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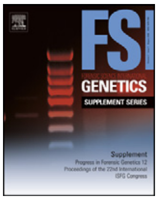

Bonaparte: Application of new software for missing persons program

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ABSTRACT

The Netherlands Forensic Institute (NFI), together with SNN at Radboud University Nijmegen, have developed new software for pedigree matching which can handle autosomal, Y chromosomal and mitochondrial DNA profiles. Initially this software, called Bonaparte, has been developed for DNA DVI. Bonaparte has been successfully applied in a real DVI case: the Afriqiyah Airways crash in Tripoli, Libya on 12 May 2010 in which 103 persons perished. The software performed excellently in terms of computational performance, stability and user-friendliness. This showed that Bonaparte is a reliable and time-saving tool which significantly simplifies and enhances a large-scale victim identification process.

Bonaparte has been applied in NFIs missing persons program. For this, the software is connected to the NFI's missing persons database (CODIS). Since Bonaparte uses XML as import format, data from any source can be imported. In the new configuration, CODIS data is automatically imported into Bonaparte. Then the software automatically performs a set of direct searches, as well as searches against both partial and full family trees. For the autosomal DNA results, exact likelihood ratios are computed. Finally, match reports can be generated on demand by Bonaparte's customized reporting modules. In this way, an advanced search strategy combined with a modern, efficient work flow is realized in NFI's missing persons program.

1. Introduction

The last decade several fatalities have caused the death of many persons. In such events, the identification of the remains of the victims is of great importance. This disaster victim identification (DVI) work is greatly facilitated by the advent of modern DNA technology. Countries have become aware of the importance of preparedness for disaster victim identification (DVI). In the Netherlands, in collaboration with SNN at Radboud University Nijmegen, the Forensic Institute (NFI) has developed new software for pedigree matching victim identification of mass fatality incidences. This software, called Bonaparte uses so-called Bayesian networks to perform the screening and the matching. Bayesian networks are very well suited to model statistical relations of genetic material of relatives in a pedigree [1]. The whole pedigree of relatives of the missing persons could be used in the screening and matching process. This will lead to much less false hits than with methods which do not take complete pedigree information into account. An additional advantage of this Bayesian network approach is their modeling flexibility. Other factors that play a role in the statistical analysis such as mutation model, missing data, uncertainty in family relations etc. are easily and transparently incorporated in the same modeling frame.

This paper describes some features of the software, the performance of the software in a real DNA DVI case and the use of the software in the on-going missing persons program in the Netherlands.

2. Features of Bonaparte

The features described here are specific to Bonaparte's current model. This model can easily be refined and enlarged. Bonaparte's computational core for autosomal DNA profiles is designed to calculate the likelihood ratio (LR). The biological model underlying these calculations is Mendelian, enriched with the possibility of mutation and allelic dropout in the profile [2–4]. It uses defined population statistics and a minimal count method for allele frequencies. Furthermore, it computes the number of mismatches in pedigrees in detail. The validation of the autosomal part of the software has been published [2]. Both simple and more complicated pedigrees, among which inbred ones have been used for this validation.

Besides autosomal DNA profiles, Bonaparte software can handle Y-chromosomal and mitochondrial DNA profiles as well. As no accurate estimations of the frequencies of Y-chromosomal or mtDNA profiles are available, the matching process in the current Bonaparte version returns the (minimal) number of mismatches,

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no LR. For autosomal profiles, the software returns both measures. For all types of profiles, one-to-one and pedigree matching are both supported.

The matches can be performed automatically (scheduled) and manually. Matching against elimination profiles can be done to find contaminated samples. Direct matching of unidentified individuals against each other to detect possible relationships between them is possible. In addition, if the pedigree contains more than one missing person, a stepwise identification can be done by replacing missing person by an individual that has been identified in the first go. For this purpose the pedigree editor has been equipped with a drag-and-drop tool.

3. Performance in a DNA DVI case

On 12 May 2010 an Afriqiyah Airways Flight crashed upon landing near the Tripoli airport in Libya. One hundred and three persons perished. Among the victims were a number of blood relatives. The NFI performed the identification work by DNA techniques and applied the Bonaparte software for the first time in a real DVI case.

Dutch DVI teams collected samples from the victims in Tripoli and samples from the missing persons in the Netherlands. In total 149 tissue samples from bodies or body parts and 220 reference samples from (relatives of) 77 missing persons were sent to the NFI. Sixteen DNA profiles from personal effects and/or from relatives of 7 missing persons were typed in foreign labs and were sent to the NFI. The NFI received no reference samples from 19 non-Dutch national missing persons.

The samples arrived in batches from day 8 to day 25 after the crash.

Upon delivery at the NFI the samples were processed. After isolation and quantification DNA profiles were obtained containing 15 autosomal loci and amelogenin using the Identifiler kit (AB). The isolation, quantification and DNA profiling process took 3–4 days per batch.

After DNA profiling, the DNA profiles were entered into the Bonaparte software and the matching process was started. This matching process took only several minutes per batch. Then, matching reports were generated and were issued the same day.

The total identification process took 25 days, 129 bodies or body parts were matched to a missing person. Matching with Bonaparte took only a small time period in the whole identification process.

It appeared that the Bonaparte software performed excellently in terms of computational performance, stability and user-friendliness. This showed that Bonaparte is a reliable and time-saving tool which significantly simplifies and enhances a large-scale victim identification process.

4. Missing persons program

Since April 2007 the NFI has a national DNA database for missing persons. The CODIS software is used as database. In 2011 the database has more than 900 DNA profiles. It contains besides DNA profiles from unidentified persons and missing persons, DNA profiles from relatives of missing persons as well.

For indirect comparisons - i.e. looking for matches between unidentified persons and relatives of missing persons - the Bonaparte software has been applied.

Bonaparte can communicate with other data transport systems via standard data interfaces which make it flexible. At the NFI the CODIS database is coupled to Bonaparte via an in-house program (so called Napoleon). By this coupling DNA profiles and pedigree information from the CODIS database are imported to Bonaparte. The software automatically performs a set of direct searches, as well as searches against both partial and full family trees. For all cases, exact likelihood ratios (for autosomal profiles) and/or number of mismatches (for autosomal, Y-chromosomal and mitochondrial DNA profiles) are computed. Finally, match reports can be generated on demand by Bonaparte's customized reporting modules. In this way, an advanced search strategy combined with a modern, efficient work flow is realized in NFI's missing persons program.

5. Conclusion

Bonaparte software can effectively handle the identification process in case of large disaster with many victims and it can be applied in the missing persons program.

Conflict of interest

None.

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