

when prodⁿ leaves of mafes quoted so diff. Sires are diff.
 at the bulle & hence if it subjected to the blase
 himitation: If doesn't take into account the prodⁿ leaves of the mafes
 which findet if the simplest measure is a single head under same pen
 \bar{P} = mean avg. of all daughters of under a sire

$$\bar{I} = \bar{P}$$

proposed by ← Edmards in 1932

f. Simple daughter avg. index:
 as per need a few of them are discussed here -
 Qdly. methods for finding the sire have developed time to time
 so as to select the best sire.

program tested it requires ranking all sires for their genetic worth
 indicates the prodⁿ ability of the sire. Since, a no. of sires are
 based on sire index a numerical value is obtained which
 is a mathematical expression of a breeding worth of a sire
 genetic worth of sire & such an index is kth sire index.
 In form of a index which is the index of the
 genetic worth of sire

2. Equivalent/ Intermediate Index: Given by Hensson in 1931

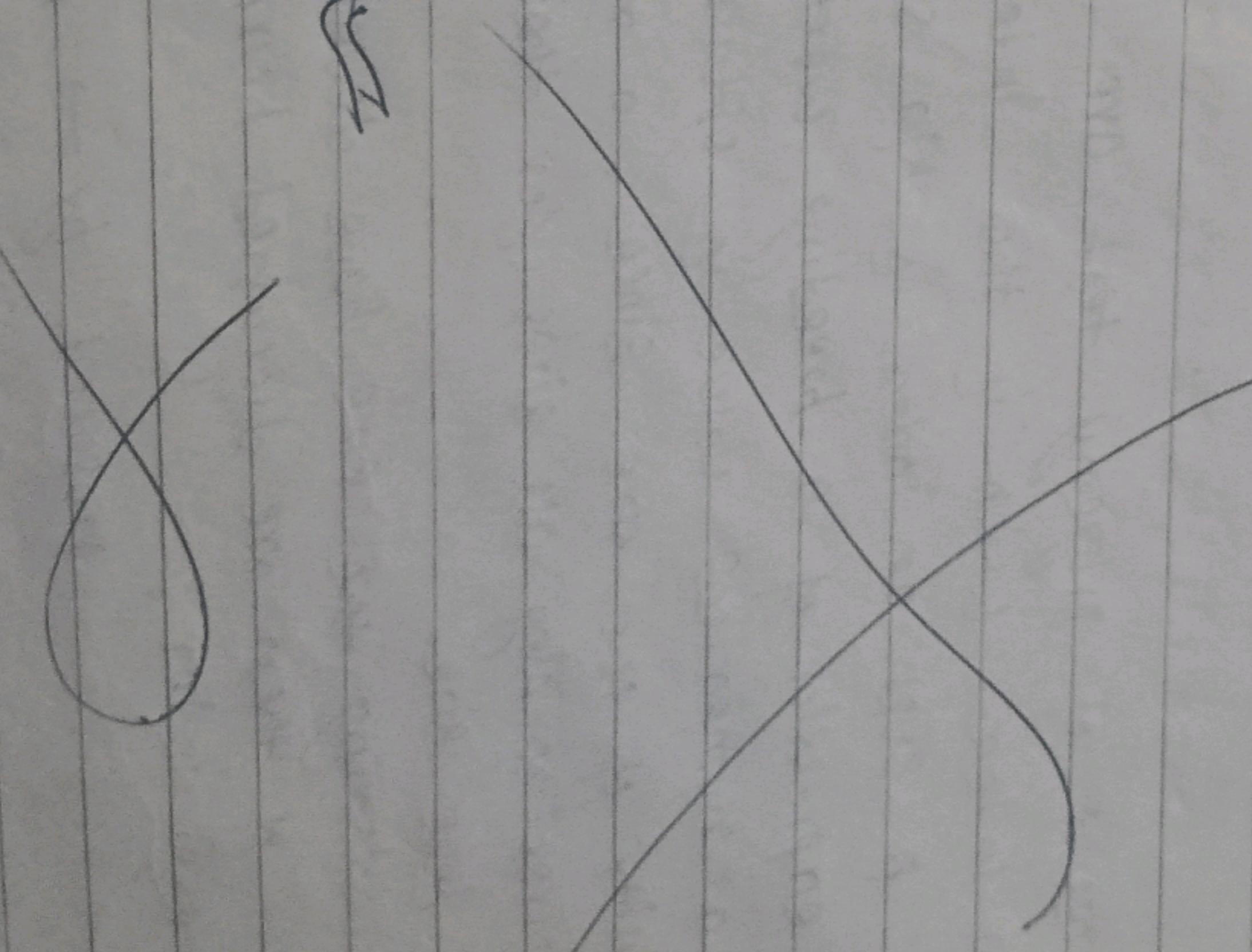
→ Also kpa yapp's index or Mount hope index b/c it was 1st use at mount hope farm in 1928

$$I_2 = 2\bar{D} - \bar{M}$$

\bar{M} = mean of the mates/dame sgs.

→ This index makes adjustment for the variation in prod' level of the dams. However, It does not correct the prod' level of mates allotted to diff. sires. If inferior dams are allotted to a sire there is over estimation of sires B.V. But in case superior dams are allotted than avg., it under estimate the sires B.V.

(3) # Rice Index.



(4) Tomar Index: 1965 by Tomar.

It depends on dam daygster comparison with simultaneous we of their contemporaries herd avg.

(iv) Corrected daughter avg. Index: Given by Krishnan (1956)

It corrects the daughter avg. for the influence of differential pred'n level of dams mated by bulls on the basis of regression of daughter records on dams and it is 4 times as efficient as the Intermediate Index

$$I_s = \bar{D} - b(\bar{m} - \bar{H})$$

b = regression coefficient whose value is $b = 0.5 h^2$

\bar{H} = Herd avg.

The term $b(\bar{m} - \bar{H})$ appearing in the Index is the correction for the genetic superiority or inferiority of the set of dams allotted to the sire over the herd avg.

(v) Contemporary daughter avg. Index: Given by Sundaresan.

It takes into account the variation in no. of daughters in progeny groups

& also corrects for period variation in conve condn to which the record might have been subjected.

$$I_c = \bar{H} + bQ(\bar{D} - C_p)$$

$$\bar{H} = \text{herd avg. } \downarrow \text{contemporary avg.}$$

\bar{D} = ~~daughter~~ avg.

n = no. of progeny of sire under test

k = constant based on sire error variance.

(vi) Corrected Contemporary daughter avg. Index: Sundaresan

for the differences in the progeny no. & period to period variation adjust for the unequal pred'n level of dam mated to diff. sires.

$$I_7 = \bar{H} + bQ(\bar{D} - C_p) - b(\bar{m} - C_m)$$

(iii) Dairy search 'index': Sunderason (1965)

$$T = \bar{H} + \frac{n}{n+12} (\bar{D} - C_2) - b (\bar{M} - \bar{C}_M)$$

cix) Least square constants.

cx) Maximum likelihood method

cxi) Restricted maximum likelihood method [REML]

cxi) BLUP (Best linear unbiased prediction method) by C.R. Henderson.

~~#~~ Inbreeding Coefficient:

- It is the probability that 2 alleles in a genotype are identical by descent.
- It is denoted by ' F' ' & its value ranges from 0-1
- It is also expressed in terms of % genes (0-100%)
- Inbreeding coefficient tells about the relative 'P' in homozygosity in comparison to the base popn.
- ' F' ' is an individual property means it has to be calculated for each individual separately.

To calculate ' F' :

1. Path diagram method:

$$F_x = \frac{1}{2} \sum_{i=1}^n (1 + f_{i,i})$$

^{through}
 $n = \text{no. of arrows connecting the sire of dam of individual}$

$\sum_{i=1}^n$ ~~X~~ sum of all the paths.

* The ' F' ' will be 'zero' in following cases:

c.i) When both parents are unknown for an individual.

c.ii) The individual whose only one parent is known.

ciii) When both parents are known but they are not related by

civ) When both parents are known but they don't have any common ancestor. In that case ' F' ' will be zero.

Correlated response to selection:-

When selection is applied on a trait for eg 'X' then there will be change in the mean genotypic level of the genetically correlated response to selection. This is k/a Correlated response to selection.

The response to selection in character 'X' which is directly selected is = $R_X = h_X \cdot h_Y \cdot \sigma_A(X)$

Here the character 'X' is like independent variable of character 'Y', is dependable variable therefore, the change in 'Y' due to change in 'X' can be estimated by simple linear regression.

$$\text{by}_X = r_A \cdot \frac{\sigma_A(Y)}{\sigma_A(X)} \cdot R_X$$

$$C_R_Y = b_{YX} \cdot R_X$$

$$C_R_Y = r_A \cdot \frac{\sigma_A(Y)}{\sigma_A(X)} \cdot R_X$$

Thus the term b_{YX} , $b_{YX} = r_A$ is called as co-henitability b/c it is equivalent to r_A in response to direct selection.

Hence, the correlated response can be estimated if the ' r_A ' is of both characters - genetic correlation & S.D. of character 'Y' are known.

Sometimes it becomes necessary to improve character 'X' indirectly by applying selection to some correlated character 'Y'. This procedure of selection is k/a Indirect selection.

In other words the selection applied to some character other than the one it is desired to improve is k/a Indirect selection.

The selection The character on which selection is applied

is k/a Secondary or Auxiliary character. The indirect selection is applied in following situation -

NOTES

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(i) If the desired character is difficult to measure with precision but the secondary character is measurable in one set only then the high intensity of selection will be possible by indirect selection.

(ii) The desired character may be costly to measure for e.g. the FCE (fast conversion efficiency) than it may be economical better to select for an easily measured character such as growth rate.

(iii) When the desired character is measured at a low stage in life of an individual but the auxiliary character is measurable

of an early stage

in which selection would be advantageous

Co-ancestry :- The degree of relationship by descent b/w the two parents is k/a Co-ancestry. or of coefficient of kinship or of Consanguinity.

~~Hustave malecot~~

- It is symbolised by ' f '.
- The co-ancestry of any two individual is identical with the Inbreeding coefficient of their progeny if they were mated. Thus, the co-ancestry of two individuals is the probability that two gametes, taken at random one from each carry alleles that are identical by descent.
- The co-ancestry of an individual with itself is equal to $\frac{1}{2}$ or 0.5.
- Coancestry of two individuals is equivalent to the mean co-ancestry of one individual with the two parents of the other.

* 50% Inbreeding coefficient is achieved by selfing in 1st gen by full sib in 3rd gen & by half sib mating in 6th generation.

By Gustav malecot. parents \rightarrow -/2000 A- A- B/c

A	B	C	D
A	1	$\frac{1}{2}$	$\frac{1}{2}$
B	$\frac{1}{2}$	1	$\frac{1}{4}$
C	$\frac{1}{2}$	$\frac{1}{4}$	1
D	$\frac{1}{2}$	$\frac{5}{8}$	$\frac{5}{8}$
		$\frac{5}{8}$	$\frac{9}{8}$

Genetic variance = $1 + \frac{1}{2}$ Genetic cov. b/w parents)

Always 1 or more than one.

Genetic cov. = $\frac{1}{2}$ Genetic cov. on one indiv. with parents of other individual

↳ always less than 1.

Inbreeding Co-efficient = Genetic variance - 1

Relationship Co-efficient = $\frac{\text{Genetic cov}}{\sqrt{\text{Genetic variance of } X} \times \sqrt{\text{Genetic var. of } Y}}$