Summary

(1) Seven cultivated species and 226 wild species have been described as potato and its relatives (Hawkes 1990). In this study, the nature of genetic differentiation in the Andean cultivated potatoes and putative ancestral wild species was investigated using chloroplast DNA (ctDNA) and nuclear DNA (nDNA) markers, and the species differentiation and domestication were discussed.

(2) Five basic ctDNA types (T, W, C, S and A types) have been previously distinguished (Hosaka 1986), which showed extensive overlaps in their frequencies among cultivated species and between cultivated and putative ancestral wild species (Hosaka 1995). First, 76 accessions of cultivated and 19 accessions of wild species were evaluated for ctDNA types and examined by ctDNA high-resolution markers (ctDNA microsatellites and H3 marker) and nDNA restriction fragment length polymorphism (RFLP) markers. ctDNA high-resolution markers identified 25 different ctDNA haplotypes. The S- and A-type ctDNAs were discriminated as unique haplotypes from 12 haplotypes having C-type ctDNA, and T-type ctDNA from 10 haplotypes having W-type ctDNA. Differences among ctDNA types were strongly correlated with those of ctDNA high-resolution markers (r=0.822). Differentiation between W-type ctDNA and C-, S- and A-type ctDNAs was supported by nDNA RFLPs in most species except for those of recent or immediate hybrid origin. However, differentiation among C, S and A-type ctDNA was not

clearly supported by nDNA RFLPs, suggesting that frequent genetic exchange occurred among them and/or they shared the same gene pool due to common ancestry.

(3) *Solanum stenotomum* Juz. et Buk. (2*n*=2*x*=24) is considered to be the most primitive diploid cultivated species from which all the other Andean cultivated potatoes were originated (Hawkes 1990). To disclose ctDNA variability and the maternal origin of *S. stenotomum*, 36 accessions of *S. stenotomum* and 86 accessions of putative wild ancestral species were determined for ctDNA types and analyzed by high-resolution markers (seven ctDNA microsatellites and an H3 marker). High-resolution markers discriminated 57 different ctDNA haplotypes, which were classified into the W-type ctDNA group and C-, S- and A-type ctDNA group, and within the latter group S- and A-type ctDNAs were distinct from each other among many different haplotypes mostly having C-type ctDNA. Compared with other putative ancestral wild species, *S. stenotomum* showed somewhat limited ctDNA diversity, having two major haplotypes found in different wild species in different places.

(4) Andigena potatoes (*S. tuberosum* L. subspecies *andigena* Hawkes, 2*n*=4*x*=48) are native farmer-selected, important cultivars, which form a primary gene pool of the common potato (*S. tuberosum* ssp. *tuberosum*). The genetic diversity of 185 Andigena accessions and six Chilean native potatoes (*S. tuberosum* ssp. *tuberosum*) was studied using ctDNA microsatellites and nDNA RFLP markers. Andigena potatoes had 14 ctDNA haplotyes and showed higher variability in central Andes, particularly in Bolivia, whereas those in the northern regions of the

distribution area were remarkably uniform with A1 ctDNA and Chilean ssp. *tuberosum* with T ctDNA. Most of 123 clearly scored RFLPs using 30 single-copy probes seemed randomly sampled and proved the same gene pool shared among these widely collected accessions. Nevertheless, the geographic trend of the nDNA differentiation from north to south along the Andes and the correlated differentiation between nDNA and ctDNA (r=0.120) could also be revealed by Canonical variates analysis.

(5) It is concluded that the species having C-, S- or A-type ctDNA are genetically differentiated from those having W-type ctDNA. Potatoes were possibly domesticated from a broadly-defined ancestral species complex with multiple, or at least dual origins. Andigena was likely originated as tetraploid forms from *S. stenotomum*, but its genetic diversity was considerably modified through sexual polyploidization and introgressive hybridization, and throughly mixed by inter-varietal hybridization and exchange of superior genotypes by humans.