People of the *British Isles*

Newsletter Issue 5 - June 2012

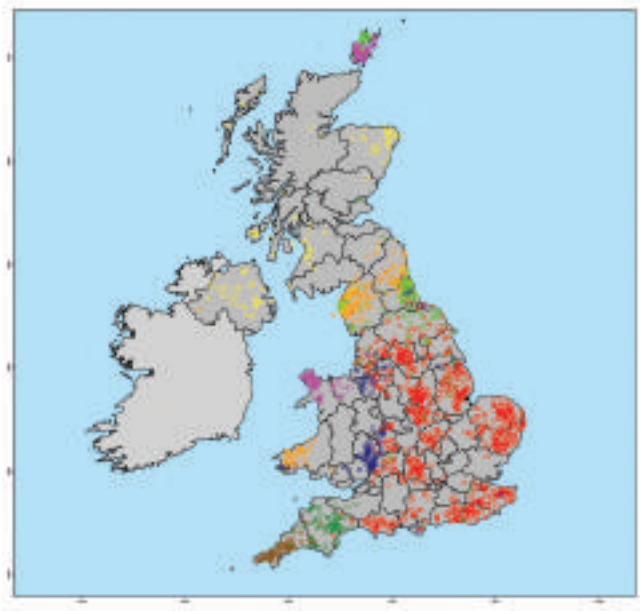
Welcome

Well it is time for the annual newsletter of "The People of the British Isles". We would like to update you on our progress over the last year and tell you about an exciting event we are taking part in. We have spent a fruitful year returning to our volunteers and collecting 3D face photographs and our first paper (People of the British Isles: preliminary analysis of genotypes and surnames in a UK-control population) was published in the European Journal of Human Genetics earlier this year. It is available for download from our website. This effectively announces PoBI to the scientific world and attracted a favourable commentary from Chris Tyler-Smith and Yali Xue. The link to that paper is also on our website. This is a good start and we are now currently preparing a major paper based on analysis of about 2,000 samples. More about that later.

The Royal Society Summer Science Exhibition 2012

The project has been invited to be one of 21 that will be exhibiting their work at the Royal Society Summer Science Exhibition in July. This is a week-long event at the Royal Society open to the public and includes two evening soirees, which are open only to Royal Society fellows and invited VIP guests. This is an annual event that has been running in one form or another since about 1778 with the aim of showing off cutting edge science to the public. We will be displaying some of our genetic maps from our latest analyses and will also have the 3D camera there. The Exhibition will be open to the public from Tuesday 3rd July until Sunday 8th from 10am to 9pm (apart from Wednesday, Thursday and Sunday when it closes at 5pm or 6pm). If any of you are around in London during that period and want to pop in, we would love to see you again! You can get further details from **http://sse.royalsociety.org/2012/exhibits.** We are the "Genetic Maps" exhibit and will be in the main hall.

Prof. Peter Donnelly, Director of the Welcome Trust Centre for Human Genetics, and Professor of Statistical Science, University of Oxford, has been a co-applicant on the grants funding both phases of the project. Peter organised the genotyping of the samples and has led the statistical analysis of geographical structure from genetic data, for the forthcoming paper



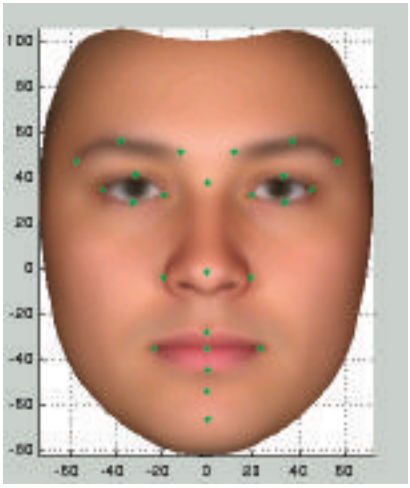
A genetic map of the UK. Each symbol is the place where a sample comes from. Individuals who belong to a genetically similar group are distinguished by colour

Our forthcoming paper

We are working on final analyses and writing up of a really exciting paper. It is based on 2,031 of our samples on which we have examined about 500,000 genetic markers across the genome. We have used a new approach to group individual samples together by genetic similarity into a number of clusters. These are then colour coded and placed on a map of the UK at the average position of where the grandparents were born. This new method of analysis, combined with our careful collection strategy, means that we can detect amazing fine scale population structure within the UK (see map). Indeed the detail of the geographic differences astonished us. For example, the genetic boundaries between Cornwall, Devon and the rest of England remarkably fall on the County boundaries, whilst in Orkney there are obvious differences between Westray and Mainland. This level of detail is unprecedented in human population genetics - until now it has been difficult to even differentiate reliably between North and South Europe.

Furthermore, by collaborating with a couple of other large projects (within the Wellcome Trust Case Control Consortium 2), we have access to genetic data from about 6,300 more samples from throughout Europe. With these, we are currently looking to see if we can detect those European regions that contributed to the clusters that we observe in the UK. The results are looking promising and will be an important part of our paper.

Where are we now?



Face landmarks that need to be annotated by hand

The current collection stage of the project has been going well over the last year. We have done a number of collection events round the country (and have more planned), ranging from Cornwall to Orkney. So far we have managed to collect 3D face photographs from about 920 volunteers, most of whom have been people kind enough to respond to us getting in contact after the initial blood collection. Of these, we have genetic data for about 820 and should soon be in a position to start looking for genes involved in specific facial features.

The whole process is quite complicated and will take a bit of time. Briefly, when we get the photographs, we have to mark by hand 26 specific points on the face (see figure). This is currently being done three times for each individual and these points are then used by a computer program to place many thousands more points, which define the face digitally. These can then be used to compare, for example, distances between specific points on the face across many different people. Our collaborators in Surrey then look at how aspects of features are distributed amongst the volunteers. Once we have some sort of ranking of these features, we can then start to look for associations between the features and genes.

Our collaborators at KCL have also had a productive time collecting 3D face photographs from their collection of twin volunteers and have collected about 1,500 photos. These will help us to determine the heritability of the features we are interested in (see box below) and can also be used to corroborate any genetic findings we make.

A busy day in Bangor

The 3D camera means that we don't work in tents now!

Are you a night owl or a morning person

Why use Twins?

The observation that identical (monozygotic, MZ) look so much more alike than non-identical (dizygotic, DZ) twins, or siblings, suggests that facial features have a strong genetic basis. They can be used to provide an idea as to which features are most likely to have a strong genetic basis and will also be helpful in assessing the accuracy of our face classifications.

When looking at DNA, MZ twins are identical whereas DZ twins only share half their DNA. This means that if both twins in an MZ pair almost always share the same feature, whilst DZ pairs don't, then the feature has a strong genetic component. On the other hand if MZ twins share a feature about the same amount as DZ twins then a strong environmental component is involved.

We are collaborating with TwinsUK, which was set up by Professor Tim Spector, Consultant Rheumatologist in 1992, based at the Department of Twin Research, St Thomas' Hospital, King's College London. They have over 12,000 volunteers registered and have collected a great deal of data from them that has been used in research into many traits and diseases, with over 600 publications to date. They are still recruiting, in particular for a new London based study, and can be contacted through:

www.twinsuk.ac.uk, www.facebook.com/twinsuk, twinsuk@kcl.ac.uk, 020 7188 5555

And if you are willing to be a part of the second phase of the project please do get in contact with our event organiser, Tammy Day (tammy.day@oncology.ox.ac.uk, or 01865 863819).