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DETERMINATION OF GENETIC VARIATION FOR MODELLING EFFICIENT GERMPLASM COLLECTION STRATEGIES

Final Report
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TABLE OF CONTENTS **PAGE**

2. Table of Contents	1
3. Executive Summary	2
4. Research Objectives	3
5. Methods and Results	4
a. collection	4
b. wild barley	5
c. wild onions	39
d. melons	40
6. Impact, Relevance and Technology Transfer	52
7. Project Activity/Outputs	52
8. Project Productivity	53
9. Future Work	53

3. EXECUTIVE SUMMARY

Due to an array of causes, over the past 70 years Central Asia, considered to be one of the world's most important centers for genetic diversity in many crops, underwent and is still undergoing serious genetic erosion. In this trilateral program between scientists from Israel, Turkmenistan and Kazakhstan, the primary objective is to obtain quantitative data on the extent and structure of genetic variation and diversity in the gene pool of representative plant crops and species in order to understand the mechanisms of genetic erosion. This will allow the formation of efficient strategies for genetic conservation. Three species were examined: melons, wild barley and wild onions.

The program included collecting germplasm and determining the extent and structure of genetic variation present. Collections of the three species were made in all three countries. Most collection trips included participants from at least two of the countries.

For wild barley, 10 Israeli and 36 Turkmenian populations were collected; no wild barley was found in Kazakhstan. Genetic variation was determined using field trials and starch gel electrophoresis. Extensive amounts of genetic variation was present. The Turkmenian populations had a different structure of genetic variation than did populations from the Near East and eastern Mediterranean.

For melons, over 100 accessions were collected from Central Asia. Extensive variation was found in fruit appearance, quality and taste. Several accessions are being incorporated into breeding programs.

Collaboration, and with it the strengthening of the scientific capabilities of the CARs, was considerable in this project. The planning of all collection trips was conducted by the P.I.s of the three countries with the CAR P.I.s learning appropriate collecting strategies. The training in Israel of CAR junior scientists was an important goal (4 from Kazakhstan, 2 from Turkmenistan) and they often worked together with Israeli students. The scientific infrastructure of the CARs was improved.

4. RESEARCH OBJECTIVES

For the past 70 years, i.e. during most of the Soviet period, Central Asia underwent, and is still undergoing, serious loss of indigenous germplasm; i.e. genetic erosion. This was due to an array of causes including: (i) severe industrial pollution; (ii) radiation fallout and pollution; (iii) misguided agricultural policies; (iv) urbanization; (v) monocultural agricultural practices; and (vi) the introduction of new cultivars that were required to be grown in place of indigenous landraces or cultivars. Only since the breakup of the Soviet Union has it become possible to examine the extent of genetic erosion.

This is a trilateral program between scientists from Israel, Turkmenistan and Kazakhstan. Its primary objective is to obtain quantitative information on the extent and structure of genetic variation and genetic diversity in the gene pool of important crops from Central Asia. This is necessary in order to: (i) have a base to quantify the extent of genetic erosion over time; (ii) understand the effects of the loss of genetic diversity on the extent and structure of existing genetic variation and diversity in the Central Asian gene pool; (iii) develop efficient collecting and evaluation strategies that maximize the number of genes and gene complexes that can be collected and evaluated with the minimum number of plants needed to be collected and evaluated in order to minimize cost, space and infrastructure.

In order to have as useful a program as possible, it was agreed by all P.I.s to examine one species or species groups in each of the three levels of genetic resource utilization:

a. primary - the existing weedy forms, landraces, primitive cultivars and varieties and breeding lines of a crop. Melons, *Cucumis melo* was chosen. It is widely grown throughout Central Asia and the region is considered to be one of the species' most important centers of genetic diversity;

b. secondary - the wild progenitors of a crop. Wild barley, *Hordeum spontaneum*, which is the progenitor of cultivated barley, was chosen. It is widely found throughout Israel and Turkmenistan and reportedly in southern Kazakhstan and can easily be crossed with cultivated barley for genetic exchange.

c. tertiary - several wild species that are related to domesticated onions and with special breeding techniques can be hybridized with the crop were chosen.

5. METHODS AND RESULTS

It was decided by all P.I.s to develop integrated collecting and research programs.

A. COLLECTION OF GERMPLASM

The germplasm was to be collected using a strategy developed by one of us (S.M.) for collecting populations of annual wild grasses and for vegetable landraces and/or populations (Mendlinger and Zohary, 1995; Mendlinger et al, 1993). Seeds from each plant from each population or primitive variety were separately bagged. Each barley population was classified as to: (i) its geographical position in the species range (whether it is in the core or the periphery); (ii) to its ecological position (whether it is in the central or main ecological niche or in a marginal niche); and (iii) region (Israel, Turkmenistan or Kazakhstan). Important ecological and climatological information and data were obtained for each population. The *Allium* ssp. were collected as populations with both seeds and bulbs collected. When possible *Cucumis melo* was collected as landraces and each fruit initiated the beginning of an accession.

1. Israel

In April-May, 1993, Dr, Mendlinger collected populations of wild barley from populations representing both mesic and xeric environments.

In April-May 1994 Dr. Mendlinger further collected populations of wild barley from the mesic and xeric environments of Israel. The collected populations included both central and marginal as well as core and peripheral populations. Each population consisted of between 50-70 individual plants. The collections were planned and conducted with Dr. Yerlan Turuspekov and Mr. Usken Batilova of Kazakhstan and Mr. Azat Nourberdyev of Turkmenistan; the junior scientists were spending a six-eight month training period in Dr. Mendlinger's laboratory for determining genetic variation in barley.

2. Turkmenistan

In May-June 1993 a collection trip lasting almost a month was conducted for wild barley and onions. The trip covered most of southern, western and central Turkmenistan plus sections of the Karakum desert and western Turkmenistan. An extensive collection was made for barley (18 populations) and a moderate one for several wild onion species. Participating were the Israeli and Turkmenistan P.I.s plus Azat Nourberdyev, Sergei Volis and Irina Safronova (from the Institute of Botany, St. Petersburg).

In May 1994 a collecting trip for wild barley and wild onions was conducted in eastern, southern and western Kazakhstan. The collecting team consisted of scientists from Turkmenistan and Israel and was planed and coordinated by Drs. Orlovsky, Durikov and Mendlinger. Twenty one populations of barley and eight of onions were collected. During the summer of 1994, the Turkmen P.I.s, either alone or with Israeli scientists, collected 51 landraces or primitive varieties of melons. (Unfortunately, the origin of many of the landraces is unknown). Seed was given to Israel and to Kazakhstan for evaluation.

In 1995, the Turkmenistan P.I.s, after coordinating with the Israeli and Kazakh P.I.s, conducted a collecting trip in eastern and northern Turkmenistan for all three targeted species groups. The region is primarily semi-arid and arid but in some areas an extensive canal system exists for irrigation. Collected were:

a. barley - four populations were collected, but all turned out to be primitive cultivars of cultivated barley;

b. melons - Twenty-one primitive varieties or landraces were collected, most at or near the Turkmenistan-Uzbekistan border;

c. onions - no populations were found.

3. Kazakhstan

In 1993 two collection trips were conducted by Kazakh scientists, the first for melons and the second for wild barley and onions. The collecting trip for melons covered southern Kazakhstan. This collection of melons were only made available to the other P.I.s in 1995.

In July 1993, Dr. Irina Ivanchenko of the Kazakh Botanical Garden conducted an extensive search for wild barley and onions in southern Kazakhstan. She failed to locate any

populations of *H. spontaneum* and did not know if the species is absent or the spikes had already shattered. She did collect several populations of wild onions.

In 1994 Dr. Sarsenbaev collected 27 varieties of melons from southern Kazakhstan.

In 1995 the Dr. Sarsenbaev conducted three collecting trip. The first was for wild barley and onions and was conducted in June, 1995 in the southern mountains and foothills of Kazakhstan. No populations of wild barley were found and he believes that they are either absent or very rare and isolated in Kazakhstan. This is against the conventional wisdom of the species' range and is an important finding. Eight populations of wild onions were found and collected. Plants from these populations were subsequently planted for evaluation in Kazakhstan and Israel

The second trip, in July 1995, was for melons and covered southern Kazakhstan and northern Uzbekistan. He collected 34 primitive varieties, most from Kazakhstan.

The third collecting trip, also for melons, was conducted with Dr. Mendlinger in August and covered south-western Kazakhstan and the Aral Sea region. They collected almost twenty primitive varieties, including some from soils which are very saline.

B. GENETIC ANALYSIS- THE EXTENT AND STRUCTURE OF GENETIC VARIATION IN THE THREE SPECIES

1. *Hordeum spontaneum,* wild barley

The genetic analysis for Hordeum spontaneum was conducted, due to logistical limitations, primarily in Israel However, the personal conducting the research program included scientists form all three countries, often working together as a team on the same project. The scientists included:

Kazakhstan - Yerlan Turuspekov, Saule Abugalieva, Uzken Batilova and Umuzat Bertova;
Turkmenistan - Azat Nourberdyev and Irina Pirogova;
Israel - Sergei Volis, Yvonne Ventura and Haim Kooperman.

The genetic analysis included three integrated field trials and electrophoretic evaluation of 13 water soluble structural proteins from 31 Turkmenian and 6 Israeli populations.

a. Field Trials

Three field trials were conducted over the three years of the program. The field trials were an integrated program in which we attempted to quantify and understand the genetic variation and diversity present in the collected populations.

1 .The first field trial was designed to examine the effects of different sowing dates on phenological and morphological variation in wild barley. Sixteen and ten populations from Turkmenistan and Israel respectively were examined; the populations represented different ecological and geographical areas in each country. Fifteen mother plants from each population were chosen at random and three seeds from each plant were used (almost all seed from the same plant are homozygote and identical). Three sowing dates were chosen: November 1, November 25 and December 20. For each sowing date, one seed/mother plant was sown in the greenhouse and transplanted into the field at three weeks old. Each sowing date consisted of three blocks with 5 plants per population in a row (each representing a different mother plant) per block. The field consisted of 1.5 meter wide raised beds with a single drip line containing 2-liter per hour drippers spaced 0.5 meters apart in each bed. One seedling per mother plant was transplanted next to each dripper. The plants received irrigation and fertilization as needed via the drippers.

The plants were examined for an array of vegetative and reproductive traits including: a longitudinal study of the number and height of vegetative and reproductive tillers, time of reproductive tillers, date of harvest, the height, number of nodes, number of spikelets and yield of the first three shoots.

2. The second field trial was conducted for determining the potential drought tolerance of the collected populations. Populations originating in both Turkmenistan and Israel from mesic and xeric environments were examined. Due to space limitations, only 12 Turkmenian and 6 Israeli populations were used. The plants were grown in pure sand. Two irrigation treatments, low and high, were given twice a week. The same traits as in the first field trial were examined.

3. The third field trial used the agromanagement protocols of the first but examined the populations collected in the second year with some of the first year's collections.

The results of the three field trials presented a more or less similar picture of genetic variation in phenological and morphological traits. Rather then repeat similar types of data over all three experiments, we are presenting a paper which we wrote on the results of the second field trial. Its conclusions would be the same for the other field trials.

Phenotypic variation and stress resistance in core and peripheral populations of H. spontaneum

Introduction

Rapid environmental changes/deterioration occurring, either as a result of human activity or natural causes, pose population biology question of whether populations of the same species may differ in their persistence to such changes.

If an area is undergoing an environmental change and its indigenous plant population therefore becomes extinct, the populations from the areas that have already undergone this or a similar stress should be better candidates for recolonization in this stressed area. As many aspects of plant physiology and ecology differ across a species' distribution (Parsons, 1980,1991; Antonovics, 1994; Trevis, 1994) it is unlikely that the persistence of populations under environmental changes will be uniform regardless of a population's position in a species range. Persistence of a population under environmental stress can be attained either by the stress resistance of specific genotypes or by high phenotypic plasticity. Genetic variability in such populations may be either low (most individuals are resistant or phenotypically plastic) or high (resistant and nonresistant genotypes are common). A combined genetic-demographic mathematical model predicts population persistence with an increase in overall genetic variance (Pease et al., 1989). As individuals may vary in their persistence, either through adaptation or through phenotypic plasticity, to conditions that can never occur within most of the species range, it is plausible that genetic variability with respect to resistance and plasticity varies across the range of species distribution.

It has been shown that the genetic structure of populations from the boundary of the species distribution ('peripheral' sensu Brussard, 1984) and those away from the boundary ('core' populations) may differ (Soule, 1973; Brussard, 1984; Parsons, 1991). Three hypotheses have been developed to explain potential differences in selection processes and genetic variation patterns between peripheral and core populations and are discussed elsewhere (Safriel et al., 1994). They can be briefly described as the following:

(a) the **"Carson" hypothesis:** core populations undergo balancing selection and have high genetic variation, whereas in peripheral areas with fewer suitable ecological niches populations are adapted to a narrower range of ecological conditions and hence are less genetically variable than core populations (Carson, 1959; da Cunha and Dobzhansky, 1954);

(b) the **"Fisher" hypothesis:** core populations undergo stabilizing selection and therefore within-population genetic variability is low, whereas peripheral populations constantly undergo fluctuating selection, induced by variable and unstable environmental conditions, and consequently have high within-population genetic variability (Fisher 1930);

(c) the **"Mayr" hypothesis:** gene flow from the core to the periphery is stronger than selection in the periphery, hence genetic variability is homogeneous throughout the range (Mayr 1965, 1970).

Each hypothesis has different implications for conservation strategy and emphasizes a different allocation strategy for conservation in respect to a species core and periphery.

In this study we compared the genetic variation and phenotypic plasticity in core and peripheral populations of *Hordeum spontaneum* Koch. and asked two questions: i) are there differences in the response to environmental changes between peripheral and core populations; and ii) whether these differences are associated with differences in genetic (phenotypic) variability. Genetic variability in *H. spontaneum* across its distribution range was intensively studied for many characteristics, including disease resistance, isozymes and DNA sequences (Brown et al. 1978; Nevo et al. 1986; Jana and Pietrzak 1988; Saghai Maroof

and Allard 1990; Chalmers et al. 1992), but surprisingly few studies were devoted to variability in phenotypic traits (Nevo et al. 1984; Snow and Brody 1984). Study of phenotypic variability representing the whole plant level of genetic variability has an advantage over study of enzymatic and DNA variability as a study of adaptive variation while enzymatic and DNA polymorphism in many cases is selectively neutral.

Materials and methods

Species studied

Hordeum spontaneum Koch. is a morphologically diverse, widespread annual grass species with ecotypic differentiation (Snow and Brody, 1984). It is abundantly distributed in open park forests and herbaceous formations of the Near East, Turkey, western Iran, Afghanistan and Turkmenistan and reaches its distribution boundary in patchy and sporadic formations in southern Israel, the Aegean region, the Egyptian coast, eastern Iran, India, Kazakhstan and China (Harlan and Zohary, 1966; Zohary, 1973; personal observations) (Fig. 1).

Experimental methods

Between 30-50 plants each from 23 Turkmenian and 7 Israeli populations were collected during two expeditions in Turkmenistan (May 1992 and 1993) and in central and southern Israel (April-May 1992 and 1993). From these, 12 Turkmenian and 6 Israeli populations representing the different environmental conditions of their countries were chosen for this study. We used the degree of aridity to differentiate populations into core and peripheral, which was similar to differentiation of Israeli populations into mesic and xeric ones used by Nevo et al. (1984) for *H. spontaneum* and Mendlinger and Zohary for *Aegilops* species (1995). In this study five Israeli populations were from the southern periphery (The Negev and Judean Deserts), and one Turkmenian population was from the northern periphery of the species distribution (annual rainfall 100-150 mm). The other eleven Turkmenian populations (foothills of Kopet-Dag mountain chain and Badhis Highland) and one Israeli population from the Mediterranean coast represent the species core (200-500 mm rainfall) (Table 1). Thus the segregation of populations into core and peripheral ones employed two criteria: (i) population position in a species range (at the border of species distribution and away from it); and (ii) aridity with annual rainfall of 200 mm as the cutoff point. Plants from each population were collected along a transect(s) with the collected plants spaced between 1-3 m apart and one spike per plant harvested and separately bagged (Marshall and Brown, 1975; Mendlinger and Zohary, 1995).

One seed per mother plant was sown in a greenhouse on November 1, 1993 and the plantlets were transplanted into an experimental sand garden at the Institute of Desert Research in Sede Boqer on November 15. Each plantlet was transplanted into a 1/4 m^2 framed plot, placed in the ground and filled with sterile sand to a depth of 1m. A complete randomized block design was used with 6-10 plants per treatment per population.

Two water treatments were examined: low (LW) and high (HW) irrigation. In addition to 14.5 liters/plant of rainfall (58 mm rainfall fell during the growing season), the plants in the low water treatment received 9.25 liters and in the high 18.5 liters of irrigation water during the season. The amount of water supplied was calculated using the Pan A transevaporation rate during the season, with the low treatment representing a water stress (i.e. drought conditions) and high treatment relatively favorable conditions. Irrigation was done by hand-watering twice a week. The fertilizer NPK 20:20:20 was supplied at each irrigation with each plant receiving the same amount of fertilizer.

After establishment, the number of days to appearance of the second vegetative tiller was recorded and the number of tillers per individual plant and tiller height were counted and measured respectively every ten days until the plants initiated bolting. After the appearance of reproductive tillers, the first three reproductive tillers of each plant were tagged with colored tags representing the first, second and third tiller in order of awn appearance and each tiller was measured for: culm length, flag and penultimate leaf length, spike length, awn length, number of nodes, internode length and total tiller height and the number of days to anthesis and awning were recorded. At senescence all spikes were

harvested and the total number of reproductive tillers was counted. After harvest the number of spikelets per spike and the average spikelet and seed weight were measured.

Statistical analysis

A Nested Analysis of Variance (ANOVA) on the morphological characters was used to partition the total variance between population groups (i.e. species core and periphery), between populations of a group and between individuals within a population. A 2-Way ANOVA was carried out for all phenological and morphological traits between population groups and water treatment (HW and LW). A significant interaction between population groups and treatments was presumed to reflect the different amount of phenotypic plasticity between groups of populations. The relationship of found population plasticity with environmental factors (climatic and geographic) was studied by multiple regression analysis. Using the coefficient of variation, CV, comparison of variation in phenotypic traits between population groups was carried out using the Wilcoxon matched-pairs signed-ranks test for each trait. Principal Component analysis (PCA) using the program 'CANOCO' (Ter Braak 1987) was done to determine the pattern of interpopulation variation in phenotypic traits.

Results

Trait values

In both irrigation treatments peripheral populations started reproduction (days to anthesis and days to awn appearance) significantly earlier than core ones (Table 2). Under both treatments plants from peripheral populations had significantly fewer nodes and spikelets per spike and lighter seeds but heavier spikelets than core populations. Spike and awn length, flag and penultimate leaf length and internode length did not differ between the two population groups under HW but were significantly different under LW with all reproductive traits being smaller in core than in peripheral populations.

Days to awn appearance and days to anthesis, the phenological traits associated with the start of reproduction, were not affected by irrigation but depended upon each population's original location, i.e. Turkmenistan or Israel (Table 3). The number of days until tillering was not affected by water treatment or by the origin of the populations. The interaction between treatment and population group was not significant in any phenological trait, indicating that the phenotypic plasticity of phenological traits did not differ in populations of *H. spontaneum*. Vegetative traits were not affected by any factor.

All reproductive traits except number of nodes and spike weight were strongly affected by both water treatment and the origin of populations. Interaction between the two factors were significant in 8 of the 13 traits related to plant reproduction and grain filling (Table 3). A plant's relative response to water stress as expressed in reduction in size (in total height, spike length, internode length etc.) or number (in number of nodes and number of spikelets in a spike) was greater in core than peripheral populations (22.6% vs. 10.3% , $p < 0.01$, Wilcoxon signed-ranks test) (Table 4).

Regression analysis revealed that phenotypic plasticity in populations was negatively related to annual and January temperature and positively related to annual rainfall and latitude (which is negatively correlated with annual temperature, $R^2 = 0.86$, $p < 0.001$). As wild barley's environmental favorability decreases with a decrease in annual rainfall or an increase in temperature, the latter suggests a negative relationship of plasticity with environmental severity (Table 5).

Trait variability expressed as CV

Phenotypic variability, expressed as the coefficient of variation (CV), was calculated and compared and contrasted in the two water treatments (HW and LW) for each trait in the two population groups (Table 6). Group CVs (variation in trait values over all populations of a group) ranged between 4% (days to awn appearance in core populations grown under conditions of high water availability) to 74% (number of reproductive tillers in peripheral populations grown under conditions of water stress). Core and peripheral populations were significantly different in HW treatment with more phenotypic variation in peripheral than

in core populations ($p < 0.01$, Wilcoxon signed-ranks test). Variability increased with stress (LW treatment) in core populations in all traits except the number and height of vegetative tillers whereas in peripheral populations variability increased in nine and decreased in nine traits (Table 6).

Partitioning of Variation

In all traits examined, the within population component of variation was larger than the other two components (mean values 66% vs. 25% and 9%) (Table 7). Population groups contributed the least to the total variance (9%) except in number of days to awn appearance and anthesis and the number of nodes. However, there was a relatively high percentage of between population groups variance for days to awn appearance and days to anthesis (36.3 and 32.8%) which even exceeded the within population group component (21.2 and 24.6%, respectively). The substantial amount of between populations/population groups component of variation (together around 50% of total variation) in such traits as days to awn appearance and days to anthesis, the number of nodes and seed weight suggests their importance in *H. spontaneum* population differentiation.

Trait complexes

PCA was performed to analyze the pattern of phenotypic variation between populations. The data matrices for HW and LW treatments contained identical variables and comprised only the traits with total between populations and population group variation exceeding 40% (days to awn appearance, number of nodes, number of spikelets in a spike and seed weight). (Days to anthesis was not used as it was highly correlated with days to awn appearance). The trait that contributed the most to PC I under both HW and LW treatments was number of nodes (Table 8). The first principal component explained 65 and 53% of trait variation of HW and LW, respectively.

The scattergram of population means on the first two principal components appears to group plant ecotypes by their core or peripheral position in a species distribution (Fig. 2). In both HW and LW treatments core and peripheral populations are skewed to opposite sites of the PC I. Under HW treatment there is a trend for core populations to clump together whereas peripheral populations are rather scattered. Under LW treatment this pattern is less pronounced.

Discussion

Phenotypic differentiation of *H. spontaneum* within a species range was detected for plant phenology with 36.3 and 32.8% of the total phenotypic variation contributed to the variation between populations from the species core and periphery (in days to awn appearance and anthesis, respectively). At the same time plant morphology was less important for determining this differentiation as only two traits, seed weight and number of nodes (25.8 and 26.5% of the population groups contribution to the total variance, respectively) were important. Thus core and peripheral populations differed with respect to the onset of reproduction (days to anthesis and awning), in traits related to plant growth (number of nodes) and plant fecundity (seed weight). This suggests a difference between core and peripheral population strategies with plants from peripheral populations starting reproduction earlier, growing faster and having lighter seeds than from core populations. In addition, since there were fewer spikelets per spike in peripheral than in core populations, but no significant difference between population groups in the number of spikes per plant, the decrease in seed weight is not compensated by an increase in the number of seeds produced. Hence fast plant growth in peripheral populations appears to have a lower reproductive allocation as a tradeoff. This strategy is what one would expect as the result of an unpredictable and unstable climate in peripheral areas requiring a high correlation of reproduction with stochastic weather patterns and a shortening of the vegetation period.

In most traits there was some contribution of the between-population group component to the total variance with peripheral populations harboring significantly more variation than core ones (inter- and intrapopulation phenotypic variation were pooled). In

addition PCA revealed a trend of interpopulation variation to be higher in peripheral versus core populations as expressed in the clumping of populations in the scattergrams. As phenotypic variability under conditions of water stress increased much more in core than in peripheral populations, this may indicate that peripheral populations not only are phenotypically more diverse, but are less affected by stress.

Phenotypic plasticity significantly differed between core and peripheral populations in eight traits and was positively related with favorability of a population's local environment (i.e. annual rainfall and temperature) in seven of these traits. The consistency of these results points to aridity changing from a species core to its periphery as a factor in determining the level of plasticity in barley populations. This also may mean that not only significant difference in aridity between core and periphery, but also relatively small differences between population localities may play an important role in determining the population's level of phenotypic plasticity.

As the phenotypic variability, which is at least partly genetic, is shown to be higher in peripheral than in core populations, the results best fit the "Fisher" hypothesis, although an estimation of intrapopulation variation is lacking. Higher plasticity of core vs. peripheral populations would initially appear to favor the "Carson" hypothesis, but as it is associated with greater decreases in fitness of core vs. peripheral populations (reflected in number of reproductive tillers and spikelets in a spike) the "Carson" hypothesis is not supported. The inequality of the total population group variation goes against the "Mayr" hypothesis.

Persistence of populations under conditions of water stress resulted not from high phenotypic plasticity but from genetically fixed drought resistance. This suggests that in new and stressful environmental conditions which a population may face in a case of rapid environmental change/deterioration the population persistence will be achieved not by acclimatization but by adaptation or preadaptation.

Higher resistance to water stress of peripheral populations was associated with their higher phenotypic variation as compared with core populations. The lower amount of phenotypic plasticity in peripheral versus core populations supports the hypothesis of antagonistic selection for phenotypic flexibility and genetic diversity (Lewontin, 1957; Bradshaw, 1965; Marshall and Jain, 1968). It is plausible that the higher plasticity found in core populations is the result of limited genetic diversity due to stabilizing selection. Another explanation may employ the hypothesis of Grime, Crick and Rincon (1986) that morphological plasticity in plants from productive and unproductive habitats have different patterns. According to Grime, Crick and Rincon (1986), high plasticity associated with high competitive ability will be favored in productive habitats as it enables plants to escape from depletion zones and to utilize resources fast and efficient. Unproductive and stressed habitats will require conservative strategy of resource utilization with good synchronization of life cycle with seasonally and low morphological plasticity. Thus core populations from more productive environments are expected to have higher plasticity than populations from species periphery exposed to severe stresses and resource deficiency. A test of this hypothesis is underway.

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Table 1. Ecogeographical data for 18 populations of *H. spontaneum* sampled in Turkmenistan and Israel in 1992-1993 and used in a field trial at Sede Boqer (1993/1994)

Population site	Country	Latitude	January temperature (t° C)	Annual temperature (t° C)	Annual rainfall (mm)
Core					
1	Turkmenistan	37.85	0.7	15.4	383
2	- " -	38.65	0.0	14.4	295
3	- " -	38.25	1.0	12.9	457
4	- " -	38.80	3.2	16.0	238
5	- " -	38.00	0.9	16.1	220
6	- " -	37.80	0.9	16.1	220
7	- " -	37.40	1.4	16.3	245
8	- " -	36.85	1.8	16.7	205
9	- " -	36.50	3.0	16.6	225
10	- " -	35.95	2.4	14.5	290
11	- " -	35.80	2.4	14.5	285
12	Israel	31.90	14.0	21.0	400
Periphery					
13	Israel	30.90	10.0	21.0	100
14	- " -	30.80	10.0	21.0	90
15	- " -	30.95	10.0	21.0	105
16	- " -	31.80	14.0	23.0	150
17	- " -	31.60	14.0	23.0	100
18	Turkmenistan	40.00	1.7	14.2	150

Table 2. The means of 18 phenotypic traits in two groups of populations of *H. spontaneum* (core and periphery) grown under high (HW) and low (LW) water treatments and compared by an orthogonal polynomial test. Differences between population groups are shown with corresponding levels of significance. Lengths are in cm.

Traits	LW			HW		
	core	periphery		core	periphery	
I. Phenological:						
days till tillering	23.7	22.6	ns	24.3	22.7	ns
days to awn appearance	161.0	149.4	* * *	160.9	150.1	* * *
days to anthesis	167.6	158.2	* * *	167.4	158.9	* * *
II. Morphological:						
Vegetative:						
vegetative tillers	28.8	26.8	ns	27.2	25.8	ns
height of veg. tillers	29.3	31.8	ns	27.7	29.5	ns
Reproductive:						
total height	49.4	51.4	ns	68.8	60.8	* * *
spike length	16.5	18.1	* * *	19.5	19.2	ns
awn length	7.4	8.1	* * *	8.3	8.5	ns
culm length	32.9	33.2	ns	49.2	41.5	* * *
number of nodes	4.5	3.9	* * *	4.6	3.7	* * *
internode length	7.4	8.6	* * *	10.8	11.1	ns
flag leaf length	5.0	6.4	* * *	7.4	7.5	ns
penultimate leaf length	10.6	13.4	* * *	14.4	14.8	ns
spikelets in a spike	25.4	24.3	*	29.6	24.6	* * *
spike weight (g)	0.89	0.94	ns	1.25	1.20	ns
spikelet weight (mg)	34.1	39.1	* * *	41.9	49.2	* * *
number of rep. tillers	10.9	12.9	ns	18.5	21.5	ns
seed weight (mg)	21.2	16.0	* * *	22.7	19.1	* * *

Levels of significance: *** $p < 0.001$; ** $p < 0.01$; * $p < 0.05$; n.s. not significant

Table 3. Two-way ANOVA for phenotypic traits in two groups of populations of *H. spontaneum* (core-periphery) grown under high (HW) and low (LW) water treatments. Differences between treatments, population groups and their interactions are shown with corresponding levels of significance.

Traits	irrigation treatment		population groups		interaction treatment * groups	
	F[z]		F		F	
I. Phenological:						
days till tillering	0.1	n.s.	1.8	n.s.	0.1	n.s.
days to awn appearance	0.1	n.s.	117.3	* * *	0.1	n.s.
days to anthesis	0.1	n.s.	80.9	* * *	0.2	n.s.
II. Morphological:						
Vegetative:						
vegetative tillers	1.2	n.s.	2.1	n.s.	0.1	n.s.
height of veg. tillers	2.3	n.s.	2.9	n.s.	0.1	n.s.
Reproductive:						
total height	164.0	* * *	7.2	* *	19.8	* * *
spike length	102.7	* * *	9.9	* *	2.3	* * *
awn length	15.1	* * *	7.7	* *	2.5	n.s.
culm length	153.8	* * *	13.5	* * *	16.4	* * *
number of nodes	0.2	n.s.	177.7	* * *	5.2	*
internode length	188.7	* * *	14.2	* * *	4.6	*
flag leaf length	70.2	* * *	12.9	* * *	9.3	* *
penultimate leaf length	58.6	* * *	22.6	* * *	12.9	* * *
spikelets in a spike	33.7	* * *	66.8	* * *	26.9	* * *
spike weight	120.4	* * *	0	n.s.	3.1	n.s.
spikelet weight	115.4	* * *	54.6	* * *	1.8	n.s.
reproductive tillers	42.2	* * *	3.9	*	0.2	n.s.
seed weight	9.9	* *	34.9	* * *	1.2	n.s.

z. Levels of significance: *** $p < 0.001$; ** $p < 0.01$; $p < 0.05$; n.s. not significant

Table 4. Means of morphological traits of *H. spontaneum* population groups and the effect of experimental water stress. The traits shown are those demonstrating significant interaction between population groups and treatment (2-way ANOVA), arranged in a decreasing order of % reduction in core populations. Lengths are in cm.

Traits	Population groups					
	core			peripheral		
	mean value		red.	mean value		red.
	HW	LW	(%)	HW	LW	(%)
culm length	49.2	32.9	33	41.6	33.3	20
flag leaf length	7.4	5.0	32	7.5	6.4	15
internode length	10.8	7.4	32	11.1	8.6	22
total height	68.8	49.4	28	60.8	51.4	15
penultimate leaf length	14.4	10.6	26	14.8	13.5	9
spike length	19.6	16.5	15	19.2	18.1	6
number of spikelets in a spike	29.6	25.5	14	24.6	24.3	1
number of nodes	4.6	4.5	2	3.7	3.9	- 4

Wilcoxon matched-pairs signed-ranks test:

Ts	n	p
0	8	**

Level of significance: ** $p < 0.01$

Table 5. Coefficients of multiple determination (R^2) employing as dependent variable the amount of a population's relative response to water stress, expressed as percentage of reduction in trait size or number in 12 Turkmenian and 6 Israeli populations of *H. spontaneum* grown under two water treatments (HW and LW, respectively). Independent variables were climatic and geographic factors*. Slope is represented for regression line of the factor contributed the most to the total explained variance.

Trait	$X_1X_2X_3$	R^2_1	R^2_{12}	R^2_{123}	slope
spike length	TjLt	0.46**	0.47**		-1.0
total height	Tm	0.33*			-2.8
internode length	Tm	0.24*			-2.5
culm length	Tm	0.29*			-3.2
flag leaf length	RnLt	0.27*	0.36*		0.1
penultimate leaf length	LtRnTm	0.41*	0.50*	0.52*	2.3
spikelets in a spike	Tm	0.51***			-2.3

* Climatic values were taken from the Atlas of Israel (1970), The USSR climate reference book. Part 30. Turkmenistan. vol. 2,4,5 (1967, 1968, 1969) and from multiple-year records of the Meteorological Service of Turkmenistan.

Symbols of variables : Lt = latitude; Tm = mean annual temperature; Tj = mean January temperature; Rn = mean annual rainfall;

Levels of significance: *** $p< 0.001$; ** $p< 0.01$; * $p< 0.05$

Table 6. Variation in phenotypic traits in *H. spontaneum* population groups for two water treatments (HW and LW, respectively), expressed through Coefficient of Variation (CV), and the periphery/core ratio of coefficients of variation.

	HW			LW		
Traits	periphery	core	ratio	periphery	core	ratio
I. Phenological:						
days till tillering	33.5	33.7	0.99	35.5	37.1	0.96
days to awn appearance	6.7	3.9	1.70	8.4	4.8	1.74
days to anthesis	5.2	4.0	1.29	6.9	4.6	1.48
II. Morphological:						
Vegetative:						
number of vegetative tillers	39.1	37.5	1.04	45.4	29.5	1.54
height of vegetative tillers	42.0	33.9	1.24	41.0	32.5	1.26
Reproductive:						
total height	31.9	23.1	1.38	25.9	31.4	0.83
spike length	18.2	12.8	1.42	15.5	17.6	0.88
awn length	40.0	22.9	1.75	37.0	24.3	1.52
culm length	41.2	29.1	1.42	36.7	40.4	0.91
number of nodes	24.3	15.2	1.60	23.1	17.8	1.30
internode length	33.3	27.8	1.20	33.7	37.8	0.89
flag leaf length	45.3	43.2	1.05	51.6	44.0	1.17
penultimate leaf length	39.2	29.2	1.34	50.0	35.8	1.39
number of spikelets in a spike	23.6	16.6	1.42	19.8	22.4	0.88
number of reproductive tillers	70.7	57.3	1.23	74.1	66.7	1.11
spike weight	29.1	35.2	0.83	28.7	48.3	0.59
spikelet weight	21.5	28.6	0.75	26.7	37.1	0.72
seed weight	28.8	29.1	0.99	26.3	31.1	0.84

Wilcoxon matched-pairs signed-ranks test:

Ts	p	Ts	p
17	**	70	n.s.

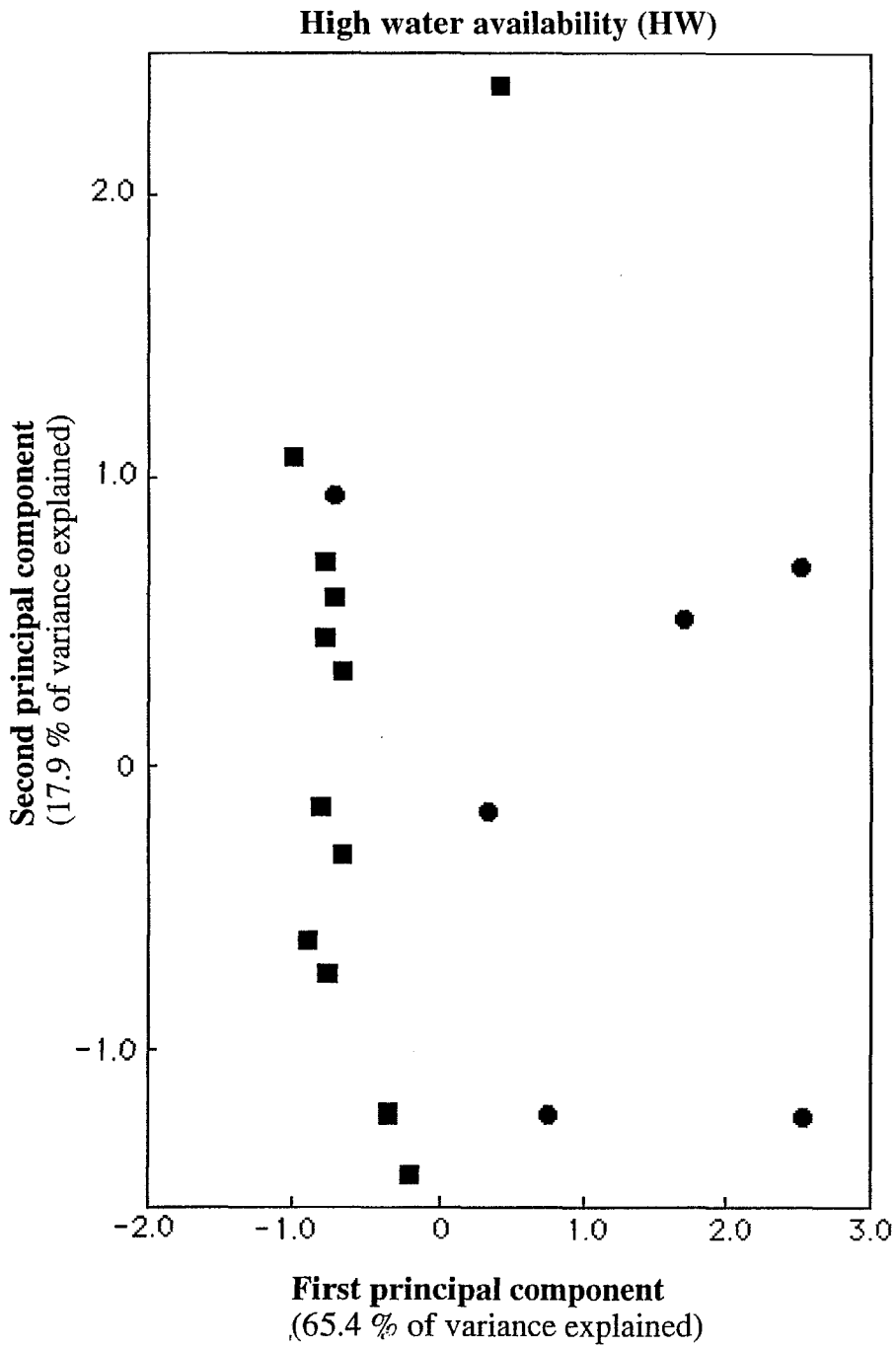
Levels of significance: ** $p < 0.01$; * $p < 0.05$; n.s. not significant

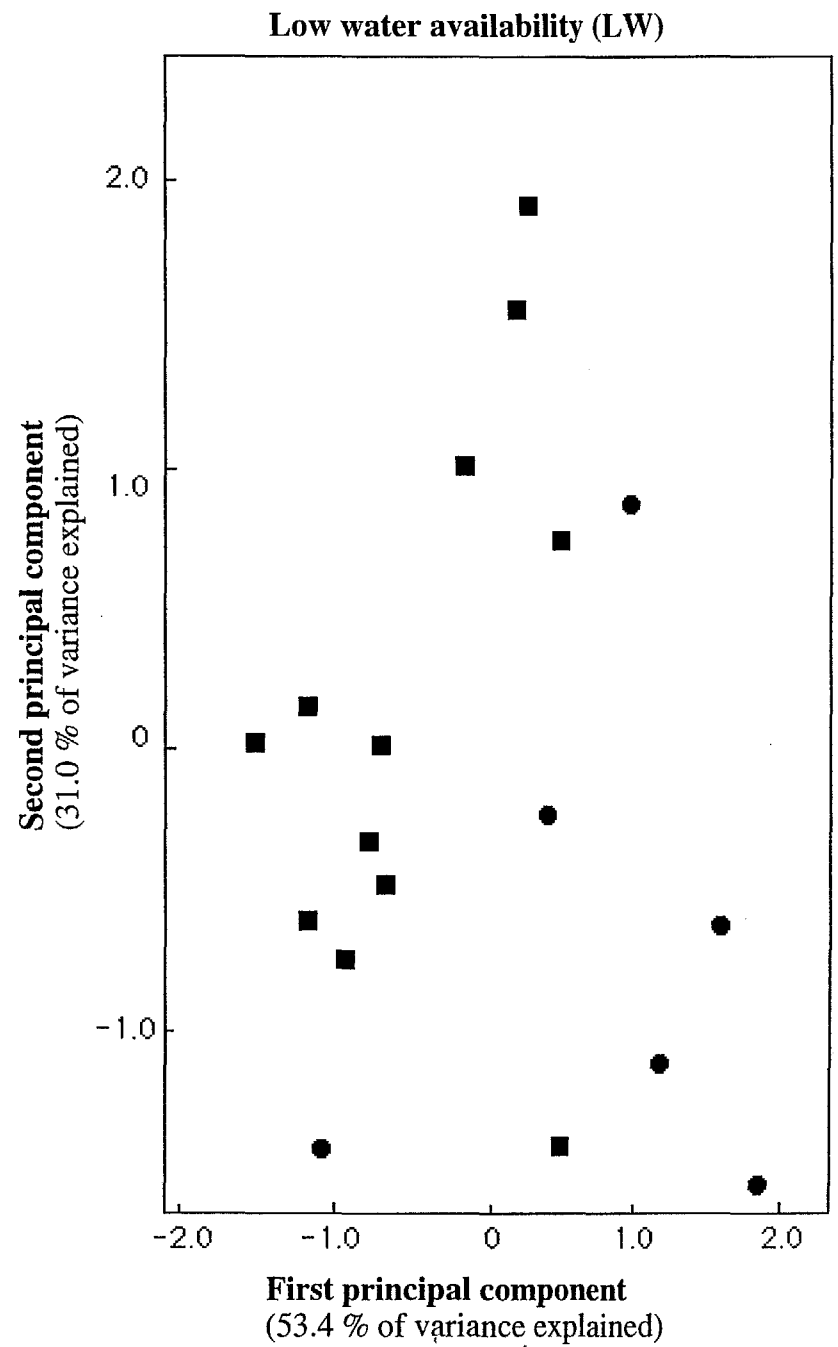
Table 7. Variance components (in percentage) between population groups (core and periphery), between populations within a group and within populations for phenotypic traits in populations of *H. spontaneum* grown in a field trial at Sede Boqer, (1993/1994)

Traits	Variance components		
	between groups	*between* populations	*within* populations
I. Phenological:			
days till tillering	0	16	84
days to awn appearance	36	21	42
days to anthesis	33	25	43
mean	23	21	56
II. Morphological:			
Vegetative:			
number of vegetative tillers	0	16	84
height of veg. tillers	0	28	72
mean	0	22	78
Reproductive:			
total height	3	30	67
spike length	3	21	76
awn length	0	30	70
culm length	3	30	66
number of nodes	26	23	51
internode length	2	19	79
flag leaf length	7	15	79
penultimate leaf length	2	24	73
number of spikelets in a spike	15	27	58
spike weight	0	25	75
spikelet weight	9	27	65
number of reproductive tillers	0	25	75
seed weight	26	30	44
mean	7	25	67
total mean	9	25	66

Table 7. Variance components (in percentage) between population groups (core and periphery), between populations within a group and within populations for phenotypic traits in populations of *H. spontaneum* grown in a field trial at Sede Boqer, (1993/1994)

Traits	Variance components		
	between groups	between populations	within populations
I. Phenological:			
days till tillering	0	16	84
days to awn appearance	36	21	42
days to anthesis	33	25	43
mean	23	21	56
II. Morphological:			
Vegetative:			
number of vegetative tillers	0	16	84
height of veg. tillers	0	28	72
mean	0	22	78
Reproductive:			
total height	3	30	67
spike length	3	21	76
awn length	0	30	70
culm length	3	30	66
number of nodes	26	23	51
internode length	2	19	79
flag leaf length	7	15	79
penultimate leaf length	2	24	73
number of spikelets in a spike	15	27	58
spike weight	0	25	75
spikelet weight	9	27	65
number of reproductive tillers	0	25	75
seed weight	26	30	44
mean	7	25	67
total mean	9	25	66


High water availability (HW)
Second principal component
(17.9 % of variance explained)
2.0
1.0
0
-1.0
-2.0
-1.0
0
1.0
2.0
3.0
First principal component
(65.4 % of variance explained)


Low water availability (LW)
Second principal component
(31.0 % of variance explained)
2.0
1.0
0
-1.0
-2.0
-1.0
0
1.0
2.0
First principal component
(53.4 % of variance explained)

2. Electrophoresis

In order to investigate the extent and structure of genetic variation in wild barley and its relationship to: (i) species distribution (core vs. periphery); and (ii) local environmental conditions (favorable or central vs. unfavorable or marginal) structural proteins from plants from thirty three populations of *H. spontaneum* from Turkmenistan (27) and Israel (6) were examined electrophoretically. The populations were chosen from those collected to represent the total area and ecological diversity that was found. (Logistical and financial limitations did not allow us to examine all of the populations).

Starch gel electrophoresis was performed on 20-25 seedlings/population for 16 water soluble structural loci. Most of these populations were also used in the various field trials. Electrophoretic analyses were conducted using 2-3 week old leafs. The loci examined were PGM (1 locus), PGI (2), MDH (2), 6-PGD (2), EST (3), ACPH (3), GP (1), GDH (1) and CAT (1). For each population, the allele frequencies, the mean number of alleles per locus (A) and the proportion of loci polymorphic (P) were calculated and the degree of genetic similarity determined. The structure of genetic variation was determined using Shannon's information index to partition the total genetic diversity in a manner similar to the field data; i.e. into its within population, between populations of a region and between region components.

As for the field data, we are presenting a manuscript on the genetic variation found in the Turkmenian populations. The results of the Israeli populations were similar to that previously found by Nevo et al. (1986a).

The Extent and Structure of Genetic Variation in Wild Barley form Turkmenistan

Introduction

Wild barley, *Hordeum spontaneum*, Koch., the progenitor of cultivated barley, is a dominant or common species in much of the Middle East and eastern Mediterranean, Central Asia and the Afghanistan and Tibetan plateaus. Over the past 20 years, the extent and structure of genetic variation and diversity has been extensively studied, but only from populations originating in the Middle East and eastern Mediterranean parts of its range, mostly from Israel, Syria, Jordan, Turkey, Greece and Iran (Nevo et al., 1979, 1986a, 1986b; Moseman, et al., 1980; Snow and Brody, 1984; Jana and Pietrzak 1988; Saghi Maroof et al., 1990).

No comparable genetic information is available from populations from the northern or eastern parts of *H. spontaneum's* distribution; i.e. from Turkmenistan, Afghanistan, or Tibet. This lack of information on the genetic variation in wild barley populations across its range has not allowed us: (i) to fully understand the extent and structure of genetic variation and diversity and the variation's relationship to ecological and environmental factors; and (ii) the development of an effective and efficient sampling strategy for germplasm collection and preservation of agronomically important genes. The first reason is important if we are to fully utilize this species as a model for understanding the interrelationship between population genetics and ecology. The second reason is important to efficiently utilize this species for its breeding potential.

The present work was aimed to investigate the extent and structure of genetic variation in 36 Turkmenian populations of *H. spontaneum* which originates from the northern part of the its range. Genetic variation was examined using electrophoretic analysis of 13 water soluble leaf proteins. The populations examined covered various ecological/environmental regions .

Materials and Methods

Collecting

About 50 spikes, each from a separate plant, were collected from each of thirty six Turkmenian populations during two expeditions in Turkmenistan (May 1992 and 1993). The areas and the populations collected represented, as close as we could estimate, the distribution and density of wild barley in Turkmenistan. The localities and important geographical, meteorological and ecological data of each population are given in Tables 1a and 1b and their distribution is shown in Fig. 1. The populations were divided into six ecological or environmental regions : (i) Kopet-Dag mountains (13 populations); (ii) Kopet-Dag foothills (8); (iii) Karakum desert (3); (iv) Kugitang mountains (4); (v) Kugitang foothills (5); and (vi) Badhyz plateau (2). The first three regions also represent the western and the last three regions the eastern part of Turkmenistan. Population size was estimated and each population was characterized as small (< 500 plants), medium (500-10,000 plants) or large (> 10,000 plants).

Sampled populations were chosen using a mixed sampling strategy over the distribution area to represent differences in soil and climatic factors (Marshall and Brown, 1975; Mendlinger and Zohary, 1995). The collection protocols in each population followed Mendlinger and Zohary (1995). Collection was made via one or more linear transects covering as much of a population's area as possible. In each population, plants at least 2 meters apart were sampled by collecting one spike from each plant. The number of plants collected from each site was independent of levels of observable diversity and abundance.

Electrophoresis

Twelve water soluble loci encoded by seven enzyme systems plus one general protein locus were examined using horizontal starch gel electrophoresis. The protocol and recipes followed Brody and Mendlinger (1980). Leaves from two week old seedlings were cut, macerated in two drops of distilled water and a drop of bromophenol blue and the extract absorbed on filter paper wicks. The starch gel was prepared by boiling 39g of hydrolyzed potato starch (Sigma, S-4501) dissolved in 300 ml gel buffer with subsequent degassing by a vacuum pump. Three buffer systems (Tris-citrate (TC), Tris-malate (TM) and Poulik discontinuous buffer) were used. Preparation procedures followed Brown (1978) and Brody and Mendlinger (1980).

Samples from 15 different plants, five each from three populations, and a control were placed on each gel. Gels were run in a refrigerator at 4°C on a current of 100 mA and voltage of 100 (TM), 110 (TC) or 200 (Poulik) for 3-4 hours. After electrophoresis, each gel was sectioned into three slices with each slice stained for a different enzyme. The list of enzymes tested, the abbreviations employed, E.C. numbers, number of loci in each enzyme system and the buffer used are:

1. Catalase, *Cat* ; E. C. 1.11.1.6; 1 locus. Poulik buffer
2. General Protein, *Gp* ; E. C. 4.1.1.39; 1 locus. TM and TC buffer.
3. Glutamate dehydrogenase, *Gdh* ; E. C. 1.4.1.2; 1 locus. TC and Poulik buffer.
4. Esterase, *Est* ; E.C. 3.1.1.2; 3 loci. TC buffer.
5. Malate dehydrogenase, *Mdh* ; E.C.1.1.1.37; 2 loci. TM and TC buffer.
6. Phosphoglucomutase, *Pgm* ; E. C. 2.7.5.1; 1 locus. TM buffer.
7. Phosphoglucose isomerase, *Pgi* ; E. C. 5.3.1.9; 2 loci. TM buffer.
8. 6-Phosphogluconate dehydrogenase, *6-Pgd* ; E. C. 1.1.1.44; 2 loci. TM buffer.

After staining the gels were scored by the same two people, then fixed in 10% glacial acetic acid for 24 hours and stored at 4°C. Alleles were scored according to their mobility on the gel with "a" being the fastest, "b" next, etc. All gels were scored a second time at the end of the experiment.

Statistical analysis

The extent of genetic variation for each population was determined by calculating the as mean number of alleles per locus, A; the proportion of polymorphic loci, P; and the expected percent heterozygosity, H_e. Nei's coefficients of genetic identity, I, and genetic distance D (D = - ln I), were used to calculate the genetic relationship between the populations (Nei, 1972). The extent of genetic diversity in each locus H_e, was calculated as $H_e = 1 - \Sigma p_i^2$ where p_i is the frequency of each allele in a locus in the population. The partitioning of diversity into its three components, within populations, between

populations of a region and between the six regions, was accomplished by using Shannon's Information Index (Lewontin, 1972; Mendlinger and Zohary, 1995).

Single-linkage Cluster Analysis was performed for the determination of population genetic similarity. Stepwise Multiple Regression analysis and Canonical Correspondence Analysis were performed to determine the degree of association between environmental factors and allele frequencies.

Results

A total of forty two alleles were found over the thirteen loci in the 36 populations (Table 2). The general pattern of genetic variation over most loci was for a loci to contain an ubiquitous allele combined with 1 or 2 moderate to low frequency alleles found in several if not in many populations. Among the loci only Gdh and G.P. were weakly and locally polymorphic; the other eleven loci displayed strong polymorphism in at least one population.

The forty two alleles can be characterized using a modified classification system based on Marshall and Brown (1975) which characterizes alleles into four groups according to their frequency within populations and their extent of their geographic distribution. It was found that: (i) eleven alleles, one in each locus except Est-3 and Cat, were ubiquitous and in high frequency in all populations; (ii) seventeen alleles were widespread (in at least 5 populations) but in moderate frequency (total frequency above 2%); (iii) three alleles, Est-4d, Pgm-a and Mdh-1-a, were more localized (found in less than 5 populations) but common in these populations (at least 10% in most populations); and (iv) eleven alleles were localized and rare (less than 1% over all populations). Only one allele, Pgi-2-a, was unique to one population.

When the populations were subdivided into the six ecological regions, only 29% of the alleles were found in only one ecological zone or one part of the country (Table 3). These were: Est-1-a (only in Kugitang foothills); Est 3-d and PGH-b (only in the western half); Est-4-d (only in Kopet-Dag mountains); Est-4-c (only in the Kopet-Dag and Kugitang mountains); Gdh-a,c and Pgm-c (only the Kugitang mountains and foothills); and Pgm-a, Pgi-2-a,d and Mdh-2-a (only in Kopet-Dag mountains and foothills).

The amount and structure of genetic variation varied between populations (Table 4). The mean number of alleles per locus, A, was 1.50 but ranged between 1.23 to 2.08; the proportion of polymorphic loci per population, P, was 0.41 (range 0.23-0.77); the proportion of heterozygosity per locus per individual, H_o, was 0.001 (range 0.000-0.008); and genetic diversity, H_e, was 0.095 (ranged from 0,042 - 0.216). Significant correlations were found between A, P and H_e but no significant correlation between these three parameters and D, population size or distance. The Kugitang foothills had significantly higher A, P and H_e than the other five regions, but a similar amount of genetic diversity (Table 5). No significant differences were found between the eastern and western part of the country nor between environment.

The genetic distance was calculated between all pairs of the 36 populations (Table 6). The mean genetic distance between populations was 0.081 (range 0.053-0.192). The dendrogram derived by cluster analysis of genetic distance between populations shows that genetic distance is not related to geographic distance (Fig. 2). For example, populations that are very close geographically (e.g. populations 21 and 22 or populations 5 and 6) are very distant genetically and vice versa (e.g. populations 7 and 20) (Fig 2). The populations from the Kugitang mountains and foothills were genetically very close to each other and more distance from the others. The populations from the Kopet-Dag mountains were equally distance from each other as they were from the other populations.

The partitioning of total genetic diversity into its within population, between populations within a group and among the six ecological regions components is represented in Table 6. The largest single component was between populations within a region (39%), within populations had a smaller component (33%) and between regions the smallest component (28%).

Significant correlation was found between key environmental factors and genetic variation. Climatic and geographic factors significantly explained a substantial amount of variation in allele frequencies at 4 polymorphic loci and total H_e when analyzed by Multiple Regression Analysis (Table 7). Temperature, evaporation, rainfall and altitude were the factors correlated with allozyme variation. Canonical correspondence analysis was

applied to total allele frequencies data of 36 populations of *H. spontaneum* with 9 geographic and climatic parameters as external variables. Only longitude could significantly explain the allelic variation over the 36 barley populations (Wilks' Lambda 0,04, F 5.1, $p < 0.05$, Monte Carlo permutation test).

The association of allele frequencies with soil type was also analyzed by Canonical Correspondence Analysis (CCA). Fig. 3 represents the results of CCA in 8 alleles whose variation among populations is significantly explained by variation in soil types. The frequencies of these 8 alleles were used as dependent variables and the 7 soil types as independent variables. A significant relationship between allele frequencies with variation in soil type (Wilks' Lambda 0,013, F 4.4, $p< 0.001$) is reflected in the canonical centroid plot (Fig. 3) where soil types are quite well separated from each other.

Discussion

The pattern of the extent and structure of genetic variation and diversity found in populations from Turkmenistan was significantly different from the patterns found in populations that originating from the eastern Mediterranean and Near East. Nevo et al. (1986a; 1986b) and to a lesser extent Jana and Pietrzak (1988) found a mosaic or patchy patterns of allele distribution with sharp local differentiation. While they found that some alleles were common and somewhat widespread, few if any ubiquitous alleles were identified and many alleles were found to be unique to either a population or very localized.

In this study, from populations from the northern part of the species distribution, a different pattern was found. First, of the 13 loci examined, 11 had ubiquitous alleles which were almost always the allele in the highest frequency in all populations. Second, these populations contained a higher proportion of widespread alleles, but usually in lower frequencies, than the previous studies found . Third, only one allele was found to be unique to a single population as opposed to many such alleles found in previous studies (Nevo et al. 1986a; 1986b). .

The level of genetic diversity (H_e) found in Turkmenian populations of *H. spontaneum* (0.095) is similar to estimates of Nevo et al. (1986) for two countries in the Near East, Israel (0.103) and Turkey (0.099), but significantly lower than found in Iran (0.130). and those reported by Jana and Pietrzak (1988) for Turkey, Jordan and Syria (0.14, 0.17 and 0.15, respectively).

The different pattern of genetic variation is reflected in the genetic distances found in this study as compared to others. In this study the mean genetic distance was 0.081. This relatively low genetic distance is consistent with populations containing a large number of ubiquitous alleles in high frequencies, a large number of secondary common or widespread alleles in relatively low frequency and low number of unique or rare alleles. As opposed to this, Nevo et al. (1986a), who found few ubiquitous alleles but many unique or patchy alleles, had significantly greater genetic distances between their populations (0.119 and 0.110 for Israeli and Turkmenian populations respectively, t-test, $p<0.05$).

The different pattern of genetic variation also produced a different pattern for the partitioning of genetic variation. In this study only 33% of the total genetic variation was found within populations, 39% between populations of a region and 28% among the six regions; i.e. 33% within and 67% among populations. Nevo et al. (1986a), which showed major genetic differences between populations, found that 54% of the genetic variation was duo to within populations 39% between populations of a region and only 8% among regions. For populations originating in Turkey (Nevo et al., 1986b), 53% was within and 47% among populations. Jana and Pietrzak (1988) reported that 43% of the total variation was within and 57% among populations.

Overall, this study indicates that the strong patchiness of mosaic pattern reported in previous studies was not found in populations of *H. spontaneum* from the northern part of its range. Thus the relative importance of local or microenvironmental factors over macroenvironmental factors in directing the extent and structure of genetic variation as reported by Nevo et al. (1979; 1986a) may not be as important in Turkmenistan or in other parts of the species range. This can be seen from the number of significant correlations found between specific allele frequencies and environmental parameters. This may

influence future collecting strategies for this important source of germplasm for cultivated barley.

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Table 1A. Ecogeographical data for 36 populations of *H. spontaneum* from Turkmenistan

No.	Location	Geomorphology	Ecology		
			Soil type	Habitat	Pop. size
1	Seliysky	Kopet-Dag mountain range	mountain gray soil	defile	large
2	Chuli (2 km NW)	Kopet-Dag mountain range	mountain gray soil	south slope	large
3	Beurme (7 km S)	Kopet-Dag mountain range	mountain gray soil	east slope	large
4	Bami (10 km SW)	Kopet-Dag mountain range	mountain gray soil	wadi	medium
5	Bami (12 km SW)	Kopet-Dag mountain range	mountain gray soil	slope	medium
6	Kara-Kala (15 WNW)	Kopet-Dag mountain range	mountain gray soil	defile	small
7	Kara-Kala (7 km SSE)	Kopet-Dag mountain range	mountain gray soil	wadi	small
8	Kara-Kala (20 km SSE)	Kopet-Dag mountain range	mountain gray soil	mountain pass	large
9	Iskander (60 km SW)	Kopet-Dag mountain range	mountain gray soil	wadi	medium
10	Krasnovodsk (1 km W)	Krasnovodsk plateau	basalt	shallow wadi	small
11	Aschabad (10 km NW)	Karakum Desert	sand	roadside	medium
12	Aschabad (15 km SE)	Kopet-Dag foothill plain	gray brown desert soil	roadside	medium
13	Aschabad (20 km SE)	Kopet-Dag foothill plain	gray brown desert soil	roadside	medium
14	Aschabad (30 km SE)	Kopet-Dag foothill plain	gray brown desert soil	roadside	medium
15	Aschabad (35 km SE)	Kopet-Dag foothill plain	gray brown desert soil	roadside	medium
16	Aschabad (50 km SE)	Kopet-Dag foothill plain	gray brown desert soil	wadi	small
17	Aschabad (60 km SE)	Kopet-Dag foothill plain	gray brown desert soil	wadi	medium
18	Kaahna (2 km NW)	Kopet-Dag foothill plain	gray brown desert soil	plain and wadi	medium
19	Dushak (10 km W)	Kopet-Dag foothill plain	gray brown desert soil	shallow wadi	medium
20	Serachs (40 km NNW)	Karakum Desert	sand	ravine	medium
21	Serachs (3 km SSE)	Karakum Desert	takyr	abandoned field	medium
22	Kepelya (20 km NW)	Badhyz plateau	gray soil	plain	large
23	Kepelya (1 km S)	Badhyz plateau	mountain gray soil	east slope	large
24	Karluk (5 km W)	Kugitang foothill plain	clay	wadi	medium
25	Karluk (10 km N)	Kugitang mountain range	clay	wadi	large
26	Karluk (10 km N)	Kugitang mountain range	mountain gray soil	defile	large
27	Karluk (15 km N)	Kugitang mountain range	mountain gray soil	few ravines	small
28	Karluk (10 km E)	Kugitang mountain range	mountain gray soil	defile	medium
29	Charshanga (17 km NE)	Kugitang foothill plain	clay (salty)	plain	medium
30	Gaurdak (10 km SE)	Kugitang foothill plain	?	wadi	medium
31	Gaurdak (3 km SE)	Kugitang foothill plain	?	shallow defile	medium
32	Kara-Kala (25 km NW)	Kopet-Dag mountain range	clay	wadi	small
33	Kizil-Arvat (70 km SSW)	Kopet-Dag mountain range	clay	wadi	large
34	Kizil-Arvat (80 km SSW)	Kopet-Dag mountain range	clay	wadi	large
35	Chuli (1 km NW)	Kopet-Dag mountain range	mountain gray soil	slope	large
36	Charshanga (5 km NE)	Kugitang foothill plain	clay	wadi	medium

Table 1B. Geographical and climatic data for 36 populations of *H. spontaneum* from Turkmenistan

No.	Geography			Climate					
	Longitude	Latitude	Altitude	Average temperature			Rainfall	Humidity	Evaporation
	(Ln)	(Lt)	(Al)	Annual (Tm)	August (Ta)	January (Tj)	(mm) (Rn)	(%) (Hu)	(cm) (Ev)
1	58.60	37.85	600	15.4	27.8	0.7	383	58	132
2	58.00	38.00	670	14.1	25.2	1.8	268	58	132
3	56.90	38.60	440	14.4	27.4	0.0	270	56	136
4	56.70	38.65	500	14.4	27.4	0.0	295	56	136
5	56.75	38.60	800	14.4	27.4	0.0	295	54	136
6	56.15	38.50	480	16.1	27.6	3.6	320	54	135
7	56.45	38.35	480	15.8	27.7	3.7	404	54	135
8	56.35	38.25	1130	12.9	24.0	1.0	457	54	135
9	55.35	38.80	340	16.0	28.2	3.2	238	56	165
10	52.95	40.00	100	14.2	27.3	1.7	150	61	140
11	58.30	38.00	150	16.1	28.9	0.9	220	54	150
12	58.60	37.90	150	16.1	28.9	0.9	220	54	150
13	58.65	37.85	150	16.1	28.9	0.9	220	54	150
14	58.75	37.80	150	16.1	28.9	0.9	220	54	150
15	58.80	37.80	150	16.1	28.9	0.9	220	54	150
16	58.90	37.75	150	16.1	28.9	0.9	220	54	150
17	59.05	37.60	160	16.1	28.9	0.9	213	54	150
18	59.55	37.40	170	16.3	29.0	1.4	245	52	169
19	59.90	37.20	170	16.3	29.0	1.4	211	52	169
20	61.05	36.85	200	16.7	29.2	1.8	205	49	170
21	61.25	36.50	300	16.6	28.3	3.0	225	47	185
22	61.40	35.95	160	14.5	25.8	2.4	290	48	174
23	61.50	35.80	880	14.5	25.8	2.4	285	48	174
24	66.25	37.60	300	18.0	30.2	3.4	185	45	231
25	66.30	37.65	300	16.3	28.5	2.7	379	45	231
26	66.30	37.65	350	16.3	28.5	2.7	379	45	231
27	66.35	37.70	300	16.3	28.5	2.7	379	45	231
28	66.40	37.60	500	16.3	28.5	2.7	379	45	231
29	66.20	37.60	300	18.0	30.2	3.4	185	45	231
30	66.15	37.75	350	16.3	28.5	2.7	272	45	231
31	66.10	37.80	350	16.3	28.5	2.7	272	45	231
32	56.05	38.55	200	16.1	27.6	3.6	302	54	135
33	55.75	38.35	200	16.1	27.6	3.6	302	54	135
34	55.80	38.30	180	16.1	27.6	3.6	302	54	135
35	58.00	38.00	680	13.5	24.4	1	268	58	132
36	66.10	37.55	300	18.0	30.2	3.4	185	45	231

Table 2. Allele frequencies at 13 loci in 36 Turkmenian populations of *H. spontaneum* .

Locus	Allele	Population																
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Est-1	*a*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	b	1.00	1.00	1.00	1.00	0.90	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
	c	-	-	-	-	0.10	-	-	-	-	-	-	-	-	-	-	-	-
Est-3	*a*	-	-	-	-	-	0.50	-	0.15	-	-	-	-	0.05	-	0.10	-	-
	b	0.50	0.75	1.00	1.00	0.30	-	0.25	0.20	-	0.05	1.00	-	0.70	0.15	0.15	0.20	-
	c	0.25	0.25	-	-	0.70	0.35	0.40	0.65	-	-	-	-	0.05	0.10	-	0.30	-
	d	0.25	-	-	-	-	0.15	0.35	-	1.00	0.95	-	1.00	0.20	0.75	0.75	0.50	1.00
Est-4	*a*	-	-	-	-	-	0.70	-	-	-	-	-	-	0.05	-	0.05	-	-
	b	1.00	0.90	1.00	1.00	1.00	0.30	0.95	1.00	0.90	1.00	1.00	1.00	0.95	1.00	0.95	1.00	1.00
	c	-	0.10	-	-	-	-	0.05	-	0.10	-	-	-	-	-	-	-	-
	d	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Cat	*a*	-	-	0.15	0.05	-	-	-	-	-	-	-	-	-	-	-	-	-
	b	0.10	0.05	0.85	0.85	0.80	-	0.40	0.60	0.95	-	1.00	0.75	1.00	0.80	1.00	1.00	0.45
	c	0.90	0.95	-	0.10	0.20	1.00	0.60	0.40	0.05	1.00	-	0.25	-	0.20	-	-	0.55
GP	*b*	-	-	0.05	-	0.05	-	-	-	-	-	0.05	0.05	0.05	0.05	0.05	-	-
	c	1.00	0.85	0.95	1.00	0.95	1.00	1.00	1.00	1.00	1.00	0.95	0.95	0.95	0.95	0.95	1.00	1.00
	d	-	0.15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Gdh	*a*	-	-	0.05	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	b	1.00	1.00	0.95	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
	c	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

30

Pgm	*a*	0.25	-	-	-	-	-	-	-	0.05	-	-	0.65	-	-	-	-	0.20
	b	0.70	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.95	1.00	1.00	0.35	1.00	1.00	1.00	1.00	0.80
	c	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Pgi-1	*a*	-	-	-	-	-	-	-	-	-	-	0.05	-	-	-	-	-	-
	b	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.80	1.00	0.90	0.85	1.00	0.30	1.00
	c	-	-	-	-	-	-	-	-	-	-	0.15	-	0.10	0.15	-	0.70	-

Table 2. Continued.

18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	Mean
-	-	-	-	-	-	-	-	-	-	-	-	0.10	0.20	-	-	-	-	0.10	$0.011^{3,z}$
1.00	1.00	1.00	1.00	1.00	0.90	0.85	0.65	0.50	0.40	0.75	0.85	0.80	0.80	1.00	1.00	1.00	1.00	0.80	0.922^{36}
-	-	-	-	-	0.10	0.15	0.35	0.50	0.60	0.25	0.15	0.10	-	-	-	-	-	0.10	0.067^{10}
-	-	-	-	-	-	0.05	-	-	0.05	0.20	-	0.10	0.20	0.10	-	0.10	0.30	0.05	0.054^{13}
0.20	0.75	0.45	-	0.10	1.00	0.75	0.75	0.70	0.80	0.75	0.75	0.90	0.80	0.65	0.65	0.10	0.55	0.60	0.486^{32}
0.10	0.25	0.20	0.20	0.90	-	0.20	0.25	0.30	0.15	0.05	0.25	-	-	-	0.25	0.55	-	0.35	0.196^{24}
0.70	-	0.35	0.80	-	-	-	-	-	-	-	-	-	-	0.25	0.10	0.25	0.15	-	0.264^{19}
0.15	0.10	-	-	0.35	-	-	0.10	-	-	-	0.05	0.30	0.05	0.25	0.15	0.50	0.15	0.10	0.085^{15}
0.85	0.90	1.00	1.00	0.65	1.00	0.60	0.90	1.00	1.00	1.00	0.65	0.60	0.95	0.60	0.75	0.10	0.85	0.80	0.865^{36}
-	-	-	-	-	-	0.40	-	-	-	-	0.30	0.10	-	0.05	0.05	-	-	0.10	0.035^{9}
-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.10	0.05	0.40	-	-	0.015^{3}
-	-	-	-	-	-	-	0.10	-	-	-	-	0.10	-	-	-	-	-	-	0.011^{4}
0.85	1.00	0.50	0.45	1.00	0.95	0.85	0.80	1.00	1.00	1.00	1.00	0.80	0.80	1.00	0.95	0.90	0.95	0.80	0.755^{34}
0.15	-	0.50	0.55	-	0.05	0.15	0.10	-	-	-	-	0.10	0.20	-	0.05	0.10	0.05	0.20	0.233^{25}
-	-	0.20	-	-	-	0.10	0.05	-	-	0.05	-	-	0.05	-	-	-	-	0.05	0.024^{13}
0.95	1.00	0.80	1.00	1.00	0.95	0.85	0.95	1.00	1.00	0.95	1.00	1.00	0.95	1.00	1.00	1.00	1.00	0.95	0.968^{36}
0.05	-	-	-	-	0.05	0.05	-	-	-	-	-	-	-	-	-	-	-	-	0.008^{4}
-	-	-	-	-	-	-	0.05	-	-	-	-	0.05	-	-	-	-	-	0.05	0.006^{4}
1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.90	1.00	1.00	1.00	1.00	0.95	1.00	1.00	1.00	1.00	1.00	0.90	0.992^{36}
-	-	-	-	-	-	-	0.05	-	-	-	-	-	-	-	-	-	-	0.05	0.003^{2}

-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.032^{4}
1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.95	1.00	1.00	1.00	1.00	0.95	1.00	1.00	1.00	1.00	1.00	0.90	0.962^{36}
-	-	-	-	-	-	-	0.05	-	-	-	-	0.05	-	-	-	-	-	0.10	0.006^{3}
-	-	-	0.15	-	-	-	0.15	-	-	-	-	-	-	-	-	-	-	0.15	0.014^{4}
1.00	1.00	1.00	0.85	0.90	0.95	1.00	0.85	1.00	1.00	0.95	1.00	1.00	0.95	1.00	0.95	1.00	1.00	0.85	0.947^{36}
-	-	-	-	0.10	0.05	-	-	-	-	0.05	-	-	0.05	-	0.05	-	-	-	0.039^{9}

z = the number of populations containing the allele

Table 2. Continued.

Locus	Allele	Population 1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Pgi-2	*a*	-	-	-	-	-	0.10	-	-	-	-	-	-	-	-	-	-	-
	b	-	-	0.05	-	0.05	-	0.05	-	0.10	-	0.05	-	-	-	-	-	0.05
	c	1.00	1.00	0.95	1.00	0.95	0.90	0.95	1.00	0.90	1.00	0.95	1.00	0.95	1.00	1.00	0.95	0.95
	d	-	-	-	-	-	-	-	-	-	-	-	-	0.05	-	-	0.05	-
6 Pgd-1	*b*	-	-	0.05	0.10	-	0.10	0.05	0.15	-	-	-	-	-	0.05	0.05	-	0.05
	c	1.00	0.85	0.90	0.90	0.95	0.90	0.80	0.85	1.00	0.90	0.90	0.80	1.00	0.85	0.95	0.90	0.85
	d	-	0.15	0.05	-	0.05	-	0.15	-	-	0.10	0.10	0.20	-	0.10	-	0.10	0.10
6 Pgd-2	*a*	0.10	-	-	0.05	0.05	-	0.10	0.10	-	0.30	-	-	-	-	-	-	0.10
	b	0.90	0.95	1.00	0.95	0.95	1.00	0.85	0.90	1.00	0.70	1.00	1.00	1.00	1.00	1.00	1.00	0.90
	c	-	0.05	-	-	-	-	0.05	-	-	-	-	-	-	-	-	-	-
Mdh-1	*a*	-	-	-	-	-	0.35	-	-	-	-	-	-	-	-	-	-	-
	c	1.00	1.00	1.00	1.00	1.00	0.65	1.00	1.00	1.00	1.00	0.95	1.00	1.00	1.00	1.00	1.00	1.00
	d	-	-	-	-	-	-	-	-	-	-	0.05	-	-	-	-	-	-
Mdh-2	*a*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	b	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
	c	-	-	-	-	-	-	-	0.75	-	-	-	-	-	-	-	-	-

Table 2. Continued.

18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	Mean
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.003^{1}
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.010^{6}
1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.95	1.00	1.00	1.00	1.00	0.983^{36}
-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.05	-	-	-	-	0.004^{3}
0.05	0.05	-	-	-	0.05	0.50	-	-	-	-	0.25	-	-	0.05	-	-	-	-	0.043^{14}
0.85	0.90	1.00	0.85	0.95	0.90	0.50	1.00	1.00	1.00	1.00	0.75	0.90	1.00	0.95	0.95	1.00	1.00	1.00	0.911^{36}
0.10	0.05	-	0.15	0.05	0.05	-	-	-	-	-	-	0.10	-	-	0.05	-	-	-	0.046^{17}
-	-	0.05	0.10	-	-	0.15	0.15	-	-	-	-	0.05	-	0.05	-	-	-	0.15	0.042^{14}
0.95	1.00	0.95	0.90	0.90	1.00	0.85	0.85	1.00	1.00	1.00	1.00	0.95	1.00	0.95	1.00	1.00	0.95	0.85	0.950^{36}
0.05	-	-	-	0.10	-	-	-	-	-	-	-	-	-	-	-	-	0.05	-	0.008^{5}
-	-	-	-	-	-	-	0.25	-	-	-	-	-	0.05	-	-	-	-	0.20	0.024^{4}
1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.75	1.00	1.00	1.00	0.95	1.00	0.65	0.85	0.75	0.50	1.00	0.80	0.940^{36}
-	-	-	-	-	-	-	-	-	-	-	0.05	-	0.30	0.15	0.25	0.50	-	-	0.036^{6}
-	-	-	-	-	-	-	-	-	0.05	0.10	-	-	-	-	-	-	-	-	0.004^{2}
1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.85	0.90	0.90	1.00	1.00	0.80	1.00	0.95	1.00	0.95	1.00	0.961^{36}
-	-	-	-	-	-	-	-	0.15	0.05	-	-	-	0.20	-	0.05	-	0.05	-	0.035^{6}

Table 3. The allele frequencies in 13 loci of *H. spontaneum* from six regions in Turkmenistan.

Locus/ allele	Region					
	Kopet Dag mountains	Kopet-Dag foothills	Karakum desert	Kugitang mountains	Kugitang foothills	Badhyz plateau
Est-1 a	-	-	-	-	.08	-
b	.99	1.00	1.00	.58	.82	0.95
c	.01	-	-	.42	.10	.05
Est-3 a	.09	.02	-	.06	.08	-
b	.45	.27	.48	.75	.76	.55
c	.26	.10	.13	.19	.16	.45
d	.19	.61	.38	-	-	-
Est-4 a	.13	.04	-	.02	.10	.18
b	.80	.96	1.00	.98	.72	.82
c	.03	-	-	-	.18	-
d	.04	-	-	-	-	-
Cat a	.02	-	-	.02	.02	-
b	.65	.86	.65	.96	.85	.98
c	.34	.14	.35	.02	.13	.02
GP a	.02	.02	.08	.03	.04	-
b	.97	.97	.92	.97	.95	.97
c	.01	.01	-	-	.01	.02
Gdh a	-	-	-	.01	.02	-
b	1.00	1.00	1.00	.98	.97	100
c	-	-	-	.01	.01	-

Pgm a	.02	.11	-	-	-	-
b	.98	.89	1.00	.99	.97	1.00
c	-	-	-	.01	.03	-
Pgi-1 a	-	-	.07	.04	.03	-
b	1.00	.88	.88	.95	.96	.93
c	-	.12	.05	.01	.01	.07
Pgi-2 a	.01	-	-	-	-	-
b	.02	.01	.02	-	-	-
c	.97	.98	.98	1.00	1.00	1.00
d	.01	.01	-	-	-	-
6-pgd-1 a	.04	.03	-	-	.15	.03
b	.93	.89	.92	1.00	.83	.93
c	.03	.08	.08	-	.02	.05
6-pgd-2 a	.03	.01	.05	.04	.07	-
b	.95	.98	.95	.96	.93	.95
c	.01	.01	-	-	-	.05
Mdh-1 a	.03	-	-	.06	.05	-
b	.90	1.00	.98	.94	.88	1.00
c	.07	-	.02	-	.97	-
Mdh-2 a	-	-	-	.04	-	-
b	.03	1.00	1.00	.91	.96	1.00
c	.07	-	-	.05	.04	-

Table 3. The allele frequencies in 13 loci of *H. spontaneum* from six regions in Turkmenistan.

	Region					
Locus/ allele	Kopet Dag mountains	Kopet-Dag foothills	Karakum desert	Kugitang mountains	Kugitang foothills	Badhyz plateau
Est-1 a	-	-	-	-	.08	-
b	.99	1.00	1.00	.58	.82	0.95
c	.01	-	-	.42	.10	.05
Est-3 a	.09	.02	-	.06	.08	-
b	.45	.27	.48	.75	.76	.55
c	.26	.10	.13	.19	.16	.45
d	.19	.61	.38	-	-	-
Est-4 a	.13	.04	-	.02	.10	.18
b	.80	.96	1.00	.98	.72	.82
c	.03	-	-	-	.18	-
d	.04	-	-	-	-	-
Cat a	.02	-	-	.02	.02	-
b	.65	.86	.65	.96	.85	.98
c	.34	.14	.35	.02	.13	.02
GP a	.02	.02	.08	.03	.04	-
b	.97	.97	.92	.97	.95	.97
c	.01	.01	-	-	.01	.02
Gdh a	-	-	-	.01	.02	-
b	1.00	1.00	1.00	.98	.97	100
c	-	-	-	.01	.01	-
Pgm a	.02	.11	-	-	-	-
b	.98	.89	1.00	.99	.97	1.00
c	-	-	-	.01	.03	-
Pgi-1 a	-	-	.07	.04	.03	-
b	1.00	.88	.88	.95	.96	.93
c	-	.12	.05	.01	.01	.07
Pgi-2 a	.01	-	-	-	-	-
b	.02	.01	.02	-	-	-
c	.97	.98	.98	1.00	1.00	1.00
d	.01	.01	-	-	-	-
6-pgd-1 a	.04	.03	-	-	.15	.03
b	.93	.89	.92	1.00	.83	.93
c	.03	.08	.08	-	.02	.05
6-pgd-2 a	.03	.01	.05	.04	.07	-
b	.95	.98	.95	.96	.93	.95

38

c	.01	.01	-	-	-	.05
Mdh-1 a	.03	-	-	.06	.05	-
b	.90	1.00	.98	.94	.88	1.00
c	.07	-	.02	-	.97	-
Mdh-2 a	-	-	-	.04	-	-
b	.03	1.00	1.00	.91	.96	1.00
c	.07	-	-	.05	.04	-

Table 4. The mean number of alleles per locus (A), the number of polymorphic loci (P), the percentage of expected (He) and observed loci heterozygous (Ho), and the mean genetic distance (D) of 36 Turkmenian populations of *H. spontaneum* . n=20.

39

Population	A	P	He	Ho	D
1	1.38	0.31	0.108	0	0.099
2	1.46	0.46	0.097	0	0.106
3	1.38	0.38	0.056	0	0.060
4	1.30	0.23	0.042	0	0.058
5	1.46	0.54	0.100	0	0.060
6	1.46	0.38	0.142	0	0.192
7	1.69	0.46	0.148	0.004	0.071
8	1.46	0.38	0.139	0	0.121
9	1.31	0.31	0.042	0	0.083
10	1.23	0.23	0.053	0	0.144
11	1.46	0.38	0.062	0.008	0.085
12	1.31	0.31	0.096	0	0.063
13	1.54	0.38	0.072	0	0.126
14	1.46	0.38	0.103	0	0.055
15	1.38	0.31	0.053	0	0.074
16	1.38	0.31	0.101	0.004	0.108
17	1.46	0.38	0.104	0	0.098
18	1.62	0.46	0.110	0.008	0.065
19	1.31	0.23	0.057	0	0.053
20	1.38	0.31	0.119	0	0.058
21	1.38	0.38	0.116	0	0.092
22	1.38	0.38	0.084	0	0.098
23	1.46	0.38	0.050	0	0.075
24	1.69	0.54	0.185	0	0.070
25	1.92	0.77	0.201	0	0.062
26	1.23	0.23	0.090	0	0.073
27	1.38	0.23	0.077	0	0.087
28	1.46	0.38	0.088	0	0.061
29	1.46	0.38	0.122	0.004	0.061
30	1.85	0.61	0.143	0.008	0.061
31	1.70	0.62	0.158	0	0.066
32	1.70	0.46	0.124	0	0.059
33	1.77	0.54	0.128	0	0.053
34	1.54	0.31	0.144	0	0.123
35	1.54	0.46	0.094	0	0.054
36	2.08	0.77	0.216	0.008	0.053
Mean	1.50	0.41	0.106	0.001	0.079
St. error	0.032	0.023	0.007	0.0004	0. 005

40

Table 5. . The mean number of alleles per locus (A), the number of polymorphic loci (P), the percentage of expected (He) and observed loci heterozygous (Ho), and the mean genetic distance (D) in different geographical groupings.

Grouping	# of populations	A	P	He	Ho	D
A. Regions						
Kopet - Dag mountains	13	1.46b	.38b	.105b	.000	.088
Kopet-Dag foothills	8	1.43b	.31b	.099b	.001	.080
Karakum Desert	3	1.40b	.36b	.114b	.003	.078
Kagitang mountains	4	1.49b	.40b	.165a	.000	.071
Kugitang foothills	5	1.76a	.58a	.067b	.004	.062
Badhis plateau	2	1.42b	.38b	.067b	.000	.086
B. Country						
west	24	1.46a	.35a	.098a	.001	.084
east	11	1.60b	.48b	.129b	.002	.070
C. Environment						
mountains	17	1.49	.39	.107	.002	.084
foothills	13	1.56	.42	.117	.002	.073
plains	5	1.41	.37	.086	.002	.082

Table 6. Mean (±SE) of genetic distance, D, for six regions over 36 populations of *H. spontaneum* (Krasnovodsk plateau is excluded as represented by only population)

Regions	Kopet-Dag mountain range	Kopet-Dag foothill plain	Karakum Desert	Kugitang mountain range	Kugitang foothill plain	Badhis plateau	Mean
Kopet-Dag mountain range	0.096±0.003	0.090±0.007	0.089±0.008	0.089±0.009	0.083±0.008	0.094±0.008	0.090
Kopet-Dag foothill plain		0.058±0.007	0.058±0.005	0.068±0.005	0.067±0.005	0.072±0.007	0.069
Karakum Desert			0.063±0.012	0.054±0.009	0.051±0.008	0.077±0.008	0.065
Kugitang mountain range				0.015±0.002	0.029±0.002	0.053±0.012	0.051
Kugitang foothill plain					0.029±0.003	0.044±0.008	0.051
Badhis plateau						0.110†	0.075

† Only two populations compared

42

Table 7 The partitioning of the total genetic diversity in populations of *H. spontaneum*. into its within populations, between populations of a region and among regions components.

Loci	Within population	Between populations	Between regions
Est-1	46	35	19
Est-3	27	37	36
Est-4	30	35	35
Cat	31	32	37
G.P.	43	44	13
Gdh	42	58	0
Pgm	23	12	65
Pgi-1	42	37	21
Pgi-2	20	20	60
6 Pgd-1	38	43	19
6 Pgd-2	41	59	0
Mdh-1	26	44	30
Mdh-2	24	46	30
Mean	33	39	28
St. error	2.5	3.6	5.4

Table 8. The coefficients of multiple regression (R^2) with He and allele frequencies at 4 loci in 36 Turkmenian populations of *H. spontaneum* as the dependent variables and climatic and geographic factors as the independent variables*.

Allele	$X_1X_2X_3$	R^2_1	R^2_{12}	R^2_{123}
He	Tj	.26**		
Est-1				
b	EvRn	.62***	.76***	
c	EvRn	.47***	.63***	
Est-4				
a	TjEv	.20***	.32*	
b	TjEv	.35***	.44*	
c	TmAlRn	.22**	.35*	.47*
Mdh-1				
b	Tj	.24**		
Mdh-2				
b	AlRn	.30***	.36*	

* Climatic values were taken from the USSR climate reference book. Part 30. Turkmenistan. vol. 2,4,5 (1967, 1968, 1969) and from multiple-year records of the Meteorological Service of Turkmenistan.

Symbols of variables : Al = altitude; Tm = mean annual temperature; Tj = mean January temperature; Rn = mean annual rainfall; Ev = annual evaporation.

Levels of significance: *** $p< 0.001$; ** $p< 0.01$; * $p< 0.05$

43

Fig. 2. Dendrogram derived by single linkage cluster analysis of Nei's genetic distance values based on allele frequencies in 23 populations of *H. spontaneum* .

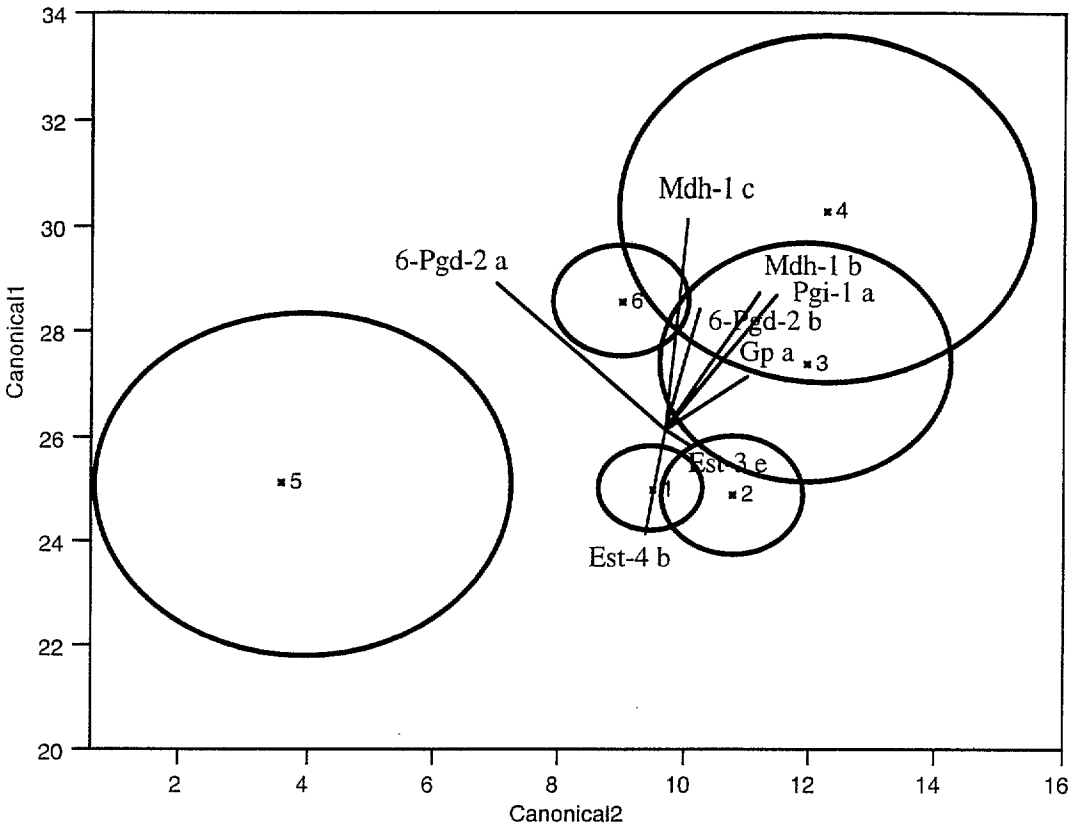

Fig. 3. Canonical centroid plot of correspondence between frequencies of 8 alleles and soil types of wild barley localities. Soil types: 1- mountain grey soil; 2- grey brown desert soil; 3- sand; 4- takyr; 5- basalt; 6- clay.

2. *Allium ssp.*- wild onions

The research program in Allium species did not provide the type and quantity of information that we had hoped at the beginning of the program. This was due to several reasons including:

(i) the selected species were much rarer than we had assumed. Therefore, we did not have as complete a collection as we needed for our initial goals;

(ii) the collection in Israel had several disease problems and according to quarantine laws some of the material had to be destroyed or maintained under quarantine;

(iii) the Israeli P.I. who was to do the research (R.K.) moved to another research institute which delayed some of her work.

Nevertheless, work was conducted in Israel and Kazakhstan and it can be summarized as:

Israel

A field plot was established in Sde Boker Israel and the collection from 1993 and 1994 were grown. An array of phenological and morphological traits were examined, but the outbreak of several diseases interfered with any good scientific conclusions.

Kazakhstan (Translated from Russian)

The research in Kazakhstan in *Allium* concentrated in two areas: (i) examining the extent and structure of genetic variation in *Allium pskemense* populations via gel electrophoresis of water soluble structural proteins; and (ii) the polypeptide content of the leaves.

The gel electrophoresis study (the protocols were similar to those used in Israel for barley) examined seven loci: Esterase-Est, Glutamic dehydrogenase- Gdh, Acid Phosphatase-Acph; Peroxidase- Per; Phosphoglucose isomerase-Pgi; Phosphoglucose mutase-Pgm; and Malate Dehydrogenase-Mdh. Genetic variation was found within most populations in most of the loci examined. Only two alleles were found in Per; the other loci had between 3-5 alleles over all populations. Only in Gdh was any differences found between populations.

The polypeptide content of leaves is heterogeneous. Overall, we can say that: (i) there are relatively few species present; (ii) most polypeptides have relatively low molecular weights (under 60kD); and (iii) there was no significant difference in polypeptides between the samples of the different populations.

3. *Cucumis melo*- **melon**

Field trials were conducted in Israel and Kazakhstan and genetic variation via starch gel electrophoresis was conducted in Israel by a Kazakh scientist.

a.Israel

1. field trials - The Turkmenian accessions were examined for an array of phenological, morphological and fruit quality analyses during summer field trials in 1993 and 1994. The Kazakh accessions were not given to Israel for evaluation until the spring of 1995. In 1995 a large scale field trial was initiated on both the Turkmenian and Kazakh accessions but had to be stopped due to an outbreak of downy mildew combined with a viral infection; the field was ordered destroyed and the plants burned by the Israeli Quarantine Service. In 1996 we repeated the field trial but the data is still being analyzed. We will report on the previous field trials. The data from 1996 will be presented in a future paper.

In 1993 and 1994 five plants of each accession (53 accessions were examined in total, but many produced no or very poor fruit) were transplanted into the field over both years. The field consisted of 1.5 meter wide raised beds with a single drip line with 2-liter/hour drippers spaced 0.5m apart running down the middle of each bed. The five plants of each accession were transplanted in a row and each plant was given a code number. During the growing season, passport data was obtained from each plant using the system developed for melons by IPBGR. These included important vegetative traits (e.g. leaf color, leaf shape, growth rates), reproductive traits (e.g. time of flowering, sex of flowers) and fruit traits (e.g. fruit weight, color, size). In addition to passport data, we also: (i) determined the number and timing of female flowers; and (ii) determined fruit quality and constituents (e.g. TSS, reducing sugars, glucose, fructose, EC, pH, acidity). The work was conducted by Yvonne Ventura (Israel), Irina Pirogova (Turkmenistan), Uzken Batilova (Kazakhstan) and Umuzat Bertova (Kazakhstan).

The overall results indicate that a large pool of genetic variation in Central Asian melons. Major differences were found in vegetative, reproductive and fruit quality traits (Tables 1 &2). For example,

1. vegetative traits - accession T-14 had a very long main stem whereas T 1 and 9 were very short;

2. reproductive - the number of female flowers varied from a low of 6 (T1) to a high of 128 (T17). The latter is one of the highest reported in the literature and most of the flowering occurred in a two week period. This corresponded with a very high number of fruits produced, all extremely small (under 150g) and all harvest at one time. This line is presently being investigated for its potential for a single harvest melon variety.

3. fruit quality - Accessions differed in their total soluble solids (TSS) from a very good 12.6% (T 1 and 10) to a low of 7.1% (T8).

2. biochemical genetic variation - the genetic profiles of 45 Central Asian accessions from Turkmenistan (T) and Kazakhstan (K) were examined in 16 loci (Table 3). The work was done by Usken Batilova and Sauli Abugalieva from (Kazakhstan). Considering that each accession originated from one or at most a few fruits, a very high amount of genetic variation was found in many of the accessions. No significant differences were found for A, P or He between the Turkmenian and Kazakh accessions (ANOVA). Significant correlation was found between the three parameters.

b. Kazakhstan (translated from Russian)

The following report is on the research conducted in Kazakhstan to examine genetic variation in melons from Central Asia.

1. field trial - Two field trials were conducted one in 1994 and the other in 1995. The first field trial was conducted at the research station at Turkistan (southern Kazakhstan) and the second at the research station at Kazlada (near the Aral Sea). Over eighty accessions or primitive varieties from Kazakhstan, Israel and Turkmenistan were sown in both localities. The agromanagement techniques were those commonly used in each region. Each

accession/variety was examined for an array of traits. These included germination rate, initial growth rate, time to flowering, days to harvest, number of fruit per plant, yield per plant, fruit weight, fruit shape (length, width and diameter), fruit color (both skin and flesh) and TSS.

In 1994, the research program in Kazakhstan focused at examining the yield, root and seed quality of melons originating in Kazakhstan. We found that the root system of all melon cultivars increased with increased age and life cycle and vegetatively larger plants had larger root systems (Table 4). In addition, the size of the root system was positively correlated with seed yield. In respect to fruit shape, we found that oval fruits were larger and contained more seed than round fruit (Table 5). Fruit with thick stems were found to have larger fruits and more seeds than fruits from thin stems (Table 6).

In 1995, we sowed 80 varieties in the filed but only 34 germinated and emerged. The vegetative period lasted 88-109 days (Table 7). The heaviest fruits were from 7355, and T-62,68,75,78 and 66 (Table 8). Major differences were also found in major agronomic (Table 9) and seed (Table 10) traits. Extensive variation was found for future breeding.

It was important for us to realize the extent of variation in indigenous varieties.

47

Table 1. Important passport and yield characters for melon accessions from Central Asia

Accession	Character					
	Main stem length (cm) 43 DAT[z]	Number of leaves 43 DAT	Internode length (cm) 43 DAT	Days to first male flower DAT	Days to first female flower DAT	Number of female flowers USDAT
T1	41	16	2.3	17	22	6
T2	165	29	5.7	14	20	25
T4	138	34	4.1	8	30	23
T5	178	31	5.6	17	20	43
T6	95	27	3.5	19	24	40
T7	159	33	4.8	14	25	25
T8	83	25	3.3	10	26	25
T9	68	26	2.3	8	30	37
T10	96	29	3.3	14	24	15
T11	108	30	3.6	12	20	31
T12	85	30	2.9	14	31	18
T13	95	25	3.7	15	22	16
T14	136	35	3.8	15	27	19
T15	152	28	5.4	13	26	46
T16	96	23	4.1	12	32	32
T17	153	35	4.3	8	21	128
T18	133	32	4.2	12	21	25
T19	103	25	4.0	15	21	20
T20	48	25	2.5	13	24	0
LSD	9	8	0.5	3	7	14

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48

Table (cont.)

Accession	Character			
	number of fruits/plant	Number of seeds/fruit	Loose seed weight (g1)	Fruit color
T1	1.4	371	1.93	orange
T2	4.3	201	1.06	green-orange
T4	6.5	262	1.09	orange
T5	6.7	651	2.73	green-orange
T6	3.5	453	2.21	green
T7	14.0	375	1.53	orange
T8	54.3	337	1.05	green-orange
T9	4.5	432	1.34	orange
T10	2.8	539	2.01	orange
T11	7.3	447	1.45	orange
T12	3.0	210	0.73	pale orange
T13	3.0	581	1.61	orange
T14	7.0	414	0.77	pale orange
T15	9.4	480	1.58	green-orange
T16	5.5	238	1.17	orange
T17	39.8	265	1.18	green
T18	8.8	609	1.83	green-orange
T19	3.3	507	2.36	orange
T20	1.5	105	2.54	pale green
LSD	19	62	0.22	

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Table 2. The mean number of alleles per locus, A, the proportion of loci polymorphic, P, and the proportion of heterogugotes (He) in 44 melon varieties from Turkmenistan (T) and Kazakhstan (K). n=3.

Variety	A	P	He	Variety	A	P	He
T-10	1.38	0.38	0.146	K13	1.06	0.06	0.021
T-13	1.13	0.06	0.042	T-66	1.00	0	0
T-20	1.13	0.13	0.042	T-95	1.31	0.25	0.063
T-18	1.19	0.19	0.063	T-65	1.19	0.19	0.063
T-1	1.19	0.19	0.083	T-72	1.25	0.25	0.083
T-15	1.31	0.31	0.125	T-67	1.00	0	0
T-17	1.44	0.44	0.167	T-81	1.06	0.06	0.021
T-25	1.00	0	0	K-20	1.00	0	0
T-11	1.06	0.06	0.021	K-9	1.00	0	0
T-7	1.19	0.19	0.063	K-21	1.00	0	0
T-12	1.06	0.06	0	K-16	1.25	0.25	0
T-19	1.25	0.19	0.042	T-82	1.00	0	0
K-4	1.13	0.13	0.083	T-63	1.13	0.13	0
K-11	1.31	0.31	0.125	T-74	1.13	0.13	0
T-72	1.19	0.19	0.063	T-74	1.06	0.06	0
T-66.7	1.31	0.31	0.167	K-19	1.19	0.19	0.063
T-60	1.06	0.06	0.021	K-22	1.00	0	0
T-69	1.06	0.06	0.021	K-7	1.13	0.13	0.063
T-19	1.00	0	0	T-18.1	1.06	0.06	0.021
T-18.2	1.06	0.06	0.063	T-16	1.13	0.13	0.083
T-7	1.25	0.25	0.042	T-4	1.00	0	0
T-76	1.00	0	0	T-61	1.06	0.06	0.021

60

Table 3 The fruit constituents of melon accessions from Turkmenistan

Accession	Fruit Constituent					
	TSS	EC	pH	Acidity	Glucose mg/g FW	percent dry matter
T1	12.6	6.9	4.84	.03	35.8	5.86
T2	8.8	8.4	5.41	.02	20.1	4.85
T4	9.6	7.5	5.75	.02	17.3	5.14
T5	8.8	8.0	4.83	.03	22.6	4.31
T6	13.8	9.4	5.07	.04	39.3	4.25
T7	9.7	7.2	5.10	.03	27.6	5.34
T8	7.1	8.1	4.81	.04	6.5	4.31
T9	7.7	7.6	4.95	.03	21.8	5.24
T10	12.6	7.2	4.83	.04	39.5	6.30
T11	10.5	7.3	5.08	.04	20.0	5.29
T12	8.3	9.7	6.01	.02	26.9	6.23
T13	11.4	7.7	5.74	.02	30.9	7.27
T14	12.2	8.,0	4.55	.06	21.0	7.29
T15	9.7	8.9	5.34	.03	30.7	5.15
T16	11.9	7.7	5.88	.02	12.9	6.84
T17	7.8	8.4	5.54	.02	12.5	4.58
T18	8,.2	9.6	5.27	.03	10.3	3.95
T19	10.5	5.7	4.91	.03	28.0	5.01
T20	11.4	5.4	5.92	.01	26.7	4.95
LSD	0.5	1.2	.23	.01	5.4	0.84

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61

Table 4 Yield and root system development (in kg/cm^2) during different phenophases in Kazakh melons

Phenophase	Degree of Development		
	Low	intermediate	high
leaf formation	5.0	6.0	7.2
side branch formation	8.0	10.4	12.2
flower bud formation	9.0	13.0	14.4
flowering	10.0	15.0	16.6
fruit set	17.0	19.0	22.0
seed yield (100 kg/ha)	1.2	1.6	2.1

Table 5. Seed quality and yield as a function of fruit shape

Trait	Fruit shape	
	round	oval
Seed length (cm)	1.2	1.3
Seed width (cm)	0.5	0.6
1000 seed weight (γ) total	45.0	49.0
embryo	28.0	30.0
endosperm	17.0	19.0
percent fruit in each group	28	72
percent germination	96	98
mean fruit weight (kg) - total	1.5	2.1
mean fruit weight (kg) - marketable	1.2	1.8
seed yield/fruit	215	248

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Table 6 Effects of fruit stem thickness on fruit and seed yield

Trait	Fruit steam thickness	
	thin	thick
Small fruits	1.2	1.3
weight/fruit (kg)	1.1	1.1
fruit thickness (cm)	1.6	1.1
seed size (cm^2)	0.79	0.48
1000 seed weight (g)	58.0	44.0
large fruits	28	72
weight/fruit (kg)	1.5	1.5
fruit thickness (cm)	2.2	1.5
seed size (cm^2)	0.84	0.55
1000 seed weight (g)	61.0	48.0
fruit yield (t/ha)	34.2	22.4
percent seed germination	94	88

52

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Table 7. THE LENGTH OF DIFFERENT PHENOLOGICAL PHASES IN MELONS GROWN IN KAZAKHSTAN

53

Variety	Sowing date	Flowering male	Flowering female	Appearance	Harvest date	Vegetative period
Revigal	12.6	23.7	1.8	20.6	6.9	88
Makdimon	12.6	23.7	21.8	20.6	6.9	88
Galia	12.6	22.7	31.7	20.6	6.9	88
Arava	12.6	22.7	31.7	20.6	6.9	88
Eureka	12.6	23.7	1.8	20.6	10.9	92
Davis	12.6	22.7	31.7	20.6	5.9	87
1007	12.6	22.7	31.7	20.6	5.9	87
Harvest Qu.	12.6	23.7	2.8	20.6	25.9	107
Early Hack.	12.6	17.7	31.7	20.6	8.9	85
Sierra Gold	12.6	17.7	31.7	20.6	27.9	109
Valencia	12.6	17.7	31.7	20.6	27.9	109
7355	12.6	19.7	1.8	20.6	21.9	103
7426	12.6	19.7	1.8	20.6	21.9	103
T-79	12.6	26.7	31.7	20.6	23.9	105
T-62	12.6	24.7	30.7	20.6	22.9	104
T-68	12.6	23.7	31.7	20.6	24.9	106
T-77	12.6	23.7	31.7	20.6	21.9	103
T-75	12.6	22.7	31.7	20.6	23.9	105
T-78	12.6	18.7	29.7	20.6	23.9	105
T-74	12.6	19.7	31.7	20.6	23.9	105
T-64	12.6	20.7	31.7	20.6	23.9	105
T-66	12.6	20.7	31.7	20.6	21.9	103
T-71	12.6	20.7	31.7	20.6	23.9	105
T-63	12.6	20.7	29.7	20.6	2.89	84

54

Variety	Sowing date	Flowering male	Flowering female	Appearance	Harvest date	Vegetative period
T-72	12.6	19.7	31.7	21.6	23.9	105
T-80	12.6	19.7	30.7	21.6	23.9	105
T-61	12.6	19.7	31.7	21.6	23.9	105
T-81	12.6	19.7	31.7	21.6	23.9	105
T-82	12.6	19.7	31.7	20.6	18.9	100
T-69	12.6	19.7	31.7	20.6	25.9	107
T-70	12.6	20.7	31.7	20.6	21.9	103
T-67	12.6	21.7	30.7	20.6	18.9	100
T-60	12.6	21.7	29.7	20.6	20.9	103
T-16.2	12.6	20.7	31.7	20.6	5.9	87

55

Table 8. AGRONOMIC CHARACTERISTICS OF MELON VARIETIES GROWN IN KAZAKHSTAN

Variety	Fruit shape	Veins	Fruit color	Fruit length cm	Fruit length cm	Fruit weight kg	Cork texture	Cork netness
Revigal	round	shallow	orange	46	44	1.5	crevices	interm
Makdimon	round	shallow	yellow	52	52	2.0	crevices	interm.
Galin	round	shallow	orange	44	44	1.2	crevices	low
Arava	round	shallow	orange	48	47	1.7	crevices	low
Eureka	round	shallow	yellow	38	38	0.89	crevices	interm
Davis	round	none	orange	51	50	2.1	crevices	interm
1007	oblate	inter	brown	45	43	1.4	crevices	interm
Harvest Qu.	oblate	none	orange	53	50	2.4	crevices	interm
Early Hack.	round	deep	brown	48	51	1-6	crevices	interm
Sierra Gold	round	none	green	24	24	1.1	crevices	interm
Valencia	round	interm	yellow	44	45	1.0	crevices	interm
7355	oval	fdeep	green	87	54	4.5	smooth	none
7426	kidney	interm	yellow	50	43	1.4	smooth	none
T-79	oval	none	yellow	70	46	3.0	smooth	none
T-62	oval	shallow	green	75	52	4.09	wrinkled	none
T-68	oval	none	yellow	83	49	4.0	crevices	low
T-77	oval	shallow	yellow	54	39	1.5	smooth	none
T-75	oval	shallow	green	84	51	4.5	smooth	none
T-78	oval	shallow	green	78	57	5.0	wrinkled	none
T-74	oval	shallow	yellow	70	60	36	smooth	none
T-64	pear	shallow	green	60	55	3.0	crevice	interm
T-66	round	none	green	61	63	4.1	smooth	none
T-71	oval	none	yellow	65	46		smooth	none
T-63	oblate	shallow	yellow	47	50	1.8	crevises	interm
T-72	oval	none	yellow	67	50	3.0	smooth	none
T-80	oval	none	green	77	53	4.0	smooth	none
T-61	kidney	none	orange	63	52	2.8	smooth	none
T-81	oval	none	yellow	75	50	3.5	crevice	high
T-82	round	interm.	yellow	60	64	43.5	smooth	none

Variety	Fruit shape	Veins	Fruit color	Fruit length cm	Fruit length cm	Fruit weight kg	Cork texture	Cork netness
T-69	kidney	low	yellow	81	66	5.5	crevice	high
T-70	oval	none	orange	71	48	3.5	crevice	low
T-67	oval	none	yellow	57	45	2.2	crevice	low
T-60	oval	none	green	75	53	3.9	smooth	none
T-16.2	round	none	yellow	22	23	1.1	smooth	none

Table 9. AGRONOMIC CHARACTERISTICS OF MELONS GROWN IN KAZAKHSTAN

Variety	Fruit Flesh					Cavity diameter	TSS %	shipping quality
	Color	thickness	surface	aroma	taste	cm		
Revigal	green	5.0	spongy	yes	average	4.2	13	inter.
Makdimon	green	4.5	rough	no	poor	6.8	11	inter.
Galia	green	4.2	spongy	yes	average	5.5	13	poor
Arava	green	4.5	spongy	yes	average	5.0	15	poor
Eureka	orange	3.3	spongy	yes	average	4.5	12	inter
Davis	orange	5.0	spongy	yes	sweet	6.0	15	inter
1007	orange	3.5	spongy	yes	average	5.0	14	inter.
Harvest Qu	orange	5.0	rough	yes	sweet	6.3	15	inter
Early Hack.	green	3.5	spongy	no	average	8.0	12	inter
Sierra Gold	green	2.0	rough	no	poor	4.0	5	inter
Valencia	green	3.5	spongy	yes	average	7.0	11	inter
7355	orange	4.0	rough	no	poor	8.0	10	inter
7426	yellow	2.8	fibrous	yes	poor	6.5	6	inter
T-79	white	3.5	fibrous	yes	sweet	6.0	15	poor
T-62	white	5.5	spongy	no	average	5.3	10	high
T-68	white	4.3	rough	no	average	6.32	12	inter
T-77	white	4.0	rough	no	poor	4.5	7	inter
T-75	white	4.7	rough	no	average	6.0	13	inter
T-78	white	5.5	rough	no	verage	6.0	9	high
T-74	orange	4.7	smooth	yes	sweet	9.0	10	inter
T-64	white	5.0	rough	no	sweet	6.0	14	high
T-66	white	6.0	smooth	yes	sweet	7.5	13	poor
T-71	green	3.6	rough	no	average	7.0	12	inter.
T-63	white	3.5	smooth	yes	average	7.0	7	poor
T-72	white	4.5	rough	no	average	7.09	11	inter
T-80	green	4.0	rough	no	sweet	7.0	13	poor
T-61	white	4.1	rough	yes	average	8.0	11	inter
T-81	green	3.8	rough	no	sweet	7.5	16	inter

Variety	Fruit Flesh					Cavity diameter	TSS %	shipping quality
	Color	thickness	surface	aroma	taste	cm		
T-82	yellow	5.3	spongy	yes	average	8.0	9	poor
T-69	white	5.0	rough	no	average	10.0	10	inter
T-70	white	4.5	rough	no	sweet	6.2	12	poor
T-67	green	4.0	rough	no	average	6.5	12	inter
T-60	white	3.5	rough	no	average	7.0	13	inter
T-16.2	white	1.5	fibrous	yes	poor	4.0	7	inter

Table 10 SEED CHARACTERISTICS FROM MELONS GROWN IN KAZAKHSTAN

Variety	Seed color	Seed size (cm)	Seed shape	Seed weight (100 seeds) g
Revigal	yellow	1.3	ellipsoid	4.10
Makdimon	yellow	1.3	ellipsoid	4.05
Galia	white	1.1	ellipsoid	4.45
Arava	yellow	1.2.	cone	4.15
Eureka	yellow	1.2	cone	2.64
Davis	yellow	1.3	ellipsoid	3.95
1007	white	1.1	cone	2.95
Harvest Qu.	yellow	1.3	cone	4.35
Early Hack.	yellow	1.1	cone	3.50
Sierra Gold	white	1.1	cone	0.50
Valencia	yellow	1.1	cone	2.95
7355	yellow	1.7	oblong	4.70
7426	yellow	1.2	cone	3.70
T-79	yellow	1.4	ellipsoid	7.10
T-62	orange	1.1	deformed	3.40
T-68	yellow	1.4	cone	5.00
T-77	yellow	1.1	deformed	2.23
T-75	yellow	1.3	cone	3.55
T-78	yellow	1.4	ellipsoid	7.15
T-74	white	1.6	ellipsoid	7.80
T-64	yellow	1.3	cone	5.40
T-66	white	1.6	cone	8.52
T-71	yellow	1.4	cone	4.55
T-63	brown	1.4	ellipsoid	4.00
T-72	yellow	1.4	ellipsoid	5.65
T-80	yellow	1.4	cone	5.45
T-61	yellow	1.4	cone	5.00
T-81	yellow	1.2	cone	3.90
T-82	yellow	1.4	cone	5.50
T-69	white	1.3	cone	6.05
T-70	orange	1.3	ellipsoid	4.65
T-67	yellow	1.3	cone	5.40

60

Variety	Seed color	Seed size (cm)	Seed shape	Seed weight (100 seeds) g
T-60	yellow	1.4	cone	5.45
T-16.2	white	1.0	cone	2.25

6. IMPACT, RELEVANCE AND TECHNOLOGY TRANSFER

The finding of this project will be useful and used by the Kazakh and Turkmenian P.I.s in several ways.:

(i) the collections made in melons and wild barley are being used as the basis for national collections. For the first time both countries have collections under their own control and not that of the Soviet Union;

(ii) the collected germplasm is presently being evaluated in both countries for their economic potential. For example, some of the collected melon landraces have been included in a breeding program for cold tolerance in Kazakhstan;

(iii) an understanding by the Turkmenian and Kazakh scientists who worked on the project on the importance of genetic variation and the treasures that they have have influenced their future work plans.

The project's impact on people and institutions was significant. It helped to train an new generation of scientists who, often for the first time, have come to understand the importance of their indigenous germplasm. They have also understood that their indigenous germplasm is disappearing and must be preserved. The institutions involved have benefited in two ways. First by having better scientists. Second, they have improved their infrastructure by purchasing equipment and chemicals that were not possible without the program.

7. PROJECT ACTIVITIES/OUTPUTS

A series of nine meetings/workshops were held between the P.I.s in order to coordinate and discuss the project. These were:

a. May 1993 - Turkmenistan
b. June 1993 Kazakhstan
c. May 1994 - Turkmenistan
d. October 1994 - Kazakhstan
e. March 1995- Israel
f. August 1995 - Kazakhstan
g. November 1995 - Turkmenistan
h. July 1996 - Kazakhstan
i. December 1996 - Turkmenistan

Six junior scientists from the CARs spent at least six months in Israel obtaining training and conducting research. These were:

a. Dr. Yerlan Turuspekov - Kazakhstan
b. Dr. Saule Abugalieva - Kazakhstan
c. Mr. Uzken Batilova - Kazakhstan
d. Mr. Umuzat Bertova - Kazakhstan
e. Mr. Azat Nourberdyev - Turkmenistan
f. Ms. Irina Pirogova - Turkmenistan

A series of papers have either been published or are in press including:

(a) Turuspekov, E.K., S.I. Abugalieva, S. Mendlinger and S. Volis. 1996. Polymorphism in populations of wild barley from Turkmenistan. Genetica (in Russian, in press).

b. Volis, S., S. Mendlinger, U. Safriel, L. Olsvig-Whittaker and N. Orlovsky. Conservancy implications of phenotypic variation and stress persistence in core and peripheral populations of *Hordeum spontaneum*. Biological Conservation (in press).

c. Mendlinger, S., Y. Ventura and S. Abugalieva. Genetic variation in melons from Central Asia. (in press).

d. Y. Ventura, S. Abugalieva and S. Mendlinger. Fruit quality of Central Asian melons. (in press).

Additional papers are presently being written or are being prepared publication.

62

8. PROJECT PRODUCTIVITY

The project accomplished most of its scientific and all of its development goals. Scientifically, the collections and research in wild barley and melons were in depth and provided us with the type of information which we had hoped to obtain. In onions, the goals were not achieved, primarily due to our not finding the targeted species in large enough numbers.

In respect to training and improving the scientific methodology and infrastructure of the CAR institutions, we accomplished our goals. As seen above, a number of junior scientists worked and received training in Israel and the CAR institutes were able to purchase needed equipment.

9. FUTURE WORK

The P.I.s from Kazakhstan, Turkmenistan and S.M. (Israel) are presently writing a major proposal for a trilateral program for the Aral Sea Basin. The program's basis is that the agricultural and economic systems established by the Soviet Union failed do to its lack of understanding the concepts of costs and profits. This led to not only an inefficient agricultural system but to catastrophic environmental damage.