O a d d a Pac c : E d c DNA Pac c a

E. Matisoo-Smith[†] **and J. H. Robins**

Department of Anthropology and Allan Wilson Centre for Molecular Ecology and Evolution, University of Auckland, P.B. 92019, Auckland, New Zealand

Communicated by R. C. Green, University of Auckland, Auckland, New Zealand, May 5, 2004 (received for review March 16, 2004)

The human settlement of the Pacific in general, and the origin of the Polynesians in particular, have been topics of debate for over two centuries. Polynesian origins are most immediately traced to people who arrived in the Fiji, Tonga, and Samoa region ≈3,000 B.P. and are clearly associated with the Lapita Cultural Complex. Although this scenario of the immediate origins of the 228(the)-22tln9cw22.8(Pacific)-322.8(O59.8med43sr65.0Eted,8med43srthe)-ed43srdebate Polynesians and the Lapita cultural complex continues. Our previous research has shown that analyses of mtDNA variation in the Pacific rat (*Rattus exulans*), often transported as a food item in the colonizing canoes, are valuable for tracing prehistoric human migration within Polynesia. Here we present mtDNA phylogenies based on ≈240 base pairs of the D-loop from both archaeological and modern samples collected from Island Southeast Asia and the Pacific. We identify three major haplogroups, two of which occur in the Pacific. Comparing our results with Lapita models of Oceanic settlement, we are able to reject two often cited but simplistic models, finding support instead for multifaceted models incorporating a more complex view of the Lapita intrusion. This study is unique and valuable in that *R. exulans* is the only organism associated with the Lapita dispersal for which there are sufficient ancient and extant populations available for genetic analysis. By tracking population changes through time, we can understand more fully the settlement process and population interactions in both Near and Remote Oceania.

Oceania | Lapita | prehistory | ancient DNA | phylogeography

T [illegible] ≈40,000 B.P., 9 [illegible] ≈3,100 B.P. (1) (F g. 1). [illegible] G [illegible] B [illegible] 33,000 B.P. [illegible] I [illegible] 29,000 B.P., [illegible] A [illegible] A [illegible]

9 G F E,

D A F 9

, *R. exulans*,

A I A E I I A (2, 6) H (7). *Rattus exulans* 9

R. exulans (8). *R. exulans*

I *R. exulans*, (*Canis familiaris*), (*Sus* .), (*Gallus gallus*) *R. exulans*, E

E 300 *R. exulans*, E (*Rattus rattus* *Rattus norvegicus*), , *R. exulans* , *R. exulans*

D A E *R. exulans* (9)

H D A I A *R. exulans*, *R. exulans*

Materials and Methods

131 A 64 *R. exulans* A H 33 64 1921 1963. H 1993. D A 87 *R. exulans* F G (9)

1, A D A / (10). F (9). ≈240 ; *Supporting Text*, A A C9 D A (11). I). F D A , C9 A A D A (A , G), " (11). A 32 27 (J) (12) 96.4( )-30

A g E 4
H g g
I
g *R. exulans* (15),
9 , *R. exulans*
9 I (16), g
gg D A
R. exulans (17)
(<0.5%) 35
g
R. exulans I
E 4

/
4 I
I
(18, 19),
(7) I EA
9 / C (20, 21).
BB H
II III
BB
9
III.
H III II
9
4 4
C
4 (1).
II, 2, III /
9,
4
R. exulans (*n* = 132),
E 4 C
IIIB. G IIIB

-H (19). *R. exulans* *R. praetor* 2 B, I, 3,120 B.C. (7). H, 4 ., I, *R. praetor* 13,000 B.C., *R. exulans* 8,000 13,000 B.C. I gg (25) *R. exulans* *in situ* g . G g g I A g H, *R. exulans* g g 10,000, 3,000 B.C. .

Alternate Routes of Dispersal? I g g III , 9 . *R. exulans* 4 gg (2) g I A , I A , F 9 , g g , , D0 B 17.6 ( )-226 (0 3. 1 9 0 6)-226 ,

F [illegible] (44). G [illegible]
[illegible] 9 [illegible]