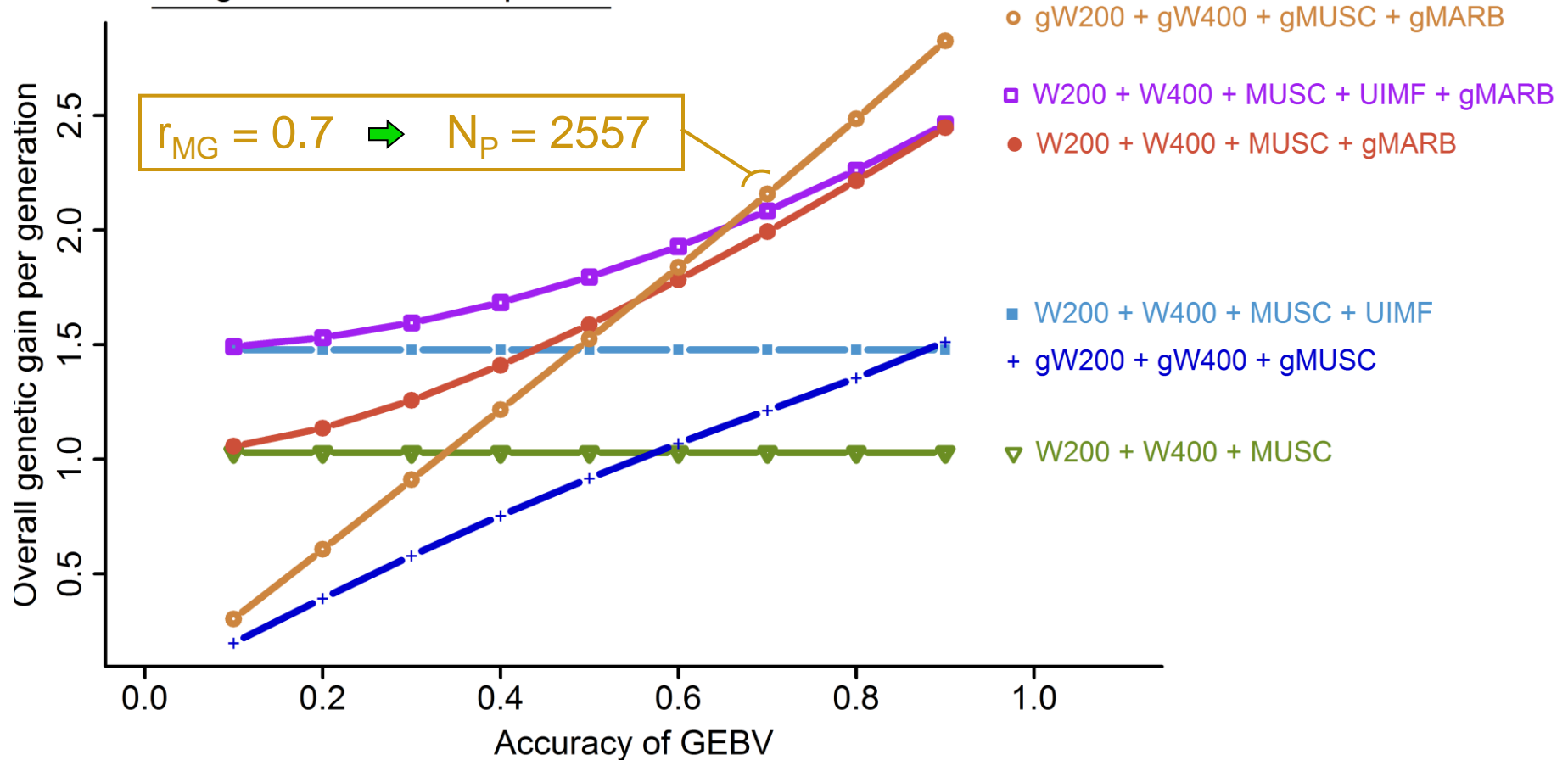
Weight on MARB is tripled





Results

Weight on MARB is tripled





Concluding remarks

- Setting up a reference population of ~500 animals for using **gMARB** could suffice to obtain larger response to selection than using **UIMF**.
- With ~2500 animals, adding **UIMF** to an index already **gMARB** would bring little benefit, unless the economic weight for **MARB** is much larger than for other traits.



Thanks

