AN INVESTIGATION OF THE MARKER PROTEINS OF COTTON SEEDS. I.

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Previously, in studying the buffer-soluble proteins of the seeds of cotton plants of the varieities Tashkent-1 (*G. hirsutum* L.) and S-6030 (*G. barbadense* L.), we detected distinctive proteins in them which, according to our hypothesis, are marker proteins of these species [1].

We have investigated the species affiliation of these proteins in different representatives of the genomic groups of the cotton plant in Mauer's classification [2] and we have also investigated the acid-soluble fraction with the aim of detecting distinctive proteins. Electrophoresis in an acid medium is used successfully for revealing the marker proteins of wheat, barley, peas, and other cereals [3-5].

The flour from the seeds of both species, separately, was defatted with chloroform–hexane (1:1) and then acetone, successively, as described in [6]. The extraction and the electrophoresis of the buffer-soluble proteins were performed by the method described in [1], and the extraction of the acid-soluble proteins as in [7, 8] with our own modifications as applied to the cotton plant after the elimination of the buffer-soluble and globulin proteins with 10% NaCl. The acid-soluble proteins were isolated with 1% acetic acid. Electrophoresis was carried out by the Ornstein-Davis method [9] after the pH of the extract had been brought to 4.3 with a 10% solution of Tris. The time of electrophoresis was 2 h, the current strength 100 mA, and the voltage 250 V. The size of the PAAG plate was 10 × 10 × 0.1 cm. Protein was determined by Lowry's method [10], and 100-150 μg of protein was placed in each well of the gel.

As can be seen from Fig. 1, the components with R_f 0.43 and 0.51 were present in the representatives of *G. hirsutum* L. ssp. *punctatum*, ssp. *paniculatum* L., Tashkent-1, and S-4727 and were absent from the representatives of *G. barbadense* L., *G. arboreum* L. and *G. herbaceum* L. The components with R_f 0.37 and 0.48 were present in all the representatives of the species *G. barbadense* L., but in a representative of *G. arboreum* L. only one component, with R_f 0.37, was found. *G. herbaceum* L. was represented by components with R_f 0.34 and 0.40, which indicates a possible greater evolutionary closeness of the species *G. arboreum* L. to the species *G. barbadense* L. than to *G. herbaceum* L. The presence in a representative of the wild

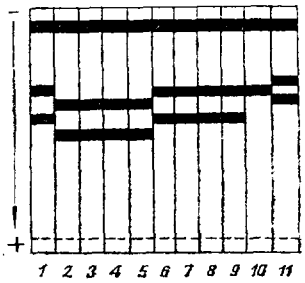

Fig. 1. Electrophoretograms of the buffer-soluble marker proteins of: 1) *G. hirsutum* L., ssp. *mexicanum* – wild; 2) ssp. *punctatum* – semiwild; 3) ssp. *paniculatum* – cultivated–tropical; 4) Tashkent-1; 5) S-4727 – cultivated; 6) *G. barbadense* L; ssp. *darvinii* – wild; 7) ssp. *ruderale* – semiwild; 8) ssp. *vitifolium* – cultivated–tropical; 9) S-6030 – cultivated; 10) *G. arboreum* L. – diploid species; 11) *G. herbaceum* L. – diploid species.

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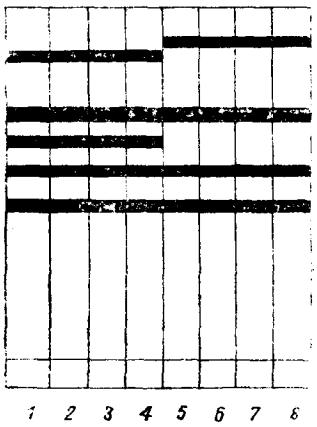

Fig. 2. Electrophoretograms of the acid-soluble proteins of: 1) *G. hirsutum* L. ssp. *mexicanum* – wild; 2) ssp. *punctatum* – semiwild; 3) ssp. *paniculatum* – cultivated–tropical; 4) Tashkent-1 – cultivated; 5) *G. barbadense* L.: ssp. *darvinii* – wild; 6) ssp. *ruderale* – semiwild; 7) ssp. *vitifolium* – cultivated–tropical; 8) S-6030 – cultivated.

form of *G. hirsutum* L., ssp. *mexicanum* of components of R_f 0.37 and 0.48 permits the suggestion of the existence of a common ancestor for these tetraploid species of the cotton plant [11].

Figure 2 shows electrophoretograms of the acid-soluble proteins. It can be seen that the first components from the start in the case of *G. hirsutum* L. and *G. barbadense* L. have different electrophoretic mobilities. Furthermore, in the proteins of *G. hirsutum* L. there is an additional, third from the start, component. These components, just like those given above, are species-specific marker proteins and they can be used for the analysis of interspecies hybrids and for the directed breeding of the cotton plant.

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