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The use of ecogeographical data in the exploitation of variation from gene banks

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Summary. As the variation of species is known to be influenced both by ecological and geographical factors, data on the origin of a sample from a given species could be used to infer some of its genetic characteristics. This concept was examined in the context of gene banks, where the assembled diversity usually represents a large range of environments and geographic locations. Results suggest that, although ecological variables in the site of origin can be useful in predicting genetic characteristics in the samples, the use of such data is neither simple nor precise. On the other hand simple geographic data, irrespective of their ecological content, were found to offer an effective method of stratifying and sampling variation in germ plasm collections.

Key words: Gene banks – Variation – Origin – Ecogeographical data

Introduction

With the rapid expansion of climatic and ecological data bases, new possibilities have emerged for the prediction of patterns of genetic variation in natural populations according to their geographical origin. The combination of climatic, ecological and geographical (or "ecogeographic") data offers potential benefits in disciplines such as conservation biology and agriculture. For example, ecogeographical principles could be used in helping to select useful samples from gene banks, where the collected diversity is often not evaluated and is described solely by its origin (Peeters and Williams 1984). The purpose of this paper is to determine whether an ecogeographical approach is useful to sample the variation in gene banks, and whether it is the ecological or the geographical component that best describes this variation.

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Materials and methods

Recently collected accessions from gene banks with precise passport data were selected from four different collections. From the available passport data, the climatic conditions at the site of collection of the original samples were determined from latitudes and longitudes, and by matching these with the nearest meteorological stations in the FAO (Food and Agriculture Organization of the United Nations) world climatic database. Adjustments were made for differences in altitude between sites of collection and climatic stations. The lines were then tested for their tolerance to salt in hydroponics solutions in growth chambers, according to the methods developed by Epstein (1972) and Forster et al. (1987). As it is well established that rainfall is negatively correlated with soil salinity (USDA 1954; Tal 1985), the assumption was that entries from arid areas would have greater resistance to salt than entries from more rainfed areas and that this potential could, therefore, be predicted solely on the basis of origin. Altogether, 160 lines were tested. A detailed description of the methods used can be found in Peeters (1988).

Results and discussion

The salinity responses of selected lines were used to regress salt tolerance on rainfall and results are shown in Fig. 1. The t-statistic for the slope was of 4.29, indicating that salt tolerance decreased with rainfall in the site of origin. However, the percentage variance accounted for was only 15.8%. Based on this and other analyses (Peeters 1988), it was found that the associations between the ecological variables and the salt responses were only weak. However, very distinct patterns emerged when the variation was partitioned by origin and particularly when

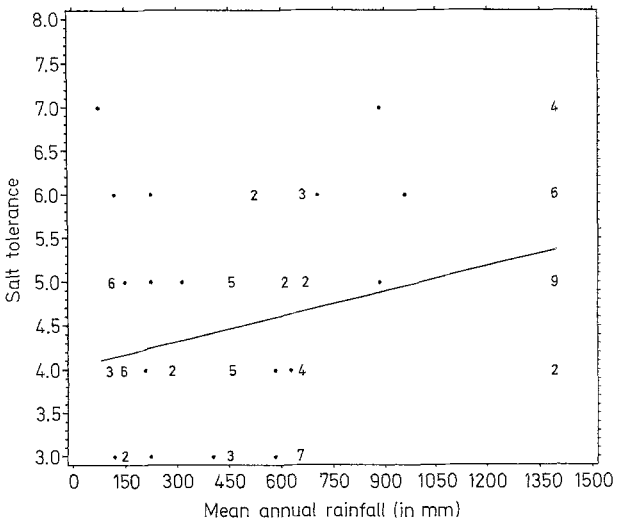

Fig. 1. Regression analysis of salt tolerance on mean annual rainfall in the site of collection for selected USDA entries

it was partitioned by country of origin. This association was first studied by means of an ANOVA on the mean salt tolerance scores, which showed that differences between samples from different countries were very highly significant ($P<0.001$).

Mean ratings for salt tolerance by country and the associated variation, together with mean rainfall values for selected countries, are presented in Table 1. This table confirms that large differences existed between the gene pools of different countries. The most resistant germ plasm overall was that of Iran. Surprisingly, the *Hordeum spontaneum* that was studied and which originated from Israel was the most susceptible material, followed by the commercial cultivars from the U.K. and then the breeding lines obtained from the International Center for Agricultural Research in the Dry Areas (ICARDA). However, in terms of variability the picture was nearly reversed with the exception of the material from ICARDA, which also possessed the least variability. The most variable germ plasm was that originating from Yemen, followed by the wild barleys from Israel and the commercial cultivars from the U.K.

The importance of precise notes in the collection site and in relation to origin was assessed by testing material, which included collector's notes on salinity. The results are shown in Table 2. The table shows that, although two out of the three lines that originated from saline environments gave the best scores for that particular group of material (score of 5/9), several other entries from that group gave the same score. Furthermore, comparisons of the scores for this material with the rest of the trial shows that it had only a low to intermediate overall degree of tolerance. Based on the collector's notes alone however, the three lines marked as originating from a

Table 1. Differences between country samples in mean responses to salt stress and in mean rainfall at the sites of collection

Country		N	Mean[a]	S.D.	CV
India	SR	14	4.928	0.997	0.202
	RF	14	410.500	315.800	0.769
Iran	SR	7	3.714	0.756	0.203
	RF	7	395.700	93.400	0.236
Nepal	SR	27	5.518	0.893	0.162
	RF	27	1357.200	136.100	0.100
Pakistan	SR	26	3.884	0.765	0.197
	RF	26	377.300	252.200	0.668
Turkey	SR	13	4.846	0.899	0.185
	RF	13	523.900	83.800	0.160
Yemen	SR	6	4.666	1.633	0.350
	RF	6	321.700	209.400	0.651
Morocco	SR	16	5.687	0.602	0.106
ICARDA	SR	10	5.900	0.568	0.096
Israel[b]	SR	6	6.333	1.211	0.191
	RF	6	417.500	416.500	0.998
C. CULT.[c]	SR	11	5.909	1.136	0.192

[a] 1 – highly resistant, 9 – highly susceptible
[b] *Hordeum spontaneum*
[c] Commercial cultivars (U.K.)
SR – mean stress response, RF – mean annual rainfall for the collection sites, by country

Table 2. Assessment of the potential for salt tolerance in germ plasm in relation to notes from the collector[a]

Entry[b]	Altitude	Collector's notes	Mean salt response[c]
NG 1020	500 m	Very dry	5
NG 1038	450 m	Salt	5
NG 1085	900 m	Very dry, sandy soil	6
NG 1096	750 m	Slightly salty	5
NG 1109	150 m	Steep slope	6
NG 1138	350 m		6
NG 1142	200 m	Salt	6
NG 1151	550 m	Very rocky soil	6
NG 1168	850 m	Very dry, sandy soil	5
NG 1204	1700 m	Short and sparse plants	7
NG 1215	1800 m	Steep and S facing slope	5
NG 1220	1400 m	Moderate N-E facing slope	6
NG 1228	2200 m	Valley bottom	5
NG 1251	2300 m	Late maturing	6
NG 1266	1200 m	Moderate N facing slope	6
NG 1285	2300 m	Poor crop on rocky slope	6

[a] Based on a 1985 wheat and barley collecting mission to Morocco sponsored by the International Board for Plant Genetic Resources (IBPGR)
[b] Collector's number. Samples currently stored at the Nordic Gene Bank
[c] 1 – highly resistant, 9 – highly susceptible

saline environment could have been selected – erroneously – for their potential tolerance.

The results from this experiment, which are presented only partially here and for only one trait, allow two important conclusions. The first is that variability of germ plasm samples was found to be strongly partitioned by country of origin, some countries being of very low diversity, others of high diversity. In addition, results show that the average expression of a trait generally varies greatly between country gene pools, since the germ plasm of some countries was found to be quite susceptible, while that from others was quite resistant overall. Quality and degree of variation by origin are, therefore, distinct. This is perhaps best illustrated by the *Hordeum spontaneum* lines, which were among the most variable on average but also the most susceptible on average.

Several studies have shown that a careful investigation of ecological variables can lead to the detection of germ plasm with useful and predictable attributes (Rick 1973; Hardacre and Eagles 1980; Klebesadel and Helm 1986). However, in this analysis it was found that climatic mapping was extremely time-consuming and results suggest that ecological variables, whether these are assembled at the collection site itself or subsequently, do not generally appear to be warranted in the context of gene banks in the attempt to facilitate the selection of the most useful variability. Nevertheless, the validity of these concepts was demonstrated, although the associations found were either complex or weak.

While ecogeographical concepts per se appear to be of limited immediate use in the context of gene banks, the use of simple passport descriptors referring to origin, on the other hand, appears to offer a genuine potential to sample and utilize effectively the variability in collections. In this and in another analysis (Peeters and Martinelli 1989), variation of gene bank samples was found to be substantially different by country of origin. Furthermore, origins showed strong differences both in the quantity and quality of their variation. This signifies that some countries are better sources in which to seek variation for a given trait than others, but since associations between traits vary strongly between origins, these other countries may be better eventual sources for the improvement of cultivars in a given breeding context. A high level of variation for a given country and for a given trait does not necessarily mean that this country will be a useful source of material for that trait. For example, in this experiment the variation found in the *Hordeum spontaneum* from Israel was among the highest. However, this germ plasm was also the most susceptible on average for the trait that was tested. Both dimensions of variation are geographically distributed and appear to follow geopolitical boundaries more precisely than ecogeographical ones. In the case of cultivated species, these patterns are likely to have been strongly influenced by the activities of the plant breeders and the farmers, who have developed and exchanged germ plasm within their own country limits. Hence, the best approach to use gene banks effectively appears to lie in first structuring the available samples carefully according to their origin and then in making small subsamples from each of the defined origins available to the breeders for detailed evaluation in their own environments.

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