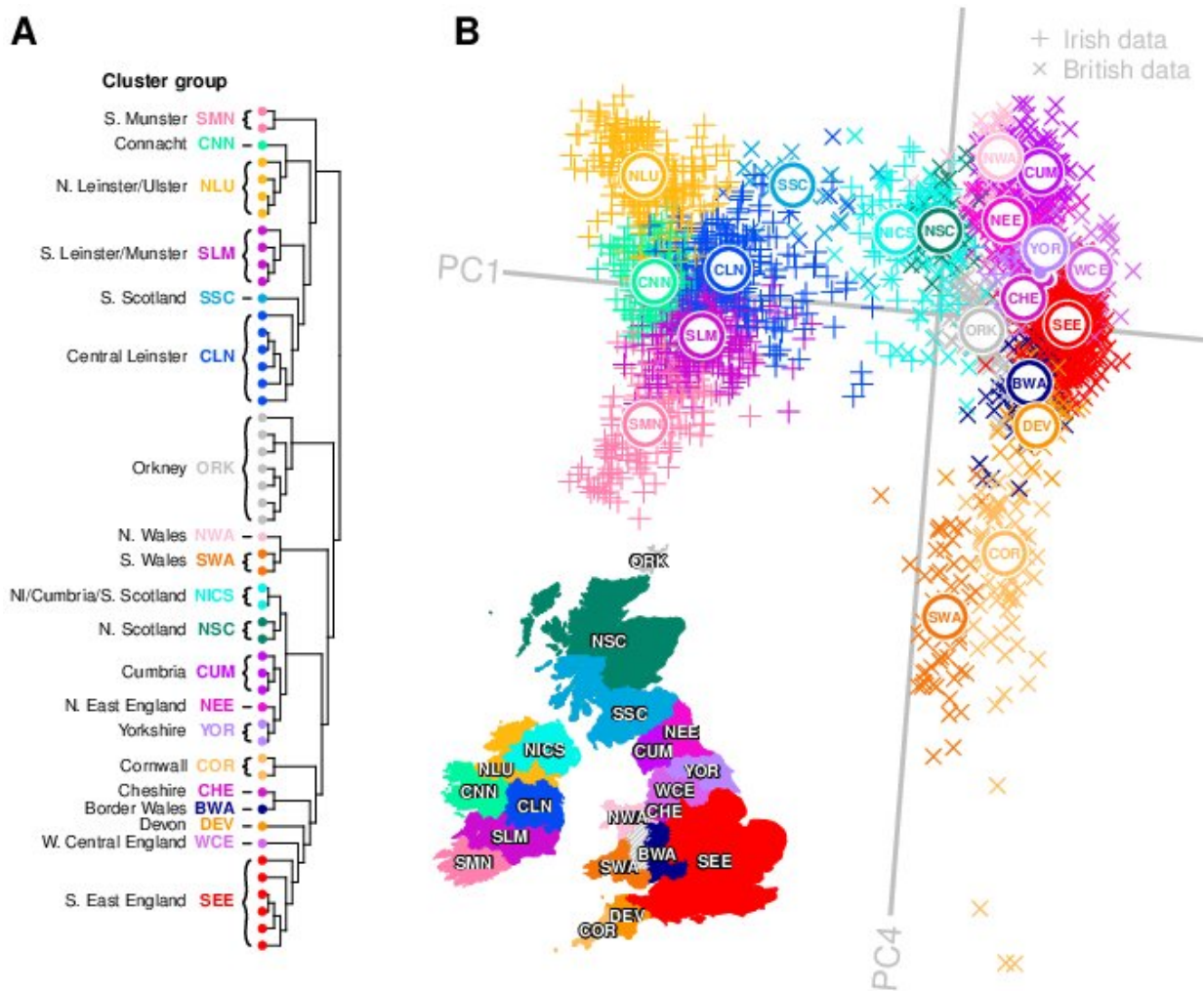


Historical migrations left genetic footprints on the Irish genome

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fineSTRUCTURE analysis demonstrates that haplotypes mirror geography across the British Isles as illustrated in A.) FineSTRUCTURE clustering dendrogram B.) Principle Component space. Administrative boundaries in map sourced from GADM (<https://gadm.org>). Credit: Ross P. Byrne and colleagues

A genome-wide study of the people of Ireland reveals a previously hidden genetic landscape, shaped through geography and historical migrations. Ross Byrne and Russell McLaughlin of Trinity College Dublin in Ireland report their findings January 25th, 2018 in *PLOS Genetics*.

In the 10,000 years that people have continuously inhabited the Emerald Isle, they have established distinct cultural and geographic regions. Previous studies, however, had found no clear genetic groups within the Irish [population](#). In the current study, researchers took a more detailed look at genetic diversity across the islands. They analyzed genetic variation across almost 1,000 Irish genomes and over 6,000 genomes from Britain and mainland Europe. The study revealed 23 distinct Irish genetic clusters, separated by geography. The clusters are most distinct in western Ireland, but less pronounced in the east, where historical migrations have erased the genetic divisions. When the researchers took into account genetic contributions from people with British ancestry, a clear trend arose, showing input from Britain dropping off in populations to the west. The researchers also detected genetic input from Europe and estimated the timing of the historical migrations of the Norse-Vikings and the Anglo-Normans to Ireland, yielding dates that were consistent with historical records.

The study paints a new and more complex picture of the genetic landscape of Ireland, and demonstrates the signatures that historical migrations have left on the modern Irish genome. The findings also show that a distinct genetic structure can exist, even within small, isolated populations. The researchers suggest that this newly revealed structure should be taken into account in future studies that use the Irish population to identify the genetics underlying various traits and diseases.

On the impact of the study, Ross P. Byrne says: "This subtle genetic structure within such a small country has implications for medical genetic association studies. As it stands current corrections for population structure in study designs may not adequately account for this within country variation, which may potentially lead to false positive results emerging. We feel this will be particularly important in the analysis of rare variants as these are expected to be less uniformly distributed throughout a country. We intend to explore this further and identify if this structure should be accounted for in corrections.

Russell McLaughlin adds: "The long and complex history of population dynamics in Ireland has left an indelible mark on the genomes of modern inhabitants of the island. We have shown that, using only genetic data, we can accurately reconstruct elements of this past and demonstrate a striking correlation between geographical provenance and genetic affinity. Understanding this fine-grained population [structure](#) is crucially important for ongoing and future studies of rare genetic variation in health and disease."

More information: Byrne RP, Martiniano R, Cassidy LM, Carrigan M, Hellenthal G, Hardiman O, et al. (2018) Insular Celtic population structure and genomic footprints of migration. *PLoS Genet* 14(1): e1007152. doi.org/10.1371/journal.pgen.1007152

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