A number of attempts have recently been made to identify the wild populations that form the founder germplasm stock of our crop plants (Huen et al. 1997; Molina-Cano et al. 1999; Ladizinsky 1999; Zhou et al. 1999; Badr et al. 2000). Some of these works were based mainly on comparative analyses and statistical treatments of genomic DNA polymorphism data (Huen et al. 1997; Molina-Cano et al. 1999; Zhou et al. 1999). This approach can lead to biased or, at times, conflicting conclusions because the criteria for comparisons are traits that are polymorphic both in the wild and among the cultivated material. Therefore, the end result of these comparisons is a set of values expressing relative difference (or similarity) between the accessions studied, presented in most cases as a dendrogram or set of dendrograms. Therefore, any relative approach analyses using isozyme, random amplified polymorphic DNA (RAPD), restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), simple sequence repeats (SSR), or single nucleotide polymorphisms might yield different results when carried out under similar conditions.

The inconclusiveness of the genetic distance approach has been demonstrated in several crops, of which lentil is one example. Ranges of genetic similarity among accessions of cultivated lentil (Lens culinaris Medikus), its wild progenitor subsp. orientalis (Boiss.) Hand.-Mazz., and a more distantly related L. odemensis Ladiz. are 0.71–1.00, 0.76–1.00, and 0.75–0.95, respectively, with 0.76–1.00 between the cultivated lentil and its wild progenitor and 0.75–0.95 between the cultivated lentil and L. odemensis (Hoffman et al. 1986). Another difficulty in using relative genetic distance to identify the wild genetic stock of a crop plant is the genetic bottleneck typical of most domestication events (Ladizinsky 1985). Usually, domesticated crops are thought to have originated as a result of mutations in the seed dispersal loci of a few individuals. In a wild population encompassing high DNA polymorphism, such mutations did not necessarily occur in the most frequent DNA motif at any one locus.

Genetic distance analysis was recently utilized to suggest Morocco as a centre of origin of domesticated barley (Hordeum vulgare L.) (Molina-Cano et al. 1999). The main problem with this contention has to do with the identification of the so-called wild barley (Hordeum spontaneum C. Koch) from Morocco. These populations were collected in a restricted area in the Djebel Siroua range, where they grow exclusively in cultivated fields and never spread into the adjacent natural habitats dominated by the wild desert plant Artemisia herba-alba Assso. (Molina-Cano et al. 1982). Moreover, in their analysis these authors included a tough rachis type, indicating their failure to take into account the differences between wild and domesticated plant forms. Yet another disturbing point (in addition to the title), is the conclusion suggesting Morocco as a possible centre of origin of cultivated barley. It is hard to understand how the high level of internal similarity of the Moroccan barley, which is likely to be a mere result of a founder effect (Ladizinsky 1985), supports such a conclusion.

In our view, the spontaneous barley types from Morocco originated from back mutations in one or two of the brittle-rachis genes (bt1, bt2) of cultivated barley grown in that area. This would provide a plausible explanation for the high degree of internal similarity of the Moroccan barley, its adaptation to cultivated fields, and its inability to survive in the surrounding natural habitats (Molina-Cano et al. 1982).

Recently, AFLP markers were used to estimate genetic distance between wild and cultivated barley (Badr et al. 2000). In this study, accessions from Israel, Jordan, Lebanon, Syria, Turkey, Iraq, Iran, northern Africa, central Asia, and the Himalayas were compared. Interestingly, the hypothesis of Molina-Cano et al. (1999) regarding Morocco as a center of origin of cultivated barley was not confirmed by Badr et al. (2000). Based on their DNA marker analyses, Badr et al. (2000) suggest that certain populations in the central and northern parts of Israel along with several Jordanian populations are the possible origin of cultivated barley. Inspection of the number of Israeli and Jordanian accessions versus the numbers of lines from the rest of the geographic regions relative to the actual area of the respective territories reveals the following: Israel and Jordan, while holding less than one thirtieth of the area of the other regions, are represented by 132 wild accessions. The remainder of the wild barley distribution range (including northern Africa, central Asia, the Himalayas, Turkey, Iran, Iraq, Syria, and Lebanon) are represented by 185 accessions. Had the Israeli–Jordanian wild barley genepool been represented by merely 6 lines in accordance with its relative area, what might have been the
result? Moreover, it looks as if Badr et al. (2000) refrained from comparing their results with previously published data on Israeli wild barley populations. Neale et al. (1988) identified several chloroplast DNA types among wild barley from Israel. Comparing the plastome types to cultivated barley, Neale et al. (1988) reached the conclusion that populations from the north of Israel, near the Sea of Galilee, most resemble the cultivated germplasm studied. This seems to contradict the suggestion of Badr et al. (2000) that wild barley from the central part of Israel contributed to the cultivated genepool.

In another recent paper, southwest Asia was proposed as the origin of cultivated oats (Avena sativa L.) (Zhou et al. 1999). These authors calculated genetic distances from RAPD polymorphism data and used the presence (or absence) of a chromosomal translocation as a diagnostic trait to trace the likely geographic origin of the A. sterilis L. accessions that most closely resemble cultivated oats. Unfortunately, their conclusion regarding the southwest Asian origin of cultivated oats is incompatible with their own data. Although common oat accessions were clustered into the same group and all possessed the chromosomal translocation, wild A. sterilis accessions from other territories, such as Afghanistan, Greece, Ethiopia, and Tunisia, showed the same characteristics.

The origin of crop plants has intrigued scientists for more than a century, and has been studied by several schools using different approaches and techniques. In the era of molecular biology, and with the advent of sophisticated diagnostic tools and statistical approaches, scientists would be well advised to compare their results with previously published data, as well as with those obtained by other methodologies, and to seek corroborative evidence from different fields, such as archaeology. Indeed, the suggestion by Huen et al. (1997) of southeast Turkey as the origin of cultivated einkorn wheat (Triticum monococcum L.), although based solely on AFLP data, is in full agreement with the archaeological evidence. For the crops discussed here, however, the archaeobotanical remains are in favor of barley domestication in a specific area of the Fertile Crescent (Lev-Yadun et al. 2000) and domestication of oats in Europe (Zohary and Hopf 1993).

Recently it has been suggested that cultivated barley is probably of polyphyletic origin (Zohary 1999). Indeed, Ladizinsky (1998) has estimated that about 100 independent mutations of tough rachis are required to explain the present-day allozyme diversity of cultivated barley. Whether such mutations had occurred only in a restricted area as recently suggested for the origin of Near Eastern agriculture (Lev-Yadun et al. 2000) is unclear. Alternatively, such mutants might have arisen over a large geographic range, thereby undermining the possibility of tracing the geographic origin of the initial cultivated stocks.

In our view, and in light of the above examples, a more reliable approach in attempting to identify the wild genetic stock of a crop plant is required. One possible approach is to make use of a set of diagnostic traits, all monomorphic in the cultigen but highly polymorphic in the wild. This will provide the student with an answer that is less dependent on sampling errors, and is not given in relative terms only. Using crossability relationships, meiotic chromosomal pairing data (as an expression of the chromosomal linear order), and chloroplast DNA restriction pattern, Ladizinsky (1999) recently suggested L. orientalis populations from northern Syria and southern Turkey as the possible genetic stock of cultivated lentil. Unlike the suggestions of Molina-Cano et al. (1999), Zhou et al. (1999), and Badr et al. (2000), this identification is fully congruent with the archaeological evidence (Lev-Yadun et al. 2000).

References


