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Plant distribution patterns in the Ryukyu Archipelago, Japan in the light of seed dispersal abilities

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The Ryukyu Archipelago is an assemblage of continental islands that lie between Taiwan and mainland Japan for approximately 1300 km. The climate is subtropical and moderate throughout the year and the islands are covered by well developed broad-leaved evergreen forests. On the basis of its submarine topography, the Ryukyu Archipelago is subdivided into three areas (the northern, central, and southern Ryukyus) at the Tokara tectonic strait (the Tokara Gap) and the Kerama Gap, where the sea bottom is more than 1000 m deep. These two gaps are the oldest channels in the Ryukyu Archipelago, which first segmented the land bridge connecting the Asian continent, via Taiwan and the Ryukyu Archipelago, with mainland Japan in the Pliocene or early Pleistocene. In consideration of this geographical characteristics, preceding floristic geographic studies in the Ryukyu Archipelago placed demarcation lines between the northern and central Ryukyus, and/or between the central and southern Ryukyus, based on distribution records of a few particular elements of the flora, such as endemics, mangrove plants and sea grasses (e.g., Hara, 1959; Good, 1974; Mackawa, 1974; Takhtajan, 1986; Kitamura *et al.*, 1994). Also, we conducted more quantitative analysis on the floristic demarcations, collecting distribution records of all the seed plants (approximately 1800 species) on major islands from several literature sources into a data matrix, and revealed that the flora of the Ryukyu Archipelago is hierarchically structured as (northern Ryukyus, (central Ryukyus, southern Ryukyus)).

This time, we use subsets of the floristic data in the light of different seed dispersal abilities and further investigate the influence of these deep oceanic channel divisions on the floristic differentiation in this archipelago, taking account of the influence of isolation by mere geographic distances among islands. We examined local patterns of the correlation between pairwise floristic dissimilarity and geographic distance among the islands; if floristic dissimilarity distance is not correlated with geographic distance locally, barriers (not isolation by geographic distance) are likely causing the differentiation of floras. Analysis on the influence of the deep oceanic channel divisions on the floristic differentiation is expected to advance our understanding of floristic plant geography in such island chains.

Oral -21

Population genetics of the Joey palms, *Johannesteijsmannia* H.E.Moore (Palmae)

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Johannesteijsmannia is a palm genus of four tropical rain forest understorey species. Only *Jt. altifrons* is widespread, ranging from southern Thailand, Peninsular Malaysia, Sumatra to western Borneo while *Jt. lanceolata*, *Jt. magnifica* and *Jt. perakensis* are endemic to Peninsular Malaysia. Their increasing commercial exploitation as ornamental plants makes conservation a priority. To conserve effectively, more understanding is needed about their genetics variation within and between populations of each species.

AFLP fingerprinting was generated using six primer combinations on DNA samples from 222 individuals collected from 27 populations throughout the distribution of *Johannesteijsmannia*. *Jt. altifrons* exhibited the highest genetic diversity of all. Populations of each species exhibited moderate genetic diversity (Nei's genetic diversity values ranged from 0.0861–0.1968 and the Shannon information index, from 0.0677–0.2355). Results of the Analysis of Molecular Variance (AMOVA) showed that all congeners partition higher genetic diversity within population (63%–88%) than between populations