GERMPLASM AVAILABILITY, SPECIES BOUNDARIES, AND INTERRELATIONSHIPS OF WILD AND CULTIVATED POTATOES (SOLANUM SECT. PETOTA)

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ABSTRACT

Solanum sect. Petota, the potato and its wild and cultivated relatives, contains 232 species, according to the latest taxonomic interpretation. Seven of these species are cultivated, and the rest are wild. The group is distributed from the southwestern United States to south central Chile, with a concentration of species in the Andes of Peru and Bolivia. There is much morphological and physiological diversity in the group. Many taxa are used in breeding programs to improve the disease resistances and agronomic traits of the world's cultivars. This diversity makes them challenging and fascinating subjects for systematic studies. Habitats range from seashore to alpine grasslands over 4500 m. Most species are diploid (2n = 2x = 24), but some are triploid, tetraploid, pentaploid, or hexaploid (2n = 6x = 72). There are some well-developed biological isolating mechanisms in the group, but many morphologically very dissimilar species placed in different taxonomic series can hybridize easily to produce fertile progeny. Many wild and cultivated species are believed to be of hybrid origin. Authors disagree regarding species boundaries, treatment of infraspecific taxa, species interrelationships, and the extent and evolutionary significance of natural interspecific hybridization.

Collecting expeditions continue to increase the germplasm resources of *Solanum* sect. *Petota*, and approximately 146 (160 taxa, including subspecies) of the 232 currently recognized species are available from genebanks. Recent morphological and molecular studies of these collections are continuing to refine our understanding of systematic relationships of the group. Integrated morphological and molecular studies are essential. Morphological studies are needed to test the taxonomic criteria and identifications of collections. Explicit morphological studies have revealed unexpected synonymy, and it is likely that the group contains fewer than 200 species. Molecular studies have used nuclear genes to address systematic questions of species boundaries, hypotheses of hybridization, and intrasectional relationships. Chloroplast DNA has been used for these types of studies, and to investigate intrasectional and intergeneric relationships. While many studies corroborate prior taxonomic interpretations, others are modifying our understanding of the group.

WILD POTATO DIVERSITY

Solanum L. sect. Petota Dumort., the potato and its wild and cultivated relatives, is a very diverse group. It is distributed entirely in the Americas, from the southwestern United States to south central Chile. Most species grow from 1500 m to 3500 m, but

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others grow at or near sea level, such as wild and landrace populations of *S. tuberosum* L. subsp. *tuberosum* at the southern range of the group in the Chonos and Guaitecas Archipelagos, Chile, and *S. chacoense* Bitter in eastern Argentina. Others, such as the Ecuadorian to Argentinian species *S. acaule* Bitter, can grow to elevations over 4500 m. Habitats of the group range from seashore, dry coastal desert lomas, humid tropics, dry scrub or semi-deserts, high-rainfall mountain forests, and high alpine grasslands (Hawkes, 1990).

Vegetatively, most wild species look much like the cultivated potato, with erect to ascending stems from 0.2 to 1 m tall; pinnately dissected leaves; lateral and pseudoterminal inflorescences with pentagonal to rotate, white to pink to violet to blue corollas; and globoid fruits. Tubers vary in size from that of a pea to nearly the size of the cultivars. The tubers of the wild species usually are bitter, and sometimes toxic, with leaves and tubers containing medium to high levels of glycoalkaloids (Deahl et al., 1993). The wild species rarely are used as food.

Morphological diversity within sect. *Petota* includes many variations from this common form. Some species grow as low rosettes, while others are upright or recumbent with stems 2 m or more long; leaves vary from entire to narrowly dissected and eglandular or with two distinct types of glands; corollas stellate to rotate; and fruits globoid to conical (Hawkes, 1990). Two species, *S. clarum* Correll and *S. morelliforme* Muench, can grow as epiphytes. This morphological diversity is paralleled by much physiological diversity of value for crop improvement. The cultivated potato is affected by many viral, bacterial, and fungal diseases, and is attacked by nematodes, insects, and affected by extremes of heat, cold, and drought. Fortunately, many wild species have moderate to extreme natural disease and stress resistances. In addition, they can impart improved agronomic traits such as increased yields and higher specific gravity of value for the potato chip industry (Hanneman, 1989; Hawkes, 1990; Hawkes & Hjerting, 1969; 1989; Plaisted & Hoopes, 1989; Ross, 1986; Spooner & Bamberg, 1994).

GERMPLASM AVAILABILITY

The economic value of sect. Petota has stimulated an international effort of collection and preservation of the wild species and indigenous cultivars. The major gene banks for potatoes (followed by their latest published accession-specific catalogues) include: Instituto Nacional de Tecnología Agropecuaria (INTA), Balcarce, Argentina (Okada, 1974); Universidad Austral de Chile, Valdivia, Chile (Contreras, 1980); Colección Central Colombiana, Bogotá, Colombia; Institut für Pflanzenbau und Pflanzenzüchtung, Germany (Hoekstra & Seidewitz, 1987); Landwirtschaftswissenschaften, Gross-Lüsewitz, Postleitzahl, Germay (Rothacker et al., 1991); Centro Internacional de Papa, Lima, Perú (Huamán, 1987; only the cultivated species listed); Commonwealth Potato Collection, Dundee, Scotland, United Kingdom (Wilkinson et al., 1994); The United States Potato Collection at the National Research Support Program-6 (NRSP-6, formerly known as the Inter-Regional Potato Introduction Project, IR-1 [Bamberg et al., 1993; Bamberg & Spooner, 1994]); and N. I. Vavilov Institute of Plant Industry, Leningrad, Russia (Budin et al., 1989). Recent collecting expeditions continue to increase the internationally available germplasm from Argentina (Okada, 1976; Spooner & Clausen, 1993); Bolivia (Hawkes & Hjerting, 1989; Ochoa, 1990; Spooner et al., 1994); Chile (Contreras et al., 1993; Spooner et al., 1991b); Colombia and Venezuela (Spooner et al., 1995a); Ecuador (Spooner et al., 1992); and Mexico (Rodríguez et al., 1995; Spooner et al., 1991a). The United States Potato Collection cooperates with other genebanks in the collection, increase, and international distribution of germplasm of these species. It is the largest genebank for the wild species, and maintains 4308 accessions of 146 (160 taxa, including species) of the 232 species accepted by Hawkes (1990) (Bamberg & Spooner, 1994).

TAXONOMIC TREATMENTS

The widespread range and economic value of sect. *Petota* has stimulated much taxonomic interest in the group. Hawkes (1990) produced the latest of eight comprehensive taxonomic treatments of sect. *Petota*, and there are ten regional ones (see Spooner & van den Berg, 1992a, for a summary). In total, 72 taxonomists have described 531 validly published basionyms, plus 67 nomina dubia or nomina nuda, and subsequent transfers to other ranks raise the number of species, subspecies, and varietal names to 664 (Spooner & van den Berg, 1992a). Hawkes (1990) recognized 232 species.

These careful workers have employed various taxonomic philosophies and practices, and their treatments differ in the placement of species into series, species boundaries, rank of infraspecific taxa, and hypotheses of hybridization (Spooner & Sytsma, 1992; Spooner & van den Berg, 1992a). An example of the taxonomic difficulty can be shown from a comparison published by Spooner et al. (1994) of the two recent independent taxonomic treatments of the Bolivian potatoes by Hawkes and Hjerting (1989) and Ochoa (1990). The identifications of identical collection numbers cited in common between these two treatments, excluding types, differed in 20% of the cases. Some identifications differed more. For example, identifications differed 38% of the time among the similar species S. brevicaule Bitter, S. gourlayi Hawkes, S. hondelmannii Hawkes & Hjert., S. leptophyes Bitter, S. oplocense Hawkes, S. pachytrichum Hawkes, S. sucrense Hawkes, S. sparsipilum (Bitter) Juz. & Buk., and S. vidaurrei Cárdenas.

PLOIDY LEVELS

Solanum sect. Petota includes diploids (2n = 2x = 24), triploids, tetraploids, pentaploids, and hexaploids (2n = 6x = 72); natural aneuploidy is unknown. Seventy-three percent of the species with chromosome counts are diploid (Hawkes, 1990). Odd-ploidy cytotypes (diploids vs. triploids) are known for nine species, and even-ploidy cytotypes (diploids vs. tetraploids or hexaploids) are known for two species (Hawkes, 1990; Spooner et al., 1994). Many wild species produce 2n gametes that may have played a role in the origin of these cytotypes (Camadro & Peloquin, 1980; den Nijs & Peloquin, 1977; Ortiz & Ehlenfeldt, 1992; Watanabe & Peloquin, 1989, 1991).

ISOLATING MECHANISMS

Many species in sect. *Petota* can be easily hybridized artificially (Hawkes, 1958; Hawkes & Hjerting, 1969, 1989; Ochoa, 1990) and are believed to hybridize freely in nature. For example, Hawkes and Hjerting (1969) identified 9.5% of the specimens they examined for the potato flora of Argentina, Brazil, Paraguay, and Uruguay as hybrids,

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and Hawkes and Hjerting (1989) identified 7% of the specimens examined for the potato flora of Bolivia as hybrids. Many species may be of hybrid origin (Grun, 1990; Hawkes, 1962, 1990; Ugent, 1970).

Despite this apparent ease of natural interspecific hybridization, most species boundaries are believed to be maintained by a combination of ecogeographical factors, advanced generation hybrid breakdown, genomic differences, and interspecific stylar incompatibilities (Fritz & Hanneman, 1989; Hawkes, 1990; Matsubayashi, 1991). In addition, some species are isolated by strong crossing barriers, governed by a process involving ratios of maternal/paternal effective ploidy in the endosperm, and evidenced by endosperm breakdown (the Endosperm Balance Number, or EBN hypothesis [Hanneman, 1994]). Under this hypothesis, normal seed development depends on a balance of genetic factors contributed to the endosperm from both parents. Within sect. *Petota*, species are 2x (1EBN), 2x (2EBN), 4x (2EBN), 4x (4EBN), and 6x (4EBN) (Hanneman, 1994; Hawkes & Jackson, 1992).

The predictive value of EBN has been useful to engineer interspecific crosses in potato breeding programs (Ehlenfeldt & Hanneman, 1984), and has been used to speculate on phylogenetic patterns in sect. *Petota* (Hawkes, 1994). Although EBN acts as an effective isolating mechanism between some sympatric species, the EBN barrier may have been bridged naturally by 2n gametes. Doubling ploidy level doubles EBN, and unilateral and bilateral sexual polyploidization may have been operative in the evolution of the polyploids (Ortiz & Ehlenfeldt, 1992).

RECENT SYSTEMATIC DISCOVERIES—MORPHOLOGICAL DATA

Most determinations of species boundaries in sect. *Petota* have been intuitive. Some have been tested by explicit morphological analyses (Clausen & Crisci, 1989; Giannattasio & Spooner, 1994a; Johns et al., 1987; Kardolus, in press; Spooner & van den Berg, 1992b; Spooner et al., 1995b; van den Berg et al., 1996; van den Berg & Spooner, 1992). Most of these studies have investigated difficult species complexes. Morphological support for taxa in these studies is usually only through multivariate approaches, and there are few, if any, species-specific morphological characters.

This lack of definitive characters poses problems for construction of keys and repeatability of identifications. This complex pattern of character state variability may be the cause of the lack of concordance of independent identifications of identical herbarium specimens mentioned above. It is unknown if such complex patterns of variability are caused by primary divergence, secondary hybridization and introgression, or a combination of both.

RECENT SYSTEMATIC DISCOVERIES—MOLECULAR DATA

The complex pattern of morphological variability in sect. *Petota* has made phylogenetic reconstructions difficult, and molecular characters are sought to provide additional insights. Hawkes (1994) and Spooner and van den Berg (1992a) review systematic studies using flavonoids, total protein electrophoresis, isozymes, immunology, chloroplast DNA (cpDNA), and single- to low-copy nuclear DNA restriction fragment length polymorphisms (nRFLPs). Flavonoid and immunological data have provided few, and often conflicting, insights into the evolution of the group. Total protein

electrophoresis (Desborough & Peloquin, 1968; Stegemann & Schick, 1985) and isozymes (Douches & Ludlum, 1991; Douches et al., 1991; Oliver & Martínez-Zapater, 1985) have helped resolve some low taxonomic-level questions of cultivar or species identity, hypotheses of hybridization, and genetic diversity. Random amplified polymorphic DNA (RAPDs) have been used for cultivar identification (Cribb & Hawkes, 1986; Demeke et al., 1993; Mori et al., 1993), and phylogeny of the cultivars (Hosaka et al., 1994).

Chloroplast DNA has resolved outgroup relationships (Spooner et al., 1993) to show that tomatoes [Solanum sect. Lycopersicum (Mill.) Wettst.)] are nested within Solanum and are sister taxa to potatoes, and that the series Etuberosa Bukasov & Kameraz and series Juglandifolia (Rydb.) Hawkes do not belong in sect. Petota, as treated by Hawkes (1990). Chloroplast DNA also has helped resolve some major clades in sect. Petota (Hosaka et al., 1984; Spooner & Sytsma, 1992), but resolution within the clades is poor. Chloroplast DNA also has addressed questions of origin of the cultivated species (Hosaka & Hanneman, 1988a, b), and hypotheses of hybridization (Spooner et al., 1991c). Data from nRFLPs have been useful to resolve intrasectional relationships (Bonierbale et al., 1990; Debener et al., 1990), species boundaries, and hypotheses of hybridization (Debener et al., 1991; Hosaka & Spooner, 1992; Giannattasio & Spooner, 1994b), and cultivar identification (Görg et al., 1992).

It is crucial in these molecular studies to conduct parallel morphological studies to reevaluate species boundaries. Identifications in taxonomic treatments and germplasm catalogues have been provided by taxonomists with different taxonomic philosophies and practices, and some identifications will change. For example, the nRFLP study of Hosaka and Spooner (1992) used identifications in Hanneman and Bamberg (1986; superseded by Bamberg et al. [1993]). This nRFLP study distinguished all subspecies of *S. acaule* except subsp. *acaule* and subsp. *punae* (Juz.) Hawkes & Hjert. A later explicit morphological study showed misidentifications of some germplasm accessions of *S. acaule* (Kardolus, in press), and showed *S. acaule* subsp. *acaule* and subsp. *punae* to be distinguished by the nRFLP results.

DIRECTIONS FOR FUTURE SYSTEMATIC RESEARCH

Spooner and van den Berg (1992a) provided the latest suggestions for future research in sect. *Petota*. They stressed the need for explicit morphological studies of species boundaries, DNA studies to investigate species boundaries and interrelationships, a clearer use of terms to distinguish cladistic from phenetic concepts, and more controlled crossing studies with inter- and intraspecific crossing controls and statistical analyses. Additional ideas are provided below.

Solanum sect. Petota has been one of the most intensively studied groups of angiosperms, and therefore provides many independent data sets for comparison. An area of general systematic interest is the development of statistical methods for evaluating and comparing independent data sets (Olmstead & Sweere, 1994; Smith & Smith, 1992; Williams, 1994). Explicit morphological and molecular data sets are rapidly appearing in sect. Petota, and explicit comparisons of diverse results will be needed.

Chloroplast DNA, RAPDs, and nRFLPs have much potential to investigate hypotheses of hybridization (Rieseberg & Ellstrand, 1993). Such data have been used to support (Rabinowitz et al., 1990) and fail to support (Spooner et al., 1991c) such

hypotheses in sect. *Petota*. These studies need to be extended to the many other hypotheses of hybridization in sect. *Petota* (see Spooner & van den Berg [1992b] for a compilation of hybridization hypotheses in sect. *Petota*).

Comparative genome rearrangement (synteny) studies using mainly nRFLPs showed five paracentric inversions, but with conservation of gene order, in a comparison of tomato and potato (Bonierbale et al., 1988; Tanksley et al., 1992). Synteny studies are progressing within sect. *Petota*. The results will test hypotheses of genome evolution generated by cytogenetic data (Matsubayashi, 1991) and help to design successful interspecific crosses and breeding strategies.

The ranges of taxonomic applicability of various molecular data sets need to be explored in sect. *Petota*. For example, RAPDs provide a cheap and quick way to screen large numbers of accessions for diversity and systematics, and have only been used at low taxonomic levels in potatoes and other taxa. Molecular sequence data from cpDNA (Johnson & Soltis, 1994) and the internal non-transcribed spacer regions of nuclear ribosomal DNA (Baldwin, 1992) have potential systematic utility at the genus level (Sytsma & Hahn, 1994). To date, the sequence phylogenies in sect. *Petota* that are needed to test the existing molecular and non-molecular phylogenies in the group are lacking.

I suspect that future studies will quantify and clarify the following patterns and processes in sect. *Petota*: (1) common hybridization and introgression, (2) highly polymorphic polythetic taxa, and (3) genetic similarity between many species. These factors have been invoked by past workers (e.g., Hawkes, 1990; Ochoa, 1990), have bedeviled attempts at systematic interpretations, and are likely to provide continuing difficulties. Future taxonomies probably will recognize fewer species, and interpretations of intrasectional relationships (as series) will be very different.

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