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QUALITY CHARACTERISTICS AND ITS USE
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GENETIC VARIATION AND INHERITANCE OF CERTAIN QUALITY CHARACTERISTICS AND ITS USE IN BREEDING OF CABBAGE

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In future breeding plans of Norwegian cabbage, we have set our sights on a number of goals (NLVF-report no. 109). Three important characters concerned with quality are:

1. Storage qualities

2. Length of the stem inside the head (Inner stem)

3. Length of the stem above the ground (Outer stem)

Storage quality is a very important quality character because the aim, in the future, is that Norway should be self-sufficient with cabbage for most part of the year.

With regard to the length of the inner stem, it is desirable that this is short. A long inner stem gives rise to a less compact head and thus a lower quality.

It is also probable that future breeding programmes will include demands on the size of the outer stem. If the outer stem is too long, cabbage plants have e tendency to lodge and therefore making harvesting more difficult. On the other hand, if the outer-stem is too short, this would result in the head touching the ground and making it susceptible to soil pests and diseases. It is also possible that future mechanical harvesters will set special demands on the length of the outer-stem.

Materials and methods

To study the interitance of a number of characters in cabbage, The Department of Vegetable Crops, at the Agricultural University of Norway laid out a 10 x 10 crossing where 10 genotypes were crossed diallelic (Table 1).

Genotype 0-7 originate from the Department of Vegetable Crops own breeding material. Genotype 8 comes from the American variety 'Badger Shipper', while the last genotype is from the Norwegian commercial variety 'Aglo'.

Before starting on the diallel crossings, all the genotypes were cloned from leaf shoots (NORTH 1952, SNEDDON 1962, HANSEN 1981).

None of the parental clones, except clone 8, were inbred before they were included in the present experiment. The diallel cross was complete, that means that all the individual combinations were fertile.

In 1980, plants were produced from each crossing. They were planted out in a randomised block experiment. In addition to the 100 F_1 families, the 10 parental clones were also vegetatively propagated and included in the block experiment.

Each plot had two rows of 6 plants spaced at 50 cm between plants and the rows were set 60 cm apart.

A number of observations were made on several different characters. However, from here on we shall be concentrating on the three characters that were mentioned in the introduction.

The storage quality was estimated by storing 4 heads from each

of the F_1 families and parental clones in a cooling rom. The heads were weighed before storage. During the storage period the heads were taken out, cleaned and weighed and put back again. This was done after about 75 and about 150 days of storage. Results show that the saleable yield was reduced linearly with storage time (Figure 1). As a measure of storage quality, the percentage of fall in the saleable yield after 100 days was calculated (Figure 1). The storage experiment has 4 replications.

The length of the inner stem was measured at harvest. 8 heads from each F_1 family and parental clones were divided vertically and the inner stem measured. This experiment had 5 replications.

The length of the outer stem was measured on all the plants in the block experiment two weeks before harvest. This experiment had 5 replications too.

Results

In the figures 2, 3 and 4, the distribution of family means for storage quality, length of the inner stem and length of the outer stem are presented in a graphic form. The diagrams show a good approach to a nearly normal continuous distribution. This continuous distribution shows that these three characters must be considered as quantitative characters. In other words, there must be a number of genes that control these characteres.

The regression of covariances between the diagonal families and arrays $(W_{p2/r})$ on variances of arrays (V_r) is deduced by DICKINSON & JINKS (1956). Figure 5 shows the $W_{p2/r}/V_r$ - graph for storage quality. From this graph we can see that the

genotypes 5, 6 and 9 have most dominant alleles with regard to storage quality. In addition, the regression line cuts the $W_{p2/r}$ - axis above origo. This means that the character for storage quality shows incomplete dominance.

The $W_{p2/r}/V_r$ - graph for the character length of the inner stem (Figure 6), shows that also this character shows incomplete dominance. Genotype 9 has most dominant alleles for this character.

From the $W_{p2/r}/V_r$ - graph for the length of the outer stem (Figure 7), one can see that this character too shows incomplete dominance, and that the genotypes 2 and 9 have most dominant alleles.

The $W_{p2/r}/V_r$ - graphs show that genotype 8 is the most recessive for all the three characters.

Table 2 shows the expectations for array variance (V_r), covariance between parent clones and arrays ($W_{p1/r}$) and covariance between inbred lines (diagonal families) and arrays ($W_{p2/r}$), in a diploid heterozygous diallel cross.

I have found a linear regression between $W_{p1/r}$ and $W_{p2/r}$. The expectation for the regression coefficient is:

$$b_{W_{p1/r}/W_{p2/r}} = \frac{W_{p1/r_{AA}}}{W_{p2/r_{AA}}} = \frac{W_{p1/r_{Aa}}}{W_{p2/r_{Aa}}} = \frac{W_{p1/r_{aa}}}{W_{p2/r_{aa}}} = \frac{d + h(1-2u)}{d + \frac{1}{2}h(1-2u)}$$

The slope of the regression line is determined by the level of dominance and the gene frequency. From the regression coefficient one can see that when the gene frequencies are equal ($u = v = 0.5$), the regression coefficient is equal to 1.

We can also see that when u is greater than v, the regression coefficient becomes less than 1. The regression coefficient is larger than 1 if u is less than v.

Figure 8 shows the $W_{p1/r}/W_{p2/r}$ - graph when h = ½d for the gene frequencies u = 0.2, 0.5 and 0.8 respectively. Figure 9 shows the $W_{p1/r}/W_{p2/r}$ - graph when h = d for the same gene frequencies, while figure 10 shows the $W_{p1/r}/W_{p2/r}$ - graph when h = d and gene frequencies u = 0.2, 0.5 and 0.8 respectively.

We see that irrespective of the level of dominance or the gene frequency, we can expect the regression line to go through the point of origo. At full dominance (h = d), the observations are expected to circle around origo. In the case of over-dominance (h > d), the observations are expected to fall in the third quadrant, while at incomplete dominance (h < d), the observations will arrive at a point above origo. Observations for the most recessive genotypes will in all cases be located furthest away from origo in the first or second quadrant.

With incomplete dominance, an alteration in the gene frequency will lead to only a small change in the regression coefficient. If h is large, an alteration in the gene frequency would lead to a larger change in the regression coefficient. If h = 0, there will be no significant regression at all.

Figure 11 shows the $W_{p1/r}/W_{p2/r}$ - graph for storage quality. The distribution of the points along the regression line shows incomplete dominance. This graph also shows that the genotype 5 has most dominant alleles while genotype 8 has most recessive alleles. The $W_{p1/r}/W_{p2/r}$ - graph for the character length of

the inner stem (Figure 12) shows that genotype 9 has most dominant alleles for this character. It is also genotype 9 that is most dominant with regard to the character length of the outer stem (Figure 13). Genotype 8 is most recessive in all of these three characters. The regression coefficients show that there is a surplus of dominant alleles for all the three characters.

In tables 3 and 4, D_R, H_R and the heretability in broad and narrow sense are estimated from the variance components (AASTVEIT 1966, MATHER & JINKS 1977).

The D_R's is estimated from the variances of array means ($V_{\bar{r}}$), the mean covariances between parental clones and arrays ($\bar{W}_{pl/r}$) and the covariances, between the means of parental clones and the means of their offspring families ($W_{\bar{pl}/\bar{o}}$). The H_R's are estimated by substitution in the equations for the variances of parental clones (V_{pl}), the mean variances arrays ($\bar{V}_r$) and the variances of offspring families around the total means ($V_{\bar{o}}$).

Conclusions

The results from the analysis of the diallel cross show that the three characters in question are inherited quantitatively, and that a large part of the variation is additive. One can thus expect a great response to selection.

It should be possible, from the progeny of the diallel cross, to create new varieties with storage qualities that are above average. Following this, one can carry out stabilized selection for the characters for length of the inner stem and length

of the outer stem, so that these characters are expressed properly in new varieties.

As can be seen from the results, the genotype 8 (from 'Badger Shipper') is the most recessive for all the three characters. However, genotype 8 is evidently the most recessive genotype for all the characters examined in this diallel experiment. From this, we can expect that this genotype should be a suitable common tester if one wanted to use the top cross as a method for progeny testing.

References

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   ved kombinasjonsforedling og gjentatt seleksjon på

   Plasmodiophora-infisert jord.

   Forskn. Fors. Landbr. 19: 233-54.

Table 1. Parental clones in the diallel cross.

Geno-type	Origin	References
0	'Resista' ('Jåtunsalgets v. k. ' x 'Bøhmer-wald')	Weisæth 1968
1	"	"
2	"	"
3	"	"
4	"	"
5	TK 704 ('Rossebø' x 'Bøhmerwald') x 'Bindsachsen'	"
6	"	"
7	K 707 ('Rossebø' x 'Bøhmerwald')	"
8	'Badger Shipper' (Brassica oleracea capitata x B.o. acephala)	Chiang & Grant 1975
9	'Aglo' (Selected in 'Toten Amager')	

YIELD, KG

% LOSS IN WEIGHT AFTER 100 DAYS
IS DEFINED AS STORAGE QUALITY

STORAGE TIME
(DAYS)
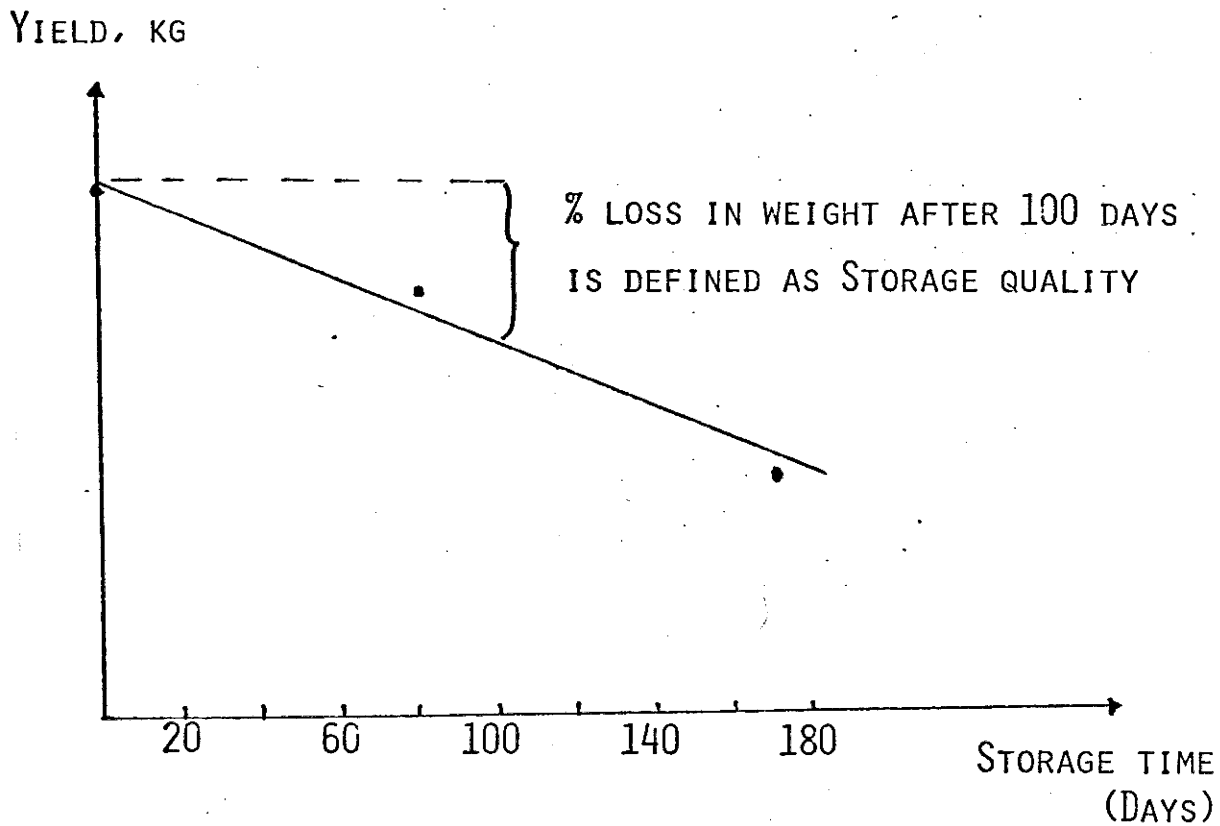
FIG. 1 . ESTIMATION OF STORAGE QUALITY
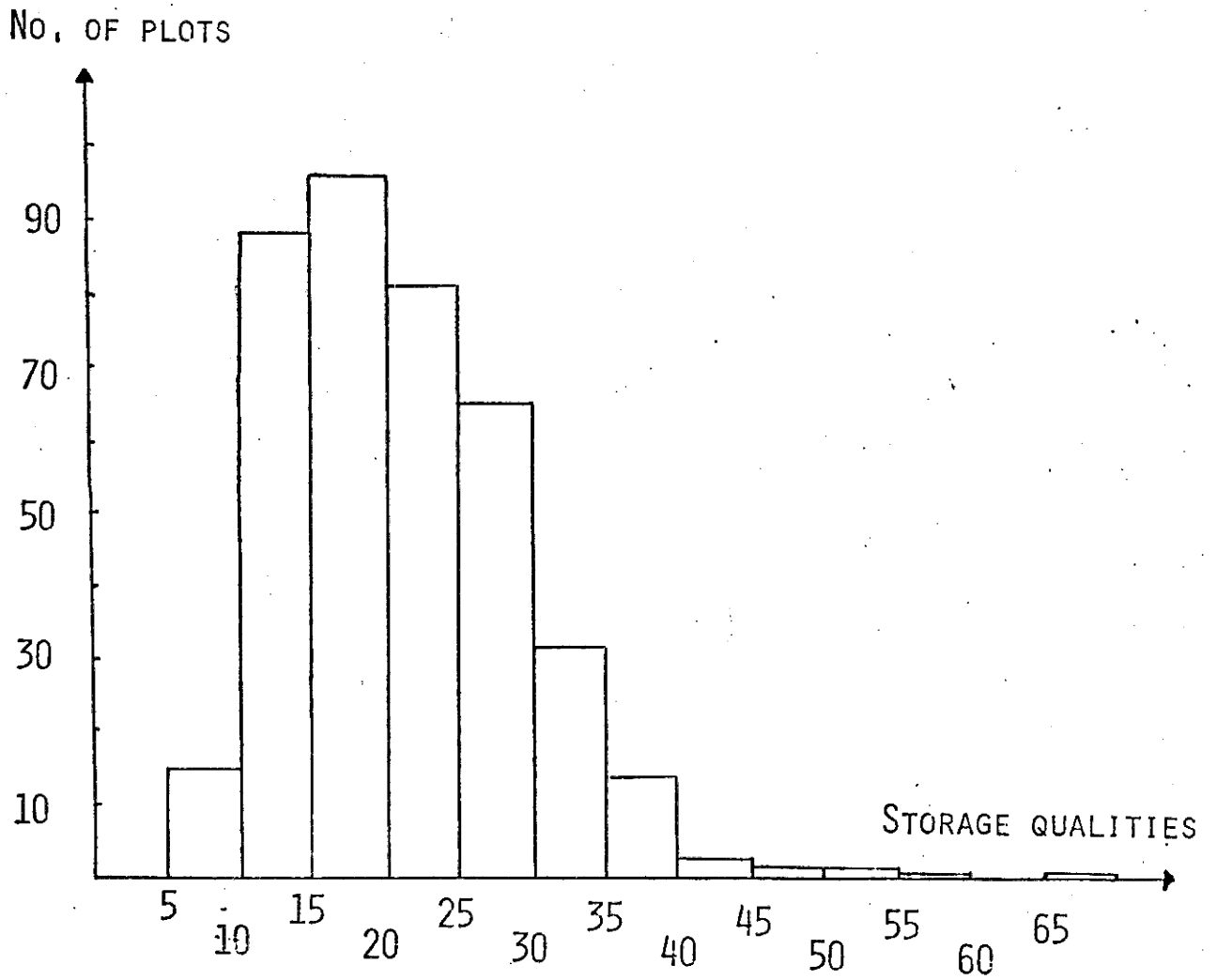
FIG. 2 . DISTRIBUTION OF STORAGE QUALITIES
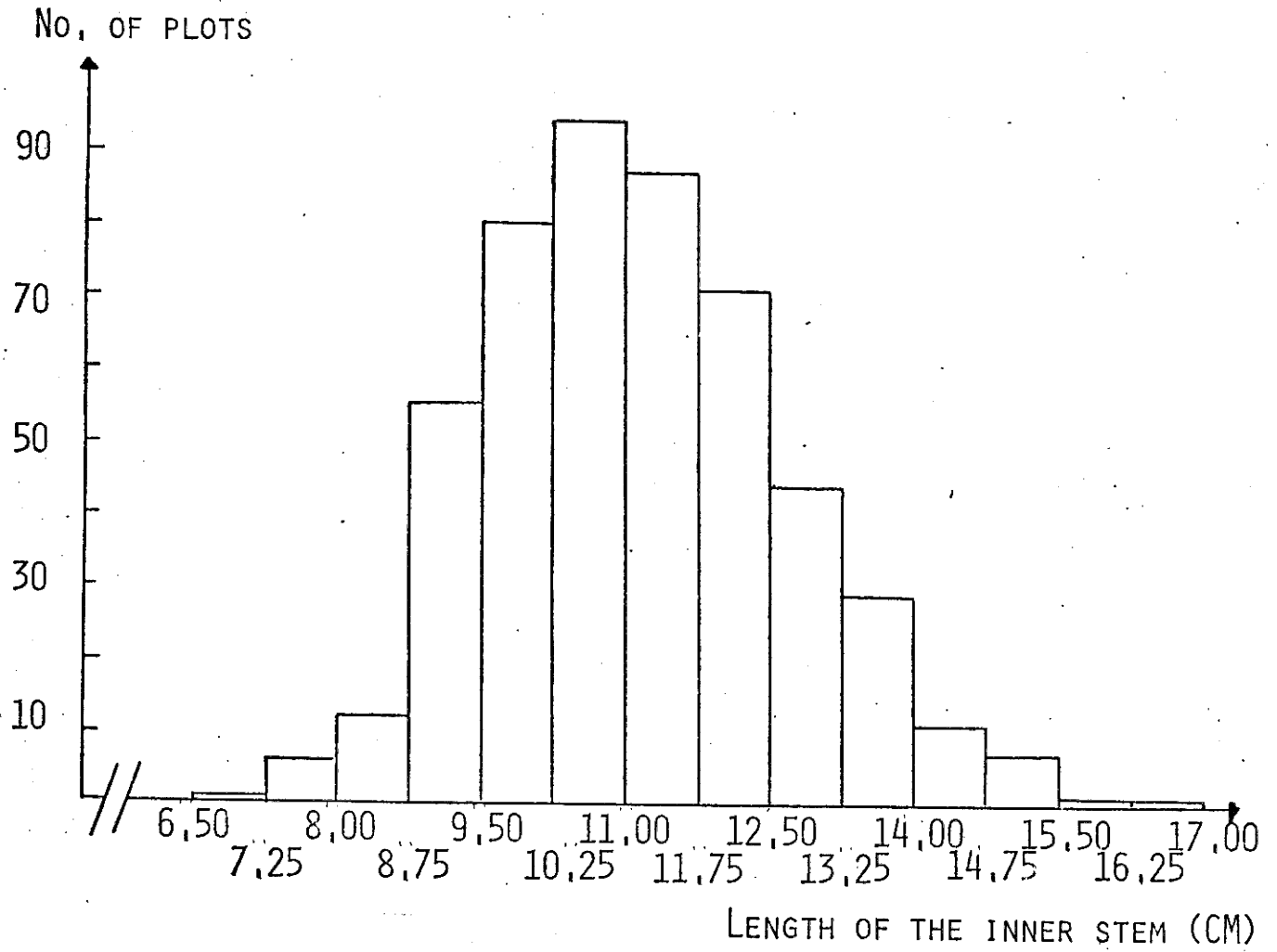
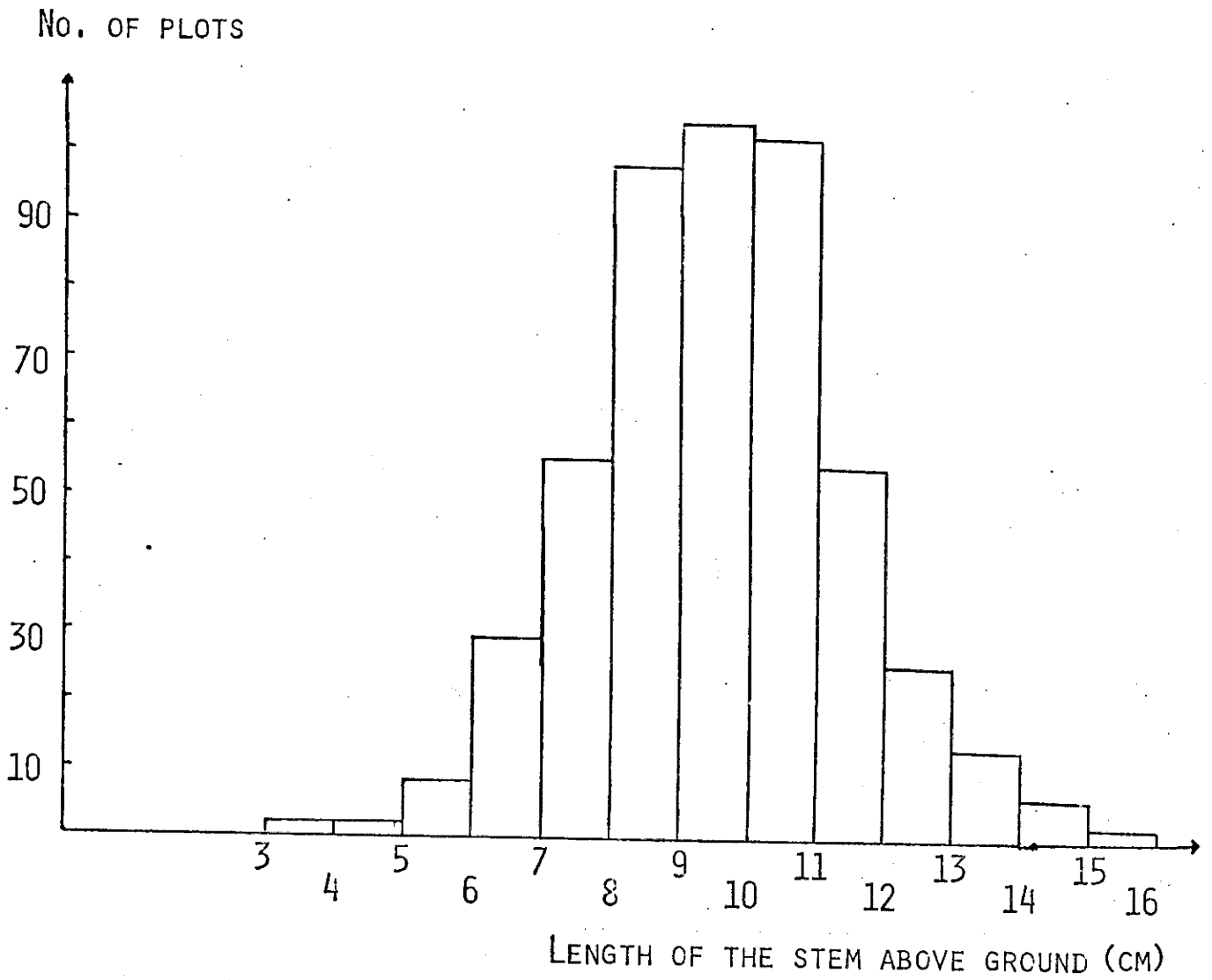FIG. 3 . DISTRIBUTION OF LENGTH OF THE STEM INSIDE THE HEAD

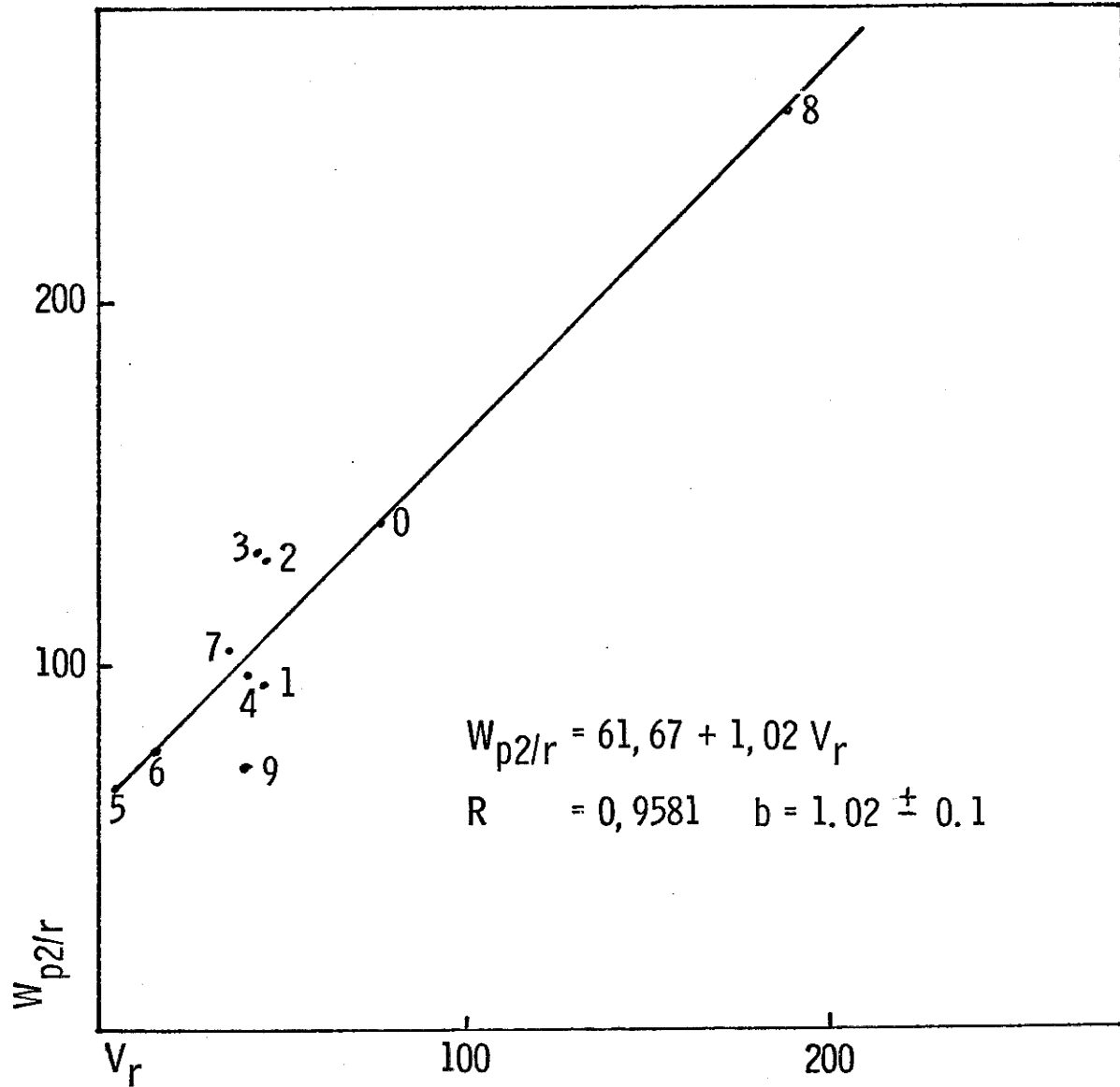FIG. 4 . DISTRIBUTION OF LENGTH OF THE STEM ABOVE GROUND

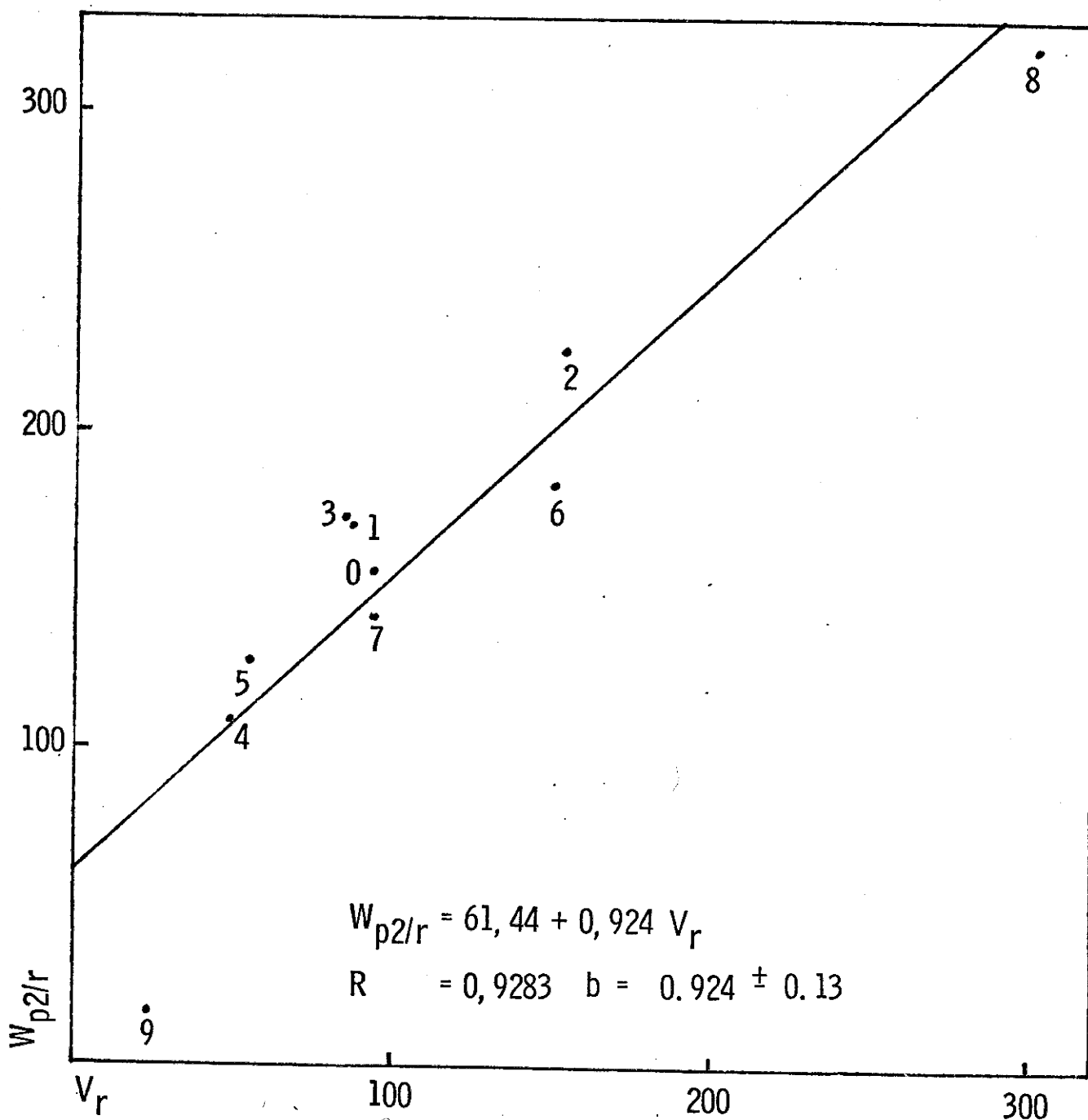Fig. 5. $(W_{p2/r}/V_r)$ – graph for storage quality

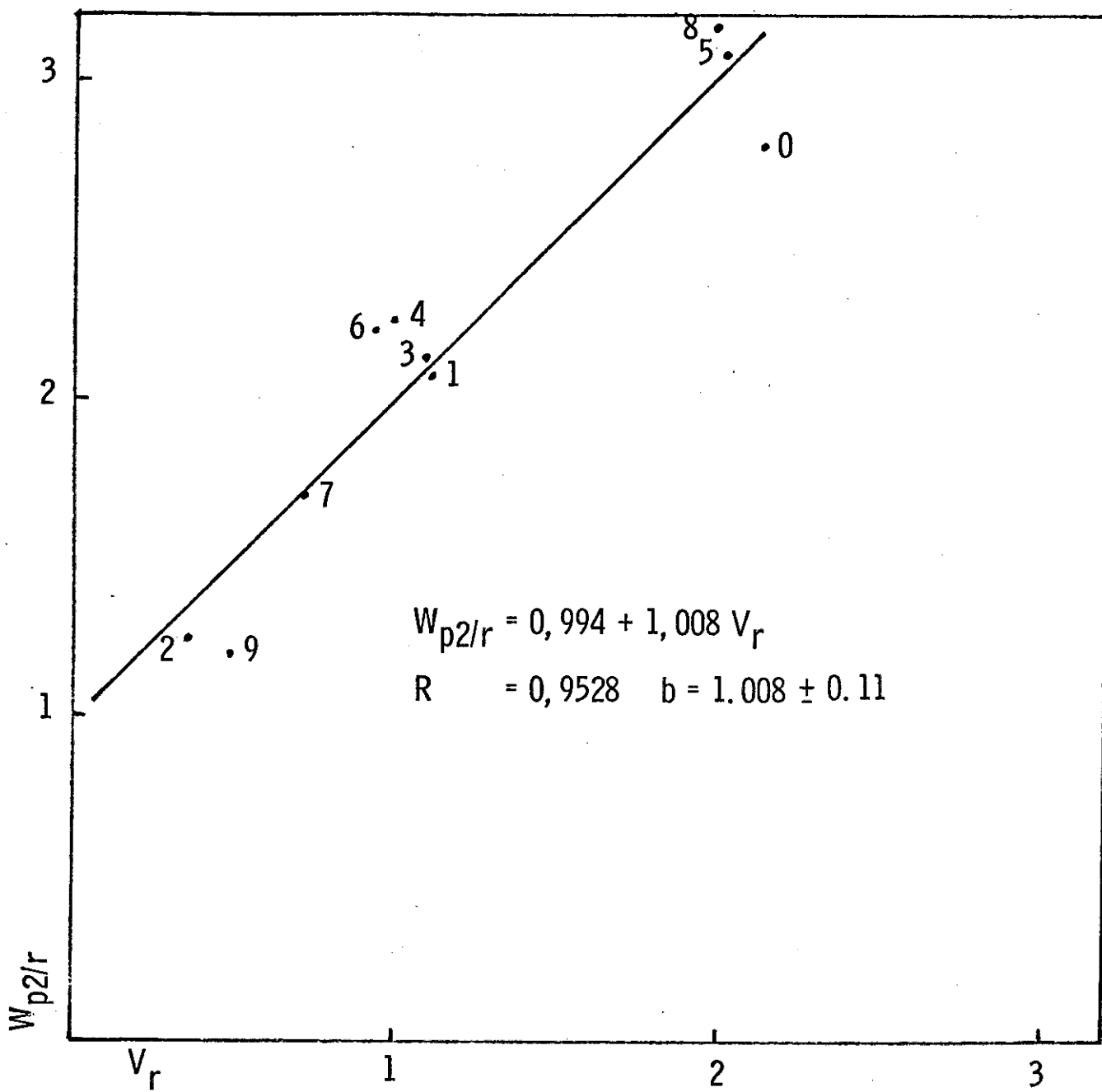Fig. 6. $(W_{p2/r}/V_r)$ - graph for length of the inner stem

The figure contains:

$$W_{p2/r} = 61,44 + 0,924\ V_r$$

$$R = 0,9283 \quad b = 0.924 \pm 0.13$$

The plotted points and fit line, with the annotations:

$$W_{p2/r} = 0,994 + 1,008\ V_r$$

$$R = 0,9528 \qquad b = 1.008 \pm 0.11$$

Fig. 7. $(W_{p2/r}/V_r)$ - graph for length of the outer stem

Table 2 . Variances of arrays (V_r), covariances between parents and arrays $(W_{pl/r})$ and covariances between the diagonal and arrays $(W_{r_2/r})$ in a heterozygous diallel cross.

Genotype Fenotype Frequency	V_r	$W_{pl/r}$	$W_{p2/r}$
AA d u^2	$\frac{1}{2}uv(d-h)^2$	$uv(d^2-2udh$ $+(1-2v)h^2)$	$uv(d^2-\frac{1}{2}(1+2u)dh$ $+\frac{1}{2}(1-2v)h^2)$
AA h 2uv	$\frac{1}{2}uvd^2$	$uv(d^2+(v-u)$ $dh)$	$uv(d^2+\frac{1}{2}(v-u)dh)$
aa -d v^2	$\frac{1}{2}uv(d+h)^2$	$uv(d^2+2vdh$ $+(1-2u)h^2)$	$uv(d^2+\frac{1}{2}(1+2v)dh$ $+\frac{1}{2}(1-2u)h^2)$

$$^b W_{pl/r}/W_{p2/r} = \frac{W_{pl/r_{AA}}}{W_{p2/r_{AA}}} = \frac{W_{pl/r_{Aa}}}{W_{p2/r_{Aa}}} = \frac{W_{pl/r_{aa}}}{W_{p2/r_{aa}}} = \frac{d+h(1-2u)}{d+\frac{1}{2}h(1-2u)}$$
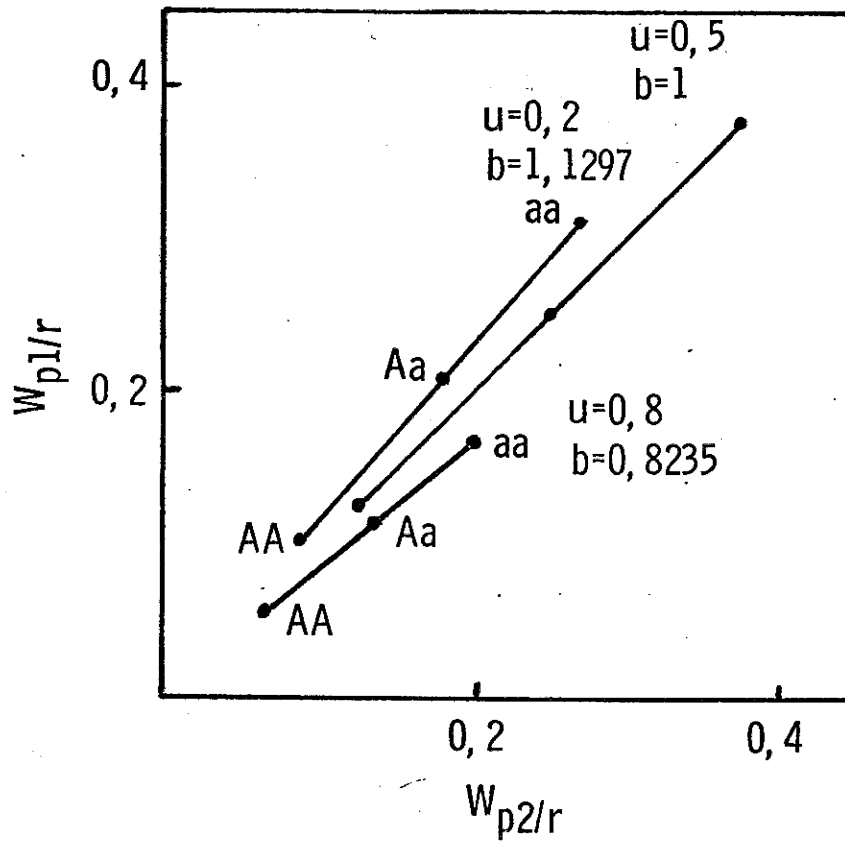
Fig. 8. The relation between $W_{p1/r}$ and $W_{p2/r}$ in a one-gene heterozygous diploid diallel cross. $h = \frac{1}{2}d.$ $u = 0.2, 0.5$ and $0.8.$
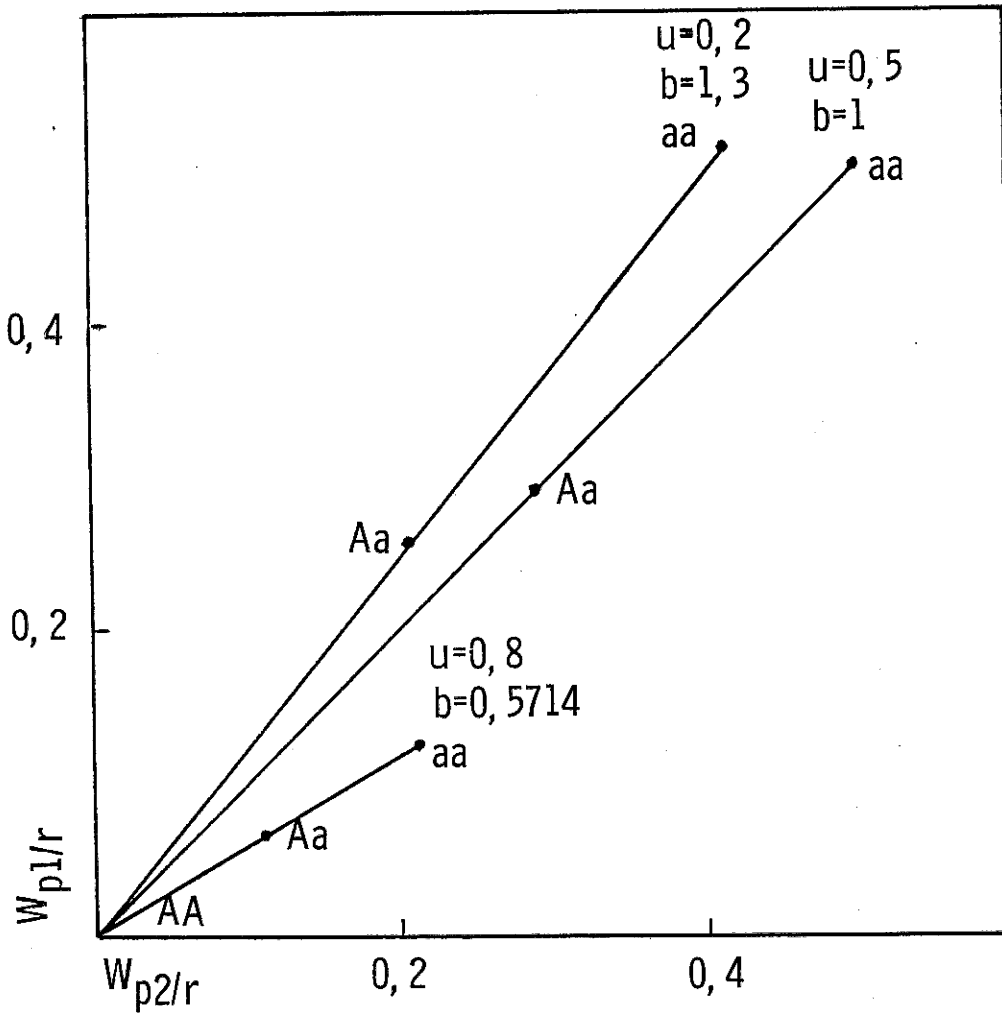
Fig. 9. The relation between $W_{p1/r}$ and $W_{p2/r}$ in a one-gene heterozygous diploid diallel cross.
h = d. u = 0.2, 0.5 and 0.8.

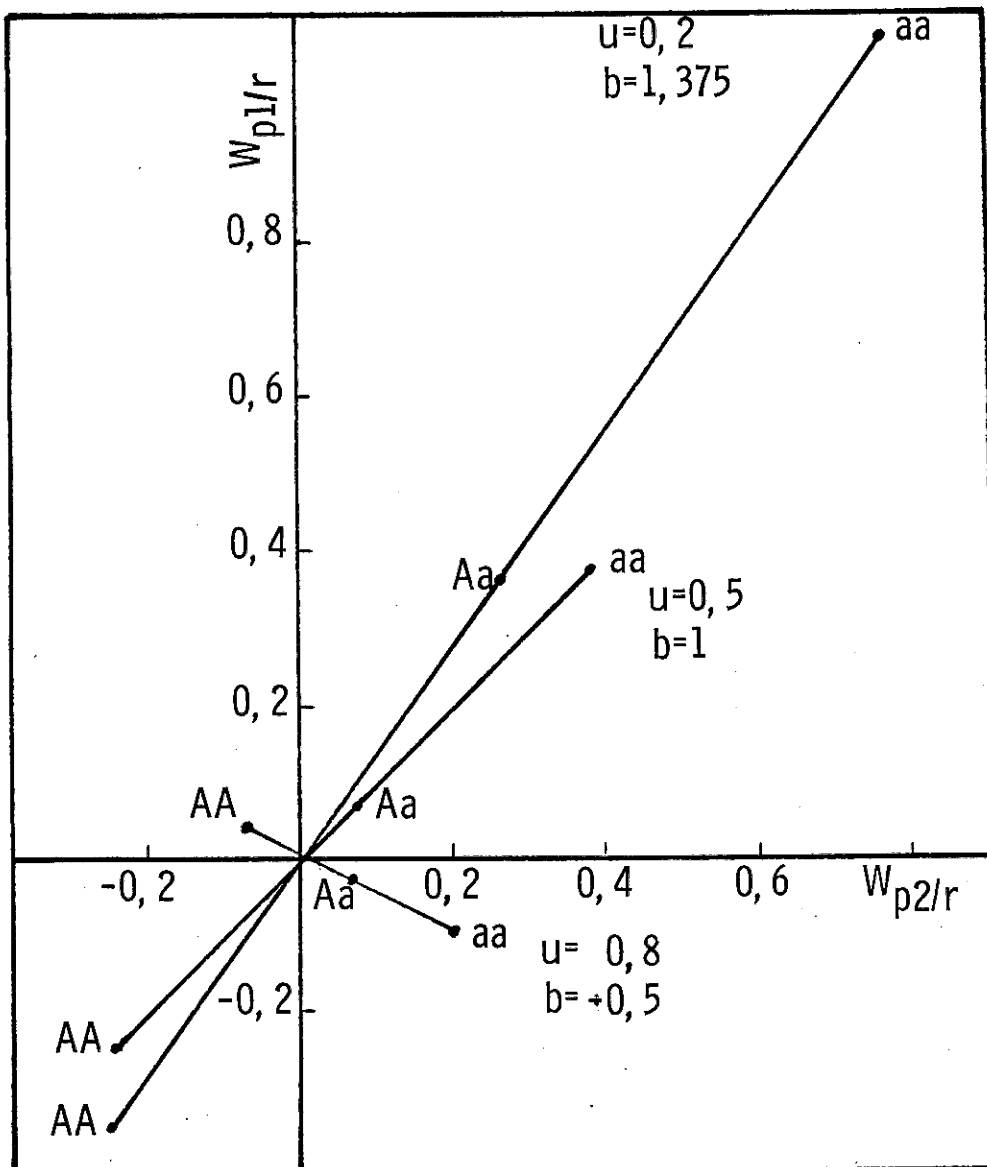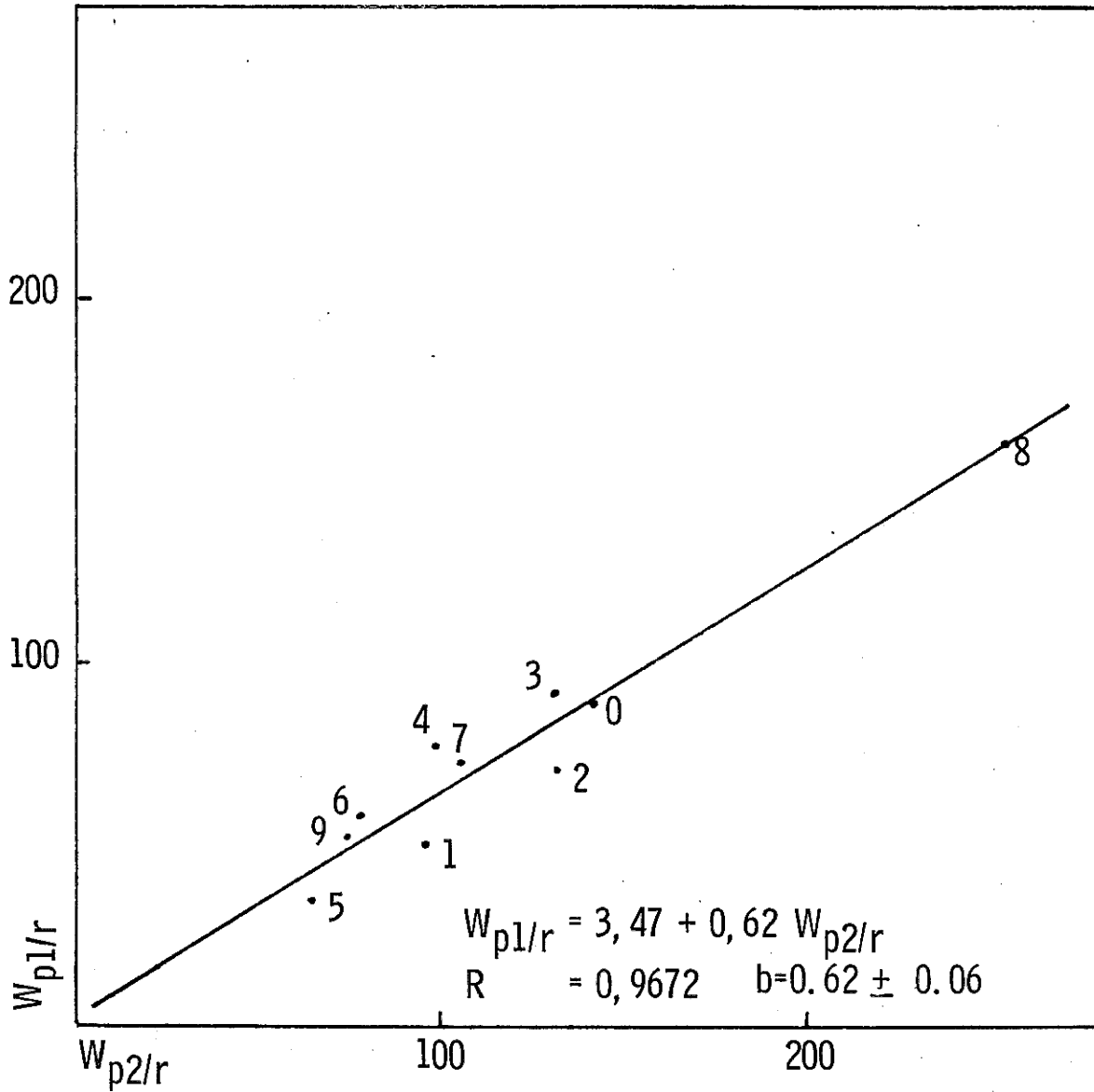Fig. 10. The relation between $W_{p1/r}$ and $W_{p2/r}$ in a one-gene heterozygous diploid diallel cross.
h = 2d.   u = 0.2, 0.5 and 0.8.
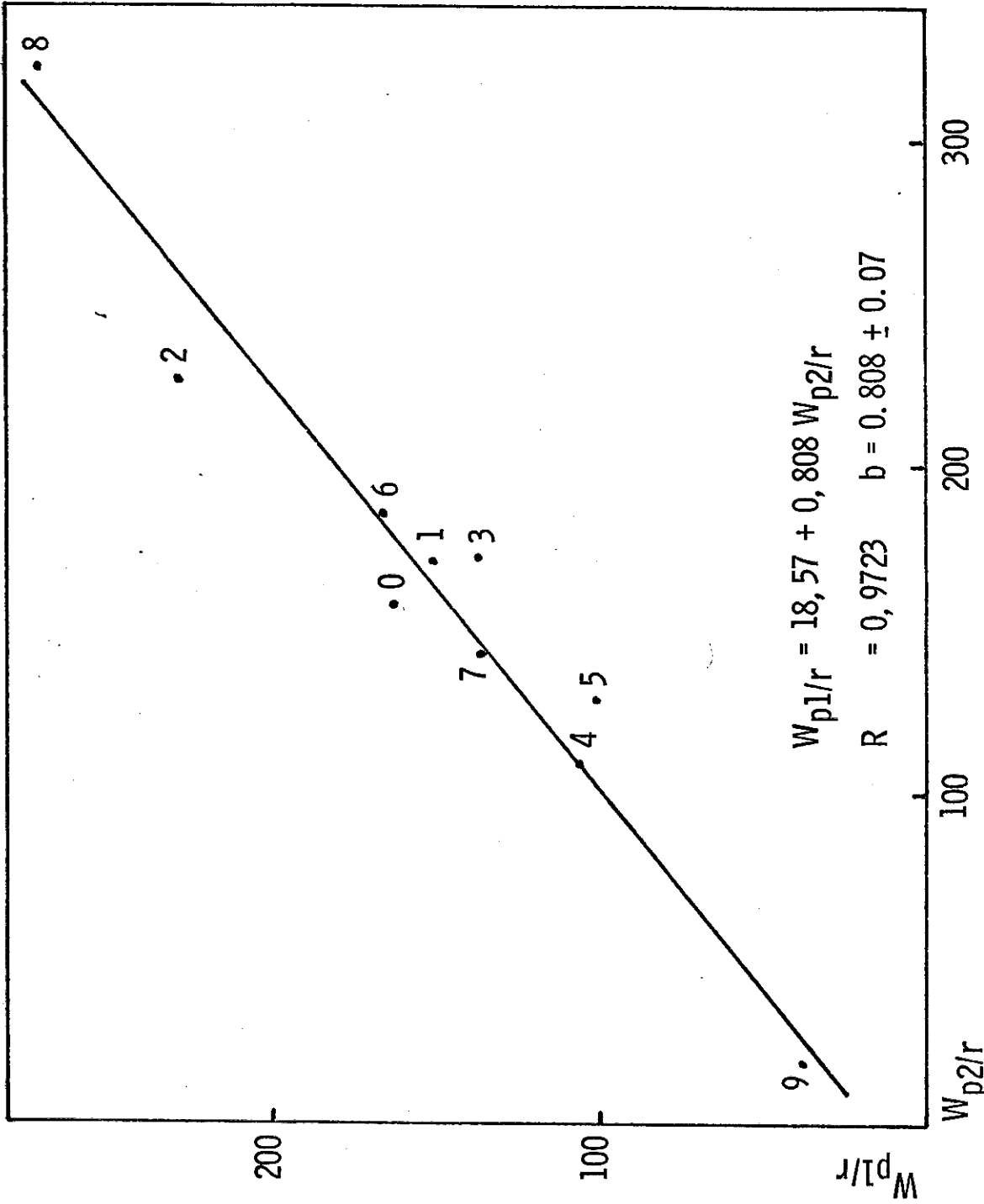
Fig. 11. $(W_{p1/r}/W_{p2/r})$ - graph for storage quality

Fig. 12. $(W_{p1/r}/W_{p2/r})$ - graph for length of the inner stem

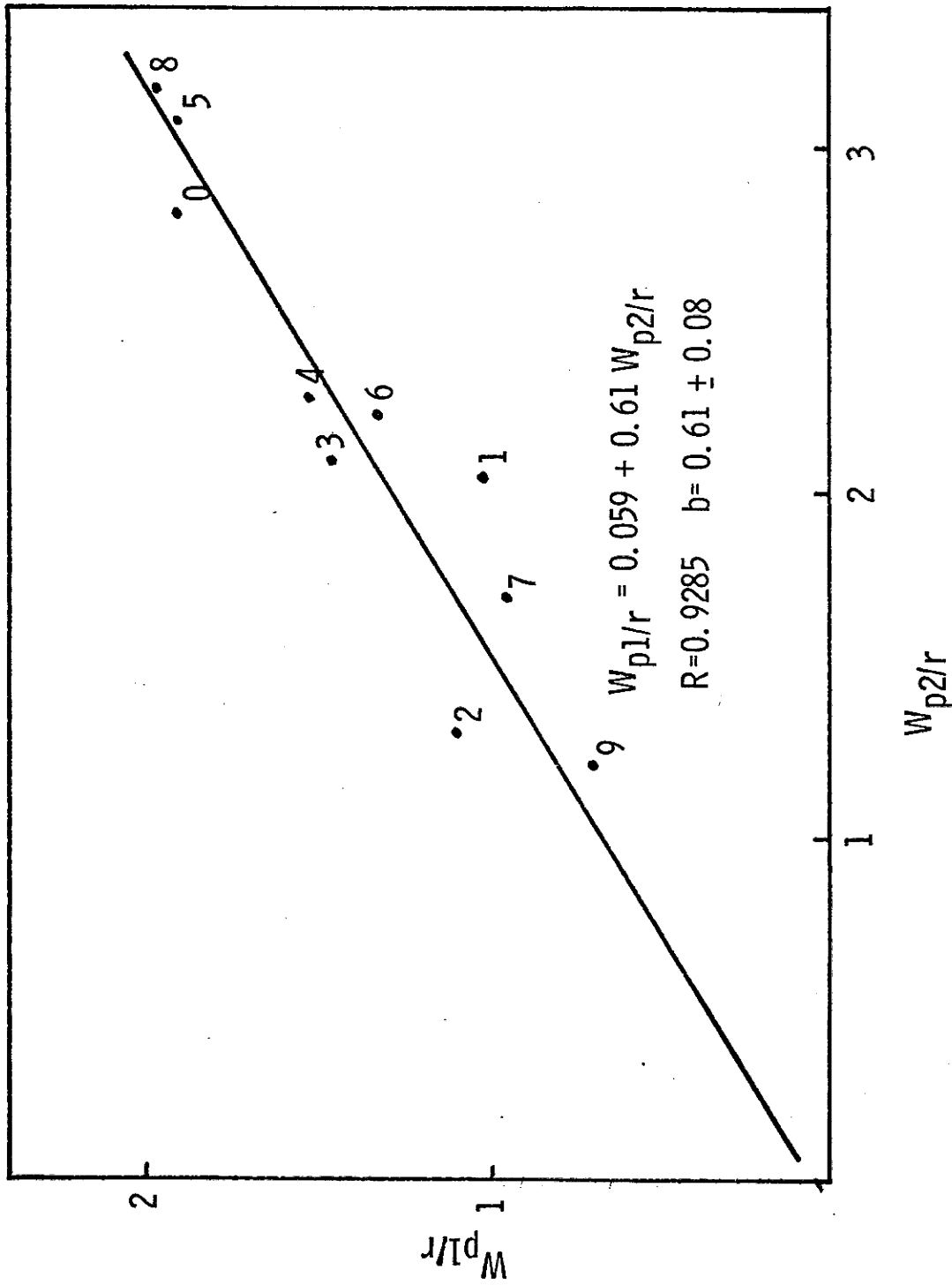$W_{p1/r} = 18,57 + 0,808 \ W_{p2/r}$

$R = 0,9723 \quad b = 0.808 \pm 0.07$

Fig. 13. $(W_{p1}/r / W_{p2}/r)$ - graph for length of the outer stem

$$W_{p1}/r = 0.059 + 0.61 \, W_{p2}/r$$

$$R = 0.9285 \quad b = 0.61 \pm 0.08$$

Table 3. Estimation of genetic and environmental components

Statistic	Description	Genetic composition	Storage qualities	Inner stem	Outer stem
V_{pl}	Variance of parents	$1/2D_R + 1/4H_R + E$	168.15	357.90	2.872
$\bar{V}_r$	Mean variance of arrays	$1/8D_R + 1/16H_R + E$	72.15	124.90	1.398
$V_{\bar{r}}$	Variance of array means	$1/8D_R \quad + 1/10E$	41.95	78.10	1.437
$V_{\bar{o}}$	Variance of offspring families around the total mean	$1/4D_R + 1/8H_R + E$	103.80	184.70	2.577
$\bar{W}_{pl/r}$	Mean covariance of arrays with p_1	$1/4D_R$	75.50	150.20	1.391
$W_{pl/\bar{o}}$	Covariance between p_1 means and the means of their offspring families	$1/4D_R$	72.80	135.40	1.390
E (Estimated from analysis of variance)			18.44	15.21	0.22

Table 4. The heritability in broad sense ($h^2_{b.s.}$) and narrow sense ($h^2_{n.s.}$) and D_R and H_R, estimated from the genetical and environmental components.

Statistic	Storage qualities	Inner stem	Outer stem
D_R	308.7	591.9	8.44
H_R	103.8	310.8	1.32
$h^2_{b.s.}$	0.91	0.96	0.95
$h^2_{n.s.}$	0.77	0.76	0.88

$D_R = (4uv(d + d(v-u))^2)$

$H_R = (16u^2v^2h^2)$