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Datasheet for the decision of 1 April 2014

Case Number: T 0984/11 - 3.5.01

Application Number: 03813461.5

Publication Number: 1579013

IPC: C12Q1/68

Language of the proceedings: EN

Title of invention:
METHOD FOR PROFILING AND IDENTIFYING PERSONS BY USING DATA SAMPLES

Applicant:
Gene Codes Forensics, Inc.

Headword:
DNA Profiling/Gene Codes Forensics

Relevant legal provisions:
EPC 1973 Art. 56

Keyword:
Inventive step - (no)

Decisions cited:
T 0641/00

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Case Number: T 0984/11 - 3.5.01

D E C I S I O N
of Technical Board of Appeal 3.5.01
of 1 April 2014

Appellant: (Applicant)	Gene Codes Forensics, Inc. 775 Technology Drive, Suite 100A Ann Arbor, MI 48108 (US)
Representative:	Bradbury, Simon Timothy Nicholas Appleyard Lees 15 Clare Road Halifax HX1 2HY (GB)
Decision under appeal:	**Decision of the Examining Division of the European Patent Office posted on 14 December 2010 refusing European patent application No. 03813461.5 pursuant to Article 97(2) EPC.**

Composition of the Board:

Chairman:	S. Wibergh
Members:	P. Scriven
	P. Schmitz
	B. Stolz
	D. Prietzel-Funk

Summary of Facts and Submissions

I. The Examining Division refused European patent application 03813461.5 on the grounds of a lack of clarity (Article 84 EPC 1973) (main request) and of inventive step (Article 56 EPC 1973) (main request and auxiliary requests 1 and 2). The applicant appeals that decision.

II. The Board arranged oral proceedings and set out its preliminary view of the case in a communication sent with the summons. The Board referred, in particular, to documents D1' (a translation into English of a document, denoted D1, in Russian, namely Gavrilei et al., 2002, "Design of the mDNAbase, an automated system for analysing mitochondrial DNA sequencing data, for the expert identification of unidentified bodies in cases of mass reception of human remains") and D5 (Leclair et al., 2000, "Enhanced kinship analysis and STR-based DNA typing for human identification in mass disasters") as apparently disclosing the aggregation of profiles. The Board also set out its provisional view that the invention amounted to a presentation of data in a manner that helped an operator to analyze them.

III. The appellant responded by letter dated 4 March 2014. With that letter, the appellant withdrew the pending requests and submitted a new main and four new auxiliary requests.

IV. Claim 1 according to the main request read as follows:

A method for profiling and assisting identification of at least one person by using data samples, comprising:

providing a reference DNA profile of at least one person;

providing a plurality of degraded member DNA samples requiring identification;

matching a plurality of member DNA samples together so as to form at least one aggregated matching sample (106), the matched member DNA samples of an aggregated matching sample having DNA profiles matched on the basis of one or more selected criteria consistent with potentially identifying a single individual and each of the plurality of member DNA samples (114) comprising a partial DNA profile exhibiting no discrepancy or only an allowed discrepancy with any other of the plurality of member DNA samples (114) and the at least one aggregated matching sample (106) comprising a DNA profile at least as complete as each of the plurality of member DNA samples;

organizing the at least one aggregated matching sample (106) into a collapsed list (100);

presenting the at least one aggregated matching sample (106) on a one-line display, the one-line display displaying a composite profile representative of the DNA profiles of all the member DNA samples in the same aggregated matching sample (106);

allowing the one-line display of each of the at least one aggregated matching samples (106) to be expanded, the expanded one-line display providing a view of all member DNA samples (114) in the same aggregated matching sample (106); and

allowing the at least one aggregated matching sample (106) to be compared with the reference DNA profile so as to profile and assist in the

identification of the person.

V. On 31 March 2014, the day before oral proceedings, the appellant submitted further evidence in the form of a statement by Professor J. A. Lorente of the University of Granada, and a graph depicting the numbers of identified victims of the attack on the World Trade Centre in New York at various dates.

VI. During oral proceedings on 1 April 2014, the appellant filed an amended version of claim 1 for the main request. In essence, the amendment removed the final step ("allowing ... to be compared ...") and the reference to "at least one aggregated matching sample ... at least as complete as ... member DNA samples". Claim 1 as amended reads as follows (bold text indicating modifications):

A method for profiling and assisting identification of at least one person by using data samples, comprising:
providing a reference DNA profile of at least one person;
providing a plurality of degraded member DNA samples requiring identification;
matching a plurality of member DNA samples together **into** *at least one aggregated matching sample (106), the matched member DNA samples of an aggregated matching sample having DNA profiles matched on the basis of one or more selected criteria consistent with potentially identifying a single individual and each of the plurality of member DNA samples (114) comprising a partial DNA profile exhibiting no discrepancy or only an allowed discrepancy with any other of the plurality of member DNA samples (114)* ***[deleted];***

providing a collapsed list (100) of at least one aggregated matching sample (106); and

presenting the at least one aggregated matching sample (106) on a one-line display, the one-line display displaying a composite profile representative of the DNA profiles of all the member DNA samples in the same aggregated matching sample (106); ***and***

*allowing the one-line display of each of the at least one aggregated matching samples (106) to be expanded, the expanded one-line display providing a view of all member DNA samples (114) in the same aggregated matching sample (106)****[deleted].***

VII. The appellant requested that the decision under appeal be set aside and that a patent be granted on the basis of claim 1 according to the main request submitted during the oral proceedings or on the basis of the claims of one of the first to fourth auxiliary requests, submitted with the letter dated 4 March 2014, all auxiliary requests being amended with the corresponding amendments as applied to the main request submitted during the oral proceedings.

VIII. The appellant's arguments can be summarized as follows.

The inventors had set out to devise an entirely new protocol for profiling, and for assisting in the identification of persons on the basis of a large number of very small, highly degraded samples. It was the aggregation of several samples that were individually insufficient, that allowed positive identifications to be made in such cases. By presenting the aggregates in an expandable collapsed list, it was possible to perform DNA-based identification efficiently. That was a

technical effect. The building of a "virtual profile" from the results of multiple assays on a single tissue sample was not known from the prior art.

The Examining Division referred to documents which showed the general possibility of expandable and collapsible lists, but the skilled person, seeking a solution to a problem in the field of DNA profiling would have had no reason to consult them. There was no reason to expect the solution to any profiling problem in such documents.

The present invention had been applied with great success to the identification of victims of the World Trade Centre attacks. Rather few identifications had been made before the present invention was introduced, but the invention had made many more identifications possible.

Document D1' disclosed a "family group" but that did not have the potential to identify an individual. D1' also failed to disclose the presentation of an expandable collapsed list with a composite profile. Indeed, D1' taught away from the invention: following D1', the skilled person, faced with highly degraded DNA, would turn to mitochondrial DNA. The present invention, however, taught that highly degraded nuclear DNA could be useful, if treated properly, namely by using aggregation.

Document D5 related to the identification of victims of an air crash. There was a small number of individuals, known from the passenger list. That was very different from the present invention, which applied when there were large numbers of unknown individuals.

Reasons for the Decision

Introduction

1. The attacks on the World Trade Centre are too well known to need introduction. More than a decade has passed, and many victims have still not been identified.

2. The invention was designed to help identification in these and related circumstances. It provides an aid for DNA profiling. At the priority date (13 December 2002), several techniques of profiling were known. It is necessary to consider two. The first, and the one with which the present invention is mainly concerned, is the analysis of "short tandem repeat" profiles ("STR"). The second is based on a comparison of hypervariable regions of mitochondrial DNA.

3. STR profiling is based on sequences of nucleotides found at specific locations ("loci") of a person's chromosomes. At these loci, there are sequences of nucleotides that repeat. The number of repetitions varies, and the pattern of repetitions across enough loci can be used to identify an individual with a high degree of certainty. Thirteen loci is a typical number.

4. An identification based on STR profiles might proceed from a known sample, perhaps taken from a person's hairbrush or toothbrush. The pattern of repetitions (e.g. 7 repetitions at locus 1, 12 at locus 2, ...) is noted. A similar analysis is carried out using DNA from a tissue sample, perhaps one found at the site of an accident. If the pattern of repetitions match, then it

is highly likely that the sample belongs to the owner of the toothbrush.

5. There is a difficulty with such a comparison: the DNA available from an accident site (as it may be) is sometimes not in good condition. It is "degraded", which means that the number of repetitions cannot be ascertained for all the loci. If twelve loci out of thirteen give results and match a reference sample, that may still be enough to be sure of an identification; but as the number of available loci is reduced, so too is the certainty with which identifications can be made. It is this problem that lies behind the invention's use of aggregation (explained further, below).

6. STR profiles are based on DNA found in the nuclei of cells, but DNA is also found in a cell's mitochondria. Mitochondria contain much less DNA than do nuclei, and identifications based on mitochondrial DNA cannot reach the same degree of certainty as identifications based on STRs. Nevertheless, mitochondrial DNA can be used. It has the advantage that it degrades less easily than nuclear DNA. It may be, for example, that although the nuclear DNA is too badly damaged for STR analysis, mitochondrial DNA is still in good condition.

The invention

7. Claim 1 according to the various requests, defines a part of a larger method set out in the description and drawings. It is useful to set out something regarding the larger method, as it provides the context for understanding what is claimed.

8. The invention provides a computer - implemented aid to STR profiling (in principle, other forms of processing could be used, but the main examples concentrate on STR and there is no harm in doing likewise here).

9. The user starts with a display showing a list of "aggregates", each shown on one line (Figure 1). Each aggregate is a logical container, in which there are one or more profiles, and the user can select an aggregate and expand the view so as to see what it contains (e.g. Figure 2). The members of an aggregate belong to it because they are sufficiently similar to one another. The criteria by which similarity is judged are chosen by the user. The user may, for example, ask the computer to collect profiles which agree on ten or more loci.

10. The profiles which form the aggregates come from a variety of sources. Some may be associated with a particular person. That would be the case if it came from the analysis of DNA from a missing person's toothbrush. Other profiles may come from samples at, say, the scene of an accident. One aim would be to find out whether any samples from an accident scene match any of the former type. If so, it may be possible to say with confidence that the missing person was involved in the accident. There can be another aim, however, which is to match samples from an accident site to one another; one might, for example, want to establish how many victims there are.

11. The user, presented with the list of aggregates, can peruse them to see what positive identifications or associations can be made. In doing this, he may simply look to how well profiles match; but he may also consider factors other than DNA evidence. The user is

able, therefore, to take a profile and put it, or a copy of it, into a particular aggregate; or to remove it from one; or to merge aggregates together. It is for the user to decide whether and on what basis to do such things.

12. One way in which the invention may help the user is by providing an indication (called an "ambiguity flag") that a particular profile is to be found in more than one aggregate. That might happen if a profile matches the other profiles in the first aggregate, but also the other profiles in the second, and so on. The ambiguity flag thus indicates that some extra attention might be needed. It might be that the profile clearly matches one aggregate better than the other, and the operator can remove it from the latter; it might be that the two aggregates really ought to be combined into a single one. Such questions are for the user to decide.

13. A point much emphasized by the appellant was that the computer generates a "composite profile" from the various individual profiles it contains. In the "collapsed list", in which each aggregate gets one line on the display, it is this composite profile that is displayed. The composite profile represents "the consensus of all the STR results for that aggregate's samples," (published application, page 3, lines 7 - 8).

The main request, inventive step

14. Claim 1 according to the main request defines a method. A reference sample and some degraded samples are provided, and samples are matched. Then, a collapsed list is provided and a display is generated with one line for each aggregate. For each aggregate, its

composite profile is displayed. The single line for an aggregate can be expanded so that all its member samples can be seen.

15. The Board is satisfied that it is reasonable to read this claim as implying the use of a computer. Accordingly, it does not fall under the exclusion of Article 52(2)(d) EPC.

16. The step of matching is somewhat obscure. The appellant explained that it is this step which produces aggregates by grouping samples together according to whatever criteria the user has chosen. The claim defines some limits as to what sorts of matching are allowed: the criteria must be "consistent with potentially identifying a single individual", and the partial DNA profiles must exhibit "no discrepancy or only an allowed discrepancy" with any of the other samples in an aggregate.

17. STR profiling was well established at the priority date. The obtaining of STR profiles themselves is not part of the invention, and the application was written on the assumption that such profiles were obtainable. The properties of STR loci which allow them to be used for identification were likewise known. The appellant claims to have realised that DNA fragments that do not in themselves provide sufficient information, can be used jointly to make an identification possible.

18. The Board, therefore, takes STR profiling for the purposes of identification of individuals as part of the prior art. It was, indeed, the subject of D5, which also discloses the provision of reference samples (from relatives or from personal effects) and samples from what D5 terms a "mass disaster". In the Board's view,

such samples can be taken to include degraded samples. Matching samples from the accident site with reference samples, which D5 does, is a form of aggregation. It is a form consistent with identifying an individual, and only allowed discrepancies are, of course, allowed.

19. What D5 does not disclose is any display of the aggregates, whether as a collapsed list or otherwise, but some form of display is, naturally, implicit. The invention, therefore, differs from what is disclosed in D5, by the choice of what is displayed and how it is displayed.

20. It is by now well established that non-technical features do not contribute to inventive step (T 0641/00, Two identities/COMVIK, OJ 2003, 352). Choices of what data to display and of how to display them do not normally contribute to produce a technical effect, and so qualify as non-technical. The Board must consider, however, whether, in the present case, these choices do produce some technical effect, either in themselves or in conjunction with the other features of the claimed method and accordingly can be taken into account for inventive step.

21. The appellant argued that the aggregation allowed the use of DNA samples that would otherwise be too degraded. The Board, however, cannot see anything in the claim that supports that contention. The aggregation according to the claim amounts to neither more nor less than grouping profiles as the operator wishes, either by specifying criteria and having the computer do it, or by manual assignment. The operator might, to be sure, choose to group together profiles which a different analyst might think useless, but

there is nothing in the claim that makes it happen.

22. Thus, if the claimed invention chooses different data to display, it is because the operator makes the choice. A choice producing a technical effect is not part of the invention.

23. The display of a list of items and allowing individual items to be expanded is well known. It is done for the convenience of the operator, providing a convenient view of a list of lists. It does not make the computer itself any better, and does not itself improve the profiling. The appellant's argument that the skilled person is seeking a solution to a profiling problem cannot be followed, simply because this manner of presenting the data does not solve a problem with profiling. It addresses the problem of how conveniently to present potentially large amounts of information.

24. The final point is that when the aggregate is displayed on one line, a "composite" profile is displayed. Again, this is a matter of choosing what to display, and amounts to providing the operator with what he wants to see. The term "composite" is defined in the claim only as being "representative" of the profiles within the aggregate. It gives the operator some idea of what is inside.

25. The appellant's further arguments do not affect this analysis. The fact that the invention has been applied with success is not a result of an improvement in the computer or in any technical aspect of profiling. Rather, it is a result of the way the analyst has chosen to work. The arguments concerning D1 are not relevant to D5. The argument that D5 is concerned with a relatively small number of known people does not aid

the appellant, because claim 1 in no way excludes such a situation.

26. The Board, therefore, is of the view that none of the differences over D5 provides a technical effect. They cannot, therefore, contribute to inventive step. As a result, the Board sees no inventive step (Article 56 EPC), and cannot allow the main request.

The first auxiliary request

27. Claim 1 differs from claim 1 of the main request in that the DNA samples are of nuclear origin. The Board's analysis of the main request is based on STR profiles as in D5, which use nuclear DNA. It applies just as well to this request, which cannot be allowed for the same reasons.

The second auxiliary request

28. Claim 1 according to this request differs from claim 1 of the main request in that "each member DNA sample represent[s] a DNA profile obtained from the same unidentified biological sample".

29. There is a problem of clarity in that the step of "presenting" refers to "the nuclear DNA" whereas the remainder of the claim does not restrict the source of DNA. As noted above, whether or not DNA is nuclear does not affect the outcome regarding inventive step. The Board, therefore, concentrates on the "same unidentified biological sample".

30. It is possible that DNA taken from a biological sample does not provide results for all STR loci. In such a case, a second assay from the same biological sample may provide results different from the first. Together, results may be obtained for more loci. This can, of course, be continued for as many assays as the analyst wishes to take.

31. The application addresses this possibility when it talks of "virtual samples", but it does not say much about them. The most detailed passage is on page 5, from line 20: "Samples with multiple experimental runs are grouped into virtual samples ... representing the results of all runs," and "In one run, BODE-DM0114805 134, only 4 loci 136, returned any results. A second assay on this same physical sample, BCB1-DM0114805 134, returned 8 loci 136, filling in many holes in the STR profile. This new virtual profile has 11 loci, and taken together have a likelihood of 3.8×10^{12} 132, high enough to be identified."

32. The application does not present such multiple attempts at retrieving enough information as new, although the appellant has argued that it was. In the Board's view, it would have been normal practise and no more than applying the idea of looking again to see if more information could be found.

33. The Board, therefore, sees no contribution to inventive step from this additional feature, and finds the second auxiliary request no more allowable than the main.

The third auxiliary request

34. Claim 1 according to this request differs from claim 1 of the second auxiliary request in that the reference profile involves nuclear DNA, the DNA contributing to a virtual sample is also nuclear, and at least one STR locus is used.

35. Since the analysis above is based on STR profiles, these differences do not affect the outcome and the Board cannot allow this request.

The fourth auxiliary request

36. Claim 1 according to this request differs from claim 1 of the third auxiliary request in that "a member DNA sample may be displayed as a member of more than one aggregated matching sample", and a flag (an "ambiguity flag") is shown when one does.

37. The way in which profiles are included in or excluded from aggregates is up to the operator. It is inherent to the process that a profile may be in more than one aggregate, so the salient feature is the ambiguity flag.

38. The operator wants to know whether any profiles are in more than one aggregate, because spotting when one could be matched in more than one way is part of the identification process. Once the operator forms the desire to know when this occurs, the invention amounts to asking the computer to do it. The technically skilled person is presented with the problem of indicating such occurrences to the user. Some sort of indication is then inevitable and would constitute a

flag.

In the Board's view, this is no more than presenting the operator with information in a convenient way. The provision of a flag would have been obvious to the skilled person, because that is just what the non-technical requirements demand.

39. The Board concludes that the subject matter of claim 1 does not involve an inventive step (Article 56 EPC 1973) and this request cannot be allowed.

Order

For these reasons it is decided that:

The appeal is dismissed.

The Registrar: The Chairman:

B. Atienza Vivancos S. Wibergh

Decision electronically authenticated