

Allopatric speciation due to 1.55 Ma isolation of the islands of Ryukyu, Japan, based on geologic and GenBank data

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The Ryukyu island arc was originally continental margin arc, but separated from the Chinese continent by the rifting of the Okinawa trough, which began at 1.55 Ma and continued to the present. Furthermore, the Ryukyu arc was simultaneously divided into the northern Amami-Okinawa and southern Yaeyama islands by the Kerama rift valley, and consequently formed two isolated islands units. The Kuroshio warm current began to inflow from the Yonaguni strait, and outflow through the Tsushima and Tokara straits also at 1.55 Ma, and effectively acted as barrier with Taiwan, China, and Japan. Through this geologic process that we newly found, vicariant speciation to generate the Ryukyu endemic animal species is expected. We tried to justify this hypothesis by drawing lineaged phylogenetic trees of these endemic species or subspecies using GenBank data, before by ourselves DNA analyses for the many other resting Ryukyu species. We can put precise branching age in these phylogenetic trees, and show simultaneous speciation at 1.55 Ma for Amami-Okinawa and Yaeyama units, respectively. The Taiwan and Tsushima straits, barriers between Taiwan-China and Japan-Korea, was insufficient during later glacial periods, and species are intermingled. Some sea embayment barrier is expected between northern and southern China. We additionally estimate the precise DNA substitution rate and justify the molecular clock.

Keywords: Ryukyu islands, 1.55 Ma synchronous isolation, lineaged phylogenetic tree, endemic species, vicariant speciation, precisely estimated molecular evolution rate