Overhead Pictures

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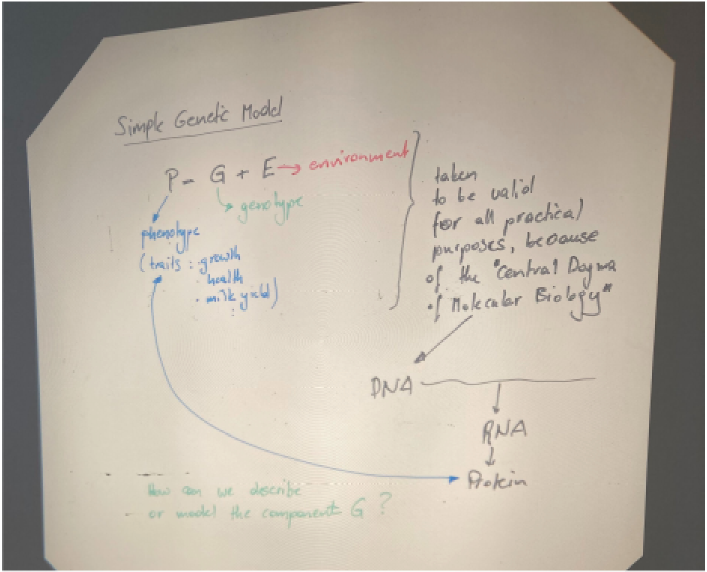
Genetic Model



Simple Genetic Model

$P = G + E$ → environment

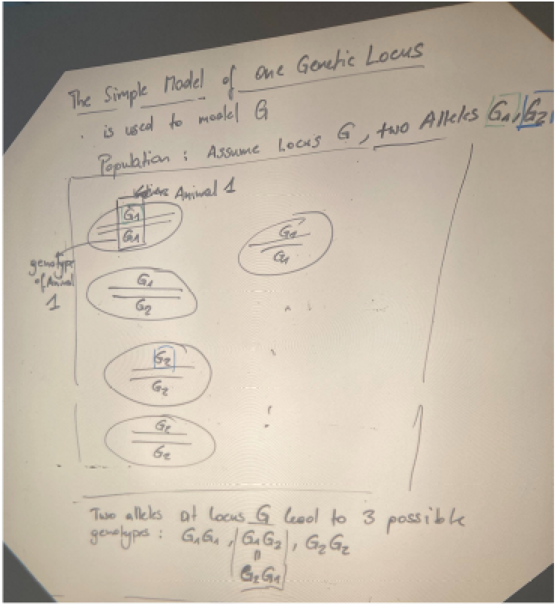
↳ genotype

phenotype
(traits : growth
· health
· milk yield)

taken
to be valid
for all practical
purposes, because
of the "Central Dogma
of Molecular Biology"

How can we describe
or model the component G ?

Single Locus



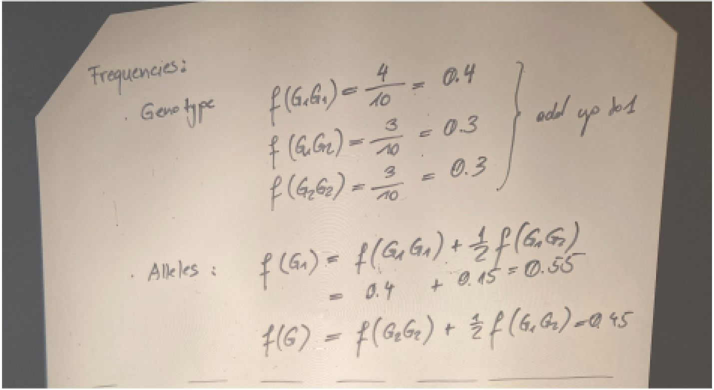
The Simple Model of one Genetic Locus

- is used to model G

Population : Assume Locus G, two Alleles G_1/G_2

Two alleles at locus G lead to 3 possible genotypes : G_1G_1, $G_1G_2 = G_2G_1$, G_2G_2

Frequencies



Frequencies:

- Genotype

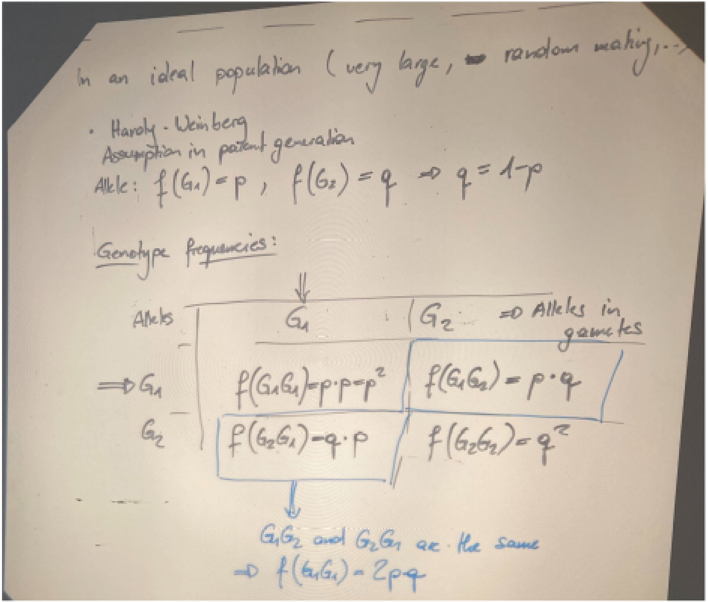
$$f(G_1G_1) = \frac{4}{10} = 0.4$$
$$f(G_1G_2) = \frac{3}{10} = 0.3$$
$$f(G_2G_2) = \frac{3}{10} = 0.3$$

add up to 1

- Alleles:

$$f(G_1) = f(G_1G_1) + \frac{1}{2} f(G_1G_2)$$
$$= 0.4 + 0.15 = 0.55$$
$$f(G) = f(G_2G_2) + \frac{1}{2} f(G_1G_2) = 0.45$$

Hardy-Weinberg



In an ideal population (very large, random mating, ...)

- Hardy-Weinberg
  Assumption in parent generation
  Allele: $f(G_1) = p$, $f(G_2) = q \Rightarrow q = 1-p$

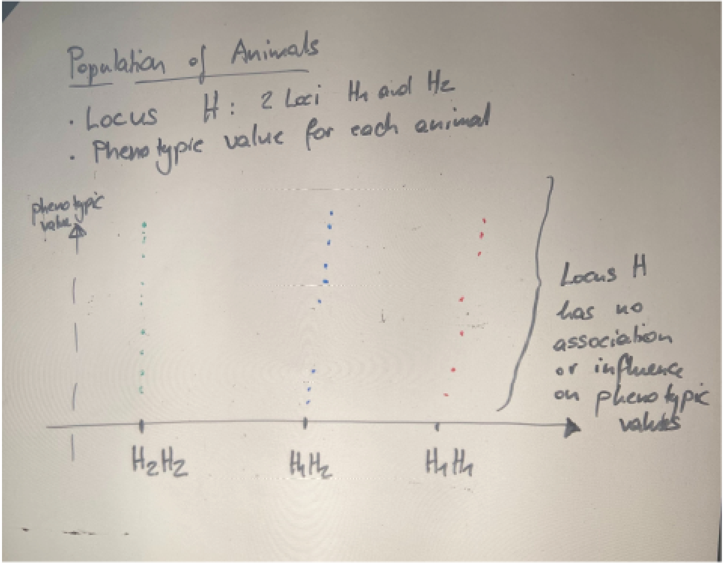
Genotype frequencies:

Alleles	G_1	G_2 ⇒ Alleles in gametes
⇒ G_1	$f(G_1G_1) = p \cdot p = p^2$	$f(G_1G_2) = p \cdot q$
G_2	$f(G_2G_1) = q \cdot p$	$f(G_2G_2) = q^2$

G_1G_2 and G_2G_1 are the same

$\Rightarrow f(G_1G_1) = 2pq$

No Association

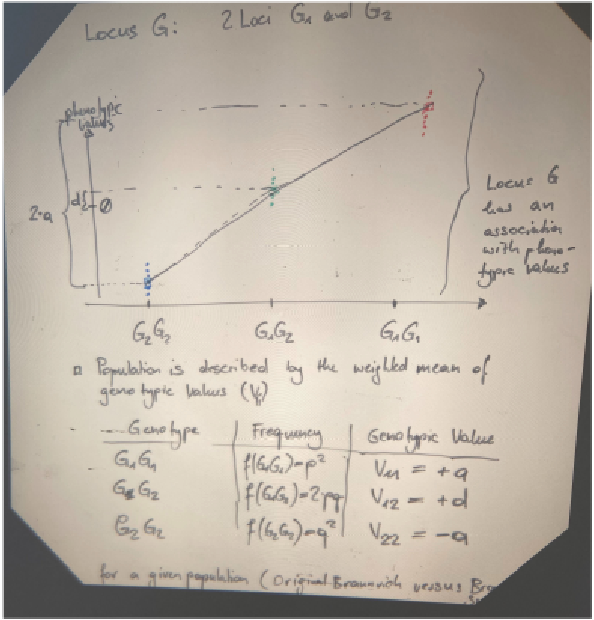


Population of Animals

- Locus H: 2 Loci H_1 and H_2
- Phenotypic value for each animal

Locus H has no association or influence on phenotypic values

Locus With Association



Locus G: 2 Loci G_1 and G_2

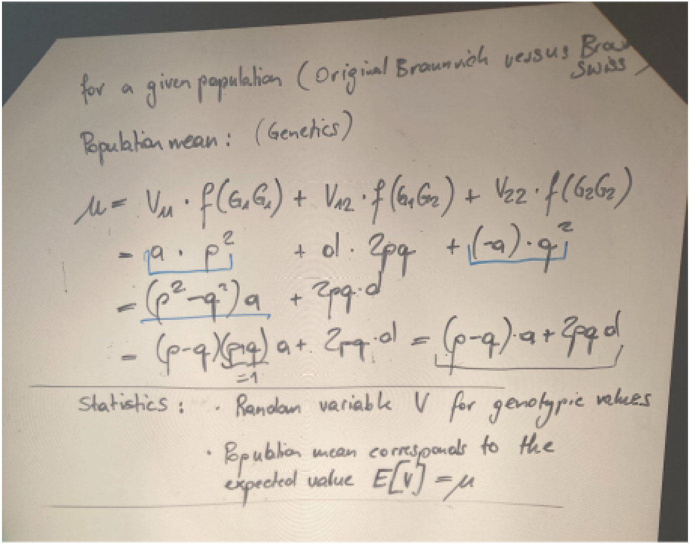
Locus G has an association with phenotype values

- Population is described by the weighted mean of genotypic values (V_{ij})

Genotype	Frequency	Genotypic Value
G_1G_1	$f(G_1G_1) = p^2$	$V_{11} = +a$
G_1G_2	$f(G_1G_2) = 2 \cdot pq$	$V_{12} = +d$
G_2G_2	$f(G_2G_2) = q^2$	$V_{22} = -a$

for a given population (Original Braunvieh versus Br

Population Mean



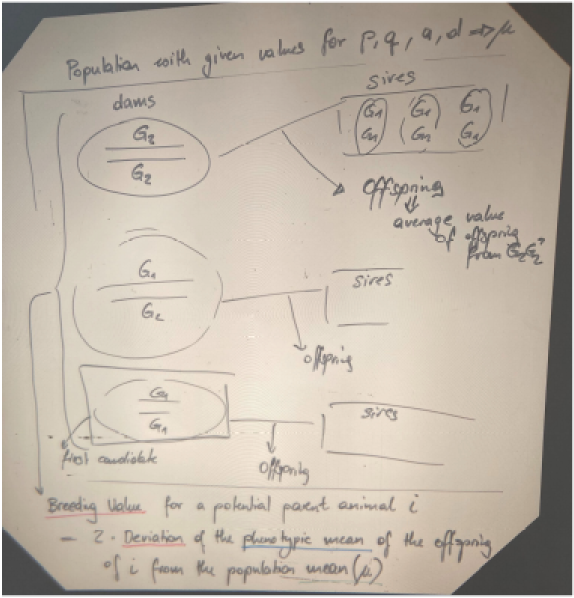
for a given population (Original Braunvieh versus Bra
Swiss)

Population mean: (Genetics)

$$\begin{aligned}\mu &= V_{11} \cdot f(G_1G_1) + V_{12} \cdot f(G_1G_2) + V_{22} \cdot f(G_2G_2)\\ &= \underbrace{a \cdot p^2}_{} + d \cdot 2pq + \underbrace{(-a) \cdot q^2}_{}\\ &= \underline{(p^2 - q^2)a} + 2pq \cdot d\\ &= (p-q)\underbrace{(p+q)}_{=1}a + 2pq \cdot d = \underbrace{(p-q) \cdot a + 2pq\,d}_{}\end{aligned}$$

Statistics:
- Random variable V for genotypic values
- Population mean corresponds to the expected value $E[V] = \mu$

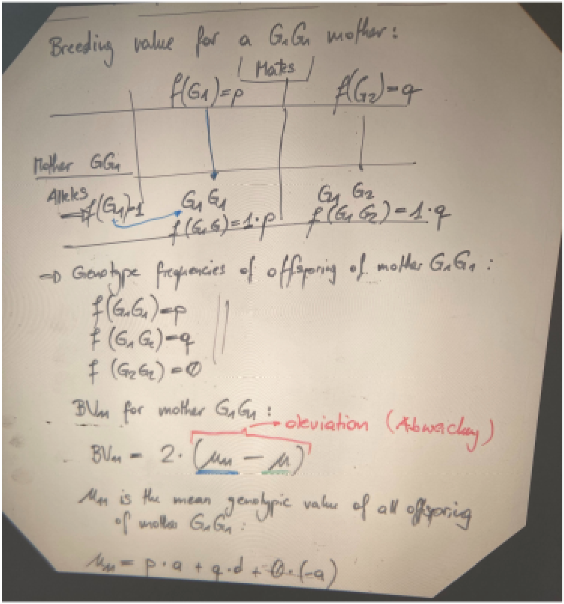
Breeding Value I



Breeding Value for a potential parent animal i

– $2 \cdot$ Deviation of the phenotypic mean of the offspring of i from the population mean (μ)

Breeding Value II



Breeding value for a G_1G_1 mother:

	Mates $f(G_1)=p$	$f(G_2)=q$
Mother G_1G_1 Alleles $f(G_1)=1$	G_1G_1 $f(G_1G_1)=1\cdot p$	G_1G_2 $f(G_1G_2)=1\cdot q$

→ Genotype frequencies of offspring of mother G_1G_1:

$f(G_1G_1)=p$

$f(G_1G_2)=q$

$f(G_2G_2)=0$

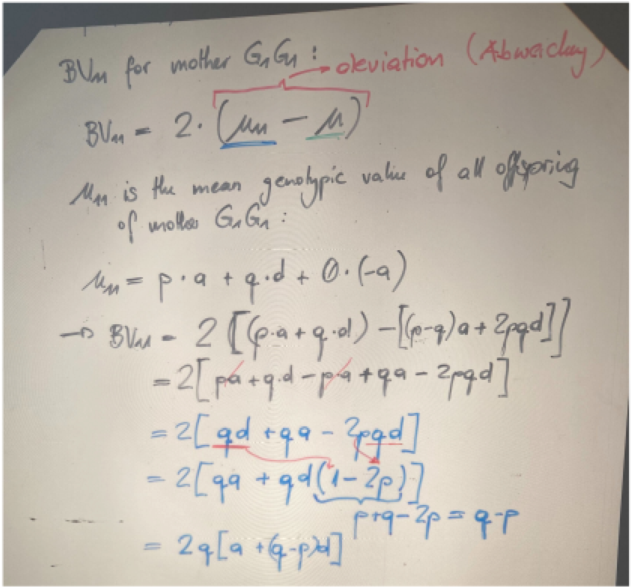
BV_{11} for mother G_1G_1:

$$BV_{11} = 2\cdot\overbrace{(\mu_{11} - \mu)}^{\text{deviation (Abweichung)}}$$

μ_{11} is the mean genotypic value of all offspring of mother G_1G_1:

$$\mu_{11} = p\cdot a + q\cdot d + 0\cdot(-a)$$

Breeding Value III



BV_M for mother G_1G_1 : → deviation (Abweichung)

$$BV_M = 2\cdot\overbrace{(\mu_M - \mu)}^{\text{deviation}}$$

μ_M is the mean genotypic value of all offspring of mother G_1G_1 :

$$\mu_M = p\cdot a + q\cdot d + 0\cdot(-a)$$

$$\rightarrow BV_M = 2\left[(p\cdot a + q\cdot d) - [(p-q)a + 2pqd]\right]$$

$$= 2[\cancel{pa} + q\cdot d - \cancel{pa} + qa - 2pqd]$$

$$= 2[qd + qa - 2pqd]$$

$$= 2[qa + qd\underbrace{(1-2p)}_{p+q-2p\,=\,q-p}]$$

$$= 2q[a + (q-p)d]$$