

F833 Secondary Structure Comparisons between Mitochondrial
12S Ribosomal RNA Gene of Genus *Hyla* and *Bufo*

이혜영*, 양동은, 이혁, 김유리, 이정은, 이현익, 양서영
인하대학교 이과대학 생물학과

The entire nucleotide sequence and secondary structure of the mitochondrial 12S ribosomal RNA gene were determined. These are the 12S rRNA from *Hyla japonica* (Korea), *H. japonica* (Japan), *H. suweonensis*, *Bufo bufo* and *B. stejnegeri*. The length of sequence differences were ranged from 931 - 937 base pairs between two genus. The maximum homologies of 12S rRNA genes were 92.6% between *Hyla* species, 97.6% between *Bufo* species.

F834 A Finger Dermatoglyphic Study of the New Zealand-Samoans

Ching Cho
Department of Premedical Course, Chosun University

Fingerprints of 100 New Zealand-Samoan males and 93 females have been analyzed. The methods used in analyzing, formulating and interpreting the fingerprint patterns were those described by Cummins and Midlo (1961). Whorls are abundant in the females (65.6%) than in the males (55.6%). The index of pattern intensity displays a higher value in the females (16.49) than in the males (15.48). The bimanual differences both in the males and females are not statistically significant for the occurrence of pattern on the digits of the right and left hands. The difference between both the sexes for the occurrence of patterns is not statistically significant. Incidences of actual symmetry on the homologous digits represented 78.2% in the males and 85.8% in the females. The mean total ridge counts showed 175.7 ± 54.6 ($M \pm SD$) in the males and 171.6 ± 49.8 ($M \pm SD$) in the females, respectively. Thus, the New Zealand-Samoans show greater affinities with the Mongoloids and the high whorl populations in quantitative dermatoglyphics.