Animal Genetics and Breeding

* Mendel was the first to explain that heredity involve transition of units from reproductive cells of the parents to the offspring.
* Mendel selected 7 varities of garden pea differing in 7 pairs of characters
* According to Mendel's Law of Dominance,
  characters which appear in F_1 called Dominant
  characters which remains hidden called Recessive.
* Pleiotrophy – Phenomen where expression of single genes affected by several characters simultaneously.
* Alleles – Alternative forms of genes

⇒ Mendel's Laws [Mendelian Genetics] Principles / Laws of inheritence :

1) Law of dominance – It concerns expression of genotype
2) Law of segregation
3) Law of independent assortment

1) Law of Dominance :

* Some alleles are dominant while others are recessive, an organism with atleast one dominant allele will display the effect of the dominant allele.

2) Law of Segregation :

* During gamete formation, the alleles for each gene segregate from each other so that each gamete carries only one allele for each gene.

3) Law of independent assortment :

* Genes for different traits can segregate independently during the formation of gametes.

→ Genotype – Genetic makeup of a individual
→ Phenotype – Physical appearance

3) "When two pairs of traits are combined in a hybrid, segregation of one pair of characters is independent of other pair of characters"

⇒ Coat color of seed Purple [B]
White [b]

* Monohybrid Cross : [MHC] – cross b/w 2 parents that differ only in one heritable character.

BB × bb

Bb — F_1 [Purple]

♂ Bb × ♀ Bb

BB Bb Bb bb — F_2

Genotypic ratio [G.R] – 1:2:1
Phenotypic ratio [P.R] – 3:1

* Backcross of MHC –
  P.R – 1:0
  G.R – 1:1
* Testcross of MHC –
  P.R – 1:1
  G.R – 1:1

→ Homozygous : An organism that has two identical alleles for a gene is called homozygous for that gene. (ex : BB)

→ Heterozygous : An organism that has two different alleles for a gene called Heterozygous for that gene (ex : Bb)

* Dihybrid Cross :

Coat colour – Brown [B] dominant
White [b] recessive
Tail length – short [S] dominant
long [s] recessive

BBss × bbSS ⇒ BbSs — F_1
[Brown, long] [White, short]

Bs BS bs bS

gametes: (Bs)(Bs) (bS)(bS) — F_1

	Bs	BS	bs	bS
Bs	BbSS	BbSS	BbSs	BbSs

— F_1

	SB	Sb	sB	sb
SB	SSBB	SSBb	SsBB	SsBb
Sb	SSBb	SSbb	SsBb	Ssbb
sB	SsBB	SsBb	ssBB	ssBb
sb	SsBb	Ssbb	ssBb	ssbb

→ F_2

9 – brown & short
3 – White & short
3 – Brown & long
1 – Whit & long

* Phenotypic ratio – 9:3:3:1
→ Genotypic ratio – 1:2:1:2:4:2:1:2:1

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⇒ Trihybrid Cross :-

Phenotypic ratio [PR] – 27:9:9:3:9:3:3:1

* To get the phenotypic ratio of a cross write PR of its precedent cross and its multiplication with 3 such as

⇒ PR of MHC [3:1]

PR of DHC
3 [3:1] : [3:1]
9:3:3:1

⇒ PR of DHC [9:3:3:1]

PR of THC
3 [9:3:3:1] : 9:3:3:1
27:9:9:3:9:3:3:1

* If there are 'n' no. of pairs of genes in a cross then

→ Type of Gamet formed in F_1 – 2^n
→ Type of Gamet formed in F_2 – 4^n
→ Type of phenotype in F_2 – 2^n
→ Type of Genotype in F_2 – 3^n
→ No. of Homozygotes in F_2 – 2^n
→ No. of Heterozygotes in F_2 – $[4^n - 2^n]$

* Phenotypic Ratio in interaction of genes / alleles

1) Intragenic / intraallelic [Monohybrid cross]

	P.R	G.R
* Incomplete dominance [MHC]	1:2:1	1:2:1
* Dominance [MHC]	3:1	1:2:1
* Co dominance [MHC]	1:2:1	1:2:1

2) Intergenic / Non-allelic [Dihybrid cross]

a) Collaborative gene action – 9:3:3:1

b) Epistasis

⇒ Dominant epistasis [masking gene action] – 12:3:1 A epistatic to B, b

⇒ Recessive epistasis [Suplementary gene action] – 9:3:4 aa epistatic to B, b

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⇒ Inhibitory gene action – 13:3 Dominant & Recessive epistasis

⇒ Complementry gene action – 9:7 [Duplicate recessive epistasis (or) Double recessive epistasis]

⇒ Pseudo allele – 15:1 → Double dominant epistasis

* If a gene have 'n' no. of multiple allele then total possible different genotype will be

$$\frac{n(n+1)}{2}$$

⇒ Hardy Weinberg Law :-

* In a large random mating population gene & genotype frequencies remain constant from generation to generation in the absence of Mutation, Migration & selection
* It was proposed by Hardy (ENG) & Weinberg [Germany] in 1908.

⇒ Change in gene frequency due to Migration is

$$\Delta q = m(q_m - q_0)$$

q_m – Gene frequency in immigrants
q_0 – Gene frequency in base population
m – Proportion of immigrants.

⇒ Sex-Linked :-

Genes present on x-chromosome & can express in both sex then they are called "sex linked."

⇒ Sex-Limited :-

Genes present on autosomes but expressed in only one sex due to hormonal influences they are called "Sex limited." eg:- Beard in man & dev. of breast in Woman

⇒ Sex-influenced :-

Genes present on autosomes but expressed upto varying degree in both sex they are called "sex-influenced."

In sex-influenced inheritence, the genes behave differently in the two sexes
eg:- Baldness in humans & Horn formation in some breeds of sheep
eg:- Dorset horn sheep

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S.No.	Scientist	Contribution.
1)	G.J Mendel Father of genetics	Father of Modern Genetics Discovered basic principles of heredity.
2)	Hugo de Vries, Correns & Van T Shermark	* Rediscover Mendelian Work
3)	Bateson Term Genetics	* Term Genetics & Allele.
4)	T.H Morgan Chromosome theory of sex determination	* Sex Linked inheritence, Theory of Linkage * chromosomal basis of "Linkage & concept of gene
5)	Fedrick Wolf	* Epigenesis
6)	J.L Lush	* Father of Modern scientific Animal genetics & breeding
7)	Robert Bakewell	* Father of Animal Breeding.
8)	Charles Darwin	* Pangensis theory
9)	* August Weismann	* Germ plasm theory
10)	* Hugo devries	* Mutation theory
11)	* Sutton & Boveri	* chromosomal theory of Heredity
12)	* Johansson	* Term Gene, Genotype & phenotype
13)	C.B Bridge	* chromosomal abberation
14)	J.H Shull Term Heterosis	* Heterosis / Hybrid vigour
15)	Beadle & Tatum	* One gene one enzyme
16)	Robert Hooke	* Discovery of cell
17)	Robert Brown	* Discovery of Nucleus & Brownian movement
18)	M.J Schleiden & T. Schwann	* Cell theory
19)	W. Fleming	* Word Chromatin & Mitosis
20)	J.B Farmer & Moore	* Word Meiosis
21)	E. Strausburger	* structure of Nucleus, Word cytoplasm & Nucleoplasm

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S.No	Scientist	Contribution
22)	M. Knoll & R. Ruska	* Electron Microscope.
23)	W.M Stanley	* Crystalised form of TMV
24)	F. Sanger	* Amino acid sequence of insulin
25)	R. Holley, H.G. Khorana	* Genetic code & Base sequence of tRNA
26)	Fedrick Griffith	* Transformation in Diplococcus pneumoniae
27)	Lederberg & zinder	* Transduction in Salmonella typhimurium
28)	Lederberg & Tatum	* Conjugation in E.coli
29)	* Waldeyer	* Word chromosome Term chromosome
30)	Jacob & Monad	* Discovery of mRNA
31)	Hoagland	* Discovery of t RNA
32)	Kurland	* Discovery of r RNA
33)	E.C Galton	* Polygenic Inheritence
34)	Holley	* clover leaf model of t-RNA
35)	Landsteiner & Wiener	* Rh factor discovery
36)	Mc. clung & Wilson	* Sex chromosomes

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* Back Cross :- Back cross of MHC — PR - 1:0, GR - 1:1

→ The cross of a progeny individual with one of its parent's.

* Test Cross :- Test cross of MHC - PR - 1:1, GR - 1:1

→ Cross of an individual with one having recessive phenotype

* Dominant :-

Pertaining to the member of a pair of alleles that express itself in heterozygotes to the complete exclusion of other member of the pair.

* Co- Dominance :-

The condition in heterozygotes when both members of an allelic pair contribute to phenotype, and it is mixture of phenotypic traits produced in either homozygous conditions.

* Epistasis :-

The masking of phenotypic effect of either or both of alleles by a gene of different pair

Masked gene is said to be hypostatic

* Locus :-

Position on chromosone occupied by particular gene.

* Crossing over :- Exchange of genetic material b/w 2 homologous chromosomes

→ Inversion provides the proof of occurence of crossing over

→ only two of four chromatids take part in crossing over.

→ Crossing over takes place b/w non-sister chromatid in which exchange of genetic material takes place.

* In birds & some reptiles,

Females (♀) → Heterogametic (WZ)

Males (♂) → Homogametic (WW)

* Morgan concluded that genes are located on chromosomes in a linear fashion & are held together in Linkage groups

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⇒ Deviations from Mendelian concept of Dominance :

1) **Incomplete Dominance** :- eg:- Short horn cattle breed — Red × White (RR) (rr)

Red-flowered [RR] × White flowered [rr]

Rr — F_1 Roan (intermediate)

Rr — F_1 Pink

Rr × Rr

RR Rr Rr rr — F_2

Red pink pink White

RR Rr Rr rr — F_2
Red Roan white

Phenotype ratio = Genotype

P.R 1:2:1
G.R 1:2:1

* Incomplete dominance

Genotypic ratio — 1:2:1

Phenotypic ratio — 1:2:1

eg:- Fowl — Feather type
Black × White
Blue — F_1

2) **Co-dominance** :- resembles both parent

eg:- Different types of red blood cells that determine ABO blood grouping.

$C^S C^S$ — Spotted ↓ C^S

$C^D C^D$ — Dotted ↓ C^D

$C^S C^D$ (Both spotted & Dotted)

	C^S	C^D
C^S	$C^S C^S$	$C^S C^D$
C^D	$C^S C^D$	$C^D C^D$

Phenotypic ratio — 1:2:1
Genotypic ratio — 1:2:1

Dominance — resembled one of the two parents } PR — 3:1, GR — 1:2:1

Incomplete dominance — Was in between

Co Dominance — Resembles both parents } PR & GR ⇒ 1:2:1

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Heterosis :- Term coined by Shull

The superiority of outbreds / crossbreds over the Avg. of their parents is called Heterosis / Hybrid vigour.

* Heterosis / Hybrid vigour is opposite to inbreeding depression
* The outbreds are heterozygotes in which the effects of undesirable recessive genes are hidden by the effect of favourable dominant genes.
* Heterosis may be positive / negative.
* positive heterosis is called Hybrid vigour
* Heterosis is observed for traits governed by non-additive gene action (Dominance, over-dominance & epistasis).
* No heterosis for additive gene action.

$$\text{Heterosis} = \text{Mean of } F_1 \text{ progeny} - \text{Mean of parental breeds}$$

$$\% \text{ Heterosis} = \frac{\text{Mean of } F_1 \text{ Progeny} - \text{Mean of parent breeds}}{\text{Mean of parent breed}} \times 100\%$$

⇒ Genetic basis of heterosis :-

* When additive gene action affects the character the mean of F_1 progeny is exactly same as the mean of the parents

Additive gene action	- No heterosis
Non additive gene action	- Heterosis

i) Dominance hypothesis :-

Favourable dominant genes in the offspring will mask the unfavourable recessive genes.

ii) Over dominance theory :-

eg: For a gene locus, there will be 3 different genotypes i.e

A_1A_1, A_1A_2 & A_2A_2

* If overdominance is present, the alleles A_1 & A_2 coming together (A_1A_2) produce a reaction which is not produced by them separately.

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iii) Epistatic effects :- It is a phenomen of interacting genes which are not alleles

* It is the effect of genes resulting from the new combination of genes from different loci.
* The different genes coming together in the hybrid interact with each other & produce greater effect than when they are alone in different parents

eg:- In a plant, one dominant gene governs - length of internodes
another domind gene governs - No. of internodes

When these two gene pairs present in single hybrid,
Offspring is taller than expected from the avg. height of parents with many internodes.

⇒ Optimum level of exotic inheritance - 50-62.5%

⇒ Types of Gene Action :-

* Recurrent selection - AGA - GCA
* Reciprocal recurrent selection - NAGA - SCA

2 Types

1) Additive - Individual effect of each gene
2) Non-additive - Interaction effect / combination effect of genes

* Additive effect of all genes which influence character - Additive genetic value (or) Breeding value.

→ Non-additive gene action may be
allelic i.e interaction b/w genes within locus (Dominance & over dominance)
or Non allelic i.e, interaction of genes b/w loci present on the same or on different chromosomes (epistasis)

* Genotype value (G) = A + D + I

A - additive value
D - Dominance
I - Epistasis.

* Dominance, & epistatic effects are known as Non-additive gene effects

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Epistasis :-

Genes present at one locus may interact with genes present at other locus of the same chromosome or of the different chromosome. This type of inter-allelic interaction is called as epistasis

Selection Methods for Additive gene Action :-

Genetic gain (ΔG) = h^2 x selection differential

h^2 – Additive genetic Variability

1) Single trait selection
   - → Individual selection – Individual's own phenotype
   - → Pedigree selection – relatives of individual i.e parent & grand parent
   - → Progeny testing – Its progeny
   - → Family selection – Half sib, full sib, Aunts, uncles
2) Multi trait selection
   - → ~~Multi~~ Tandem selection – one trait at a time
   - → Independent culling level selection [I.C.L] – 2 or more traits at a time
   - → Index selection (Total score Method) – several traits simultaneously And the highest score is selected

⇒ Selection Methods for Non-additive gene action

1) Cross breeding
2) Recurrent selection
3) Reciprocal recurrent selection

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* General Combining Ability [GCA] – Additive gene action [AGA]
* Specific Combining Ability [SCA] – Non-additive gene action [NAGA] → Heterosis (Dominance, over dominance, epistasis)

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Systems of Breeding

1) Inbreeding - Breeding of related animals within 4-6 generations
2) out breeding - Breeding of unrelated animals

* In breeding :- 2 types

1) close breeding - Mating of more closely related individuals

eg:- Sire to daughter, Son to Dam, Full brother & sister

2) Line breeding - Mating of an/s which are more distantly related

eg:- Cousin mating.

* Genetic effects of Inbreeding :-
  * Increased homozygosity
  * expression of recessive genes
  * changes genetic structure of population by changing the genotypic frequencies without changing gene frequency
* Phenotypic effects :-
  * Depress growth rate, reproductive efficiency
  * Increased death rate
  * occurence of genetic defects which are recessive in inheritence.
  * Phenotypic uniformity in inbred lines is increased

⇒ Inbreeding depression does not occur when there is additive gene action

Sire x Daughter
Dam x Son
> Progeny - 75% inheritence of parent

* Use of inbreeding for commercial produn is practiced in poultry & pigs.

Coefficient of inbreeding :- The avg. percentage increase in homozygosity or decrease in heterozygosity in an inbred animal in relation to an avg animal of same breed of foundation stock is called coefficient of inbreeding

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2) Out - breeding :- Types

1) Out crossing - Mating the unrelated individuals of same breed.

2) Cross breeding - Mating the animals of different breeds

a) Two breed cross i) Two pure bred cross

ii)* (Inter se mating) - crossing the cross breds

b) Tripple crossing - AB ♀ × C ♂

c) Four breed cross - AB × CD

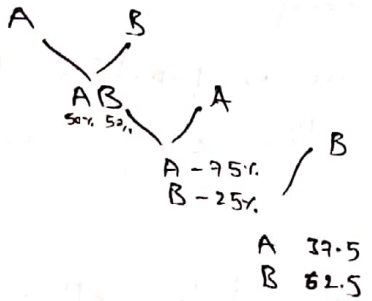
d) Back crossing - F_1 crossbred progeny × P_1

or

$F_1 \times P_2$

(P_1 & P_2 - Pure bred parents)

e) Criss crossing - Two breeds are crossed alternatively



Rotational crossing :- Males of 2/3 breeds are used in regular sequence (rotation) in successive generations on crossbred female of previous generation

3) Grading up :-

* Sires of a pure breed are mated to the female of non-discript
* Cross bred females are back crossed to pure bred sires to produce the progeny with 75% genes from pure breed.

** ⇒ After 6 generations of crossing the progeny will recieve 98.4% genes of pure bred.

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4) Species Hybridisation :- Cross b/w 2 species

Mule – Jack x Mare
Hinny – stallion x Jennet
Zebroid – Zebra x Horse
Asbra – Ass x Zebra
Pienniu – Cattle x yak in Tibet
Cattalo – American buffalo bull x cow
(F1 male) Jasta – Mithun x cow
(F1 ♀) Jastamin – Mithun x cow
(F1 ♂) Jechha – Mithun x Siri cow
(F1 ♀) Jessam – Mithun x Siri cow

Geep – Goat x sheep

⇒ Top Crossing :- It is a form of outcrossing & is like grading up system
It is the mating of female to last male in the top side of pedigree.

Ex:- Mating of Female Karan Fries with purebred sire of H.F
Top crossing ⇒ Inbred male x Non-inbred female of diff. breed

* The response for selection combined with out crossing declines after 10-15 generations & after 20-30 generations of continuous selection the response is ceased

* The point / Level at which there is a failure to respond is often called as plateau & population is called plateaued population.

** ⇒ % of inheritance in Grading up :-

	% of purebred inheritance	% of Non discript
1st generation	50	50
2nd	75	25
3rd	87.5	12.5
4th	93.75	6.25
5th	96.87	3.13
6th	98.44	1.56
7th	99.22	0.78
8th	99.6	0.39

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⇒ Breeding Efficiency :-

① Tomar's formula :- zebu cows = $\frac{n\,365 + 1020}{AFC + CI} \times 100$

Buffalow = $\frac{n\,365 + 1040}{AFC + CI} \times 100$

Where – n = no. of calving intervals

② Wilcox Formula :- $B.E = \frac{365\,(n-1)}{D} \times 100$

n = no. of total calvings

D = no. of days from first to last calving.

⇒ Response to selection :- $R = h^2 . S$ selection differential $S = i\sigma_p$ intensity of selection $i = \frac{S}{\sigma_p}$

* The change in the performance of progeny generation due to artificial selection is called response to selection / genetic change or genetic gain.

* The genetic effect of selection is frequency of desired genes is increased in a population through selection at the expense of the frequency of undesirable genes.

Selection differential :- It is denoted by 'S'

* The superiority of the selected parents over the population mean is phenotypic superiority it is called as selection differential

$S = \bar{P}_s - \bar{P}$

Where :- $\bar{P}_s$ – mean of selected parents

$\bar{P}$ – Population mean by selection was made.

* Predicted response to selection :- (R)

$R = h^2 (\bar{P}_s - \bar{P})$ (or) $R = h^2 . S$ if $h^2 = 0$ then $R = 0$, $h^2 = 1$ then $R = S$

h^2 – heritability

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⇒ Accuracy of Selection :-

I) * Accuracy of selection (based on single record) on individual itself is* h

II) * Based on pedigree performance

1) one parent record = $\frac{1}{2}h$

Both parents = $\sqrt{\frac{1}{2}h} = 0.71h$

2) One grand parent's record = $\frac{1}{4}h = 0.125h$

All four grand parents = $\sqrt{\frac{1}{4}h} = 0.5h$

3) one great grand parent record = $0.125h$

All 8 great grand " = $\sqrt{\frac{1}{8}h} = 0.35h$

III) Based on Family records

Full Sib 1) F.S = $\frac{1}{2}h$

Half Sib 2) HS = $\frac{1}{4}h$

IV) Based on Progeny record = $\frac{1}{2}h$

* Factors affecting Response to selection

1) Additive genetic variability in trait (σ_A)
2) Intensity of selection (i) $i = s/\sigma_p$ s- standard deviation, σ_p- Selection differential
3) Accuracy of selection (r_{AP})
4) Population size
5) Generation interval

* Measurement of Response :-

$$\Delta P = \Delta G + \Delta E$$

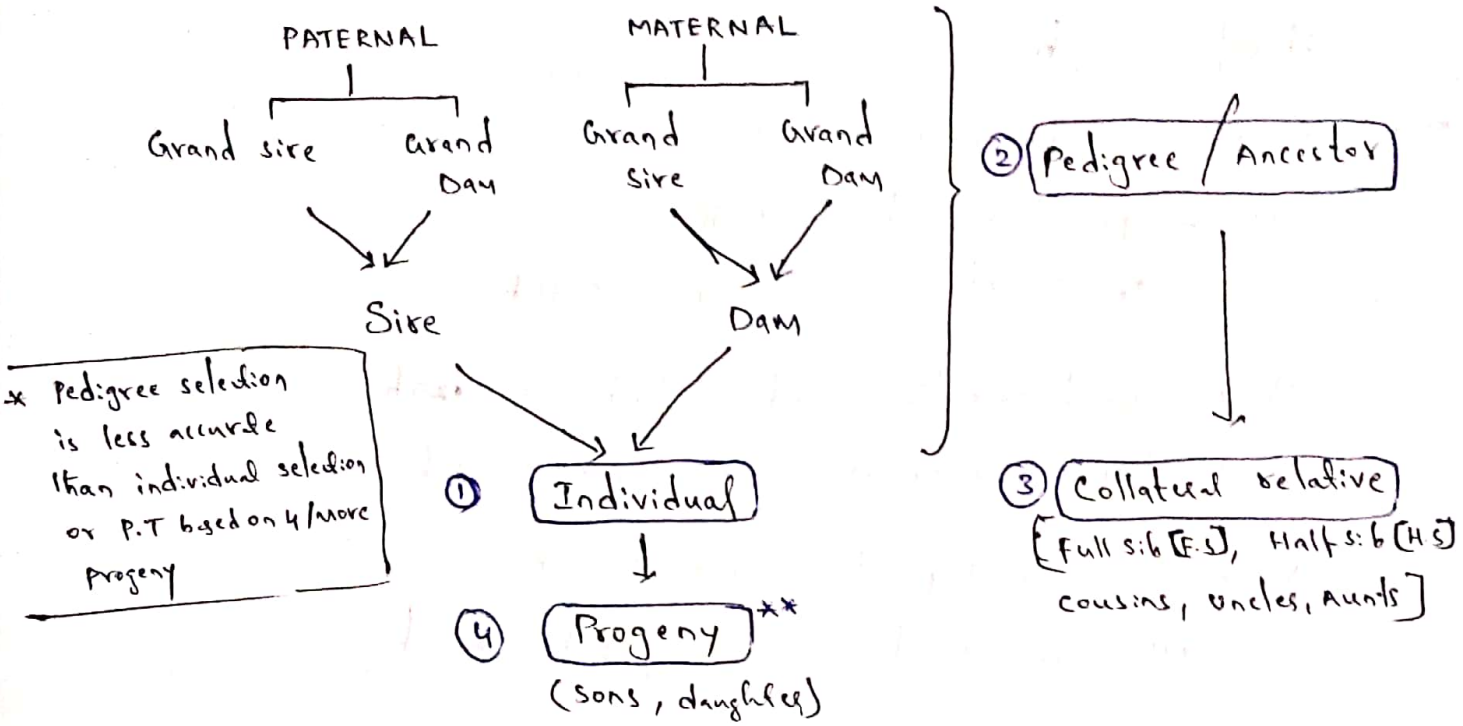
ΔP – change in phenotype

ΔG – genetic change

ΔE – Environmental change

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⇒ Different Selection Criteria to estimate Breeding value of an Individual for single trait
[B.V]



* Individual selection
estimation of B.V of an individual based on individual's own phenotypic value

* Pedigree selection / Progeny Testing :-
Estimation of B.V of an individual based on ancestors performance (parents + grand parents)

* Collateral relative / Family selection
Based on collateral relatives i.e family members (sibs - etc)

* Progeny selection
Based on progeny performance

⇒ Selection of Female :- In this individual selection is advocated
Simple method given by Lush is MPPA - Most probable producing ability

* Acuracy of selection based on single record $= h$

* Based on more records $= \sqrt{nh^2 / [1+(n-1)r]}$

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⇒ Male selection :-

* Individual selection is not possible in case of males
* Males are selected based on the performance of relatives

* Sire selection criteria — includes 3 steps

1) selection of males based on pedigree
   * Accuracy of male selection based on dam's records
   $$= 0.5 \sqrt{nh^2 / 1+(n-1)r}$$
2) Preliminary / phenotypic selection
3) Sire evaluation based on progeny testing

⇒ Individual selection is not possible for

- Traits of low h^2
- sex limited traits
- Traits expressed after death

} In P.T possible
In Ind. selectn not possible

* Progeny selection / P.T is superior over other selection criteria
P.T gives the best & most reliable information about genetic merit of parent & it overcomes the limitation of Mendelian error of gene segregation
* pedigree selection is done for traits with high heritability

⇒ Breeding strategies for cattle :-

* Grading up of non-discript cattle ~ zebu breeds
* Grading up / cross breeding of non-discript cattle ~ exotic breeds
* Selective breeding within zebu breeds

⇒ For Buffaloes :-

* Grading up for non-discript buffaloe
* selective breeding

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Cell Division / Multiplication

* DNA synthesis - S-Phase (Stage)
* Crossing over - Pachytene stage of Prophase-I (Meiosis I)

2 Types - 1) Mitosis - Division of somatic cells & chromosome no. is same as that of parent

2) Meiosis - Reduction division & daughter nuclei have half of the chromosomes
* Takes place in gonads.

Mitosis :

1) Prophase - * chromosomes become shortened & thickened
* centrosome divides into two parts, each containing centriole

2) Metaphase - * chromosomes arrange in equitorial region of spindle
* Each chromosome has two chromatids & functionally held by single ~~chromosom~~ centromere.

3) Anaphase - * centromere of each chromosome divides into two & 2 sister chromatids are converted into 2 independent chromes which moves to opposite poles.

4) Telophase - * spindle disappears & 2 daughter nuclei are reconstituted

Meiosis :

Meiosis - I — Prophase - I - 5 stages
Meiosis - II

1) Leptonema
2) Zygonema
3) Pachynema
4) Diplonema
5) Diakinesis

Meiosis-I :

1) Prophase - I :

1) Leptonema - chromosomes are highly stretched & bead like

2) Zygonema - Pairing / synapsis of Homologous chromosomes takes place.

3) *Pachynema - * Each bivalent chromosome divides longitudinally into two chromatids
* Crossing over occurs in this stage (Genetic recombination) i.e, exchange of genetic material b/w Homologous chromosomes

4) Diplonema - Bivalent chromosomes start separating & separation is not complete bcoz chromatids are held together at certain points called as chiasmata
Bivalents become shorter & thicker

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III) Metaphase – I

* Nuclear membrane disappears & bivalents are aranged at equator
* Each bivalent has 2 undivided centromeres which are on longitudinal axis of spindle Where as in mitotic Metaphase each chromosome has one undivided centromere lying on equatorial plane

III Anaphase – I

* Bivalent homologous chromosomes seperate & move to the two opposite poles.

IV) Telophase – I

* seperated chromosomes reconstitute 2 daughter nuclei

Meiosis – II — similar to mitotic division.

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* Pleiotrophy – single gene produces 2/more phenotypic effects
* Polygenic inheritence – inheritence of phenotype is determined by 2/more genes at different loci

⇒ LAW OF INDEPENDENT ASSORTMENT :-

Parents — Yellow round [YYRR] × Green wrinkled [yyrr]

F — Yellow round YyRr

F_1 – Gametes ♂

♀	YR	Yr	yR	yr
YR	① YYRR	② YYRr	② YyRR	④ YyRr
Yr	② YYRr	① Yyrr	④ YyRr	② yyrr
yR	② YyRR	④ YyRr	① yyRR	② yyRr
yr	④ YyRr	② Yyrr	② yyRr	① yyrr

Pheno.R – 9:3:3:1

G.R – 1:2:1:2:4:2:1:2:1

9 – Yellow-round
3 – Yellow-wrinkled
3 – Green-round
1 – Green wrinkled

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⇒ Multiple Alleles

* If a gene have more than 2 alleles at a single locus – called multiple alleles
* Multiple alleles arise due to mutation.
* Possible no. of genotypes for multiple alleles given by

$$\frac{n(n+1)}{2}$$ where n = no. of alleles.

Eg: Albino series of coat colour in Rabbit

* Genes at single locus govern coat colour, have 5 alternative expressions, They are

(C) Albinos → White coat & pink eyes
(C^h) Himalayan → White coat & black nose, ears & feet
(C) Wild → Grey coat colour
(C^{ch}) Chinchilla →
[C^{ah}] Light grey

$CC \times C^aC^a$
CC^a

* Albino is recessive to all other expressions
* Wild type is dominant over the others
* Chinchilla is recessive to Wild but incompletely dominant over Himalayan & albino.

1) Wild type – { CC, Cc^{ch}, Cc^h, Cc^a
2) Chinchilla – $c^{ch}c^{ch}$
3) Light grey – $c^{ch}c^{ah}$, $c^{ah}c^a$
4) Himalayan – { c^hc^h, c^hc^a
5) Albino – c^ac^a

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I) Modified Mono Hybrid Ratio

	Phenotypic ratio	Genotypic ratio
1) Dominance (Normal) –	3:1	1:2:1
2) Incomplete dominance –	1:2:1	1:2:1
3) Co-dominance –	1:2:1	1:2:1

II) Modified Dihybrid Ratio due to interaction of genes

	P.R	G.R.
1) Collaborative gene action –	9:3:3:1	1:2:1:2:4:2:1:2:1

2) Epistasis

a) Dominant epistasis – 12:3:1

b) Recessive epistasis – 9:3:4

c) Dominant - Recessive epistasis – 13:3

d) Double Dominant epistasis – 15:1 eg: Feathered & unfeathered shank in poultry

e) Double recessive epistasis – 9:7

* Pleiotrophy – Single gene – effects 2/more characters
* Polygenic inheritence : Many genes – one character
* Polygenes are the basis of inheritance of quantitative traits.

⇒ Qualitative And Quantitative Traits :

Qualitative Traits	Quantitative traits
1) These traits exhibit Discontinous variation	1) exhibit continous variation
2) Variation in this traits attributed to one or few major genes	2) shows polygenic inheritence
3) These traits least affected by environmental conditions	3) Large environmental effects
eg: Inheritance of blood group	eg: Body wt, egg production, milk yeild & growth rate

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Linkage :-

* It is the phenomen by which the parental types appear in greater frequency than is expected in F_2 is known as Linkage
* Mainly due to location of genes on the same chromosome.
* Linkage is exception to Mendel's Law of independent Assortment

eg :- Purple Long × Red round

PL Pl

PpLl — F_1 Purple Long

	observed ratio	Expected ratio.
Purple long	11	9
Purple round	1	3
Red long	1	3
Red round	3	1

* Here it is observed that parental combination viz, Purple long & red round are in great excess while the recombination or new combn viz, purple round & red long are less than expected.
* Purple & long from one grand parent and red & round from other, tend to hold together, so that more of these combinations are obtained than the expected ratio in F_2 where as new combinations are observed in lesser quantity
* Since the parental characters tend to stay together, this feature of heredity is called Linkage.
* Morgan said that coupling (when dominants entered from same parent) and repulsion (when dominants entered from different parent) are two aspects of single phenomen called linkage.
* The tendency of linked genes to remain in their original combination was due to their presence in same chromosome.
* The degree of strength of linkage depends upon the distance b/w linked genes on the chromosomes.
* No. of Linkage groups is equal to no. of pairs of chromosomes in an individual

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* An example of Linkage in poultry :

Linkage of comb shape & Leg length in chickens

Rose comb is dominant to single comb

Creeper is dominant to normal leg length

* Linkage can be classified in 2 ways :-

1) According to type of chromosome

a) Autosomal – When genes are linked on autosomes

b) Heterosomal / sex linkage – When genes located in sex chromosomes

eg :- Colourblindness & Haemophilia in mans.

2) According to distance b/w linked genes.

* Synapsis / pairing of chromosomes occurs during zygotene stage

* The chiasmata are cytological indications of crossing over

⇒ Crossing over value - Frequency of crossing over b/w 2 genes

⇒ Effective crossing over - That which is detectable in breeding experiments

⇒ Somatic crossing over - Crossing over at mitosis as opposed to meiosis

Lethal Factor :-

Cutain factors when present in particular combination in an organism causes its death, by blocking certain vital developmental or metabolic process of organism. These action of gene called lethal action & such a gene is called lethal gene.

eg :- Inheritance of coat colour in mice

Yellow mice are always heterozygotes

On homozygous dominant condition mice will die.

Yy (Yellow) × Yy (Yellow)

YY Yy Yy yy

* YY - combination is fatal because it prevents pigment formation of red blood cells of animals

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Detrimental genes :

* These are some other genes which do not cause death, but definitely reduce vigour. called detrimental genes.

→ Semi lethal genes – are responsible for some death losses in farm animals.

eg:- Dwarfism in Herefords
Creeper condn in poultry

* Most detrimental and lethal genes are either recessive or partially dominant & must be present in homozygous state to have their full effect.

⇒ Lethals in cattle :

1) Umbilical hernia — Limited to males & is dominant
2) Achondroplasia -I – Mode of inheritance is dominant, to have lethal effect
3) Achondroplasia -II – Recessive
4) Achondroplasia -III – Recessive
5) Agnatha — sex linked recessive
6) Cerebral hernia – Recessive
7) Bulldog head (Prognathism) – Recessive
8) Prolonged gestation – Recessive
9) Albino Heifer disease – Sex limited recessive gene

* Hymen is constricted, the anterior vagina & cervix are missing & the uterine body is rudimentary

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⇒ Sex Chromosome & Sex Linkage :-

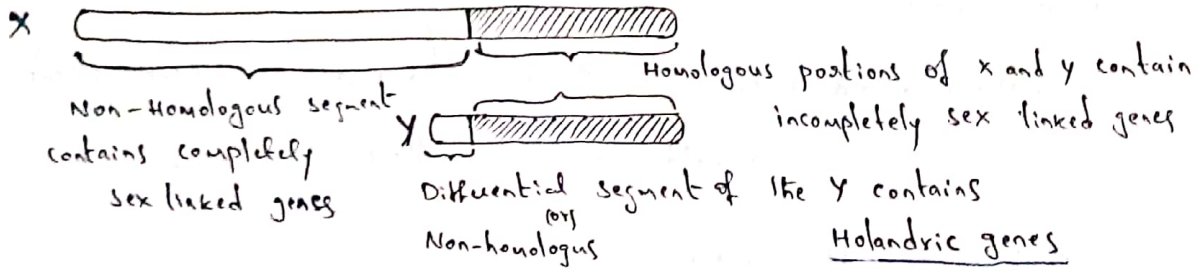
* Autosomes – chromosomes having no relation with sex
* Heterosomes / Allosomes – Sex chromosomes

⇒ In mammals – Male – XY chromosomes
Female – XX

[* Y-chromosome is different from X- in size]

⇒ In birds (including poultry) – Male – ZZ (Homozygous)
– Female – ZW (Heterozygous)

* Genes on the homologous segments are said to be incompletely or Partially sex linked.
* Genes on NON-Homologous segments contains completely sex linked ge



* Homologous / Differential segment of the Y – contains Holandric genes
These are completely Y-linked genes & inheritance of such gene is called as holandric inheritance.

* In mammals – somatic cells have 46 chromosomes
♀ – Each egg carries 22 autosomes & an X-chromosome
♂ – spermatozoa – Half carry X & other half Y-chromosome.
* In poultry (Birds) – ♀ – Heterogametic (ZW) & ♂ is Homogametic (ZZ)

♀ – Forms 2 types of eggs Half with Z-chromosome
Half with W-chromosome

♂ – produces All spermatozoa ē Z chromosome

* If Egg ē Z-chromosome fertilise with Z chromosome sperm → Male
Egg ē W fertilise with Z → Female

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is due to genes present in the sex chromosomes.

Sex Linkage :- eg:- Red-Green colour blindness in man

* It occurs due to x-linked recessive gene
* Father transmits his 'x' chromosomes to all his daughters but not to his sons & Mother passes one of her two 'x's to each of her children
* Therefore all the sons of colour blind mother are colour blind regardless of what kind of colour vision her husband have, but if the husband has normal vision all the daughters have normal vision
* If a carrier daughter (contain recessive gene covered by dominant allele) married to a men with normal colour vision produce all normal girls but among the boys 1/2 will be normal & other half will be colour blind.
* Colour blind man × Carrier / Homozygous colourblind woman results in Colourblind daughter.

* Sex-Influence Heredity :-

* Sex-influenced heredity is due to genes in the autosomes.

eg:- Baldness in man

Genotypes	Phenotypes	
	Men	Women
BB	Bald	Bald
Bb	Bald	Non-bald
bb	non-bald	Non-bald.

* Homozygous condition is same in both male & female, but heterozygous condition behaves differently in males & females
* The dev. of this sort of behaviour has been attributed to different types of hormones present in male & female.

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⇒ Mutations : Sudden & heritable changes

* The phenomen causing sudden heritable change in genotype of an organism is called mutation.

⇒ Types of mutations :

1) Gene mutations – like Deletion, Addition & substitution
2) chromosomal mutation

* Mutation may take place in a somatic or geminal tissue
* Mutation may be dominant – produces immediate effect
  or Recessive – can't express effect immediately
  express only when Homozygous recessive condition
* The rate of mutation is very low.
* Transition : Mutation of purine to another purine or pyramidine to another Pyramidine
* Transversion : Mutation of a purine into a pyramidine or vice versa
* Frameshift Mutation :
  Caused due to shifting of entire reading frame by loss or addition of single base or a segment of DNA.
* Silent mutation – which does not cause any change in protein
* Muton – smallest unit of gene capable of mutation

→ Discontinous genetic variations were called mutations
  Continous genetic variations were called Fluctuations

* Hugo de Vries proposed mutation theory of Evolution which states that evolution is a discontinous & jerky process
* Mutant – Individuals with mutations.
* ~~Gene~~ mutants are Lethal, the offsprings never reach maturity.
  Best eg for mutant in farm animals – Polledness / Hornlessness

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* Mutation generally occurs in one gene at a time
* Mutations are usually recessive & generally harmfull or lethal

Types of Mutagen :-

1) Physical
   a) Ionising radiation eg:- X-rays, γ-rays
   b) Non-ionising radiation
      eg:- U.V rays

2) chemical
   a) Base analogue
      5-Bromouracil
      5-chlorouracil
      5-Iodouracil
   b) Deamination agent HNO_2
   c) Acridine dyes
      Proflavin, Acriflavin
      5-amino acridine
   d) Other
      LSD (Lysergic acid diethyl amide)

⇒ Chromosomal Abberations :-

* Abnormal behaviour of chromosomes

A) Non-Disjunction :-

* one or more homologous pairs of chromosomes fail to seperate during gamete formation. This results in formation of chromosome gamete with lack of chromosome or have an extra chromosome.

B) Abnormalities due to Chromosome breakage :-

1) Deletion :- loss of segment of chromosome containing one / more genes
2) Inversion :- when segment of chromosome breaks off & rejoins the opposite ends, results in inverse order of genes
   * It change the gene orders but do not result in loss of genes.

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3) Duplication :- If a part of one chromosome breaks & the part gets attached to the homologous pair.

* Certain genes are present in double dose in one chromosome while the same genes are deficient in other chromosome

4) Translocation :- When a piece of chromosome becomes broken off and attached to another chromosome, usually of another pair, the phenomen called translocation

* New sex linkage is formed when translocation occurs in sex chromosome bcoz it causes change in relation of linkage group

⇒ Reciprocal translocation :- Exchange of parts b/w non-homologous chromosome.

⇒ Polypoidy :-

* occasional increase in no. of chromosomes adding or substracting a part or the whole set of haploid complement.

1) Genetic Variation :-

* It is the result of differences among the paired genes at the same locus from one animal to next

⇒ Causes of genetic variation

1) Recombination of genes
2) Gene interactions
3) Mutations
4) chromosome aberrations
5) chromosome no. changes

2) Environmental variation :-

* Result of environmental variation is masking of genetic differences

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$H^2_B = V_G / V_P$

$h^2_N = V_A / V_P$

HERITABILITY :- (h^2)

The fraction of superiority of parents which is, on the average, transmitted to ~~parents~~ their offspring.

* The non-transmittable part of the parent superiority is due to environmental effects & gene interactions.

Heritability of milk yeild in cattle — 0.2 - 0.3

* Heritability measures the ability of the trait to respond to selection.
* High heritability show much stronger response to selection than those with low heritability
* Reproductive traits have low heritability — Low h^2
* Production traits — Medium h^2
* Growth traits — High h^2

REPEATABILITY :- (r)

$$r = \frac{V_G + V_{E_P}}{V_P}$$

* The correlation b/w measurements on the same animal for traits, which are measured more than once.
* It ranges from 0 to 1 or 0 to 100 %
* Repeatability can be estimated by Intraclass correlation method.
* Repeatability estimate sets upper limits to Heritability in broad sense

Repeatability of milk yeild in cattle — 0.50

Note :

* Reproductive traits are governed by Non-additive gene action
  eg:- Fetility, Viability, Hatchability, Litter size
* Reproductive traits have low heritability
* If heritability (h^2) of a trait is low, then heterosis will be high

$\Rightarrow$ Reproductive traits — Low heritability & High heterosis

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PRINCIPLES OF POPULATION GENETICS

* Population genetics concerned with the genetic constitution (Allele & genotype frequencies) of population, their relationship & how this constitution changes with time.
* The genes carried by population have continuity from generation to generation, but genotypes in which they appear do not.
* Gene pool : Sum total of genes present in Mendelian population.

→ Transfer of genes from one gene pool to another – Gene flow.

* Population genetics was first used as the basis for genetic improvement of livestock by J.L Lush

Gene Frequency or Allele Frequency :

→ It is a proportion of one allele relative to all alleles at the locus in the population.

* The frequency of phenotype in a population depends upon frequency of allele controlling it.

If 'A' & 'a' are two alleles of a locus

& f(AA), f(Aa) and f(aa) are frequencies of 3 genotypes

⇒ Frequency of A–allele

$$f(A) = p$$

⇒ Frequency of 'a'–allele

$$f(a) = q$$

$$\boxed{f(A) + f(a) = p + q = 1}$$

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Genotype Frequency :

* It is the proportion of a population that has one genotype relative to all genotypes at a specific locus.

Two alleles — A, a

Possible genotypes — AA (Homozygous dominant)
Aa (Heterozygous)
aa (Homozygous recessive)

Genotype	No. of individuals	Genotype frequency
AA	60	f (AA) = 60/200 = 0.3 / 30%
Aa	100	f (Aa) = 100/200 = 0.5 / 50%
aa	40	f (aa) = 40/200 = 0.2 / 20%
Total	200	

⇒ Hardy - Weinberg Law

Both gene & genotype frequencies in a population remain constant from generation to generation when the population is large & mating at random & in the absence of selection, mutation & migration

For 2 alleles (A_1 and A_2) of one gene

p = f (A) frequency of A_1 gene

q = f (a) Frequency of A_2 gene

* Frequency of Homozygotes is equal to gene frequency squared

Frequency of A_1A_1 genotype = p^2

Frequency of A_2A_2 genotype = q^2

* Frequency of Heterozygotes is equal to twice the product of 2 gene frequ

Frequency of A_1A_2 genotype = $2pq$

$$\boxed{p^2 + 2pq + q^2 = 1}$$

p - Freq. of dominant gene
q - Freq. of recessive gene
p^2 - Freq. of dominant homozygo
q^2 - Fre. of recessive homozygo

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* For a single locus with 2 alleles, the maximum frequency of heterozygote will be 0.5. Then $P = q = 0.5$

$$P + q = 1$$

$$\boxed{P = 1 - q}$$

Freq. of heterozygote $= 2pq$

$$= 2q(1-q)$$

Forces changing gene & genotype Frequencies :-

1) **Migration :-**

Movement of individuals from one breeding population to another

Immigration – inward migration of individuals

Emmigration – outward migration of individuals – It brings reduction in size of gene pool.

* Migration of breeding animals cause changes in gene frequency

$$\boxed{\Delta q = m(q_m - q_o)}$$

2) **Mutation :-** sudden heritable change

* It lead to occurence of new alleles & thereby it changes the gene pool of population

$$\boxed{\begin{aligned} * \quad q &= u/(u+v) \\ * \quad p &= v/(v+u) \end{aligned}}$$

* Mutation changes gene frequency slowest

3) **Selection :-**

* Selection changes gene frequency fastest

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Breeding Value :

If an individual is mated to a no. of individuals at random, from the population then its breeding value is twice the mean deviation of the progeny from the population mean

Breeding value - value of genes to progeny
Genetic value - value of genes to self

* The value of an individual judged by the mean value of its progeny is called breeding value of the individual

* Inheritance of characters

1) Sex-Limited - Eg: milk production
Egg production
semen production

2) Sex-influenced : Eg: Baldness
Polled & Horned Dorset sheep

3) Sex-Linked : Eg: Barred plumage in poultry
Broodiness in poultry
Feather growth in poultry < rapid feathering / slow feathering
Cryptorchidism in Horses
White eye in Drosophila

* Method of sexing on the basis of sex linked characters in Poultry known as - Auto sexing. (Feather growth & colour of plumage)

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* If Correlation coefficient of full sib = 0.2 — Half sib = 4t, Full sib = 2t
  Then Heritability h^2 = 2t (t = 0.2)
  = 2 × 0.2
  = 0.4.
* Progeny testing & Family selection are effective when heritability (H^2) of trait is low
  When H^2 of trait is High — Individual selection & Pedigree selection
* Coefficient of relationship during half sib mating — 25%
  Full sib — 50%
* Realised heritability (R) / Response to selection R = $h^2 S$
* Genetic Correlation caused by — Pleiotrophy
  Linkage
  Heterozygocity
* Half sib Correlation — Best method for heritability estimation
  Full sib Correlation — Least reliable method for heritability estimation
* Polypoidy is induced by Nitrous oxide, Colchicine, Chloroform
* Linked genes — 2 genes of 2 diff. traits located on same chromosome
* Selection is most effective at intermediate gene frequency & becomes least effective at high or low gene frequencies
* Regression of breeding value (V_A) on phenotypic value (V_P) — Heritability
  $h^2_N = \frac{V_A}{V_P}$
  $H^2_B = \frac{V_G}{V_P}$
* Polygenic inheritance is governed by Additive gene Action
* Selection — Fastest change in gene frequency
* Mutation — Slowest chage in gene frequency
* Osborne index — For improving egg production in poultry
* Sire index — Index of genetic worth of sire
* Abplanalp index — For selection of pullets & cockerels
* BLUP — Most powerful method of indexing sire
* selection index — Best Method of selection

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Types of chromosomes According to the Position of Centromere

1) Telocentric (i-shape) - Terminal centromere
2) Acrocentric - Sub terminal centromere / centromere is located close to the end giving a very short arm & exceptionally long arm
3) Sub-Metacentric - Centromere is located to near to the centre
4) Metacentric (V-shape) - Centromere in the centre & chromosome with equal arms.

The Coefficient of relationship & Inbreeding Coefficient

S.No	Mating	Coefficient of relationship [Rxy]	Inbreeding Coefficient $Fx = 1/2\ Rxy$
1	Close breeding: a) Sire to daughter mating b) Son to dam mating c) Full sib mating*	0.50 or 50%	0.25 or 25%
2	a) Half sib mating* b) Grand parent - Grandson / Grand daughter mating c) Double first cousin mating	0.25 or 25%	0.125 or 12.5%
3	single first cousin mating	0.125 or 12.5%	0.0625 or 6.25%
4	Half first cousin mating	0.0625 or 6.25%	0.03125 or 3.125%

* Inbreeding is also known as genetic associative mating while out breeding is also known as genetic disassociative mating.

* Inbred line :
  - → Developed from 2 generations of Full sib mating
  - → If the inbreeding coefficient is minimum 37.5% or 0.375 then that line is called inbred line

* In Crossing :
  Crossing of two different inbred lines derived from the same breed.

* In Cross breeding :
  Crossing of two different inbred lines derived from different breeds

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Types of Outbreeding :

Sno.	Types of outbreeding	Define	special point & Examples.
1	Outcrossing	* mating b/w unrelated animals of the same breed * Progeny produced - outcross	* Simplest form of outbreeding
2	Crossbreeding	mating b/w animals of diffrt breeds within same species * Progeny produced - Cross bred	* Use to obtain Newbreed. eg: i) Kasargodu ii) Karan fries iii) Jersindh
3	Grading-Up	* Mating of pure-bred sire of descriptive breed with a local female, generation after generation	* Use to obtain pure breed. * Pure breed is obtained just after 7-8 generation.
4	Top Crossing	* Mating of pure bred male with unrelated female	* It is just like grading up but only for one generation.
5)	Species hybridisation	* mating b/w animals of different species	* Most extensive form of out breeding. eg: a) Cattalo - Buffalo x Cattle b) Pien-niu - cattle x yak c) Mule - Mare x Jack d) Hinny - Stallion x Jennet

Inheritance of characters :

S.No	Index	Sex limited traits	Sex influenced traits	Sex-linked traits
1	Genes of these traits are present on	Autosome	Autosome	Sex-Chromosomes [X-linked or Y-linked]
2	Examples	- semen production - Egg production in poultry - milk production	- Baldness in human - Polled & horned Dorset sheep	- Barred plumage in poultry - Feather growth in poultry X-linked : Hemophilia colourblindness Y-linked : Hypertrichosis
3)	Inheritance of traits through	Both ♂ & ♀	Both ♂ & ♀	* Inheritance of X-linked both ♂ & ♀ * Inheritance of Y-linked only through Male

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Inheritance of sex-linked characters :

1) Criss-Cross inheritance

* Parent of one generation passes the sex-linked character to the opposite sex in the next generation

Types :

a) Digenic

Father → Daughter → Grandson

b) Diandric

Mother → Son → Granddaughter

Non-criss-cross inheritance.

* Parent of one generation passes the sex-linked character to the same sex in the next generation.

Types :

a) Holandric

Father → son → Grandson

b) Hologenic

Mother → Daughter → Granddaughter

⇒ Central tendency, Measures of dispersion & relative measures of dispersion :

1) Central tendencies :

Eg : Mean, Median & mode.

* most stable measure of central tendancy - Mean

2) Measures of dispersion :

Eg : Range, Variance, standard deviation & mean deviation

3) Relative measures of dispersion :

eg : Standard Error (S.E), Coefficient of Variance (C.V)

* **Range** : The difference b/w the smallest & largest values in a set of data
* **Mean deviation** : Mean absolute deviation from an average.
  * Its value is always greater than mean deviation Least affected by extreme values of a series.
* **Standard deviation (S.D)** : It is ideal measure of dispersion.
  * Its value is always greater than mean deviation (M.D). (S.D = 5/4 M.D)
* **Variance** : It is equal to square of standard deviation. $V = (SD)^2$
* **Standard Error (S.E)** : $SE = \frac{S.D}{\sqrt{N}}$ where N is no. of observation.
* **Coefficient of Variance (CV)** : $CV = \frac{S.D}{A.M} \times 100$ (AM - Arithmetic mean)

A.M = 20, S.D = 10

$= \frac{10}{20} \times 100 = 50$

⇒ If mean value of mean deviation = 16 then S.D = 5/4 M.D

5/4 × 16 = 20.

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* Back cross is two types – Test cross & Out cross

⇒ (Back cross) – F1 hybrid x Any of the homozygous parent [Tt x TT or tt]

⇒ (Test cross) – F1 hybrid x Homozygous recessive parent [Tt x tt]

⇒ (Out cross) – F1 hybrid x Homozygous dominant parent [Tt x TT]

Types of Gene action :

1) Additive gene action
   * Polygenic inheritance
   * General combining ability (GCA)
   * Resemblance b/w relative

2) Non-additive gene action — Heterosis & specific combing ability (SCA)
   a) Allelic interaction / Intra-allelic interaction
      Ex: Dominance, Co-dominance, Incomplete dominance & over dominance.
   b) Non-allelic interaction / Inter-allelic int
      Ex: Epistasis

Types of Allelic interactions :

1) Dominance : When dominant is complete, then phenotype of heterozygote & dominant homozygote is same.
2) Incomplete dominance : Phenotypic value of heterozygote is lies b/w dominant & recessive homozygous.
3) Over-dominance : When the phenotypic value of heterozygous is superior to either of homozygous.

Phenotypic ratios of various gene interactions :

Types of Allelic interaction & their F_2 Phenotype ratio	Types of Non-allelic interaction & their F_2 Phenotype ratio.
1) Incomplete dominance – 1:2:1 ex: Feather colour in Andalusian fowl	1) Collaborative gene action – 9:3:3:1
2) Co-dominance – 1:2:1 ex: ABO blood group in human Roan coat colour in short horned cattle	2) Dominant epistasis / Masking gene action – 12:3:1
3) Over dominance – 1:2:1	3) Recessive epistasis / supplementary gene action – 9:3:4
	4) Complementary gene action – 9:7
	5) Duplicate gene action / Double dominant – 15:1
	6) Inhibitory gene action / Dominant-recessive epistasis – 13:3

(*) Double recessive

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Type of Non-allelic interaction	other name	ratio
1) Collaborative gene action		9:3:3:1
2) Dominant epistasis	Masking gene action	12:3:1
3) Double dominant epistasis	Duplicate gene action	15:1
4) Recessive epistasis	Supplementary gene action	9:3:4
5) Double recessive epistasis	Complementary gene action	9:7
6) Dominant & Recessive epistasis	inhibitory gene action	13:3

Sample Question :-

AABbCc genotype organism produce how many types of gametes/phenotypes genotypes & Zygotes?

1) Types of gametes or phenotypes = $2^n \longrightarrow 2^2 \longrightarrow 4$ (where n = no of heterozygote)
2) Types of genotypes = $3^n \longrightarrow 3^2 \longrightarrow 9$
3) Types of zygotes = $4^n \longrightarrow 4^2 \longrightarrow 16$.

Heterosis :- Most imp. genetic cause of heterosis - Directional dominance

* It is an increased performance of offspring over the parents
* It depends upon Non-additive gene action.
* Traits with low h^2 [Heritability] show high degree of heterosis & Vice versa
* Max. hybrid vigour is obtained in F_1 generation
* Heterosis in F_2 is diminished due to inter-se mating.

The difference b/w Heritability & Repeatability

Index	Heritability [h^2]	Repeatability [r]
Formula H^2_B - Heritability in broad sense H^2_N - Narrow sense V_G - Genetic variance V_P - Phenotypic variance V_A - Additive genetic variance / Breeding value E_P - component of Environment	1) $H^2_B = V_G / V_P$ 2) $h^2_N = V_A / V_P$ h^2_N - is regression of breeding value on phenotypic value H^2_B is ratio of genotypic variance to phenotypic variance	$r = V_G + E_P / V_P$ * It is regression of future performance on present performance * Repeatability is upper limit of heritability.
4) Define :		

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* Range of heritability & Repeatability of a trait is 0 to 1
* Most Probable Producing Ability [MPPA] / Expected real Producing Ability [ERPA] is used for estimation of repeatability.
* Repeatability is used in making culling decisions.

Heritability of different traits :-

a) Reproductive traits – Low
b) Productive traits – Medium
c) Growth traits – High

Relatives	Correlation coefficient [t]
Half sibs	$h^2 = 4t$
Full sibs	$h^2 = 2t$

⇒ If correlation coefficient of half sibs is 0.2, then heritability of a trait is?

$h^2 = 4t \quad [t = 0.2]$
$= 4 \times 0.2$
$= 0.8$

⇒ If Repeatability of a trait is 0.30, then which of the following value is not possible for its heritability.

a) 0.20 b) 0.15 c) 0.25 d) 0.45

* The value of repeatability is generally greater than Heritability

Ans :- 0.45 [Repeatability value > Heritability value]

⇒ Methods of Selection :- Given by Hazel & Lush

1) Tandem Selection :-
* It involves selection of only one trait at a time
* It is least efficient method of selection.

2) Independent Culling Method :-
* It involves selection of two or more traits at a time
* A minimum culling standard is fixing for every trait, an animal fails to meet the minimum standard for any one trait will cull irrespective of their merit in other traits.

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5) Total Score - Card / Selection Index method :

* It is the best method of selection.
* A scorecard is prepared by giving proper weight to each trait & animal with higher score card should be selected.

Basis of Selection :

1) Individual selection - Based on performance of individual
2) Pedigree selection - Based on performance of ancestors
3) Progeny testing - Based on performance of progeny
4) Family selection - Based on performance of collateral relatives

** ⇒ When Heritability of trait is high

* Individual selection & Pedigree selection are effective

** ⇒ When Heritability of trait is Low

* Progeny testing & Family selection are effective

Individual selection

* most accurate basis of selection
* It is simplest, more rapid & most commonly used basis for selection
* In individual selection, animals are selected on the basis of their own phenotype.

Progeny testing

* Most effective & best basis of selection
* This is two-way selection
* It is used for selection of sire

Nucleus Breeding Schemes :

It contains 2 types of population

1) Nucleus herd [N] : consists of elite females of high genetic merits [size = 10-15% top ranking females of total herd]
2) Test herd / Multiplier [M] : Herd from the majority of the population

Note: Generally, genetic gain achieved in Nucleus herd, it passes to Multiplier and then to village herd / Commercial herd [V]

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Differences b/w CNBS & ONBS

Closed Nucleus Breeding Scheme	Open Nucleus Breeding Scheme
1) Unidirectional gene blow [N → M → V] (top to down)	1) Bidirectional gene blow (Top to bottom & bottom to top) [N → M → V] or [V → M → N]
2) The nuclear population is entirely closed. It does not receive any gene from outside	2) Nucleus herd is open. Therefore, superior animals can enter from village herd to nucleus herd.
3) Inbreeding is more as compare to ONBS	3) It reduce the rate of inbreeding & increases genetic progress.
4) CNBS is mainly used in Pig & poultry	4) ONBS is mainly used in cattle, Buffalo & sheep.

* ONBS is better than CNBS

⇒ Types of Correlation :

1) Phenotypic Correlation
2) Genetic Correlation
3) Environmental correlation

Causes of Genetic Correlation :

a) Pleiotrophy - Permanent cause of genetic correlation
b) Linkage - Temporary cause of genetic correlation
c) Heterozygosity

Differences b/w Correlation & Regression

Correlation (r)	Regression (b)
- It is measures the degree of relationship b/w two variables	* It measures the amount of change in dependent variable per unit change in an independent variable
* Range of Correlation Coefficient -1 to +1	* Range - ∞ to + ∞
* It is relative measure	* It is an absolute measure
* $r_{xy} = r_{yx}$ (It is symmetric)	* $b_{xy} \neq b_{yx}$ (It is not symmetric)

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* Fitness/ Adaptive value/ Selective value :-

It is contribution of offspring to the next generation

Fitness (F) = 1-S Where 'S' is coefficient of selection

* Phenotypic value (P) :-

Observed value of a trait measured on an individual

$P = G + E$

G- Genotypic value

E- Environmental deviation in genotypic value

* Genotypic value (G) :-

Avg. of the phenotypic values of all individuals who have same genotype

When there is no epistasis $G = A + D$

A- Additive genetic effect / Breeding value

D- Dominance deviation

When there is epistasis $G = A + D + I$

I- interaction deviation / epistatic deviation

⇒ Breeding Value (B.V)

* B.V is value of an individual judged by the mean value of its progeny
* B.V is the twice of mean deviation of progeny from its population mean.

⇒ Response to selection (R)

$R = h^2 S$

h^2 realized heritability

S selection differential

⇒ Selection differential (S)

Superiority of selected parents over the population mean

$S = \bar{P}_s - \bar{P}$

$S = i\sigma_p$ (i = intensity of selection & σ_p phenotypic S.D)

Hence $R = h^2 S = h^2 i\sigma_p = i\sigma_A r_{AP}$

Factors affecting response to selection

1) Intensity of selection (i)
2) Additive genetic variance (σ_A)
3) Accuracy of selection (r_{AP})
4) Population size
5) Generation interval

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Crossing over :-

Exchange of segment b/w non-sister chromatids of homologous chromosomes in Pachytene stage of Meiosis-I

Translocation :-

Exchange of chromosomal segments b/w non-homologous chromosomes

Components of variance :-

$V_P = V_G + V_E$

$V_G = V_A + V_D + V_I$

$\therefore V_P = (V_A + V_D + V_I) + V_E$

Causes of genetic variation

1) Segregation - biggest cause of genetic variation
2) Crossing over - 2nd biggest cause of genetic variation
3) Mutation, Migration, Selection, Random genetic drift.

Statistical tests :- 4 tests - Z-test, T-test, chi-square test & F-test

Z-test / Large sample test	T-test / Small sample test
Apply to compare sample mean & Population mean	* Apply to compare sample mean & Population mean
1) Sample size is large ($n > 30$)	1) Sample size is small ($n < 30$)
2) Population S.D or Population variance is known	2) S.D & σ(variance) not known

* T-test are 2 types - 1) paired T-test 2) Unpaired T-test

Chi-Square test :-

* It is a non-parametric test (No population parameters are required)

Applications of χ^2 test :-

1) Test for goodness of fit

$$\chi^2 = \sum (O-E)^2 / E$$

O- observed frequencies E- Expected frequencies

2) Test for independent attribute

* Calculated value of χ^2 test is always positive

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F-test & Analysis of Variance [ANOVA]

Application :-

* Use to compare two variances
* Use to compare more than two sample mean

ANOVA - is used for testing significant difference b/w more than 2 sample means.

Mutation :-

* Sudden heritable change in genetic material

Types of mutation :-

A) Chromosomal mutation - 1) Heteroploidy 2) Chromosomal aberration

B) Gene mutation - 1) Substitution 2) Frame shift mutation

⇒ Heteroploidy - 2 types

1) Euploidy - change in set no. of sets of chromosomes
2) Aneuploidy - change in no. of chromosomes in a set

Examples of Euploidy

1) 2N-N (Monoploidy / loss of one set of chromosomes)
2) 2N+N (Triploidy / Addⁿ of one set)
3) 2N+2N (Tetraploidy / Addⁿ of 2 sets)

Aneuploidy

1) 2N-1 (Monosomy)
2) 2N-1-1 (Double monosomy)
3) 2N-2 (Nullisomy)
4) 2N+1 (Trisomy)
5) 2N+2 (Tetrasomy)

Types of Substitution :-

1) Transition - replacement of purine by purine (or) Pyramidine by Pyramide
2) Transversion - replacement of Purine by Pyramidine & Viceversa

⇒ Hardy - Weinberg law

In a large random mating population, in absence of mutation, migration & selection, the gene & genotypic frequencies remain constant from generation to generation

Gene frequency ⇒ $P+Q = 1$

Genotype frequency ⇒ $P^2+Q^2+2PQ = 1$

$\therefore P+Q+H = 1 \Rightarrow P=p^2, Q=q^2, H=2pq$

* $p = P+1/2H$
* $q = Q+1/2H$

* Frequencies of all alles at one locus must be equal to 1
* Genotypic frequency of offspring will depend only upon gene frequencies of parents.

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Forces affecting H.W Equilibrium :-

1) Systemic forces :-
Acting both in large as well as small population & can be predicted in amount as well as in direction.
Ex :- Mutation, Migration & selection.

2) Dispersive forces :-
Acting only in a small population, can be predicted only in an amount, not in direction
Ex :- Random genetic drift (Sewell wright effect)

* If gene frequency of A = 0.7 & a = 0.3, Find. out genotypic frequency of Heterozygote ? P = 0.7, q = 0.3

Genotype frequency of Heterozygote – 2pq
= 2(0.7 x 0.3)
= 0.42

* If 9 out of 100 individuals in a population suffer from a homozygous recessive disorder, frequency of disease causing allele ?

Frequency of disease causing allele – $\frac{9}{100}$ = 0.09

* If genotypic frequency of dominant homozygote is P = 0.05 & genotypic freq. of recessive homozygote is Q = 0.65, gene frequencies P & q ?

P = 0.20 & q = 0.80

* Frequency of heterozygotes among all individuals - 2q(1-q)

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* Ability of an individual to stamp its characters on its progeny is known as Prepotency

* Best method of heritability (h^2) estimation which is relatively free from biases – Half-sib correlation method

* Least reliable method of heritability (h^2) is Full sib correlation

* Exon – coding sequence
  Intron – Non-coding sequence

* No. of Autosomes & sex chromosomes normally present in Donkey egg cell
  Egg – 31+X sperm – 31+Y

Genetic covariance b/w 1) Parent-offspring – $1/2\ V_A$
2) Half sibs – $1/4\ V_A$
3) Full sibs – $1/2\ V_A + 1/4\ V_D + V_{EC}$

⇒ Covariance of relatives

S.No	Relatives	Genetic covariance	Regression (b) or Correlation (t)
1)	Offspring - one parent	$1/2\ V_A$	$h^2 = 2b$
2)	Offspring - mid parent	$1/2\ V_A$	$h^2 = b$
3)	Half sibs	$1/4\ V_A$	$h^2 = 4t$
4)	Full sibs	$1/2\ V_A + 1/4\ V_D + V_{EC}$	$h^2 = 2t$

* Unmasking of recessive genes occur in – Inbreeding.
* Inbreeding in a population reduces variance

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⇒ Probability Distributions :-

			given by
1) Normal Distribution	–	continous probability distribution	– Gaussian
2) Binomial Distribution	–	Discrete probability distribution	– Bernoulli
3) Poisson's Distribution	–	Discrete probability distribution	– Poisson.

1) Normal distribution :-

μ - Mean
σ - standard deviation

* It follows bell shaped curve
* % of items covered by Mean $\pm \sigma$ – 68%
  Mean $\pm 2\sigma$ – 95.45%
  Mean $\pm 3\sigma$ – 99.7%

2) Poisson's distribution :-

In this no. of trials is large and probability of occurence of an event is very small

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