

Ireland's position on the western edge of Europe suggests that the genetics of its population should have been relatively undisturbed by the demographic movements that have shaped variation on the mainland. We have typed 221 Y chromosomes from Irish males for seven (slowly evolving) biallelic and six (quickly evolving) simple tandem-repeat markers. When these samples are partitioned by surname, we find significant differences in genetic frequency between those of Irish Gaelic and of foreign origin, and also between those of eastern and western Irish origin. Connaught, the westernmost Irish province, lies at the geographical and genetic extreme of a Europe-wide cline.

Surnames have been used in Ireland from about AD 950 as markers of complex local kinship systems. As both surnames and Y chromosomes are paternally inherited, we divided our Irish sample into seven surname cohorts for which ancient geographical information is known, with some error. Four are of prehistoric, Gaelic origin (Ulster, Munster, Leinster and Connaught) and three are diagnostic of historical influx (Scottish, Norman/Norse and English)¹.

The biallelic markers (*SRY-1532*, *M9*, *YAP*, *SRY-2627* (ref. 2); *SRY-8299* (ref. 3); *sY81* (ref. 4); and *92R7* (ref. 5)) define nine haplogroups (clusters of genetic variants) which are highly non-randomly distributed among human populations⁶, including our samples. In particular, haplogroup 1 (hg 1) has a very high frequency in Ireland (78.1% in the island as a whole).

Surname subdivision reveals a cline in Irish samples, with exogenous samples clearly showing lower frequencies (English, 62.5%; Scottish, 52.9%; Norman/Norse, 83.0%) than Gaelic Irish samples (Leinster, 73.3%; Ulster, 81.1%; Munster, 94.6%),

which almost reach fixation in the westernmost province (Connaught, 98.3%). These highly significant differences in the frequency of hg 1 between Irish Gaelic and non-Gaelic Y chromosomes ($P < 0.001$) and between eastern and western Gaelic Y chromosomes ($P < 0.001$) persist when duplicated surnames are removed.

Eighty per cent ($n = 26$; ref. 7) of European hg 1 Y chromosomes belong to 'haplotype 15', defined by using the complex p49f/*TaqI* polymorphic system⁸. Using this relationship, we estimated that hg 1 frequencies follow a cline within Europe⁹, extending from the Near East (1.8% in Turkey) to a peak in the Spanish Basque

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