

Report from the HLA-SBT Training School, Utrecht March 2006

In March 2006 I attended an HLA-SBT Training School in Utrecht, Holland organised by Genome Diagnostics in collaboration with the University of Utrecht Medical Centre. The company offers two courses:

- a) a *basic course* – designed to provide participants with limited experience in SBT the techniques and skills necessary to perform accurate high resolution HLA typing
- b) an *advanced course* – where participants with some SBT expertise are provided with advanced instruction on how to resolve ambiguities, recognise anomalies and perform advanced data analysis and data management

I was awarded a bursary to attend the Advanced course and was very impressed with both the organisation and content of the training programme. After a warm welcome to Holland by Wietse Mulder – managing director of Genome Diagnostics – we briefly introduced ourselves to our hosts and fellow delegates from countries including Germany, Norway, Belgium, UK and Holland. We were then introduced to Dr Rozemuller, the senior scientist in bioinformatics, who gave a presentation on strategies, advantages and pitfalls of Sequencing Based HLA Typing.

For Class I genes their strategy is to amplify the entire genomic region containing the selected HLA gene and subsequently sequence both alleles simultaneously. This approach gives maximum flexibility when resolving ambiguities. For example, most 'A' locus allele ambiguities are found in exon 4, but others might be located in an intron. With the whole gene amplified it is possible to sequence different regions as needed. For genotype ambiguities, where several allele combinations result in identical heterozygous sequences they have developed a series of group specific sequence primers (GSSP) to effect resolution. This approach was shown to provide quality high resolution SBT.

After lunch we were introduced to the software designed by the company for allele assignment. Known as SBTengine®, it is designed to guide the user logically through the important or **crucial** aspects of allele assignment. We were given comprehensive training in the use of the software and, with the support of the experts were able to analyse and interpret the data generated from the practical set up for participants of the basic course which had been held earlier in the week. The preliminary analysis assigned alleles for each locus but often included genotype ambiguities. The practical component of the advanced course was to set up the appropriate GSSPs to resolve these ambiguities.

The day ended with a visit to the sequencing laboratory at the University Medical Centre. From there we were taken for dinner in the old registry of the University. The food, wine and company were excellent and a most enjoyable evening was had by all.

The second day began with a session on advanced data analysis incorporating the additional data from our GSSP exercise. It was demonstrated how SBTengine® is able to analyse all separate sequencing files belonging to a single sample simultaneously. Sequencing runs analysed earlier and sorted in 'Archive' are imported and combined with any additional data from e.g. GSSP data. Only when allele assignment is complete is the final report generated.

That the software is not dependent on the reagents used for sequencing means that data generated by other laboratories can be interpreted by SBTengine®. Some participants on the course had brought sample data 'to test out' the system and all were impressed with the results.

The course ended with a round table discussion when we had an opportunity to exchange experiences and discuss protocols used in our respective laboratories. We were joined by Marcel Tilanus, secretary of EFI and the scientific director of Genome Diagnostics. His expertise in molecular studies is widely respected and his enthusiasm for the SBT protocols developed by Genome Diagnostics and the sophisticated software was obvious.

I am very grateful to the company for awarding me the bursary to attend the Advanced training course. I found it informative, well presented and run in a very relaxed and friendly atmosphere. I am sure that their typing protocols and analysis software will play an increasing part in high resolution typing for the HLA system in the future.