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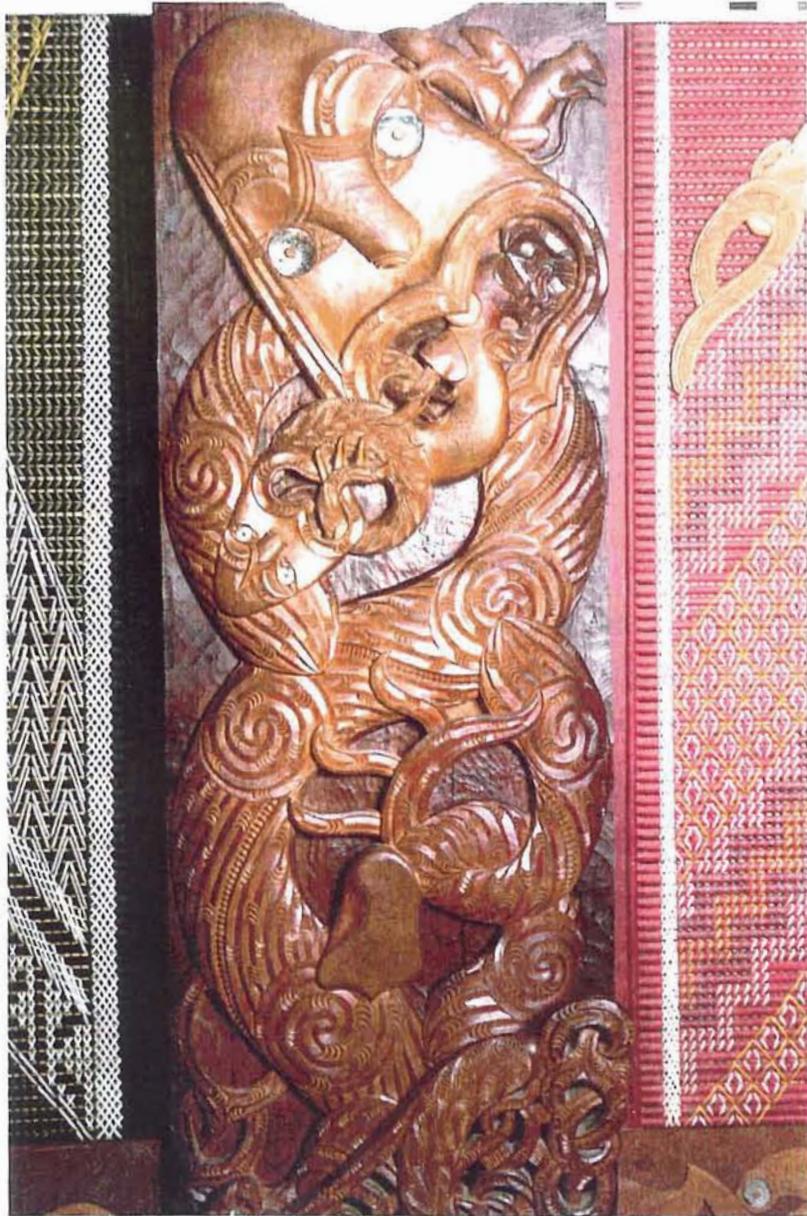
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Ruanui and the kiore - Carving from the *whare whakairo*,
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Abstract

Phylogenetic reconstruction, originally developed for biological systematics, is a tool which is increasingly being used for anthropological studies addressing the problems of population origins and settlement patterns. Given the nature of the phylogenetic model, it is expected that phylogenetic analyses only work well on populations that have stopped sharing biological information. This is particularly pertinent when looking at phylogenies of Pacific populations.

This thesis presents a unique biological approach to the study of human settlement and population mobility in Polynesia, focusing on an animal that was transported through the Pacific by the ancestral Polynesians. I argue that analyses of genetic variation of the Polynesian rat (*Rattus exulans*) are appropriate for a phylogenetic model of human colonisation and mobility. DNA phylogenies derived from 132 mitochondrial control region sequences of *R. exulans* from East Polynesia are presented. These results (1) identify a Southern Cook/Society Islands origin for all East Polynesian *R. exulans* populations, (2) indicate dual origins for Hawaiian *R. exulans*, and (3) indicate multiple origins for New Zealand *R. exulans*. These results are inconsistent with models of Pacific settlement involving substantial isolation following colonisation, and confirm the value of genetic studies of commensals for human prehistory.

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