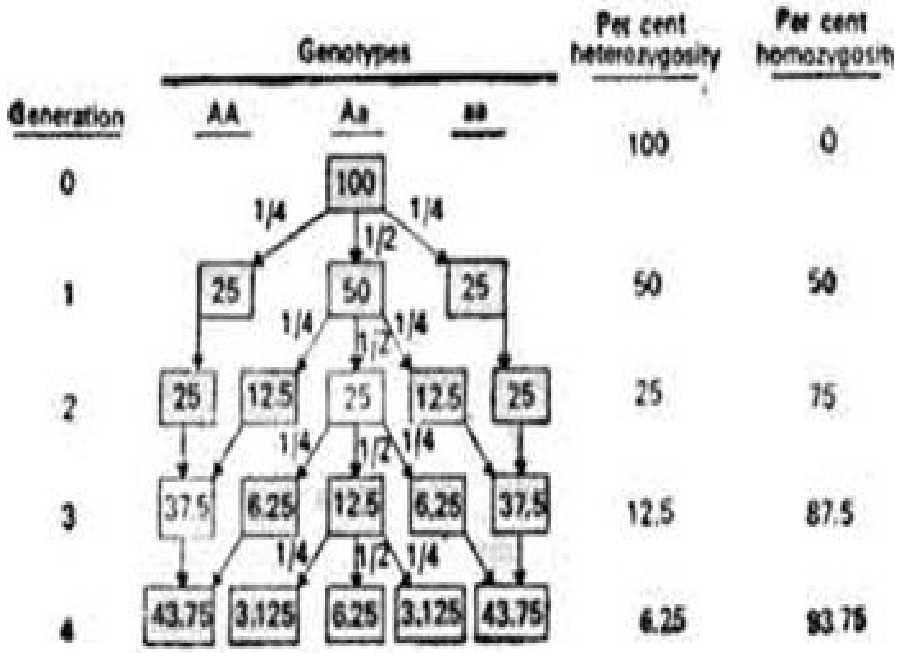
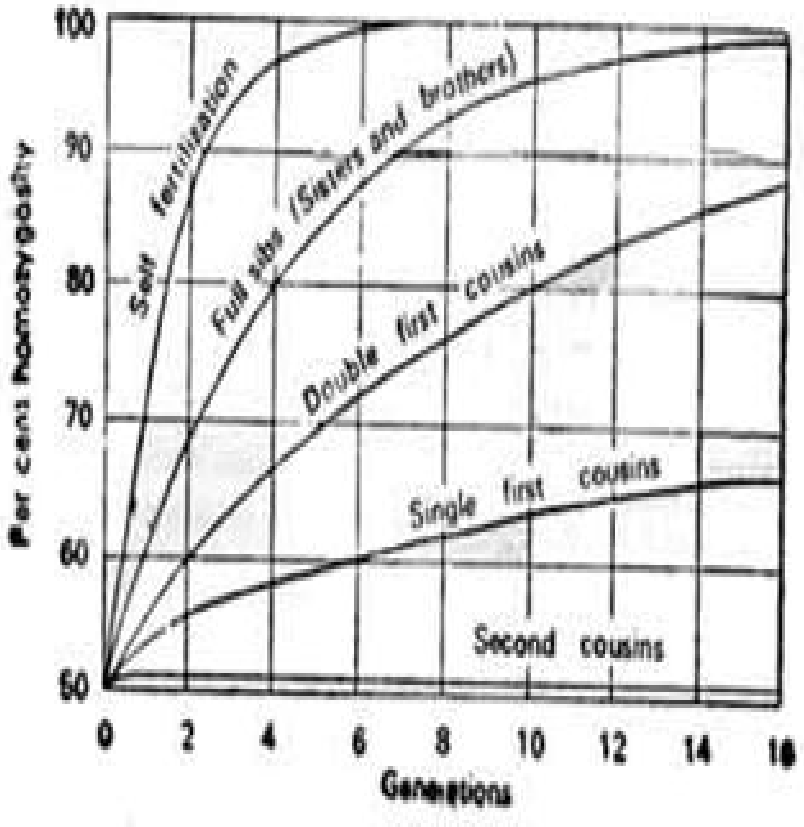
Genetic Effects of Inbreeding

The continuous inbreeding results, genetically, in homozygosity. It produces homozygous stocks of dominant or recessive genes and eliminate heterozygosity from the inbreed population. For example, if we start with a population containing 100 heterozygous individuals (Aa) as shown in figure, the expected number of homozygous genotypes is increased by 50% due to selfing or inbreeding in each generation.



Thus, due to inbreeding in each generation the heterozygosity is reduced by 50% and after10 generations we can expect the total elimination of heterozygosity from the inbred line and production of two homozygous or pure lines. But, because a heterozygous individual possesses several heterozygous allelic pairs, therefore, we can conclude that inbreeding will operate on all gene loci to produce totally pure or homozygous offsprings. In man if inbreeding continued over a number of generations it results in increasing homozygosity, but somewhat slowly. The different types of inbreedings and their corresponding increase in homozygosity have been graphically illustrated as follows:



Cross Breeding

Mating of individuals from entirely different races or even different species is called cross breeding. This represents the most extreme form of out breeding that is possible among animals. Cross breeding produces sterile hybrids in comparison to normal outbreedings.

Example- The mule is a heterotic individual which had been produced by cross breeding of a male donkey (*Equus asimus*, 2n=62) with the female horse (*Equus caballus*, 2n=64). It displays a conspicuous vigorosity and because of this it has served mankind as a patient beast of burden since time immemorial.

Genetical Basis of Heterosis

The genetical basis of heterosis is still a subject of controversy and following two theories have been propounded to explain it:

1. Over dominance theory of heterosis-The over dominance theory or physiologic stimulation hypothesis of Shull (1874-1954) considers heterozygosity to have stimulating effect on the heterosis of hybrid individual. Heterozygosity itself was thus considered to be the controlling factor.

Example-If we suppose that four gene loci are contributing to a quantitative trait, homozygous recessive genotype contribute 1 unit to the phenotype, heterozygous genotype contribute 2 units to the phenotype and homozygous dominant genotypes contribute Ii units. Then, the results can be represented as follows:

2. Dominance theory of heterosis- The dominance theory of heterosis holds that increased vigour and size in a hybrid is due to combination of favourable growth genes by crossing two inbred races. In other words, the hybrid vigour is a result of action and interaction of dominant or fitness factors or cumulative (polygenic) effect of dominant genes.

Example- If we suppose that a quantitative trait is governed by four genes. Each recessive genotype contributes on unit to the phenotype and each dominant genotype contributes two units to the phenotype. An out cross (out breeding) between two inbred lines can produce more heterotic F1, individuals than the parents. in the following manner:

Parents:	AABBccdd	X	aabbCCDD
Phenotypic value:	11/2+11/2+1+1=5	↓	1+1+11/2+11/2=5
F_1		AaBbCcDd	
		2+2+2+2=8	
Parents:	AAbbCCdd	X	aaBBccDD
Phenotypic value:	2+1+2+1=6	↓	1+2+1+2=6
F_1		AaBbCcDd	
		2+2+2+2=8	

Crossing Methods:

Convergent breeding (crossing):- Used for the improvement of a single trait or a couple of traits in an otherwise good cultivar taking cognizance of the other positive traits of that cultivar also called backcross method.

Initial crossing	A	x	B
	Recurrent parent		donor
1st backcross (50% genes from A	F_1 x A		
2nd backcross (75% A)	BC_1F_1 x A		
3rd backcross (87.5%A)	BC_2F_1 x A		
4th backcross (93.7% A)	BC_3F_1 x A		
5th backcross (96.9% A)	BC_4F_1 x A		
6th backcross (98.4% A)	BC_5F_1 x A		

Used to incorporate a resistance into a recurrent parent without changing its original trait. The above is a complete backcrossing because the current parent has been reconstituted – used when the donor parent posses a large number of negative traits but with one highly valued positive trait.

However incomplete backcrossing is recommended i.e one or two backcrosses with the recurrent parent when the donor parent posses a number of other positive traits.

Divergent Method (breeding):- Used in the evaluating of inbred lines also known as recombination because it makes use of genetically diverse parents in order to recombine their desirable traits.

(i)	the single cross method	A x B	
(ii)	three-way cross	(A x B) x C	
		F_1 x C	
(iii)	Successive cross	[(AxB)xC]xD	A x B
(iv)	Double cross	(AxB) x (C xD)	F1x C
			F1x D
(iv)	Diallel crosses		selection

Used to pinpoint parents (from a large bulk) capable of producing heterotic F_1 hybrids or those capable of producing large number of superior progencies.

One may have 6 new parents A,B,C,D,E,F.

AxB

AxC BxC 15 cross combinations

AxD BxD CxD

AxE BxE CxE DxE

AxF BxF CxF DxF ExF

6C2 = 6x5½ = 15

n – (n-1)/2

Method of diallel cross is used exclusively for genetic studies because it gives information on the effect of a number of genes, combining ability and gene interaction.

* It is not used in the breeding of self pollinated plants

(a) Genetics = science of heredity and variation (Bateson, 1906)

(b) Gene = unit of heredity e.g gene A or a

(c) Allele = (formally allelomorph meaning ‘other) is <u>one</u> of <u>the</u> two or more forms of a gene. Alternative form of a gene A, a are both alleles of the ‘A’ gene.

(d) Genotype = genetic constitution (or hereditary makeup) of an organism e.g AA, Aa, aa are genotypes

(e) Phenotype = the physical appearance of the organism in terms of colour, weight, height.

(f) Homozygousity = situation when 'both genes in an individual are the same e.g Genotype AA have both genes the same also SS, aa etc.

(g) Heterozygousity = both genes different as Aa, Ss.

Reciprocal cross does not produce different F_1 genotypes from the main cross except that a trait is inherited through the female i.e unless there is cytoplasmic inheritance e.g

AA	x	aa	=	Aa = F_1	similar
aa	x	AA	=	Aa = $F_{1(R)}$	genotypes

Both F1 and $F_{1(R)}$ are similar except the gene contributions are made by different species.

Maternal influence if F_1 in main cross differs from the F_1 in the reciprocal cross.

*The cytoplasmic content of the egg is determined by the female parent content is temporary. Phenotypic expression of homozygous, recessive condition is delayed by one generation though the genotype is expressed in the present generation; its effect are temporary.

Phenotype is not consistent with the genotype in which case, the genetic control is in the nucleus but the cytoplasm has temporary influence.

No maternal influence, no reciprocal difference if the 2 F_1s are similar.

Normal transmission (or inheritance) of character is through the sperm which contributes little or no cytoplasm, but rather through the nucleus i.e it is the nucleus that determines the genotype.

*Additive gene action = absence of dominance in the case of single locus i.e the effect of substituting gene A for a.

Both AA and Aa are dominant genotypes.

Crop Improvement by Breeding

Introduction of alien variation

An increase in the precision of selection

An increase in the speed of selection

Modification of the breeding system

A decrease in the generation time

A more precise definition of breeding objective

Hybrid Varieties

These are varieties or F_1 population obtained by crossing (hybridizing) populations [such as inbreds, clones or open-pollinated varieties] that are genetically diverse. Hybrid varieties are F_1 populations used for commercial planting because of their higher hybrid vigour (heterosis).

These can be obtained from

(a) Single cross (AxB)

(b) 3-way cross (AxB)xC

(c) Double cross (AxB) x (CxD)

In open-pollinated crop like maize Inbred lines are used (lines that are self-pollinated over a long generation i.e over generations of inbreeding). *Homozygosity is attained after 5 or 6 generations. Inbreds are never better than their parents but early testing of inbred lines for combining is used to eliminate lines that may not produce superior progenies upon further inbreeding.

To obtain inbred lines:

(1) Select plant parents

(a) that the vigorous (good vigour)

(b) that are free from diseases

(c) that have desirable characters e.g

(i) increased seed size or productiveness

(ii) earlier maturity than either parent

(iii) greater resistance to diseases, pests or environmental stress

(iv) increased number of nodes, leaves, pods in F1

(2) Self the selected plants to produce homozygous inbred lines A,B,C,D,E,F etc

(3) Cross AxB, AxC, CxD single double 3-way

Evaluation of Inbreds

(a) as single crosses early testing of inbred lines for combining

ability is used to eliminate lines that my not produce superior progenies upon further inbreeding with every n line developed evaluate. Detassel inbred Aa(n-1)/2 or single crosses over tassel A with a tassel bag. Also cover the ear of inbred B to prevent self pollination.

(b) by 3-way crosses

(c) by performing top-crosses crossing inbred with a tester to test general combining ability of the top-cross is cross between a clone, an inbred selection or line and a common pollen parent.

	Line selection	x	tester
Topcrosses	Inbred	x	tester
	Clone	x	tester

Tester may be a variety line or hybrid that has a large number of positive traits on a wide genetic base. It is used to test for general combination ability.

Common pollen parent tester

(d) by diallel analyses - to measure the GCA and SCA of inbreds ${}^{6}C_{2}$

= 6x5x4x3x2x1

2x4x3x2x1

= 15

Success of selecting inbred lines for yield depends on the diversity of the original parents. However, early testing of inbred lines for GCA will help to eliminate lines that may not produce inbreds upon further inbreeding

Note:-

- Hybrid varieties make use of heterosis to a great extent: unrelated parents give high heterosis

- Hybrid varieties from inbred crosses are highly uniform

- Hybrid varieties have narrower genetic base

- The yield ability of hybrids lack consistent superiority from year to year. i.e performance reduces with years of continuous cultivation.

- Hybrid varieties are costlier to produce.

Combining Ability In Crops Plants

Good combining ability implies the ability of a parent plant to produce superior progenies when combined with another parent.

During the process of recurrent selection- building up of minor genes, test crosses are used to measure combining ability.

The tester used here (open-pollinated parent-line, variety, single cross hybrid e.t.c) must have broad genetic base so that variations in their performance among testcrosses will be due to differences in their general combining ability (GCA).

*GCA is the average performance of a line in hybrid combination. $GCA_1 = 59.8$

Average mean performance.

Diallel cross

A **diallel cross** is a mating scheme used by plant and animal breeders, as well as geneticists, to investigate the genetic underpinnings of quantitative traits.

In a full diallel, all parents are crossed to make hybrids in all possible combinations. Variations include half diallels with and without parents, omitting reciprocal crosses. Full diallels require twice as many crosses and entries in experiments, but allow for testing for maternal and paternal effects. If such "reciprocal" effects are assumed to be negligible, then a half diallel without reciprocals can be effective.

Common analysis methods utilize general linear models to identify heterotic groups, estimate general or specific combining ability, interactions with testing environments and years, or estimates of additive, dominant, and epistatic genetic effects and genetic correlations.

There are four main types of diallel mating design:

1. Full diallel in which parents and reciprocal crosses are involved along with F1
2. Full diallel without inclusion of parents
3. Half diallel with parent and without reciprocal crosses
4. Half diallel without parents or reciprocal crosses

Diallel mating designs: when the same parents are used as females and males in breeding, the mating design is called **diallel.** Here are some commonly used diallel mating designs in forestry:

Half diallel - Each parent is mated with every other parent, excluding selfs and reciprocals.

F/M	1	2	3	4	5	6
1	-	*	*	*	*	*
2		-	*	*	*	*
3			-	*	*	*
4				-	*	*
5					-	*
6						-

Smart diallel - Parents are sorted for their breeding values from the best to the poorest and most crosses are made among the best.

F/M	1	2	3	4	5	6
1	-	*	-	*	-	*
2		-	*	-	*	-
3			-	*	-	-
4				-	-	-
5					-	-
6						-

Advantages and disadvantages of diallel mating designs

Diallel designs provide good evaluation of parents and full-sib families,

Provide estimates of both additive and dominance genetic effects,

Provide estimates of genetic gains from both additive and non-additive genetic variance,

When the number of parents mated increases, the number of crosses increases by 2N, where N is the number of parents and the design can be costly

Using the same parents as males and females make the mating design a little bit complicated to analyze.

Diallel analysis of 5 inbreds

	Lines						
	1	**2**	**3**	**4**	**5**	**Mean**	**X**

1	-	41.7	62.2	70.8	64.4	59.8	239.1
2	41.7	-	65.7	72.1	64.4	61.0	243.9
3	62.2	65.7	-	64.2	60.4	63.1	252.5
4	70.8	72.1	64.2	-	59.6	66.7	266.7
5	64.4	64.4	60.4	59.6	-	62.2	248.8
Mean	59.8	61.0	63.1	66.7	62.2	-	
	5C2 = 5x4x3x2 / 3x2x2 = 10 single crosses						

Specific Combining Ability (SCA)

*SCA is the performance (behavior) of parent (X) when crossed with another parent (Y) y= a tester i.e the performance of the line when compared with a tester.

A line with high heterosis when compared with the tester is said to have good SCA.

Mean performance of line 1 and line 4 above is given as

$M_{1,4} = GCA_1 + GCA_4 + SCA_{1,4}$

$= 59.8 + 66.7 + 70.8 = 197.3$

$M_{2,4} = GCA_2 + GCA_4 + SCA_{2,4}$

61.0 + 66.7 + 72.1 = 199.8

$SCA_{2,4} = Mean_{2,4} + GCA_2 + GCA_4$

= 61.0 + 66.7 + 72.1 = 72.1

(xi+xii) = total value for rows + mean value of parents

From the table line 4 has the highest GCA of 66.7. It also has good SCA with line 1 and 2.

Therefore,

If the mean performance of lines in hybrid combination is known, then the SCA which is either higher or lower than the mean can be calculated as

SCAxy = Meanxy - GCAx - GCA y

When carrying out selection for specific combining ability (SCA), we normally use testers with narrow genetic base.

Combining ability should therefore be examined always when we want to develop superior progenies i.e when heterosis is practically exploited or when hybridization is used to develop new cultivars.

Diallel crossing method is used when we want to test whether a line is a good or poor combiner. Hybridization is made between pans a non of selected genotypes in all possible combinations.

The number of crosses taking into consideration the reciprocal ones is n(n-1) i.e

With a set of 10 lines, it is necessary to make a 10(10-1) = 90 cross combinations. If there is no reciprocal n(n-1)/2.

*When the number of crosses to be made is practically impossible, the GCA is evaluated by testing all lines against a common parent i.e a tester – performing topcrosses.

A best hybrid or a standard variety can be used as a tester in the case of maize. The lines that perform well with the tester are selected for diallel crossing for SCA.

GCA is considered to be a result of additive gene action while SCA, is as a result of non-additive variance i.e dominance and **Epistasis.**

Epistasis (interallelic gene interaction)

Dominance (intraallelic gene interaction)

(a) Significant MS of GCA & SCA shows that the cultivars included in diallel crosses had significant differences i.e they are highly variable.

(b) Large MS for GCA compared with MS for SCA means that additive gene action played a more important role in the inheritance of a trait than non-additive gene action (dominance and epistasis)

Phenotype and Components of Phenotype Variability

P (phenotype) = G(genotype) + E(environmental effect)

Individuals differ in phenotypic values i.e in outward or physical appearance as a result of genetic differences among the individuals, environmental factors and interaction between the genotype and the environment. Thus the phenotypic value of individuals is made up of components that can be determined by the analysis of variance. From the above statements.

$V_p = V_a + V_E + V_{GE}$

Where;

V_p = Phenotypic variance, V_G = genotype variance and V_E = environmental variance.

P_1	Mean	P_2
A_1A_1	½ (A_1A_1+A_2A_2)	A_2A_2
	$F_1(A_1A_2)$	
	d	
-a	1	+a

If A_1A_1 = 6cm and A_1A_2 = 7cm

It implies that

The presence of A_2 in the F_1 causes a change of 7cm compared with meaning that the gene expression above is additive. If dominance A_2 will be recessive. If there is epistasis, there will be interaction among different gene loci e.g AA x BB. A_1A_1 expresses an additive effect when it occurs with another gene B_1B_1 but a dominant effect when it occurs with the recessive allele b_1b_1.

Therefore,

$$V_G = V_A + V_D + V_I$$

V_A = Variance with additive gene effect

V_D = Variance with dominance gene effect

V_I = Variance as a result of interaction between genes

Hence

$V_P = V_A + V_D + V_I + V_E + V_{GE}$

V_E = is the environmental variance as a result of factors of the environment

$V_E = V_{P1}+V_{P2} + V_{F1}/3$ because the three are a measure of environment variance

Let us look at the genotypic variance via F_2 and the backcross B_1 and B_2

$A_1A_1 \times A_2A_2$ $F_2 = A_1A_2 \times A_1A_2$

$A_1A_2 = F_1$ $F_2 = A_1A_1+2A_1A_2+A_2A_2$

Three genotypes; four phenotypes 1:2:1

$A_1A_1 = ¼$; $A_1A_2 = ½$; $A_2A_2 = {}^1/_4$

From the table or diagram above

(P_1)	(F_1)	(P_2)
$A_1A_1 = -a$	$A_1A_2 = d$	$A_2A_2 = +a$

Which are deviations from the parent mean

$F_2 = ¼\ A_1A_1 + ½\ A_1A_2 + ¼\ A_2A_2$

$= ¼\ (-a) + ½d + ¼a = ½d$ (F_2) deviation

Variance $(V_G) = f(x-x)^2$

$V_G = (-a-½)^2 + ½(d- ½d)^2 + ¼(a-½)^2$

$= ¼(a^2+ad+¼d^2) + ½({}^1/_4d^2) + ¼\ (a^2- ad +¼d^2)$

$= ½a^2 + ¼d^2$

$V_G = ½a^2 +¼\ d^2$ if $a^2 = A$

V_G = ½A + ¼D $d^2 = D$

V_{F2} = $V_G + V_E$ = ½A + ¼D + E (Total variance)

Note that from the cross above

B_1 = A_1A_2 x A_1A

$A_1A_1 + A_1A_2 = ½(-a) + ½d$

$½(-a – ½d)^2 + ½(d- ½d)^2 = ¼a^2 + ¼d^2$

$= ¼a^2 + ¼d^2$

Like the above

B_1 = ¼A + ¼D

V_{B1} = ¼A + ¼D + E because $VB_1 = V_G + V_E$

Also,

V_{B1} = ¼A + ¼D + E

$V_{B1}+V_{B2}$ = ½A + ½D + 2E

V_{P1} = E

V_{P2} = E $E = (V_{P1}+V_{P2}+V_{F1})/3$

V_{F1} = E

Mean values (x) and variance (∂^2) of seed germination in the parent and hybrid generations of two soybean genotypes.

Parent & hybrids	**No of plants analysed**	**Percent Germination**	
		X	∂^2
P_1 TGX 1448-2E	20	94.5	25.2
P_2 TGX 737p	20	98.0	5.5
F_1 (P_1 x P_2)	20	94.7	27.6
B_1 (F_1 x P_1)	10	95.0	161.1
B_2 (F_1 x P_2)	10	97.0	45.6
F_2 (F_1 x F_1)	126	94.9	137.2

E = (25.2 + 5.5 + 27.6)/3 = 19.4

FV_2 = 137.2 = ½A + ¼ D+E E = 19.4

½A + ¼D = 137.2 – 19.4

½A + ¼D = 117.8 …….(i)

= ∂^2g

B_1+B_2 = ½A + ½D + 2E

= ½A + ½D + 38.8 = 206.7

= ½A + ½D = 167.9 ……(ii)

½A + ¼D = 117.8

½A + ½D = 167.9

2A + D = 471.2 …….(iii)

2A + 2D = 671.6 …….(iv)

Equations 4 minus equation 3

D = 200.4

$2A + 200.4 = 471.6$

$2A = 271.2$

$A = 135.6$

From F_2 variance

$V_{F2} = ½A + ¼D + E$

$137.2 = ½(135.6) + ¼(200.4) + 19.4$

$137.2 = 67.8 + 50.1 + 19.4$

Express as a %

$100\% = 49.4 + 36.5 + 14.1$ in V_{F2}

$V_A = 49.4\%$

$V_D = 36.5\%$

$V_E = 14.1\%$

$H_B = 85.9\%$

$H_N = 49.4\%$

From the analysis, the F_2 generation that has total variance is shown to have very high genetic variability for seed viability (49.4 + 36.5%) = 85% than environmental variance (14.1%).

This suggest that there is big genetic differences between TGX 1448-2E and 737p. About 57.5% of genetic variance is due to the additive gene action and 42.5% was due to the dominance gene action.

The above shows the simplest way of calculating the components of genetic variance but note that the variances due to epistasis (interallelic interactions) which are frequently associated with quantitative traits are omitted. This is because, such calculations call for more complex formulae of biometrical genetics using the models of Mather and Jinks (1971); Falconer (1981) and others.

Calculations from diallel crosses using the methods of Jinks (1954); Haymann (1954) and Mather and Jinks (1971) may also be used. Mean and variances of six generations for height from a maize trial with completely randomized individual is presented in the table.

Generation	**No of individuals**	**(cm) mean**	**Variance**
P_1	50	69.6a	48.6
P_2	50	68.4a	40.1
F_1	100	89.6c	53.0
F_2	200	79.5b	97.3

B_1	200	77.4b	66.5
B_2	200	78.3b	84.6

P_1 & P_2 have similar means (69.6, 68.4)

F_1 mean is considerably high (89.6)

F_2 is in-between P_1P_2 and F_1 values (79.5)

P_1, P_2 and F_1 have similar variance (48.7 on average)

F_2 variance is much larger (97.3)

Environmental variance ∂^2e = 48.7 = VE = E

MP height = 69.0cm

F_1 mean height = 89.6

Heterosis = $\frac{89.6 - 69.0}{69.0} = \frac{20.6}{69.0}$ = 29.9%

If variance in the F_2 (V_{F2}) = 1/2A + ¼D+E

V_{B1} = V_{B2} = ¼A + ¼A + E

Where

A = Additive gene action

D = Dominance gene action

(a) Solve or estimate the values of A & D and hence determine whether plant height in maize is controlled by additive or dominance gene effects

(b) What effect does environment have on plant height in maize

(c) Estimate Heterosis for plant height

Q2 ANOVA of seed yield of 6 genotypes of cowpea in a particular tropical environment.\

Source	Df	Ms	Expected ms	F-ratio
Total	Rt-1			
Rep	r-1	192.0		*24.68
Treatment	t-1	69.8	$\partial^2 e + r\partial^2 t$	8.97**
Error	(t-1) (r-1)	7.78	$\partial^2 e$	

$\partial^2 e = 7.78$

$r\partial^2 t = 69.8 - 7.78 = 62.02$

$\partial^2 t = 62.02/4 = 15.51$

$\partial^2 p = \partial^2 e + \partial^2 t = 23.29$

$Hb = \partial^2 t / \partial^2 p = 66.57$

$= 66.60\%$

(a) Recopy the table if 5 treatments was planted in 4 reps in randomized complete block.

(b) What type of design is used here and why?

<u>Testing for Means of Difference</u>

Significant mean squares is an indication that variability exists among the sources under consideration. For instance, significant mean squares for genotype indicates that the genotypes are quite diverse or there is genotypic variability causing the genotypes to perform differently under similar environmental conditions.

Differences between two means can be tested using

(i) Fisher's Least Significant Difference (FLSD)

(ii) Bayer's Least Significant Difference (BLSD)

(iii) Honest Least Significant Difference (HLSD)

(iv) Duncan's Multiple Range Test (Duncan separation)

Any of the above is used when F-test has been shown to be significant

Steps

1. Perform a preliminary F-test

2. Calculate (Sd) Standard error of difference between 2 treatment means from the variances of the means (error mean squares)

3. Obtain 't' value at error df at 5% probability level

   Error variance = $\partial^2 e$

   With "r" replications OR n = no of observation

   Variance of the mean = $\frac{\partial^2 e}{r}$ or $\partial^2/r = \partial^2 x$

   Standard error of a mean = variances of mean

$\sqrt{\partial^2 x}$ = $\sqrt{\partial^2/r} = \sqrt{\partial^2/n}$

Variance of 2 treatment means

$\partial^2_1 - \partial^2_2 = \partial^2_{x1} - \partial^2_{x2} - = \partial^2_{x1} - x_2$

Standard error of 2 treatment means.

$\partial^2/r - \partial^2/r$ = $\partial^2 x_1 - x_2$ = $\partial x_1 - x_2 = 2d^2/r$

$\partial x_1 - x_2$ = $\sqrt{2}\partial^2/r$ = $\partial\sqrt{2}/r$

= ∂d

Assume $\partial^2 e$ = 1.78 and r = 4

∂x = $\partial^2 e/r$ = 1.78/4 = 0.45

$\partial x_1 - x_2$ = $\sqrt{2}\partial^2/r$ = $\underline{\sqrt{2}x\ 1.78}$

= 4 = $\sqrt{0.89} = 0.94$

See t-test and Lsd defined on loose sheet

If error df = 12 and probability level is 5%

$t_{5\%}df_{12}$ = 2.179

$Lsd_{5\%}$ = $t_{5\%}df_{12}$ x ∂ = 0.94 x 2.179

DMRT see loose sheet = 2.05

Statistical Tests

1. t-tests (Lsd) test of significant for paired observations
2. F-tests (ANOVA tests)
3. Duncan Multiple range test
4. Test of association – Correlation

   - Regression

   Path Coefficient Analysis
5. Stability tests
6. Scaling tests – test of adequacy of the additive-dominance model in the backcrosses, F_2 and F_3 populations.

   A = $2B_1 - F_1 - P_1$

   B = $2B_2 - F_1 - P_2$

   C = $4F_2 - 2F_1 - P_1 - P_2$

   OR

   C = $2F_2 - B_1 - B_2$ to test non-allelic interaction

   D = $8F_3 - 3P_1 - 3P_2 - 2F_1$

Test for reciprocal difference (maternal effects)

e.g $F_1 - F_{1(R)}$ = 96.0 – 94.7 = (1.3) observed

t-test: to test for significance in paired observations e.g two mean values

$$t = \frac{x_1 - x_2}{Sx} = \frac{F_1 - F_{1(R)}}{Sx} = 1.3$$

Sx = Standard error of the mean = $\sqrt{\partial^2}/n = \partial/\sqrt{n}$

n = no of observations, ∂^2 = variance of the means

$$Sx = \frac{27.6}{20} = 1.17$$

$$t = \frac{1.30}{1.17} = 1.10 \text{ cal (expected)}$$

A df_{19}5% (i.e $\frac{0.05}{2} = 0.025$)= 2.093 (tab)

cal < tab

No significant difference between 1.3 and 1.10

No reciprocal difference, no maternal effect.

From Question

M = ½ (P_1 + P_2) = 69.0

[d] = ½ (P_1 - P_2) = 0.60

[h] = $F_1 - M$ = 20.60

Dominance ratio (h/d) measures the degree of dominance of the allele at a locus

h/d = 1 A completely dominant to a

h/d = -1 a completely dominant to A

h/d = 0 no dominance (co dominance)

D = 87.08

H = 20.42

F = 18.1

Ew = 47.23 = Environmental variation within families

= $(VP_2 + VP_2 + VF_1)/3$

Eb = Environ. Variation between families

Variances have to be homogeneous.

*If heterogeneous, heterogeneity (though small) is caused by the fact that variances are positively correlated with the means.

Variance at F_2 = 97.3 i.e phenotypic variance

Genetic variance = 97.3 – 47.23 = 50.07

h_B = 50.07/97.3

= 51.4% = 0.51

i.e 51% of variation was due to genes and 49% was due to environment.

Mathematically: $\partial^2 g$ = ½ d2 + ¼ h2

= ½D + ¼ H

$$\partial^2 p = \frac{1}{2}D + \frac{1}{4}H + Ew$$

F= 18.1 is additional term contained in the two backcrosses

H's sign depends on the direction of dominance or dominant allele

$F = (\sum dh)$

If P_1 has dominant alleles, F will be positive and thus variance within B_1 will be less than that within B_2.

If F = 0, then both parents carry the same number of dominant alleles.

F = B_2 Variance - B_1 Variance

= 84.6 – 66.5

= 18.1