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**A Genetic Analysis of the
Kaimanawa Horses
and Comparisons with Other Equine Types.**

A thesis presented in partial fulfilment of the requirements

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of Master of Science in Genetics
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Abstract.

Recorded sightings of feral horses in the Kaimanawa ranges and the surrounding area date back to 1876. Since then, the Kaimanawa horse herd has received many different influxes and during the mid-1900s its population size increased to the thousands. However, two decades ago the herd went through a substantial reduction in size, numbering only 179 individuals. Hence they were granted legal protection within a defined geographic area. This protection served its' purpose more than adequately, for by January 1994 the population size had increased 10-fold to c.1700. Concurrently, the horse population appeared to be trampling and grazing native endangered flora. Therefore, it has been proposed that some form of population management be enforced on the feral herd. This has evoked opposition in the form of empirically unsubstantiated claims that the Kaimanawa feral horses "may constitute a unique gene pool." (Wright, 1989) This research was executed so as to determine the genetic distance of the Kaimanawa horses from other, more populous equine breeds in New Zealand.

Blood samples were taken from four hundred and eight Kaimanawa horses, and their blood types for the inherited variants of sixteen polymorphic red blood cell and plasma proteins (Al, PGD, PHI, Gc, Tf, α -1 β , Pi, Es, Hb, A, C, D, K, P, Q and U) were determined. From these blood types, the frequency of each of the ninety four alleles within the aforementioned genetic systems was calculated. These frequencies within the Kaimanawa horse sample were then compared with those of Thoroughbred, Arabian, Standardbred, Station Hack and Shire horses. This comparison took the form of genetic distances, calculated via both Roger's and Nei's genetic distance measures.

Both models demonstrated the same trends; the genetic distance is smallest between Kaimanawa horses and Station Hacks ($D_R=0.211$, $D_N=0.070$), and greatest between Kaimanawa horses and Shires ($D_R=0.337$, $D_N=0.413$). These genetic distance values were then diagrammatically represented in phylogenetic trees.

Aside from genetic distance calculations, a qualitative comparison between the Kaimanawa horses and the other equine types was conducted, based on whether each of the ninety four previously mentioned alleles are shared amongst each of the populations. It was found that all but nine alleles were shared with Thoroughbreds and Station Hacks, with the remaining alleles being found in other equine types existing in New Zealand.

All of these analyses indicated that, a) the two equine types with the greatest amount of genetic similarity to the Kaimanawa horses are the Station Hacks and Thoroughbred horses; and b) every allele present in the Kaimanawa horses can be found in another of the equine types studied. Based on this evidence, the Kaimanawa horses should not be classified as genetically unique and their preservation can not be justified based on an argument of genetic insurance. However, it must be recognised that they have aesthetic and historical value to some New Zealanders.



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