

Clark, Curtis. 1978. Evolution of the desert species of *Eschscholzia* (Papaveraceae). Botanical Society of America, Misc. Ser., Publ. 156.

SESSION 6. CONTRIBUTED PAPERS (11-113)

Section: Systematic (BSA) and American Society of Plant Taxonomists (ASPT)

Presiding: Hugh D. Wilson

Room: 100 McBryde

Monday Morning, June 26  
8:30 am.

Session 6

8:30 am.

T1

HUGH D. WILSON. Department of Biology, Texas A&M University, College Station, Texas 77843 - Relationships of *Chenopodium bushianum* Aellen. *Chenopodium bushianum* was described in 1929 from northeastern North American material which had been previously assigned to *C. album* L. and other naturalized taxa. Aellen used characteristics of fruit size, pericarp morphology, and perianth structure to distinguish between *C. bushianum* and elements of the Eurasian *C. album* complex (section *Chenopodium* subsection *Leiosperma*). He believed that *C. bushianum* is most closely related to a group of alveolate-fruited American weeds (section *Chenopodium* subsection *Cellulata*). This alignment has not been followed by regional and state floristic treatments of the northeastern United States. Aellen's taxon is generally either ignored or placed as a synonym of *C. album*.

Crossing patterns resulting from artificial hybridization indicate that *C. bushianum* is distinct from *C. album* and closely related to the alveolate-fruited *C. berlandieri* of western North America. Hybrids between these two species are completely fertile, as is the F<sub>2</sub> generation. This genomic compatibility, plus the presence of morphologically intermediate populations in areas of sympatry, suggest that *C. bushianum* may not be specifically distinct from *C. berlandieri*. Crossing data therefore conform to patterns of morphological, biochemical, and cytological variation in indicating that populations circumscribed by Aellen as *C. bushianum* are part of a native American complex of weedy chenopods, phylogenetically and taxonomically distinct from *C. album*.

8:45 am.

T2

CURTIS CLARK.\* Department of Botany, University of California, Davis, Ca 95616. --Evolution of the desert species of *Eschscholzia* (Papaveraceae).

Four closely related species of *Eschscholzia* are restricted to the deserts of southwestern North America. *E. parishii* (n = 6), *E. covillei* (n = 12), and *E. minutiflora* (n = 18) seem to constitute a polyploid series, although differences in gross morphology and seed coat microsculpturing suggest that *E. parishii* may differ somewhat from the original diploid ancestor. With increased chromosome number there is decreased flower size and greater adaptation for autogamy. *E. glyptosperma* (n = 7) hybridizes experimentally with *E. parishii* and no other *Eschscholzia*. Meiotic analysis suggests that *E. glyptosperma* arose by a chromosome duplication; it may also differ from *E. parishii* by one or more translocations. *E. glyptosperma* seeds possess at maturity a dry, air-filled multiple epidermis which provides buoyancy and is clearly an adaptation for dispersal by runoff water. All three derivative species inhabit harsher climates than *E. parishii*, and *E. glyptosperma* and *E. minutiflora* are widespread.

Monday Morning, June 26

Session 6

9:00 am.

T3

JAMES E. RODMAN. Department of Biology, Yale University, New Haven, Connecticut 06520. - Variation, hybridization, and linkage relations in sea-rockets (*Cakile*, Cruciferae): Seed glucosinolate evidence.

In the first extensive study of intra- and inter-population variability of seed glucosinolates, remarkable uniformity among individuals was found within the two chemically distinct subspecies of Atlantic coast *Cakile edentula*. Glucosinolate profiles of 11 identified compounds were determined by gas chromatography for 170 plants from ten populations and were compared with previous results for 31 samples of this species and with analyses of 36 artificially bred F<sub>1</sub> and F<sub>2</sub> plants. Seed glucosinolates were shown to be stable, genetically determined characters and were employed as taxonomic markers in a study of hybridization between northern ssp. *edentula* and southern ssp. *harperi* where they form mixed populations on the Outer Banks of North Carolina. Twelve plants with hybrid chemical profiles were detected in a sample of 77 individuals from three populations; the zone of hybridization is narrow. Artificial hybrids of the two subspecies are qualitatively additive and quantitatively intermediate in seed glucosinolate composition, and families of F<sub>2</sub>'s show a range of recombinant glucosinolate profiles. Natural hybridization was confirmed by recovering hybrid and parental types in progeny of two presumptive wild hybrids. The array of glucosinolates specific for each of the two hybridizing entities segregated as a linked unit, and independently of fruit length.

9:15 am.

T4

MARVIN L. ROBERTS. Department of Botany, The Ohio State University, Columbus, Ohio 43210. - The application of seed protein electrophoresis to the systematics of the *Orophaca Astragalii*.

Discontinuous polyacrylamide gel electrophoresis was used to determine biochemical relationships among the *Orophacas*, a group of seven perennial *Astragalus* species comprising the sections *Orophaca* and *Sericoleuci*. Native albumins and globulins from seeds could not be used for systematic comparisons owing to the poor resolution and low concentrations of the former and the large molecular weight of the latter. Electrophoresis of SDS (sodium dodecyl sulfate) derivatives of the soluble proteins allowed a high resolution of the denatured polypeptide constituents. SDS electrophoresis of single seeds showed only slight intrapopulation variation, however the interpopulation variation was significant. This distribution of the variation is concordant with that of certain minor morphological characters and leaf flavonoid profiles which vary among populations but are uniform within them. Geographic trends in this intraspecific variation could not be detected. Protein variation within species is so extensive that comparisons between species are difficult. Separation of the species into two sections is not supported by protein similarities. It is concluded that the data are more useful for illustrating the levels and patterns of genetic variation than for assessing taxonomic relationships. The patterns of intraspecific variation could be explained either by genetic drift in disjunct populations, or by the action of strong selective forces in divergent habitats. The primary function of seed proteins as a reservoir of amino acids may allow the rapid accumulation of genetic changes, which can then be maintained because of the disjunct nature of the populations.