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Breeding Progress and Performance of Wheat Cultivars in Different Environments in Israel from 1970 to 2002

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Abstract: The behaviour of wheat cultivars in environments with different yield level and the progress of wheat breeding in Israel were investigated by a statistical exploration of 353 Regional Wheat Trials, performed from 1970 to 2002. In the trials 125 experimental and commercial cultivars of *Triticum aestivum*, 11 of *T. durum* and one *Triticale* line (summarised as cultivars) were tested. The yield levels of trials ranged from 0.5 to 8.8 t/ha. The assumption of additive cultivar effects did not fit to trials differing much in yield since genetic variance within trials was closely related to the yield level of trials. The cultivars differed in grain yield by multiplicative factors that were well reproducible and highly correlated across environments. The best differentiation of cultivars, expressed as the ratio of genetic to residual variance, was found in high yielding environments. Specific adaptations of cultivars to the environmental yield level were absent or negligible and the ranking of the tested cultivars was very similar across environments. Residual variance was very low after standardisation to equal genetic variance. Statistical cultivar × environment interactions might be largely artefacts of additive yield models, applied to non-standardised data. Significant differences between cultivars were observed in relative yield, stability of relative yield, earliness, height, kernel size and hectoliter weight. Cultivar yield was significantly associated with lodging resistance, short straw and low protein content, while the association with other traits was low or non-significant. Breeding resulted in an increase of the average relative yield of cultivars in regional trials by more than 30%. The top recent bread wheat cultivar Galil is yielding approximately twice more than cv. Florence Aurore, the leading cultivar till the seventies. Breeding progress for yield was fast in the seventies, but only moderate in the last 10 years, with cv. Galil as the top yielder since 1996. Further breeding progress might be harder to achieve than in the past.

Keywords: Israel; wheat; cultivars; breeding; yield stability; adaptation; variance components

In Israel, like in European countries, regional variety trials are officially performed every year in the main wheat growing regions. Advanced experimental lines are compared in the trials for several years in a number of agronomic traits with standard commercial cultivars. Outstanding experimental lines can then be released into commercial cultivation. Data from 353 regional trials, collected since 1970, are now maintained by the second author in a database. The data from individual trials comprise information on the performance of the tested cultivars in several agronomic traits and from many trials also on rainfall, fertilisation, crop rotation and several diseases. Much information is missing in the database and the data are highly non-orthogonal since every year new cultivars enter the trials and poorly performing entries are excluded. Even so, the exploration of the database with proper methods can provide information on breeding progress, cultivar adaptation, trait correlations, effects of environmental factors and economically relevant suggestions for more efficient cultivar testing. In this paper we analyse the behaviour of cultivars at different yield levels and the progress in grain yield achieved by wheat breeding in Israel.

MATERIAL AND METHODS

The environment. Israel's environment is very diversified. Mean annual precipitation during

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the rainy season of November–April diminishes from 900 mm in the very North to almost nil at about 500 km to the South. Yearly fluctuations are considerable, with frequent drought years. About three quarters of the wheat acreage are in the 500–250 mm precipitation zone. Soils in the wheat areas are also very differentiated. We described the environment and the wheat growing regions in detail in a separate paper (ATSMON & SCHWARZBACH 2004). Wheat is sown at the onset of the rainy season, i.e. usually in November, and harvested from late April to June. In this paper "years" indicate always the harvest year.

The trials. On average 12 regional trials were performed each year in different wheat growing regions, with a variable number of experimental breeding lines and commercial cultivars. The trials of the same year were orthogonal for most entries. Since commercial cultivars and experimental lines were statistically treated equally, the term "cultivars" is used for both. Poorly performing cultivars were mostly excluded after one year. Promising cultivars were usually tested for 2–3 years. Commercial cultivars remained in the trials longer, in one case even 22 years. The trials consisted of randomised blocks with 4 replications till 1972 and with 6 replications since 1973. Up to 1984 the plots were sown with farm drills and harvested with farm combine harvesters. The sown plot size was about 100 m^2 and only a part was harvested, usually 55–70 m^2. Since 1985 plot drills and plot harvesters were used in most trials. From 1970 to 2002 a total of 125 cultivars of *T. aestivum,* 11 of *T. durum* and one *Triticale* line were sown. The summary details of the trials are given in Table 1.

Table 1. Main trial parameters

		Range	Average
Trials per year		7–15	12
Cultivars per trial		9–23	14
Net plot size (m^2)	1970–1984	55–95	65
	1985–2002	17–22	20
Years of testing		1–22	3.6
Trial yield (t/ha)		0.5–8.8	4.6
Yearly rainfall (mm)		154–1180	440
Emergence date		15.11.–12.1.	3.12.

The crops preceding the trials in the rotation were very different. The most frequent were: "hay" (17%, crop not clearly specified), cotton (14%), leguminous crops (12%), wheat (10%), fallow (9%), cucurbitaceous crops (8%) and maize (6%).

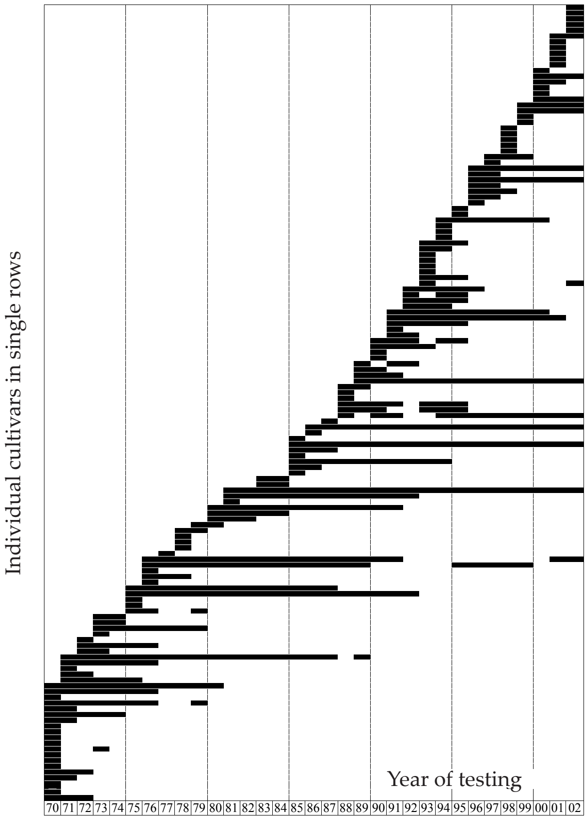

Figure 1. Testing years of cultivars in regional wheat trials (each black box represents about 12 trials in the given year)

Structure of data. As every year a part of the tested set of cultivars changed, the data were highly non-orthogonal. There was no cultivar common to all trials or all years. An impression of the non-orthogonality and structure of cultivar testing is given in Figure 1.

Statistical procedures. Since the individual plot yields were not available for most trials, cultivar means from individual trials were used as primary data. Trial sites changed during the years and the yearly environmental conditions at a site also differed. Therefore, trials were handled as unique environments regardless of years if effects of cultivars or yield levels were investigated. Because of the wide range of trial yield levels of about 1:20, the variances of the investigated factors were highly non-homogeneous. Since the data were non-orthogonal, the Least Squares technique (LS) was used to estimate the main effects, as suggested by FINNEY (1980) and by KEMPTON and FOX (1997) for unbalanced experiments. The LS technique, based on a two-way classification, consisted in forming an equation for each analysed value according to the general linear model in which a value is defined as the sum of general mean, row (cultivar), column (trial) and residual effects. The system of equations is then solved using suitable software. The cultivar means or other effects, calculated by this technique, are referred to as "LS-adjusted". For the calculations we used the FTAB spreadsheet program, written by the first author and able to solve fast very large non-orthogonal data sets, using an iterative algorithm. Where the linear model was inappropriate, the data were standardised first. Variance of cultivars and other effects was estimated by subtraction of the error variance of the respective LS-adjusted means, properly weighted, from the variance of LS-adjusted cultivar or environment means, respectively, using the same software. To obtain variance estimates for years and for trials within years, the trials were grouped by years. Within each year LS-adjusted cultivar means and trial variance were independently estimated. The pooled trial variance within years was used as the estimate of trial variance. From the LS-adjusted cultivar means for each year the variance of year effects was estimated.

RESULTS AND DISCUSSION

Exploration of the database. The first step was a test for sufficient genetic variance since no further analysis would make sense without it. The trials were randomly separated in two groups. Within each LS-adjusted cultivar means were independently estimated. Since in both groups the same cultivars were tested independently, the ranking of cultivars should be similar in the case of reproducible genetic variation. A significant correlation between the LS-adjusted cultivar means of both groups should then be expected. The obtained correlation is demonstrated in Figure 2.

The highly significant correlation shows that the ranking of cultivar means is reproducible even though the data in both trial groups are highly non-orthogonal. The calculated covariance of 0.33 can be used as a crude estimate of genetic variance, since it contains only the variance that is common to both variables, i.e. just genetic variance[1]. More interesting for agriculture is its square root, the genetic standard deviation, which is 0.57 t/ha.

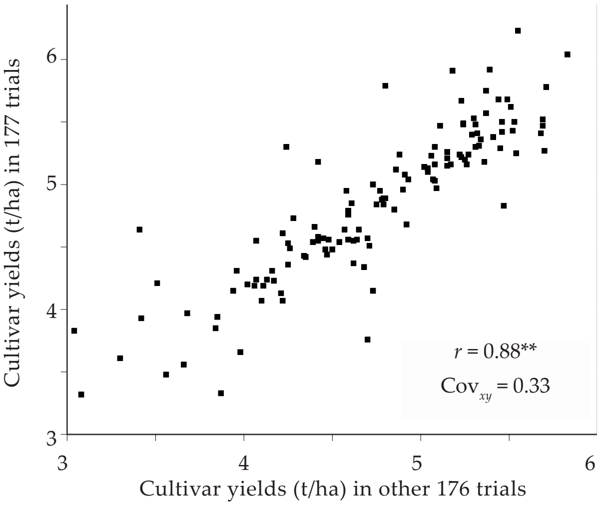

Figure 2. Correlation between LS-adjusted cultivar yields in two random trial groups

To obtain preliminary crude estimates of genetic and environmental effects, variance components from all available data of the 353 trials were estimated from non-standardised data as described earlier. The estimates are summarised in Table 2.

Although these estimates are crude, ignoring the range of yield levels from 0.5 to 8.8 t/ha and different trial quality, they show that the trial environments have a several times larger effect upon yield than cultivars and residual effects. The variance

Table 2. Preliminary estimates of variance components for grain yield (t/ha)

Source of variation	Variance	
Total	3.43	
Environments	2.87	
trial sites		2.39
years		0.50
Cultivars	0.25	
Residual	0.25	
Sum of components	3.37	

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[1] If x_i = yield of cultivar i in trial group 1, y_i = yield of the same cultivar in trial group 2 and g_i = effect of cultivar i, then in the linear model $x_i = \mu + g_i + e_1$ and $y_i = \mu + g_i + e_2$. From this it follows by simple algebra that covariance xy expresses the genetic variance σ^2_g in this special case

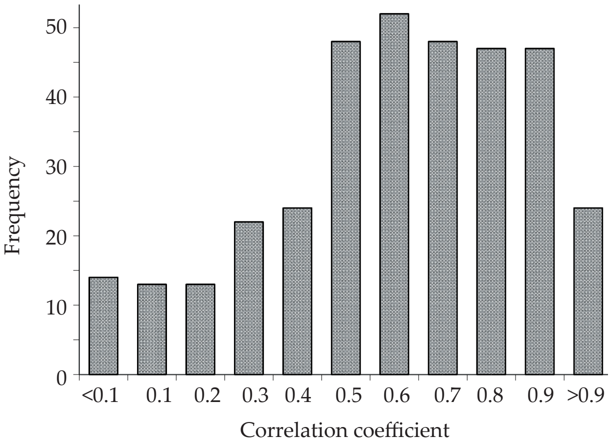


Figure 3. Distribution of correlation coefficients calculated between cultivar yields in trials and LS-adjusted general cultivar yields

estimate for cultivars is similar to the independent estimate of covariance in Figure 2, indicating the robustness of the method.

The estimates can be distorted by data from "bad" trials. We therefore tried to find and exclude trials with low reproducibility from the analysis. As a measure we used correlation coefficients between the LS-adjusted cultivar means, obtained from all trials, and the cultivar means in the individual trials. The distribution of the 353 correlation coefficients is represented in Figure 3.

The distribution shows that cultivar means in most individual trials are closely related to the general LS adjusted cultivar means. This indicates a fair reproducibility in most of the trials. Only a small number of trials had correlations lower than 0.1. These are specified here as "bad", as opposed to "good". In most of the "bad" trials the genetic variance was much lower than the residual. The correlations between individual "bad" trials were rather erratic, on average $r = 0.09$. The variance components in this group are compared in Table 3 with the group of "good" trials and with estimates for all the 353 trials.

The comparison shows an approximately four times lower genetic variance than in the "good" group. Supposing that the "bad" trials contribute more noise than useful information, and having a sufficiently large number of "good" trials, we excluded "bad" trials from further analysis. This increased the relation of genetic to residual variance by about 20%. On similar grounds Fox and Rossielle (1982) also suggested to exclude "bad" trials from analysed trial series. Because of the wide range of yield levels we first tried to analyse the effect of yield level on the differentiation of cultivars. Since data from individual trials have a large error, we separated the trials by yield level into 8 groups, the first seven with 41 trials, the last with 42 trials. Cultivars present in just one trial in a group were regarded as not present in

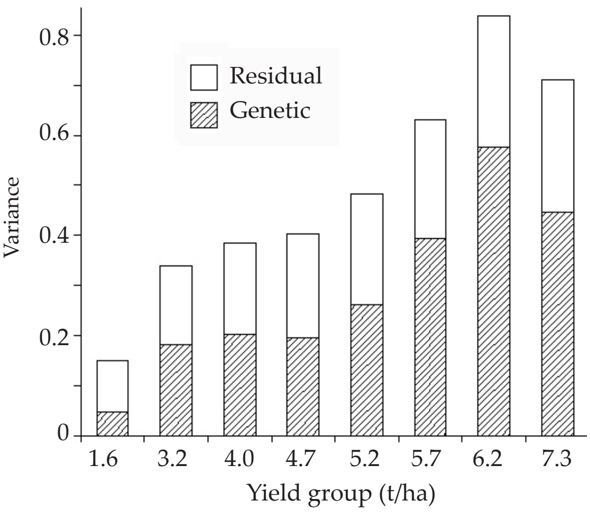


Figure 4. Genetic and residual variance estimates in trial groups with different yield levels

Table 3. Variance estimates for yield (t/ha) in groups of "good" and "bad" trials expressed relatively to the total variance

Variance	All trials	„Good“ trials	„Bad“ trials
Total	100.0	100.0	100.0
Environments	83.9	80.9	83.0
Cultivars (genetic)	7.2	**9.2**	2.4
Residual	7.3	7.5	7.7
No. of trials	353	329	24
Mean correlation to general cultivar means	0.55**	0.60**	–0.01$^{n.s.}$

Table 4. Correlations of cultivar means between trials groups differing in yield

Trial group	Mean yield (t/ha)	Mean yield (t/ha) of trial group							
		1.7	3.2	4.2	4.8	5.3	5.6	6.0	7.0
1	1.7	–	0.83[2]	0.80	0.78	0.81	0.84	0.81	0.74
2	3.2	54[1]	–	0.79	0.90	0.92	0.87	0.84	0.78
3	4.2	53	55	–	0.79	0.83	0.75	0.72	0.78
4	4.8	58	60	53	–	0.91	0.92	0.90	0.80
5	5.3	51	56	55	55	–	0.86	0.91	0.87
6	5.6	55	58	60	56	55	–	0.91	0.83
7	6.0	48	58	52	53	53	60	–	0.92
8	7.0	49	49	48	54	50	61	61	–

[1] number of available cultivars from which the correlation was calculated

[2] all correlations are highly significant at $P < 0.01$ and do not differ significantly

the group, to reduce the noise. Of the 137 cultivars 12 were present in less than four of the 329 trials and were excluded from evaluation. Within each group we calculated LS-adjusted cultivar means and estimated the variance components.

Figure 4 shows a close and highly significant association between yield level and genetic variation within trials. This means the higher the trial yield level, the more the cultivar yields diverge. Another basic finding is that the best differentiation of cultivars, i.e. the relation of genetic to residual variance, is found in the three highest yielding groups. To see if the genetic information within the groups is of similar nature, we calculated simple correlation coefficients between the LS-adjusted cultivar means of all eight trial groups (Table 4). The figures left of the diagonal indicate the number of available pairs of data.

The high correlations, even between the two most extreme trial groups, show that the genetic information is very similar at all yield levels and is expressed mainly in cultivar ranking. This supports the idea that selection for yield in low yielding environments is less effective than in high yielding environments. The practical conclusion is that cultivar testing for yield is most efficient and reliable in higher yielding environments. This, of course, does not imply that high yielding environments are the best also for the selection of other agronomic traits.

Since the spread of cultivar yields (in terms of genetic variance) is associated with the yield level of the environment, standardisation is needed to fully exploit the information from all groups. We tried three methods of standardisation:

1. To equal mean group yield, i.e. to divide the LS-adjusted cultivar means within each group by their group mean and multiply by general mean.

2. To genetic variance of general LS-adjusted cultivar means. Since the groups were non-orthogonal, the genetic variance within groups depends on the cultivars present in them. Therefore the group data were standardised to the variances of the general LS-adjusted cultivar means of the actually present cultivars, i.e. by dividing the LS-adjusted cultivar means within the group by their standard deviation and multiplication by the standard deviation of their general LS-adjusted cultivar means.

3. To equal variance of LS-adjusted cultivar means in the orthogonal kernel, i.e. dividing within each group the LS-adjusted cultivar means by the standard deviation of the orthogonal kernel of the given group and multiplication by the standard deviation of the general LS-adjusted means of cultivars in the orthogonal kernel.

After each procedure we calculated variance components from the modified groups × cultivar matrix. Table 5 summarises the relation of estimated genetic to residual variance, obtained by the different methods. Since the data were non-orthogonal, the relation was estimated also for the 36 cultivars common to all 8 groups (the "orthogonal kernel").

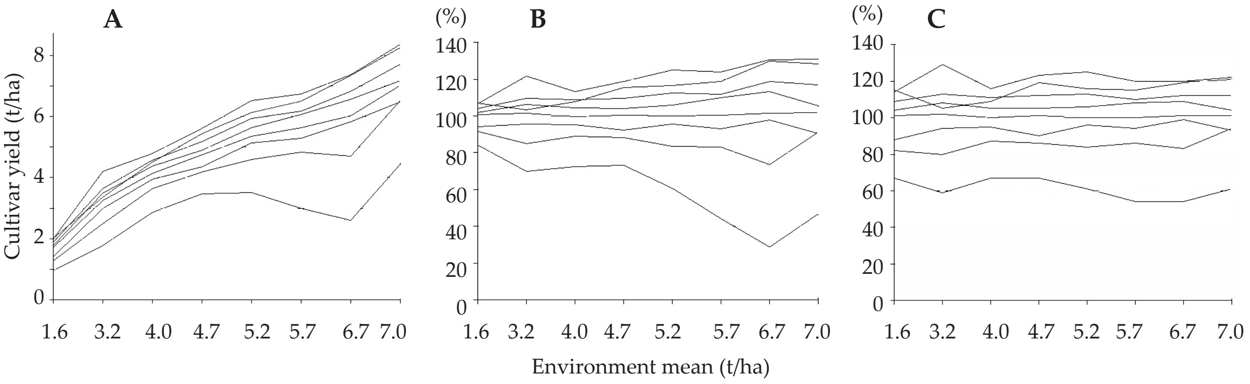
Standardisation of non-grouped primary data had only moderate effects. Standardisation, i.e. multiplication of primary data by particular fac-

Table 5. Effect of grouping trials by yield and standardisation on the relation of genetic to residual variance[1]

Trial grouping	Method of standardisation	V_g/V_r	
		125 cultivars	36 cultivars
No grouping	none	1.1	1.1
	to variance expected from the respective general means	1.2	1.2
8 groups	none	2.0	3.8
	to equal trial group yield	4.0	5.9
	to variance expected from the respective general means	4.7	7.1
	to equal cultivar variance in the orthogonal kernel	4.7	7.7

[1] variance of grain yield (t/ha)

tors, also multiplies the data error. High errors of primary data can therefore partly upset the effect of standardisation. Since means have smaller errors than the primary data, grouping alone had a larger effect than standardisation without grouping. Standardisation of LS-adjusted cultivar means of groups had a considerably larger effect. Standardisation to the variance expected from the respective general LS-adjusted means was more efficient than to equal group yields. This should be expected since apart from the environment the trial yield also depends on the tested cultivars and non-orthogonality thus introduces an additional error. The best results were obtained by standardisation to equal variance of cultivars in the orthogonal kernel. This appears to be an effect of higher precision of cultivar means in the orthogonal kernel, since in it the LS-adjusted cultivar means were based on average on 11 observations per group, compared with less than two outside it. The very low residual variance after best standardisation shows that the **performance of the tested cultivars at different yield levels can be well described by multiplicative factors that remain much the same at very different yield levels**. There is no need to suppose any real additive effects of cultivars. Estimates of cultivar yield factors are obtained after optimum standardisation by subtraction of the calculated LS-adjusted yield group effects from the standardised data and division by the general mean. Not much space is left for cultivar × yield level interactions after optimum standardisation. Only if additive cultivar effects are assumed, such interactions are necessarily generated as artefacts of the additive model, which in our case are several times larger than with a multiplicative model.



Cultivars in the figure from the top: Galil, Negev, Beth Hashita, Deganith, Shafir, Inbar, Mivhor, Florence Aurore

Figure 5. Effect of standardisation on the differentiation of LS-adjusted cultivar means in yield groups: A – not standardised; B – relative to general mean, group effects subtracted; C – standardised to equal genetic variance of the orthogonal kernel

Table 6. Standardised relative yield of 36 wheat cultivars at different yield levels

Cultivar	First tested	No. trials	Mean yield (t/ha) of trial group								s	Mean
			1.7	3.2	4.0	4.7	5.2	5.7	6.2	7.3		
Galil	1996	64	114	129	116	123	125	120	120	122	4.8	121.2
Goren	1997	30	109	108	138	114	120	113	110	118	9.7	116.3
Negev	1996	64	115	105	109	119	116	115	119	121	5.4	114.9
Bar Nir	1994	66	118	112	102	114	116	115	114	115	4.9	113.2
Yaniv	1991	97	113	108	112	108	106	119	114	113	4.2	111.6
Gedera	1992	115	113	109	114	116	112	109	110	110	2.6	111.6
Beth Hashita	1981	216	109	113	111	112	113	110	112	112	1.4	111.4
652/79/5	1990	49	114	111	110	117	110	108	112	108	3.1	111.0
W.I. 555	1991	51	113	111	113	106	113	113	107	110	2.9	110.8
Dariel	1985	170	113	107	108	110	104	112	109	115	3.5	109.8
Nirith	1989	133	111	110	106	113	109	105	105	104	3.3	107.8
Atir	1986	158	114	111	105	108	107	106	106	105	3.2	107.8
W.I.85	1992	49	107	111	95	112	107	108	109	109	5.3	107.3
H89.891	1991	21	96	108	104	112	107	112	107	108	5.1	106.8
Deganith	1980	122	104	108	105	105	106	108	109	104	2.0	106.2
W.I. 509	1990	40	104	112	109	105	103	105	104	103	3.2	105.5
748/74	1985	32	103	105	108	99	101	103	102	107	3.1	103.4
U.K. 28	1992	31	105	105	107	95	107	100	105	101	4.2	103.1
Hazera 2230	1980	47	94	102	99	106	106	103	107	99	4.5	102.0
Shafir	1976	164	101	102	100	101	100	100	101	101	0.7	100.7
Beth Lehem	1981	121	106	105	102	99	98	99	99	96	3.5	100.4
Barkaee	1975	131	104	99	100	101	100	103	98	100	2.0	100.3
Lachish	1975	181	98	99	103	99	101	98	101	100	1.7	99.8
Bareketh	1985	90	82	95	96	94	98	95	102	99	5.9	94.9
Inbar	1976	178	88	94	95	90	96	94	99	93	3.4	93.5
Cee'on	1970	111	101	92	93	95	91	93	92	91	3.3	93.5
Miriam	1971	175	98	99	90	91	89	93	90	89	4.0	92.6
Lachish 211	1971	57	94	90	94	86	94	93	91	97	3.3	92.1
Yafith	1970	66	98	88	91	93	90	92	85	81	5.2	89.7
B.D. 131	1973	67	90	77	95	79	85	94	94	96	7.5	88.8
W.I. 240	1972	44	95	87	91	80	89	84	85	76	6.1	85.7
Mivhor	1970	84	82	80	87	86	84	86	83	94	4.2	85.0
Pan	1970	54	79	82	84	89	86	82	88	88	3.6	84.5
Hai	1971	49	82	88	75	79	77	78	74	73	4.9	78.3
Gilath 182	1971	22	65	82	69	81	76	79	85	83	7.1	77.4
Florence Aurore	1970	36	67	59	67	67	61	54	54	61	5.5	61.2

Variance estimates: total 178.5, trial groups 0.0, cultivars 157.9, residual 20.5

Approximate least significant differences for cultivar means: 4.5 at $\alpha = 0.05$ and 5.9 at $\alpha = 0.01$

The effect of standardisation is demonstrated graphically on the example of eight cultivars that are all significantly different only after proper standardisation.

It can be seen that non-standardised cultivar means diverge with increasing yield level. This can be easily misinterpreted as different yield stability if regressions of cultivars on the environment mean would be calculated according to Finlay and Wilkinson (1963). Such regressions are largely determined by relative cultivar yields and disappear with proper standardisation, as can be seen in the right diagram in Figure 5. The standardised results can be then evaluated by usual statistical techniques.

The multiplicative factors of cultivar performance appear more familiar to breeders and agronomists if they are multiplied by 100. They appear then as percents of average performance and will be designated as "standardised relative yield" (SRY). The SRY of the 36 cultivars forming the orthogonal kernel, within and across the 8 trial groups, are given in Table 6. Only cultivars present at least twice in each group are included in the table.

The least significant differences in the legend of the table are very approximate since the variances within cultivars are not homogeneous and the figures within groups are based on different numbers of trials. More reliable confidence intervals can be derived for individual cultivars from the standard deviations across groups in column 12.

Yield stability can be judged according to fluctuations of relative yields across environments, as often practised by cereal breeders. It is tempting to use the standard deviation in column 12 of Table 6 as a stability measure. This is however misleading since the figures in the table are based on different numbers of observations and the figures have therefore a different error. This results in a highly significant negative correlation of $r = –0.60$ between the numbers of trials per cultivar (column 3) and the standard deviations across groups (column 12). The standard deviations across groups therefore reflect rather different precision of the cultivar means than stability. The fluctuations therefore consist largely of "noise" and are less suitable to measure yield stability. In contrast, the standard deviation of standardised relative yield is a perfect measure of stability if calculated within trial groups or from non-grouped trials, since it is then independent of the number of observations. We have found significant and reproducible differences between the cultivars in this parameter that we intend to describe in detail in a separate paper.

A different situation is with adaptation of cultivars to high or low yielding environments. A significant trend in relative yield of a cultivar with environmental yield level would indicate adaptation even with inhomogeneous trial groups. The significance of trends can be tested using the correlation between the standardised relative cultivar yields in groups and the mean yields of trial groups. To safely avoid erroneous correlations, the probability level for significance should be chosen below $1/3n$ (n being the number of cultivars). Correlations that are due just to one or two extreme values should also be rejected as artefacts. In Table 6 only two cultivars, Beth Lehem and Atir, meet these criteria and show some adaptation to low yielding environments. No significant adaptation to favourable or unfavourable environments was detected among the remaining cultivars. They might exist, but be of small magnitude and "hidden in the noise".

The absence of adaptations to yield level does not exclude adaptations based for example on resistance to diseases or on response to soil properties. Since the trials were grouped according to yield, such adaptation is levelled out by averaging. If the trials were grouped according to disease pressure or soil factors, existing adaptations would become apparent. Unfortunately not enough of such data were available in the database to justify such grouping.

The performance factors of cultivars, obtained after grouping and optimum standardisation, can be regarded as the best possible estimates of cultivar performance since they have the highest relation of cultivar to residual variance. We used them therefore to describe the progress in cultivar performance due to breeding since 1970. For better practical understanding we multiplied the factors by 100 to convert them to standardised relative cultivar yields. Regional trials usually contain the best cultivars and breeding lines available in the given year. To demonstrate the yearly progress, we replaced the actual mean cultivar yields in each year by the standardised relative cultivar yields and produced a chart (Figure 6) showing the maximum, mean and minimum performance of cultivars, tested in the given year. The progress achieved by breeding is best represented by the upper curve showing the maximum performance. The steps of this curve show the introduction of new cultivars outperforming the previous.

The breeding progress in grain yield is evident. The recent top yielder cv. Galil yields almost twice as much as cv. Florence Aurore, the leading cultivar in the seventies. The average yielding potential of cultivars included in regional trials increased by more than 30% from 1970 to 1997 and remained at this level until now. The breeding progress was fast in the mid-eighties, but slowed down in the

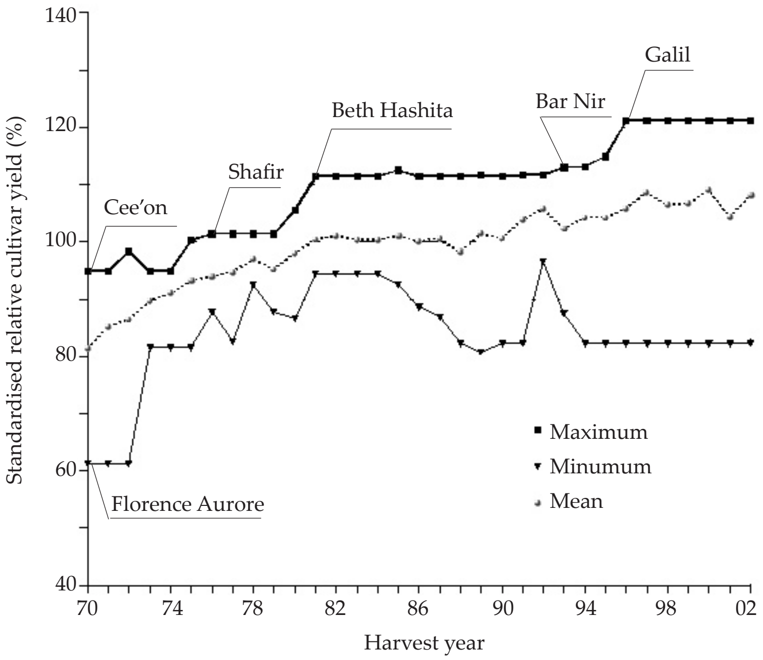


Figure 6. Progress achieved by wheat breeding in Israel from 1970 to 2002 (standardised LS-adjusted cultivar yields in regional trials)

last years. No cultivar in the regional trials has surpassed cv. Galil since 1996.

Data on other agronomic traits were also partly available from regional trials, though not unfortunately from all trials. Also, different traits were often recorded in different trials. In some cases different scales were used for the same trait and the scales had to be unified first. Protein content was usually determined by infrared spectrometry. Lodging was scored in notes from 1 (upright) to 5 (flat). Hectoliter weight was calculated from the weight of 1000 cm^3 seed volume. Shattering was estimated on a 1 to 5 scale from the quantity of kernels on the ground before harvest. The methods of determining some traits changed during the years and were not clearly described. Even so, still enough data could be explored. As with yield, we calculated LS-adjusted cultivar means for each trait from the non-orthogonal data. Trials were not grouped since much less data were available than for grain yield. Due to missing data and non-orthogonality many cultivars were without data for different traits. Therefore the individual correlation coefficients are from a different number of cultivars. In spite of all these limitations, the correlations between the obtained cultivar means for

Table 7. Correlations between wheat traits calculated from LS-adjusted cultivar means

Trait	Shattering	Lodging	TKW	Days to heading	Height	HLW	Protein	Grain yield
Shattering	–	0.26*	n.s.	–0.42**	n.s.	n.s.	n.s.	**–0.23***
Lodging score	72[†)]	–	n.s.	0.22*	0.62**	n.s.	0.23*	**–0.59****
TKW	66	96	–	n.s.	n.s.	n.s.	n.s.	**n.s.**
Days to heading	64	93	98	–	0.38**	–0.21 *	0.44**	**n.s.**
Plant height	71	79	75	72	–	0.22 *	0.27*	**–0.27****
Hectoliter weight	62	88	93	90	68	–	n.s.	**0.29****
Protein content	56	65	65	60	65	55	–	**–0.48****
Grain yield	72	102	103	102	80	93	69	–

*, ** – significant at error probability of $P = 0.05$ and $P = 0.01$, respectively

n.s. – not significant at $P = 0.05$

[†)] figures on the left from the diagonal give the number of cultivars for the respective correlation coefficient the individual traits permitted some insight into the relationship between the traits that might be of use to breeders. The obtained correlation coefficients are summarised in Table 7.

The correlations support the general experience of cereal breeders that high yielding is associated with lodging resistance and low protein content, and to a lesser extent with short straw, high hectolitre weight and resistance to shattering, and that tall cultivars tend to lodging. Earliness was not significantly related to yielding potential, but can be favourable due to its association with short straw and low protein. Although protein content is a desirable trait, it was inversely related to yield. This confirms that simultaneous breeding for yield and protein is difficult in crops that do not fix atmospheric nitrogen.

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Abstrakt

Schwarzbach E., Atsmon S. Y. (2004): **Šlechtitelský pokrok a výkonnost odrůd pšenice v různých prostředích v Izraeli v letech 1970–2002**. Czech J. Genet. Plant Breed., **40**: 1–10.

Pomocí explorativní statistické analýzy výsledků regionálních pokusů s pšenicí v Izraeli v letech 1970 až 2002, zahrnujících 353 odrůdových pokusů se 137 odrůdami, byla odhadována výnosnost, šlechtitelský pokrok ve výnosu, ekologická adaptace a další užitkové vlastnosti odrůd. Protože zkoušený sortiment byl každoročně modifikován, byla data vysoce neortogonální. V důsledku rozmanitosti prostředí kolísala výnosová hladina pokusů od 0,5 t/ha do 8,8 t/ha. Genetická variance byla úměrná výnosové hladině, takže výnos odrůd odpovídal lépe multiplikativnímu než aditivnímu modelu výnosu. Pomocí standardizace výnosového rozpětí na jednotnou genetickou varianci definovaného sortimentu a eliminací aditivních negenetických vlivů metodou nejmenších čtverců bylo možné znázornit relativní výnosnost genotypů oproštěně od vlivů výnosové hladiny. Relativní výnosnost odrůd, a tím i jejich pořadí, se na různých hladinách výnosu v podstatě nelišily. Specifické adaptace na příznivé prostředí nebyly prokázány, pouze u dvou odrůd byla zjištěna adaptace na nevýnosné prostředí. Pokud adaptace existují, mají řádově menší vliv než všeobecná výnosnost odrůd a zanikají ve statistickém šumu. Výnosnost odrůd, zkoušených v jednotlivých letech, byla použita jako míra dosaženého šlechtitelského pokroku. Odrůdy zkoušené v posledních letech jsou v průměru o více než 30 % výnosnější než ty, které byly zkoušené v roce 1970. Nejvýnosnější odrůda Galil nebyla od roku 1996 překonána a dosahuje zhruba dvojnásobného výnosu odrůdy Florence Aurore, která byla nejrozšířenější v roce 1970. Výnosnost odrůd byla silně asociována s odolností k poléhání, s nízkým obsahem bílkovin a v menší míře s nízkým vzrůstem, vysokou hektolitrovou hmotností a s odolností k výdrolu.

Klíčová slova: Izrael; pšenice; odrůdy; šlechtění; stabilita výnosu; adaptace; komponenty variance

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