

GENETIC DIVERGENCE OF THE POPULATIONS OF WILD SUNFLOWER SPECIES *H.giganteus* L. AND *H.maximiliani* SCHRADER

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Abstract

Diploid perennial species *H.giganteus* and *H.maximiliani* belong to the *Divaricati* section, *Corona-solis* series. For the purposes of this study, there was a selection of 30 populations (15 of each species) from various parts of the U.S.A..

Aimed at determining the degree of similarity between and within the two species, the study included an investigation of more than 30 traits of vegetative and generative organs. All morphometric data were statistically processed.

Dendrogrammes for particular traits, groups of traits or the traits in totality were based on hierarchical cluster analysis. Two other methods in addition to morphological analysis were applied, namely the methods of cytotaxonomy (for pollen viability) and hematahonomy (for seed tocopherol content).

The study results show that divergences are not great with regard to some of the investigated traits, whereas with regard to others, the species and populations vary notably. Dendrogrammes for groups of traits indicate a high degree of divergence both between and within the species. The dendrogramme based on all studied traits of all investigated populations (from both species) shows 3 *H.giganteus* populations to be closer to the species *H.maximiliani* than to their native one.

Key words: Sunflower, *H.giganteus*, *H.maximiliani*, populations, cluster analysis, dendrogramme

Introduction

Using cluster analysis, SCHILING AND HEISER (1981) have managed to classify the species of the genus *Helianthus*. Analysing 42 taxonomic characters, they have determined the degree of divergence between 49 species of this genus, which they classified into 4 sections and 7 series. According to this classification, diploid perennial species *H.giganteus* and *H.maximiliani* are taxonomically closely related, belonging as they do to the *Divarcati* section and *Corona-solis* series. Another classification of 23 species of the genus *Helianthus* through cluster analyses of reserve seed proteins (IVANOV and CHRISTOV, 1994) shows a genetic similarity of the species *H.giganteus* and *H.maximiliani*. At the same time, however, different positions of their populations in the dendrogramme point towards the existence of variability within the species.

Variability between various populations within the same species has been studied by many authors. Thus, HEISER (1960) determined that the populations of the species *H.petiolaris* differed in regard to numerous morphological traits, while the cytological analyses suggested a possibility of the existence of 'cytological races' within the species.

Investigating 32 morphological traits by means of cluster analysis, Dozet et al. (1993) studied genetic divergence of 63 *H.tuberosus* populations collected in Montenegro. The populations were divided into two clusters with different numbers of subgroups. Studying genetic divergence of 19 *H.tuberosus* populations collected in various parts of the United States (by means of cluster-analysing 15 morphological traits), Dozet et al. (1994) proved the existence of genetic similarities between the examined populations (3 groups with 4 populations each).

The objective of our effort was to determine the degree of genetic similarity between the species *H.giganteus* and *H.maximiliani* and the degree of variability between different populations of the species under investigation. The technique employed was cluster analyses of quantitative and qualitative biological traits.

Materials and methods

The research materials used were 15 populations of each of the species *H.giganteus* and *H.maximiliani* collected at various locations in the U.S.A. and cultivated as part of the wild species collection of the Research Institute of Field and Vegetable Crops in Novi Sad.

The following traits came under investigation: 1. Qualitative traits (branching, type of branching, stem color, leaf shape, leaf base, angle of lateral leaf veins, leaf margin, regularity of margin, head shape, shape of ray flower, color of ray flower, bract shape); 2. Quantitative traits (plant height,

number of leaves, petiole length, leaf length, leaf size, head diameter, number of achenes, number of ray flowers, length of ray flowers, length of disc flower, length of disc flower corolla, bract length, bract size); 3. Biological traits (pollen fertility, percentage of fertilization, tocopherol content).

Qualitative traits were assessed in the field at the time of flowering by means of the descriptor list (IBPGR, 1985). The values of quantitative ones were obtained by measurements or counting. Pollen fertility was determined by the stain method (ALEXANDER, 1969) and tocopherol content in the seed by thin-layer chromatography, using the response to the Emmerie-Engel method to identify tocopherol isomers.

Given the large number of investigated traits, the method employed to analyse the data was the addition method of hierarchical cluster analysis.

Marking of the traits under examination for cluster analysis was done by coding. The coding procedure, in turn, was performed on the basis of the descriptor list (IBPGR, 1985), using results of the SNK test (Costat) for metric values. The dendrogrammes were constructed by means of CLUSTER program modules of the SYSTAT statistical package.

Results and discussion

As it turned out, the most variable traits of the species *H.giganteus* and *H.maximiliani* were those of the vegetative plant organs (stem and leaf), followed by the biological ones, whereas the traits of the flower, i.e. inflorescence, proved to be stable and, consequently, important in taxonomic terms.

The traits distinguishing the two examined species are: number of leaves, petiole length, leaf length, number and length of ray flowers, number of achenes, type of branching, stem color and the color of ray flowers.

Trait analysis of the species *H.giganteus* produced a dendrogramme consisting of 4 groups (A-D) (Fig.1.). The most conspicuous population is the 2014 one, falling as it does into none of the groups. The smallest in number is group A, consisting of populations 78 and 2018. Groups C and D each consist of three populations, whereas group B is the largest (6 populations). The least divergent populations within the latter group are 1896 and 1617.

The dendrogramme of the species *h.maximiliani* consists of 3 groups (Fig.2). What is characteristic of this group is that as much as 5 populations fall into none of the groups (2115, 1645, 2226, 2214 and 2219). These are at the same time the most divergent populations, located at far ends of the dendrogramme. The most divergent of all populations is 2219. Group A (two populations) is homogenous, whereas groups B and C are heterogenous and include 4 populations each.

Figure 1. Dendrogramme of all the analyzed traits for *H. giganteus* populations

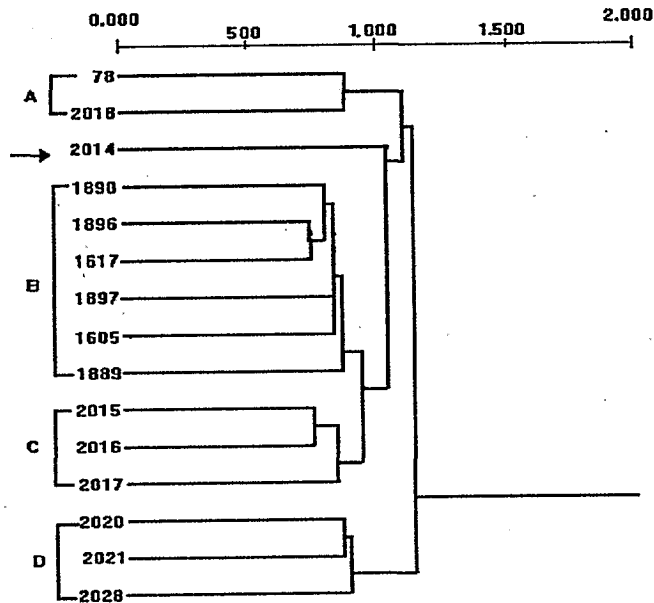
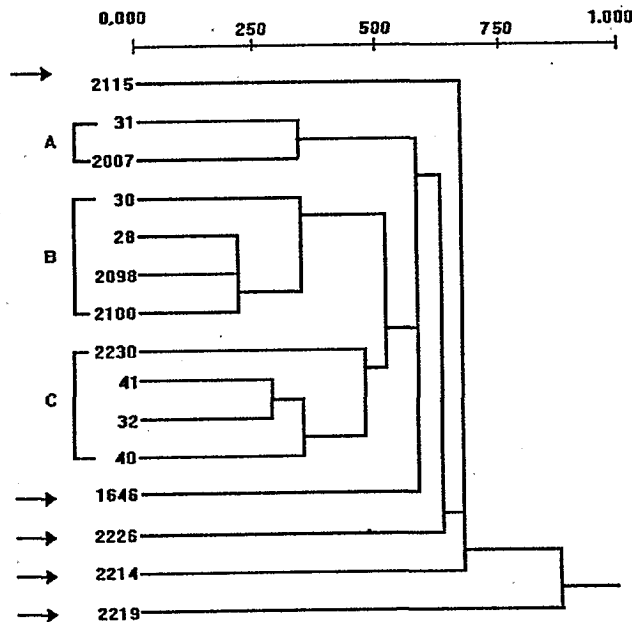
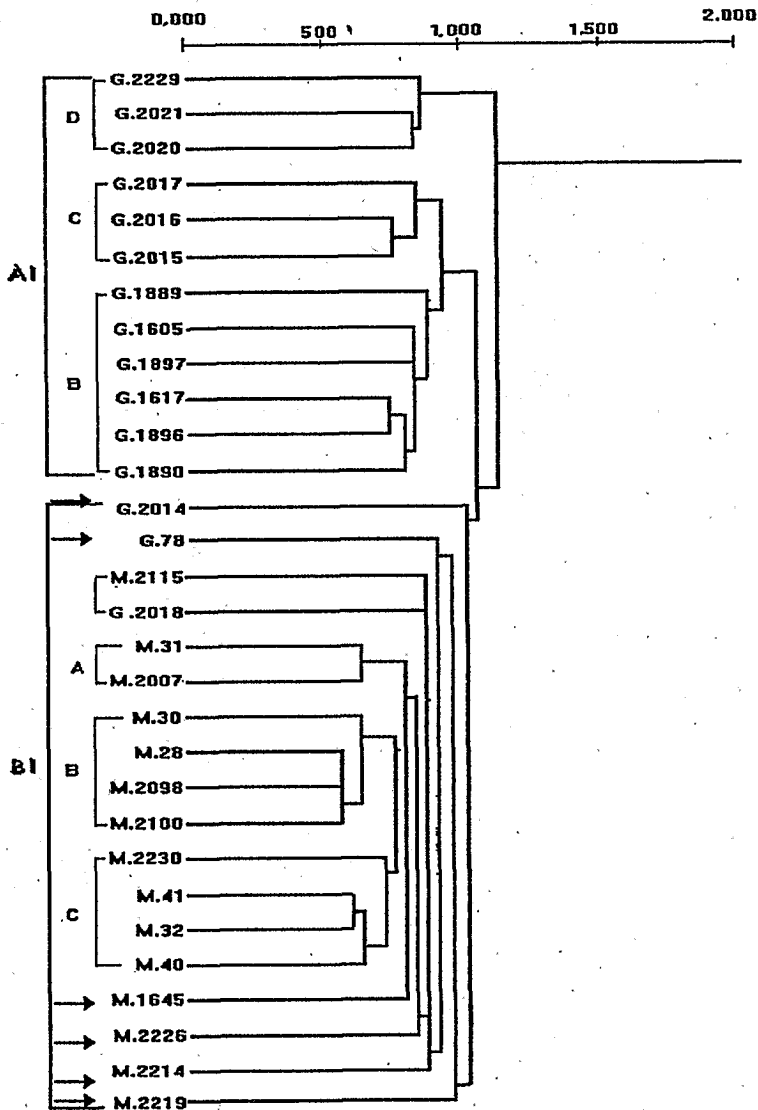


Figure 2. Dendrogramme of all the analyzed traits for *H. maximiliani* populations



A combined dendrogramme of both the species very graphically shows the interrelationships of all examined populations (Fig.3). With certain restraint, this dendrogramme can be divided into two groups (clusters: A I (12 *H.giganteus* species) and B I (15 *H.maximiliani* and 3 *H.giganteus* populations).

Figure 3. Genetic divergence of the populations of *H.giganteus* and *H.maximiliani* represented by the common dendrogramme of all the analysed traits.



In the combined dendrogramme, most of the populations retained their previous positions (Fig. 1. and Fig. 2.). Nonetheless, certain connexions between the two species have been established via 3 *H.giganteus* (2014, 78 and 2018) and 1 *H.maximiliani* (2115) population in the middle of the dendrogramme.

The disposition of the populations suggest that *H.giganteus* populations 2014, 78 and 2018 are closer to the populations of the species *H.maximiliani*. This is accounted for by the fact that the distributional ranges of the two species overlap in the eastern part of the United States (HEISER, 1969; ROGERS et al., 1982) and also by the fact that hybridization between them is possible (LONG, 1955; GEORGIEVA-TODOROVA, 1990).

Conclusion

The results of our study show that, regardless of the taxonomic closeness, these two species differ significantly on a number of traits. With respect to the majority of studied traits, variability exists between as well as within the two species (between the populations).

The dendrogrammes indicate that the degree of divergence is greater within the species *H.maximiliani*. The similarity of some populations of the species *H.giganteus* to those of the species *H.maximiliani* opens the possibility of establishing infraspecific taxons at the level of variety or form within the former species.

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