The chromosome number was determined for 25 of the 68 BC_1 F_1 plants. Of these plants fourteen had the euploid chromosome number 2n = 34. Nine plants had one extra chromosome, 2n = 35, while two plants had two extra chromosomes, 2n = 36. In some cases the extra chromosomes were telocentric and probably came from misdivision of lagging chromosomes. Extra whole chromosomes were only found in plants showing multivalents in meiosis so were probably derived from unequal segregation of multivalents in the F_1. The plants with extra chromosomes did not have decreased fertility or vigor. This indicates that sunflower is relatively tolerant of aneuploidy involving additional chromosomes.

The chromosomal relationships of the species are being investigated by meiotic analysis of the hybrids. Although the investigation is not yet completed, the main trends are clear. Six of the annual species, *H. niveus, H. debilis, H. bolanderi, H. anomalus, H. deserticola,* and *H. paradoxus* have similar chromosome end arrangements. None of these species differs by more than one translocation from any of the others. Structurally the chromosomes of these species are also very similar to the chromosomes of the perennial species (Heiser and Smith, 1964, Chandler, unpublished data). The chromosomes of the remaining five species have diverged from those of the core group by additional translocations. Clearly, the most divergent is the cultivated species *H. annuus,* a fact which has unfortunate implications for the efforts to use wild species as breeding material. *H. annuus* differs by at least four translocations from the vast majority of the annual and perennial species, and these translocation differences are one of the primary causes of sterility in the interspecific hybrids.

The multivalent configurations listed in Table 2 are within one translocation of the true maximum configuration. Some uncertainty arises concerning some rarely expressed configurations which in some crosses are difficult to distinguish from artifact chromosome associations. This problem is most serious in those hybrids exhibiting complicated configurations. For example in the hybrid *H. debilis* x *H. annuus* a chain or ring of twelve chromosomes is sometimes seen but is difficult to distinguish from a close association between the more commonly observed pair of hexavalents.

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CLUSTER ANALYSIS OF WILD *HELIANTHUS ANNUUS* ACCESSIONS.

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ABSTRACT

Wild *Helianthus annuus* L. plants are widely distributed over North America, and extensive collecting has resulted in about 400 accessions in the Davis collection. We have recorded data for 7 morphologic and 6 agronomic characters from 7 to 10 plants in each of 177 accessions. Even with these data it is an enormous task to evaluate the potential of each accession for improvement of the domestic cultivars. Consequently, the data set was analysed using cluster analysis based on the standardized Euclidean distance measure (BMDP2M). We then separated the accessions into 10 groups or 20 groups based on either morphological or agronomic data. Groups can be selected for specific characters. For instance in the morphologic data separation a cluster of 3 accessions with stem length of 72 cm can be compared to another cluster of 4 accessions with stem length of 260 cm. The cluster with the largest number of accessions (18) has a stem length of 195 cm. One group with 11 accessions was early with a mean anthesis date on May 23. There were two groups, one with 3 accessions and one of 7 accessions, with a mean of June 15 for anthesis date. The C18:2 fatty acid component of the oil for these two late groups was 62.4 and 70.5% respectively, yet the seeds apparently developed during the same period and were subjected to similar environmental conditions. These cluster results and others can be used to select likely candidates for use in a breeding program.

INTRODUCTION

Heiser *et al.,* (1969) describes six forms of uncultivated *Helianthus annuus* L., and reported that these are commonly found in every state of the United States plus areas in Canada and Mexico. Each local swarm of plants has the potential of contributing germplasm that is different from any other source. We have over 400 accessions in the USDA collection at Davis. With so many accessions, how does the plant breeder determine which might be the best for parental material?

Environmental modification of the phenotype of crop plants is well known (Goyne *et al.,* 1979). The wild *H. annuus* at different collection sites are frequently different in height, anthesis date, and other characters, but the plant breeders need to know whether these differences reflect genetic effects or phenotypic variations due to environments. The accessions can be grown in a uniform environment and morphologic and agronomic data recorded to determine the mean and variances associated with each. In most cases the agronomic data will be most important, but this will be at least partially dependent on the objectives of each breeding program.

This paper describes the use of cluster analysis to determine distinct groups containing similar types under a common set of environmental conditions. If this grouping is meaningful, one or two accessions in each group can be used as parental material to determine the possible germplasm potential which would be contributed by the collection.

Table 2. The group means of the agronomic characters for division into 10 groups.

Group no.	Anth. date	Vigor rating	Seed length	Weight 200 seeds	Oil	C18:2	Number of accessions*
		scale 1 to 5	cm	g	%	%	
1	6 — 11	2.6	4.7	1.6	28.6	69.5	40
2	6 — 10	2.7	4.9	1.7	31.6	68.3	22
3	6 — 7	2.1	4.7	1.6	28.4	67.6	30
4	6 — 13	1.7	4.2	1.3	29.4	65.6	3
5	6 — 8	3.9	5.3	2.5	29.6	63.8	8
6	6 — 15	2.3	4.7	1.4	29.2	70.5	7
7	6 — 3	2.1	4.6	1.3	26.2	63.4	12
8	6 — 2	2.7	4.8	1.6	29.3	70.0	36
9	6 — 15	3.7	5.4	2.6	30.2	62.4	3
10	5 — 23	2.6	5.1	2.2	29.9	70.2	11
Pop x	6 — 6	2.5	4.8	1.7	29.0	68.3	177

*5 accessions not included in any group

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VARIABILITY IN OIL CONTENT IN SEED OF *HELIANTHUS* SPP.

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ABSTRACT

Seed samples of a large number of wild sunflower species collected in the U.S.A. in 1980 were analysed for oil content by a NMR analyser. There was a considerable variability both among the species and among different populations of the same species. The analyses, which included all annual and a number of perennial species, found the oil contents to vary between 10 and 40%. The highest oil content, 35% on the average, was found in *H. anomalus* Blake; among the annual species, *H. annuus* L. had the lowest oil content (22%). Some populations of *H. anomalus* had as much as 40% of oil in seed which simplifies their introduction into our breeding program.

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