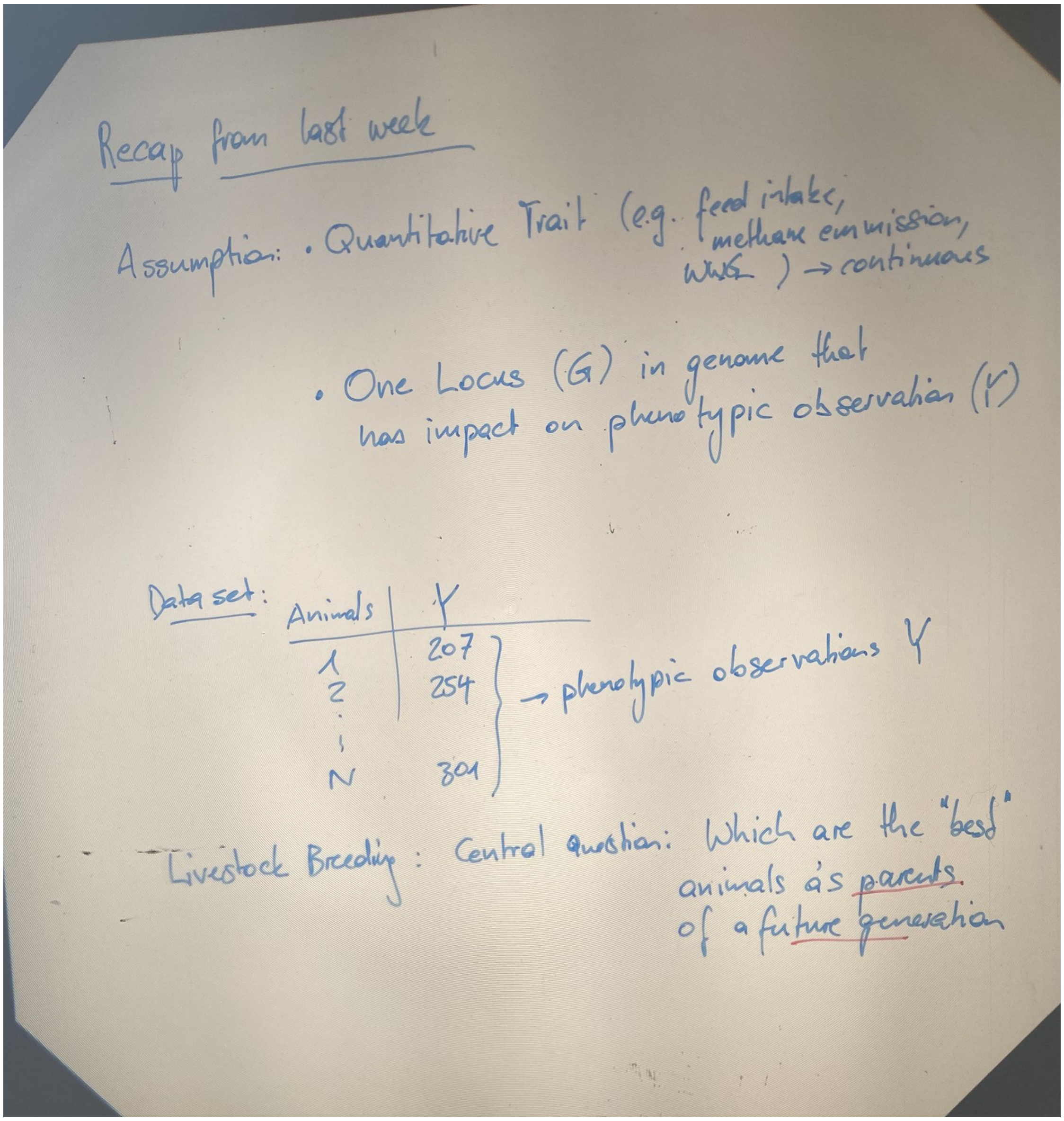
OHP Picture 1



Recap from last week

Assumption: • Quantitative Trait (e.g. feed intake, methane emission, WWG) → continuous

• One Locus (G) in genome that has impact on phenotypic observation (Y)

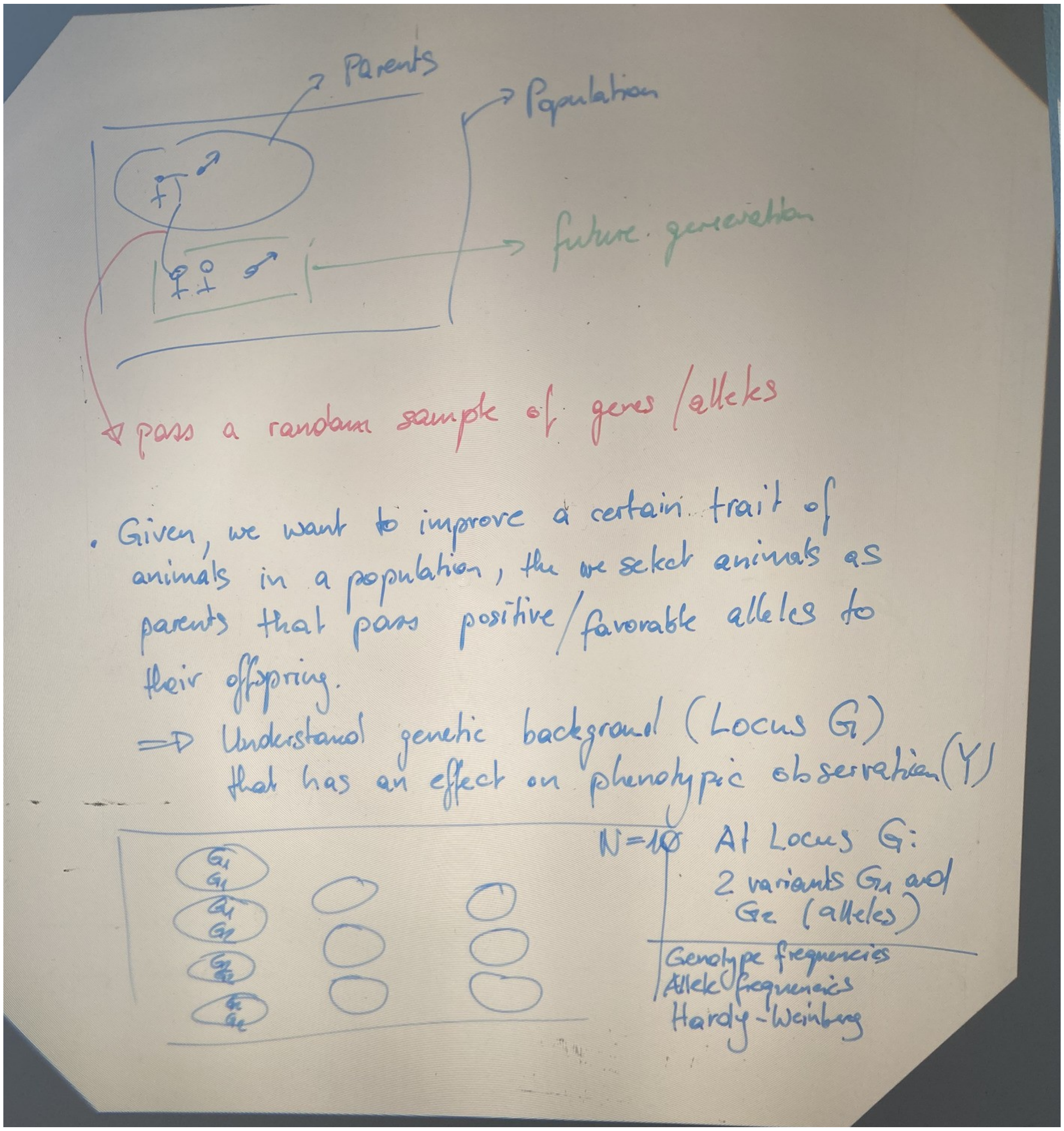
Data set:

Animals	Y
1	207
2	254
⋮	
N	301

→ phenotypic observations Y

Livestock Breeding: Central question: Which are the "best" animals as parents of a future generation

OHP Picture 2



pass a random sample of genes / alleles

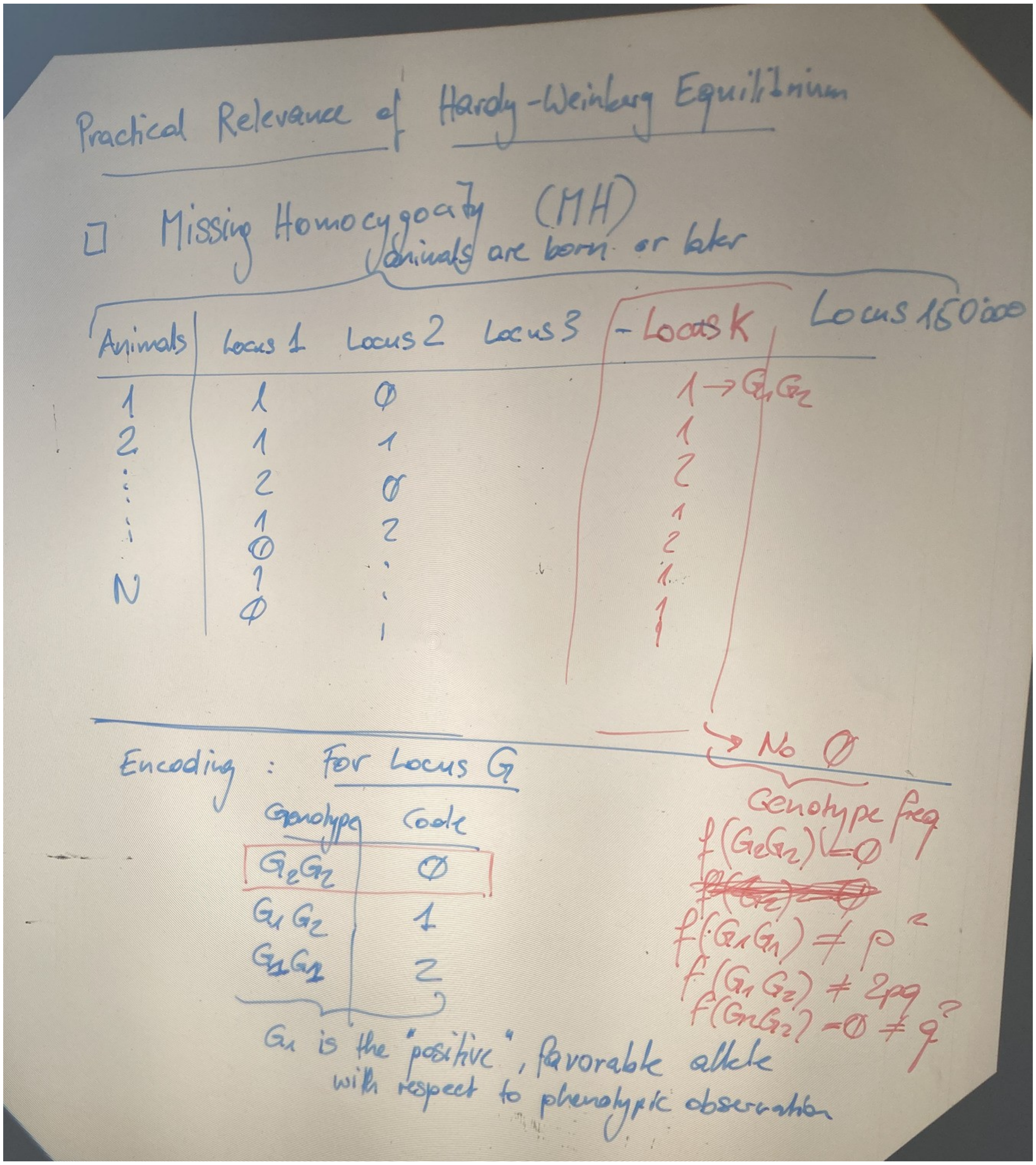
- Given, we want to improve a certain trait of animals in a population, the we select animals as parents that pass positive / favorable alleles to their offspring.

  ⇒ Understand genetic background (Locus G) that has an effect on phenotypic observation (Y)

At Locus G:
2 variants G_1 and G_2 (alleles)

Genotype frequencies
Allele frequencies
Hardy-Weinberg

OHP Picture 3



Practical Relevance of Hardy-Weinberg Equilibrium

☐ Missing Homozygosity (MH)

animals are born or later

Animals	Locus 1	Locus 2	Locus 3	- Locus k	Locus 150'000
1	1	0		$1 \rightarrow G_1G_2$	
2	1	1		1	
⋮	2	0		2	
	1	2		1	
	0	⋮		2	
N	1			1	
	0			1	

→ No 0

Encoding : For Locus G

Genotype	Code
G_2G_2	0
G_1G_2	1
G_1G_1	2

G_1 is the "positive", favorable allele with respect to phenotypic observation

Genotype freq

$f(G_2G_2) = 0$

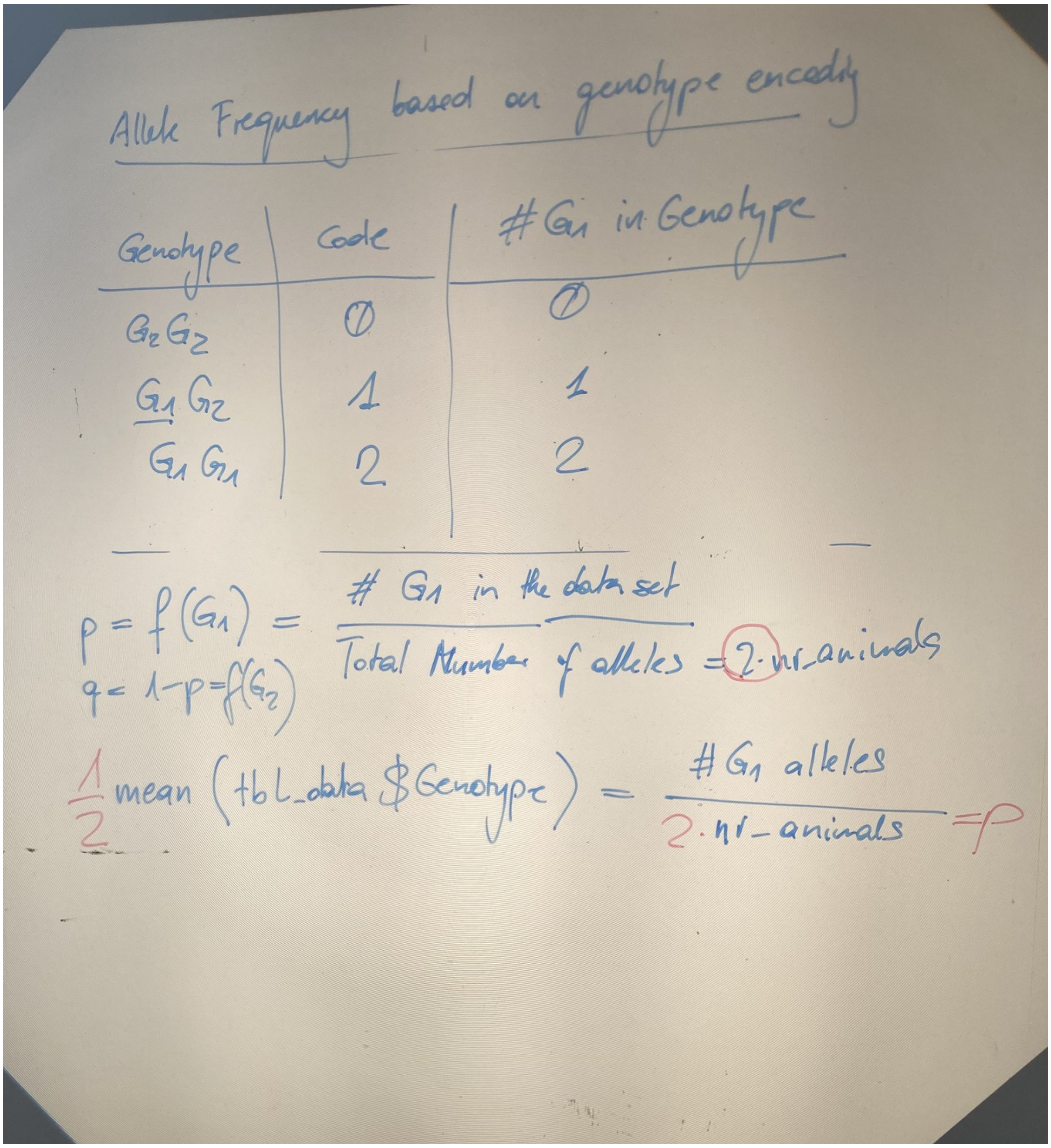
~~$f(G_2G_2) = 0$~~

$f(G_1G_1) \neq p^2$

$f(G_1G_2) \neq 2pq$

$f(G_2G_2) = 0 \neq q^2$

OHP Picture 4



Allele Frequency based on genotype encoding

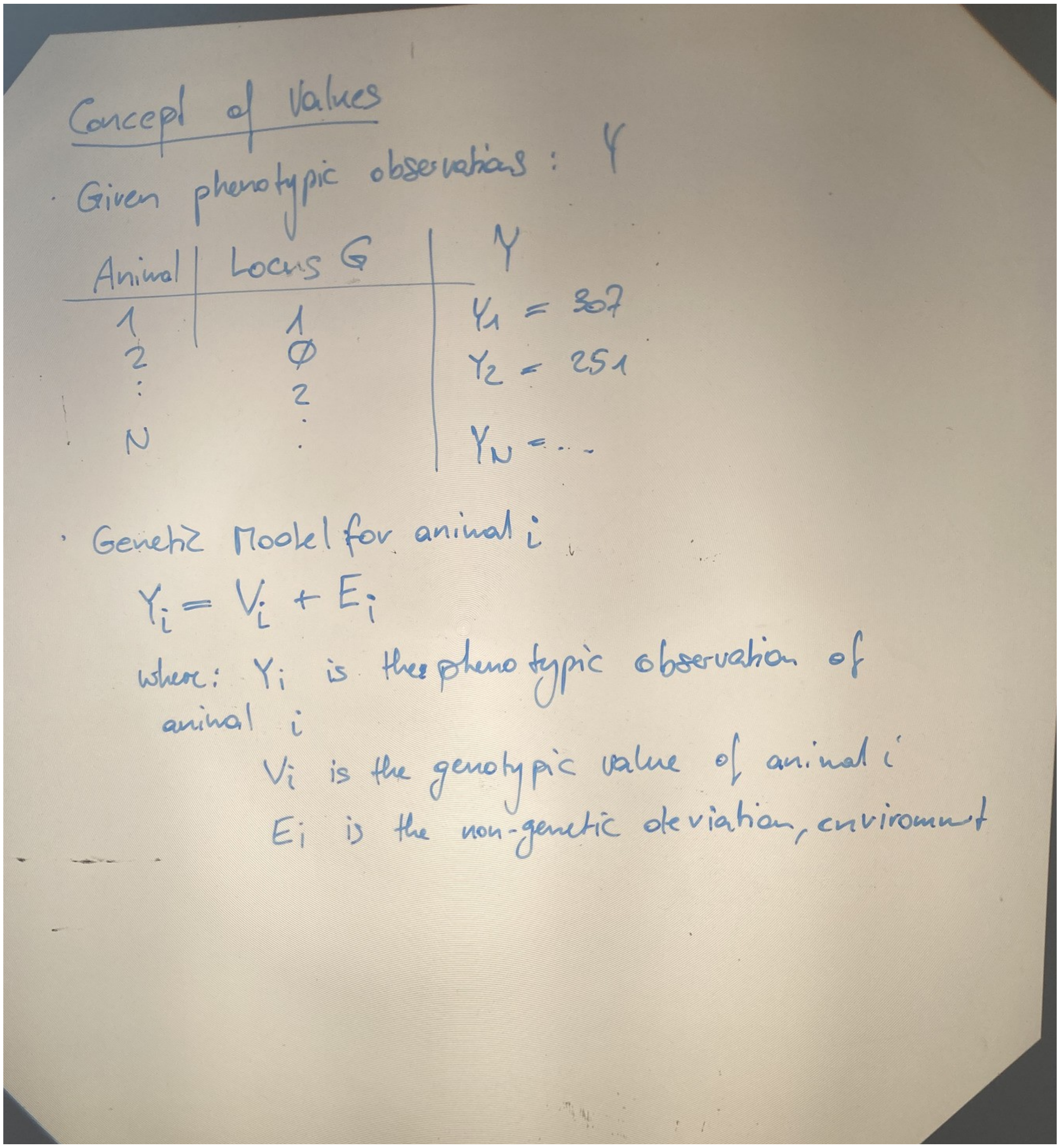
Genotype	Code	# G_1 in Genotype
G_2G_2	0	0
G_1G_2	1	1
G_1G_1	2	2

$$p = f(G_1) = \frac{\#\ G_1 \text{ in the data set}}{\text{Total Number of alleles} = \boxed{2} \cdot \text{nr\_animals}}$$

$$q = 1 - p = f(G_2)$$

$$\frac{1}{2}\,\text{mean}\left(\text{tbl\_data\$Genotype}\right) = \frac{\#\ G_1 \text{ alleles}}{2 \cdot \text{nr\_animals}} = p$$

OHP Picture 5



Concept of Values

- Given phenotypic observations : Y

Animal	Locus G	Y
1	1	$Y_1 = 307$
2	0	$Y_2 = 251$
:	2	
N	:	$Y_N = \dots$

- Genetic Model for animal i

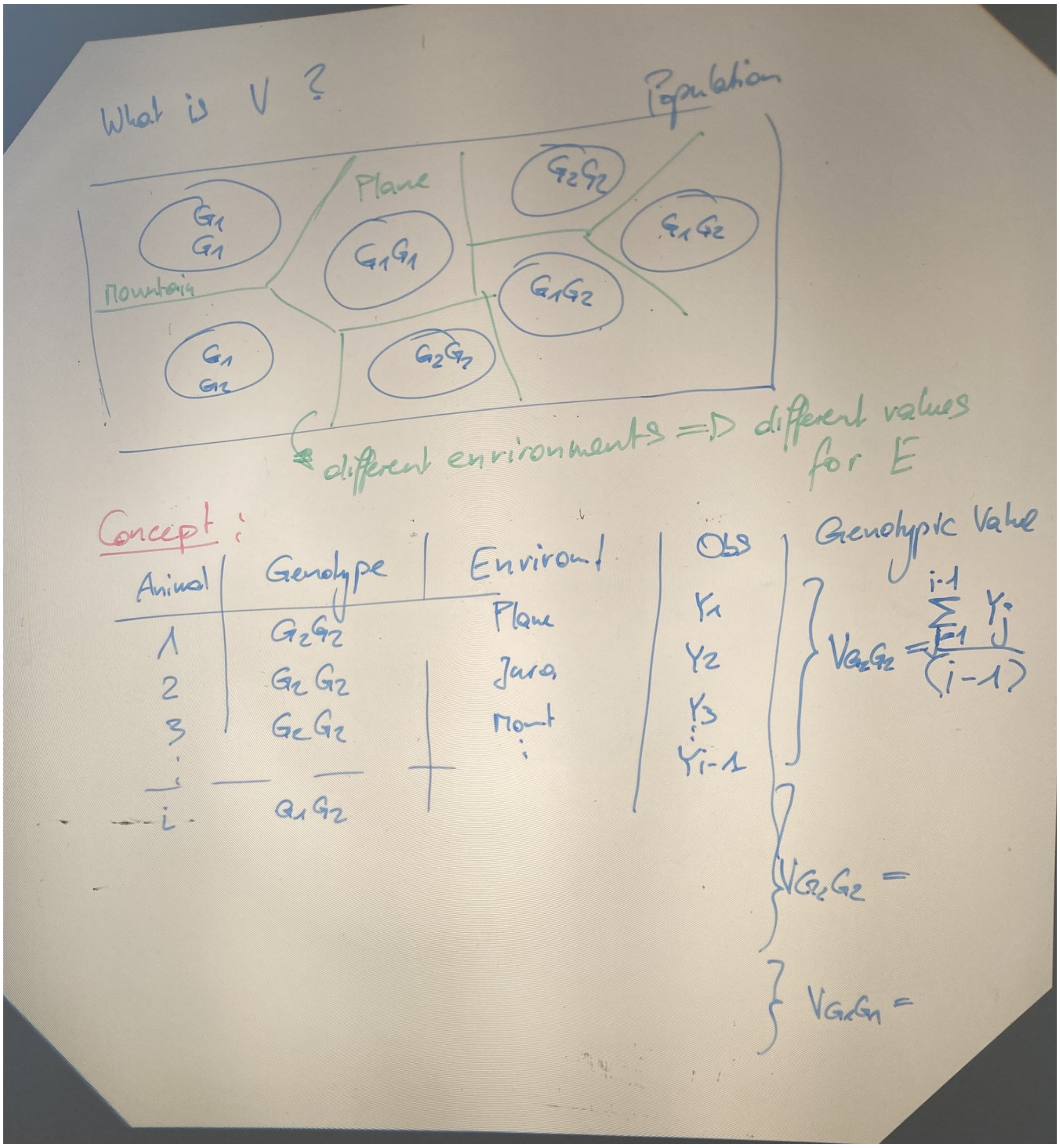
$$Y_i = V_i + E_i$$

where: Y_i is the phenotypic observation of animal i

V_i is the genotypic value of animal i

E_i is the non-genetic deviation, environment

OHP Picture 6



What is V ?

different environments => different values for E

Concept :

Animal	Genotype	Environment	Obs
1	G_2G_2	Plane	y_1
2	G_2G_2	Jura	y_2
3	G_2G_2	Mont	y_3
$\vdots$		$\vdots$	$\vdots$ y_{i-1}
i	G_1G_2		

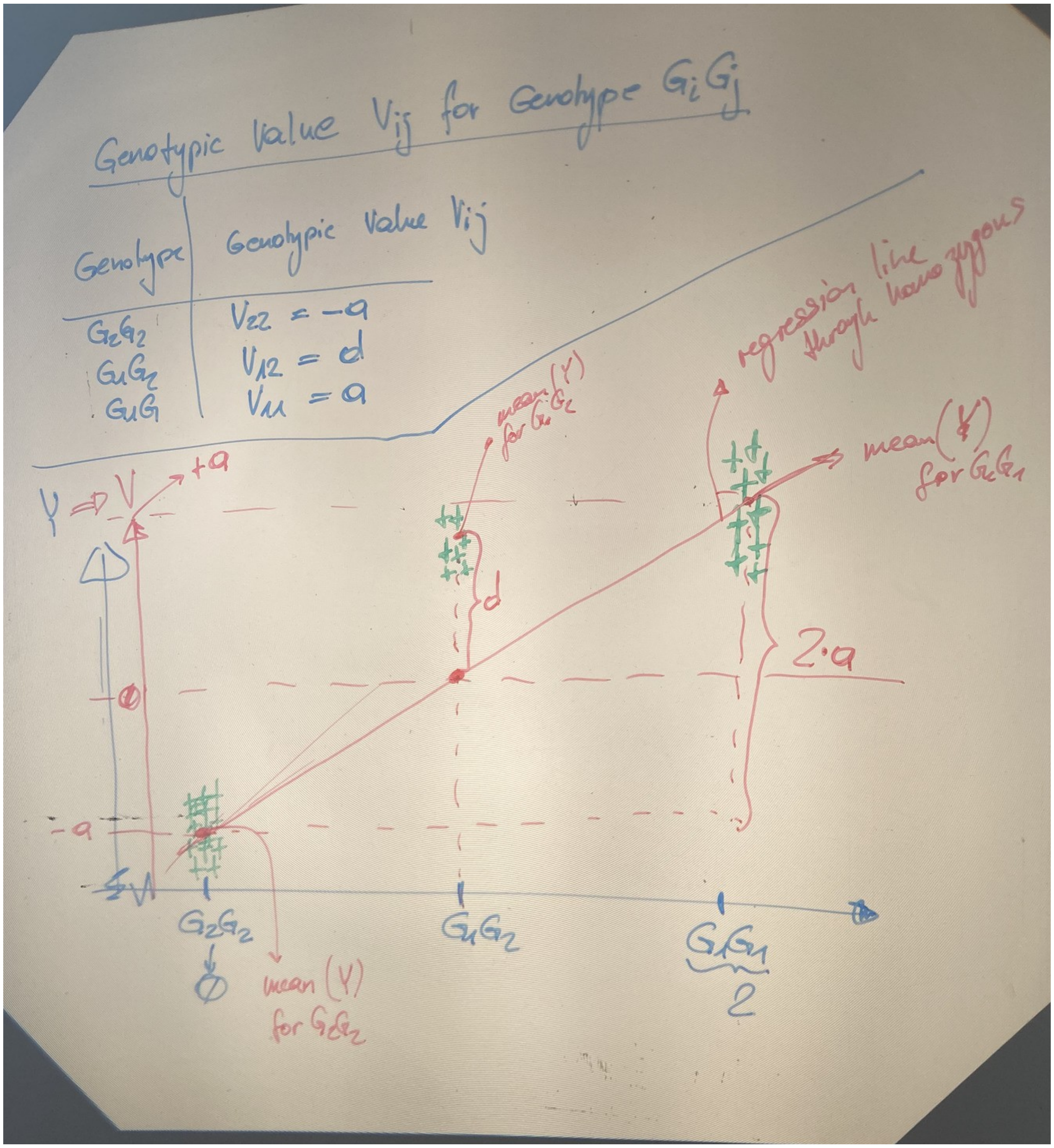
Genotypic Value

$$V_{G_2G_2} = \frac{\sum_{j=1}^{i-1} y_j}{(i-1)}$$

$$V_{G_1G_2} =$$

$$V_{G_1G_1} =$$

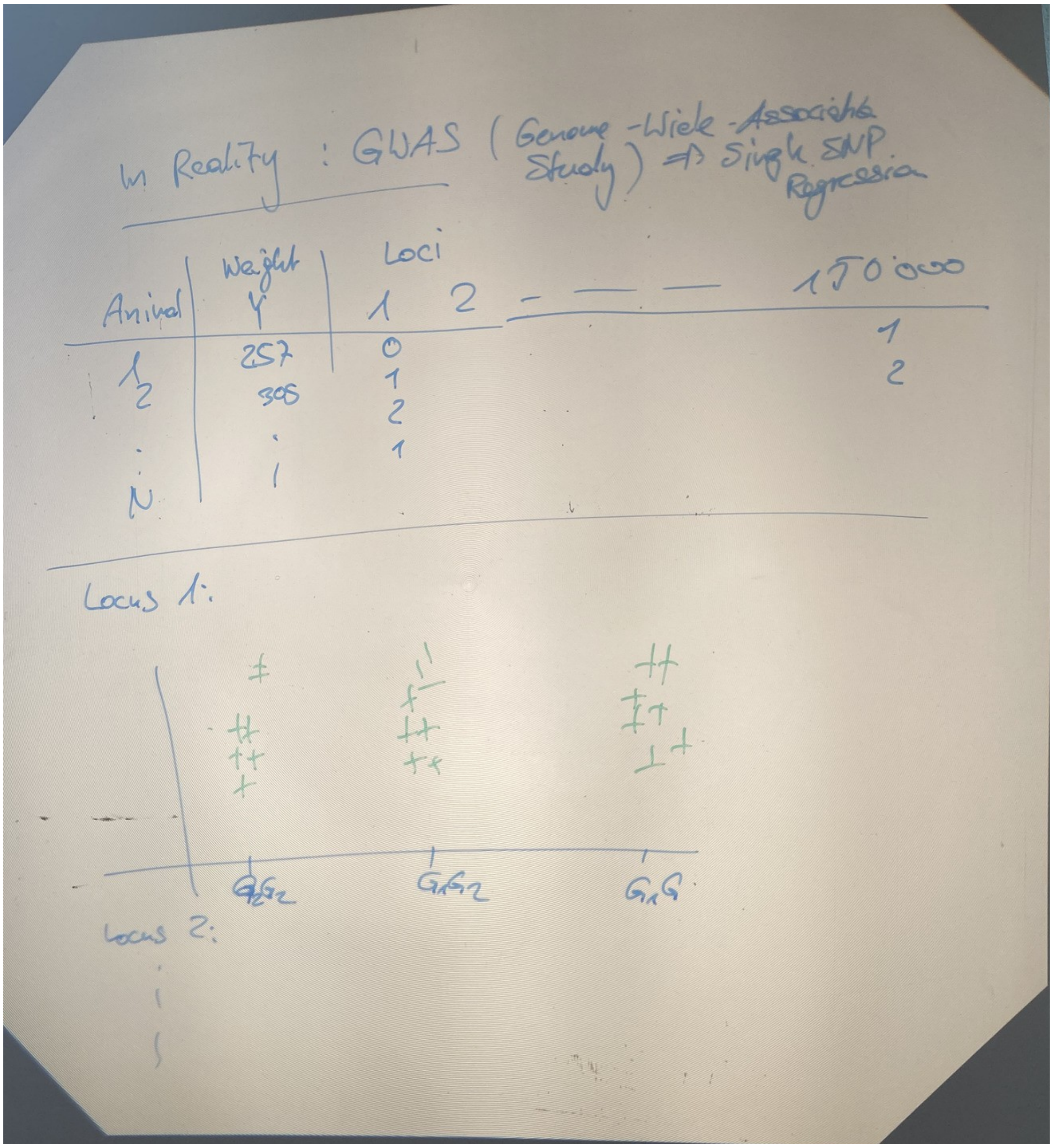
OHP Picture 7



Genotypic Value V_{ij} for Genotype G_iG_j

Genotype	Genotypic Value V_{ij}
G_2G_2	$V_{22} = -a$
G_1G_2	$V_{12} = d$
G_1G_1	$V_{11} = a$

OHP Picture 8



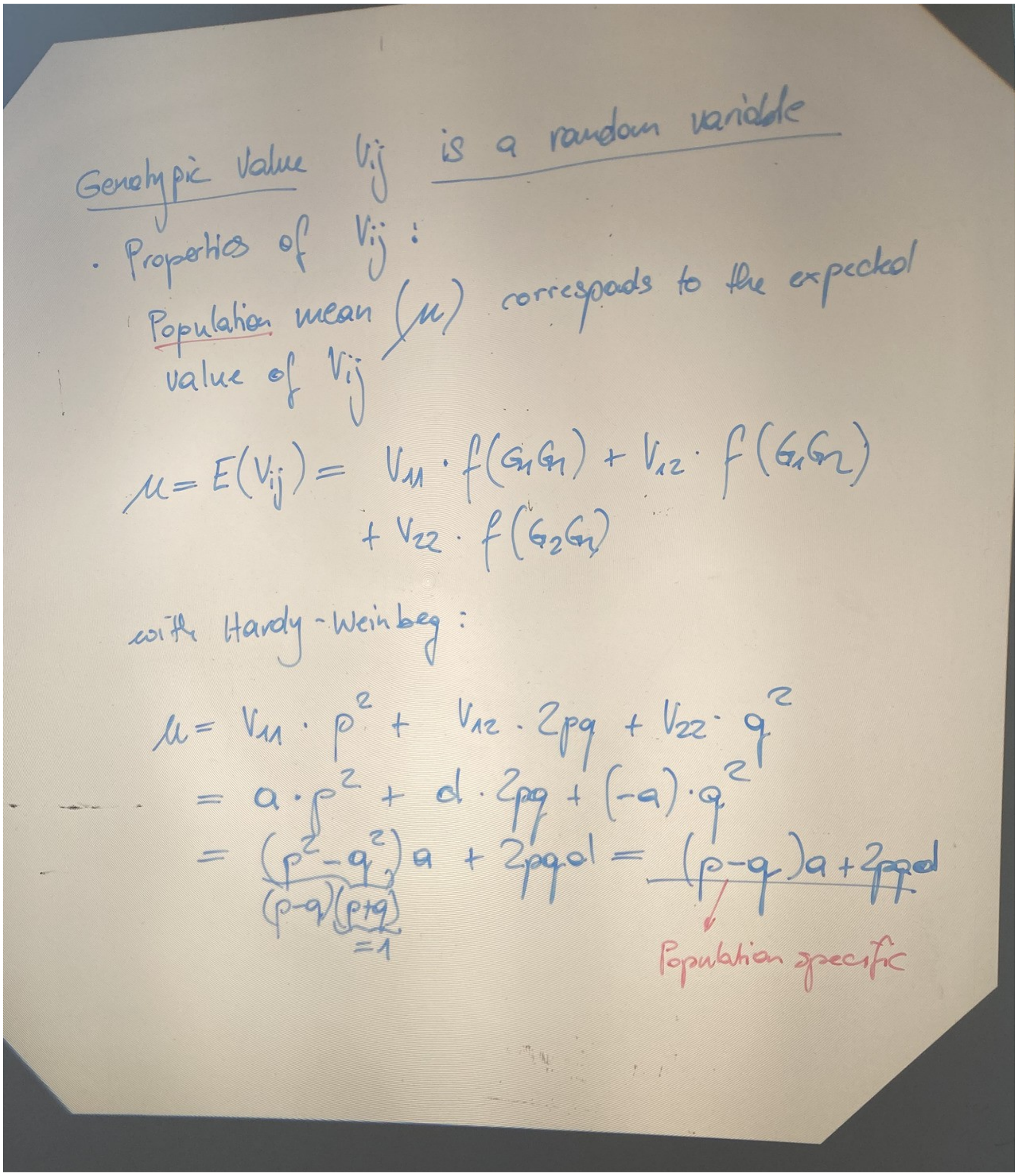
In Reality : GWAS (Genome-Wide-Association Study) ⇒ Single SNP Regression

Animal	Weight Y	Loci 1	2	— — —	150'000
1	257	0			1
2	305	1			2
.	.	2			
.	.	1			
N					

Locus 1:

Locus 2:

OHP Picture 9



Genotypic Value V_{ij} is a random variable

- Properties of V_{ij}:

Population mean (μ) corresponds to the expected value of V_{ij}

$$\mu = E(V_{ij}) = V_{11} \cdot f(G_1G_1) + V_{12} \cdot f(G_1G_2) + V_{22} \cdot f(G_2G_2)$$

with Hardy-Weinberg:

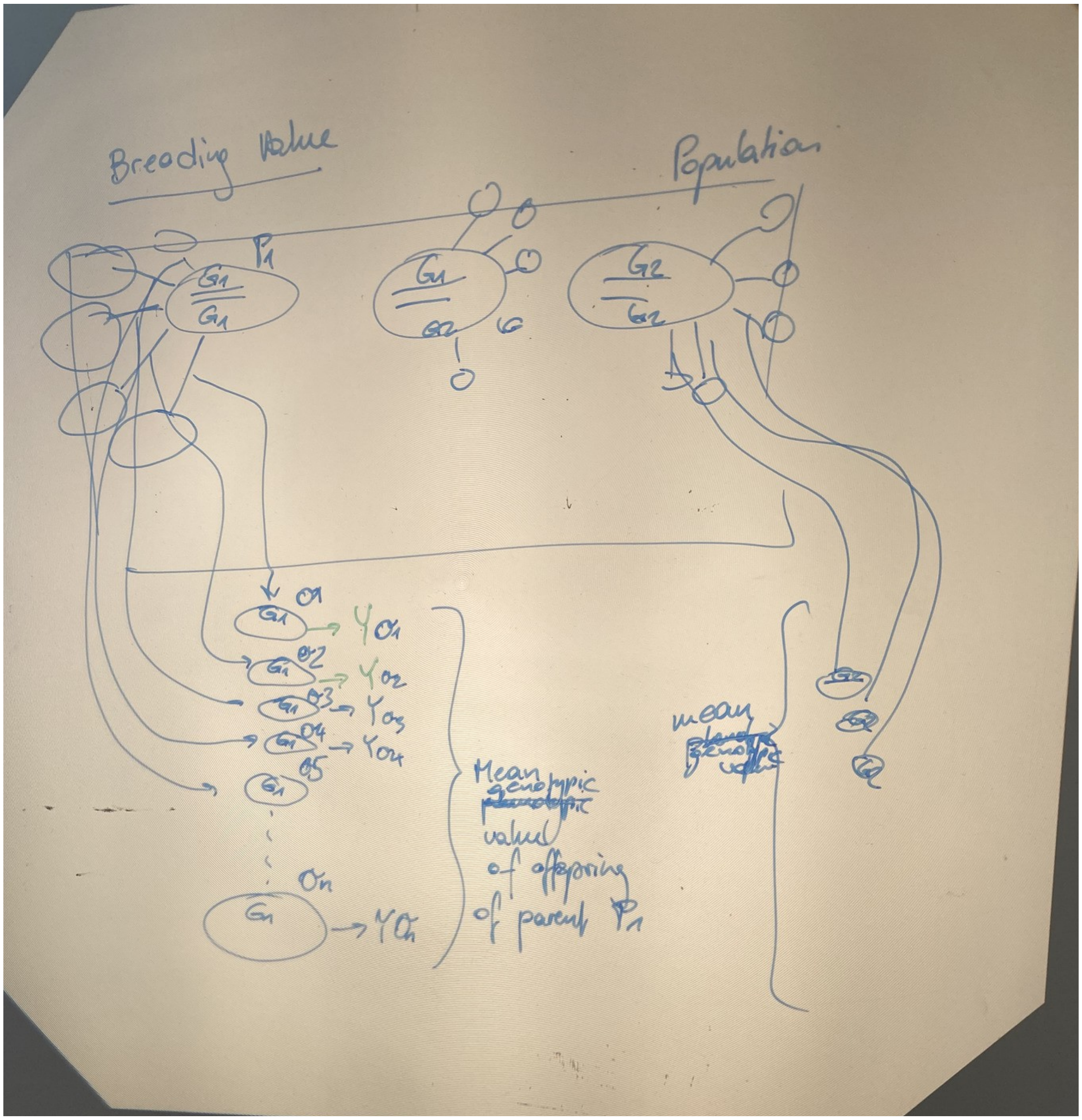
$$\mu = V_{11} \cdot p^2 + V_{12} \cdot 2pq + V_{22} \cdot q^2$$

$$= a \cdot p^2 + d \cdot 2pq + (-a) \cdot q^2$$

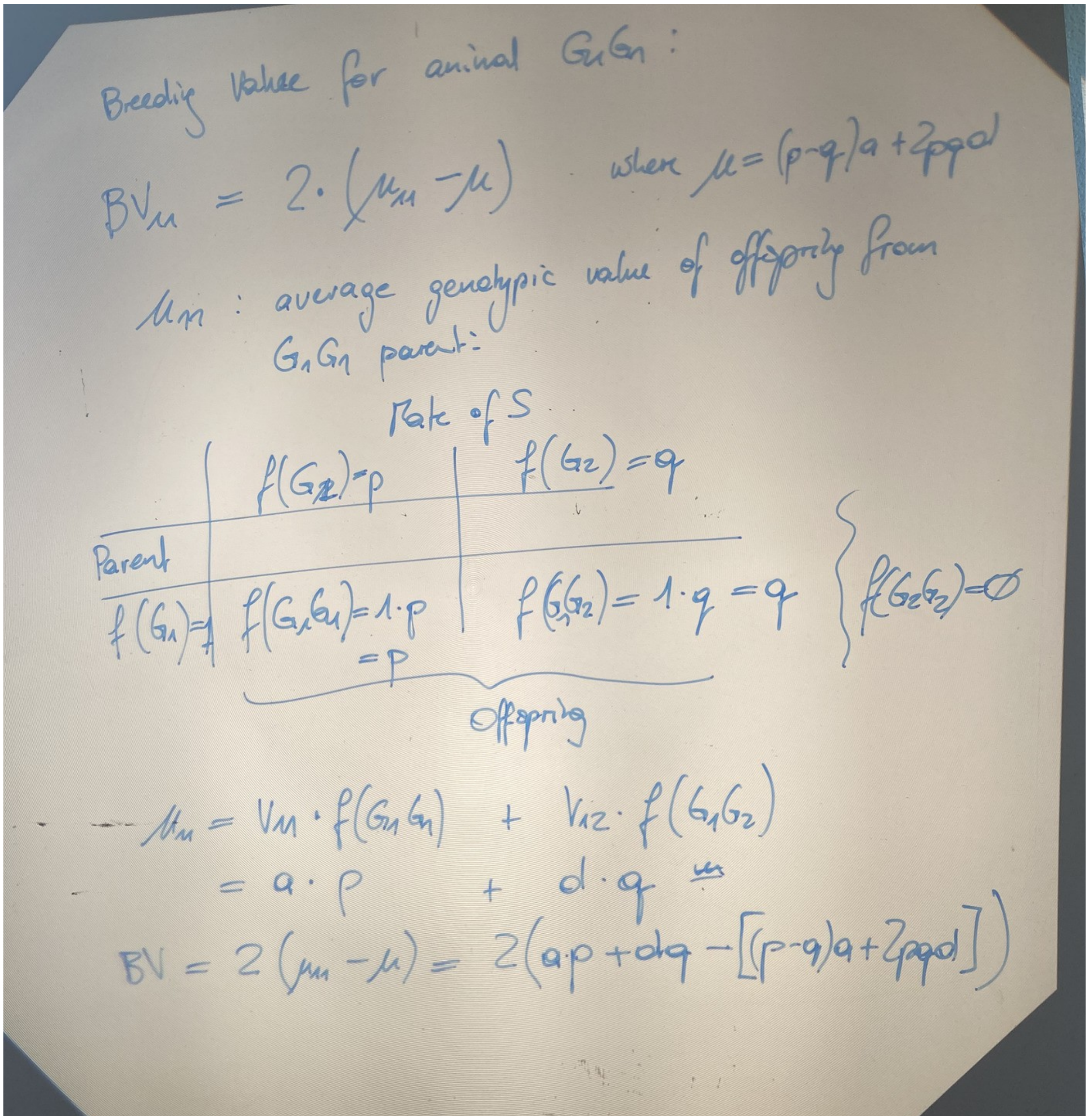
$$= \underbrace{(p^2 - q^2)}_{(p-q)\underbrace{(p+q)}_{=1}} a + 2pq \cdot d = \underline{(p-q)a + 2pqd}$$

Population specific

OHP Picture 10



OHP Picture 11



Breeding Value for animal G_1G_1:

$$BV_{11} = 2 \cdot (\mu_{11} - \mu) \quad \text{where } \mu = (p-q)a + 2pqd$$

μ_{11} : average genotypic value of offspring from G_1G_1 parent:

Mate of S

Parent	$f(G_1)=p$	$f(G_2)=q$
$f(G_1)=1$	$f(G_1G_1)=1 \cdot p$ $=p$	$f(G_1G_2) = 1 \cdot q = q$

Offspring

$f(G_2G_2)=0$

$$\begin{aligned} \mu_{11} &= V_{11} \cdot f(G_1G_1) + V_{12} \cdot f(G_1G_2) \\ &= a \cdot p + d \cdot q \end{aligned}$$

$$BV = 2(\mu_{11} - \mu) = 2\left(ap + dq - [(p-q)a + 2pqd]\right)$$