FISHING FOR VIKINGS IN THE GENE POOL OF BRITAIN

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The British Isles were profoundly affected by the era of Viking migrations, during the 8th-11th centuries AD. Any visitor can see the extent of Scandinavian influence in the place-names (with plentiful *–by* and *–thorpe* endings), and it is also plain in dialect words, and the historical and archaeological record. Yet the demographic influence of Vikings on the modern population of Britain remains debated.

Genetic analysis has evidence to offer, and past studies have used mostly mitochondrial and Y-chromosomal typing to estimate Viking admixture in various parts of the Isles [1]. A problem with studies of the British mainland is recent population movement, particularly since the Industrial Revolution. To address this problem, we have exploited the link between Y-chromosome haplotypes and patrilineal surnames [2].

Like surnames, Y chromosomes are passed from father to son, and we might therefore expect a link between a particular surname and a particular set of related Y haplotypes, descending from a shared paternal ancestor since the time of surname establishment (about 700 years ago in Britain). Analysis of Y diversity in different surnames shows this to be true [3], and generally speaking, the rarer a surname, the more likely it is that two sampled men carry the same Y haplotype. This relationship is of potential forensic utility, since it suggests that there may be some power to predict a surname from a Y-STR profile, given suitable databases [4].

In the historical context, we can exploit the surname-Y link by sampling men whose ancestry is in an area of Viking settlement, but who also bear a surname known to have existed there in the distant past. By doing this, we hope to bypass the recent post-industrial migration.

Our pilot study of West Lancashire and the Wirral peninsula [5], where history tells us of Norse settlers and the place-name evidence agrees, shows that the approach is valid. Based on frequencies of SNP-based Y-haplogroup and STR-based haplotypes, surname-ascertained population samples are significantly different from samples based only on two generations of residence. Furthermore, an admixture approach indicates that this difference can be explained by a higher level of Norwegian ancestry in the surname-based samples – they more closely reflect the population prior to the arrival of recent immigrants in the last two centuries.

To extend this work, we are now pursuing a similar approach more widely in northern Britain, with the hope of mapping the distribution of Norwegian Viking ancestry; mapping that of the Danes will be more difficult, because of earlier Anglo-Saxon migrations from the same region.

REFERENCES

1. Goodacre S, Helgason A, Nicholson J, Southam L, Ferguson L, Hickey E, Vega E, Stefansson K, Ward R, Sykes B: **Genetic evidence for a family-based Scandinavian settlement of Shetland and Orkney during the Viking periods**. *Heredity* 2005, **95**:129-135.

2. King TE, Jobling MA: **What's in a name? Y chromosomes, surnames and the genetic genealogy revolution**. *Trends Genet* 2009, **25**:351-360.

3. King TE, Jobling MA: **Founders, drift and infidelity: the relationship between Y chromosome diversity and patrilineal surnames**. *Mol Biol Evol* 2009, **26**:1093-1102.

4. King TE, Ballereau SJ, Schürer K, Jobling MA: **Genetic signatures of coancestry within surnames**. *Curr Biol* 2006, **16**:384-388.

5. Bowden GR, Balaresque P, King TE, Hansen Z, Lee AC, Pergl-Wilson G, Hurley E, Roberts SJ, Waite P, Jesch J *et al*: **Excavating past population structures by surname-based sampling: the genetic legacy of the Vikings in northwest England**. *Mol Biol Evol* 2008, **25**:301-309.