W494 The Dual Origin of Cultivation in Coconut and Its Implications for Breeding

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Coconut is cultivated throughout the tropical coasts and is integral part of the way of life of many human communities. There is no related wild species. Many coconut varieties were identified. Stature and mating system distinguish selfpollinating Dwarfs and cross-pollinating Talls. Within these types, varieties differ in terms of fruit color, size and morphology. Our work aimed to identify the genetic relationships between these varieties as well as the region where cultivation was initiated. It was also to elucidate its dissemination pathways. DNA was collected from 1322 individuals representing more than 100 populations from most of the producing countries. It was analyzed using a microsatellite kit. Results were interpreted in the light of historical information on human population movements. Software Structure identified two major groups. The largest and most diverse group (A) extended from South-east Asia to the whole Pacific. The other group (B) was present in India and on the Atlantic coasts. East Africa and the Western Indian Ocean showed evidence of introgression among groups. The frequency of group A alleles was higher in Madagascar and in the Comoros than in East Africa, reflecting austronesian migrations and arab trade in the region. Attempts to subdivide further diversity preserved group B but split group A into 4 populations. Three of them were centered on South-East Asia, Papua New Guinea (PNG) and the South Pacific without definite limit between them. Virtually all self-pollinating Dwarf coconuts were in the South-East Asian group suggesting that this region was the place of origin of dwarfism. The last population was found on the Pacific coast of Central America and was brought from the Philippines, probably at pre-Columbian times. Our results suggest that coconut cultivation was initiated separately in South Asia and in a region extending from South-East Asian and PNG. The high level of molecular differentiation between groups A and B suggests that gene exchange between India and Pacific was interrupted for a long period. Identifying QT alleles that were fixed during this period would provide breeders with efficient improvement strategies.

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