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Datasheet for the decision of 14 April 2015

Case Number: T 1286/10 - 3.5.05

Application Number: 06022934.1

Publication Number: 1783646

IPC: G06F19/00

Language of the proceedings: EN

Title of invention:
System for detection and correction of errors in input data for genotype analysis

Applicant:
Hitachi Solutions, Ltd.

Headword:
Detection and correction of false descriptions in IUB code input data for linkage disequilibrium genotype analysis

Relevant legal provisions:
EPC Art. 52(1), 52(2)(c), 56

Keyword:
Patentable invention - computer implemented invention
Patentable invention - technical character of the invention
Patentable invention - field of technology
Inventive step - after amendment
Inventive step - auxiliary request (yes)

Decisions cited:
T 1194/97

Catchword:

Europäisches Patentamt
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Case Number: T 1286/10 - 3.5.05

D E C I S I O N
of Technical Board of Appeal 3.5.05
of 14 April 2015

Appellant: (Applicant)	Hitachi Solutions, Ltd. 4-12-7, Higashishinagawa, Shinagawa-ku, Tokyo 140-0002 (JP)
Representative:	Liesegang, Roland Boehmert & Boehmert Anwaltspartnerschaft mbB Patentanwälte Rechtsanwälte Pettenkoferstrasse 20-22 80336 München (DE)
Decision under appeal:	**Decision of the Examining Division of the European Patent Office posted on 28 January 2010 refusing European patent application No. 06022934.1 pursuant to Article 97(2) EPC.**

Composition of the Board:

Chair	A. Ritzka
Members:	M. Höhn
	D. Prietzel-Funk

Summary of Facts and Submissions

I. This appeal is against the decision of the examining division, delivered during oral proceedings held on 15 December 2009 and with written reasons being dispatched on 28 January 2010, refusing European patent application No. 06022934.1 on the grounds of lack of clarity (Article 84 EPC) and lack of inventive step (Article 56 EPC) with regard to prior-art publications:

D1: J.R. O'CONNELL, D.E. WEEKS: "PedCheck: A Program for Identification of Genotype Incompatibilities in Linkage Analysis", AMERICAN JOURNAL OF HUMAN GENETICS, vol. 63, 22 May 1998, pages 259-266;
D2: M. SATIO, A. SATIO, N. KAMATANI: "Web-based detection of genotype errors in pedigree data", JOURNAL OF HUMAN GENETICS, vol. 47, July 2002, pages 377-379;
D3: J.E. WIGGINTON, G.R. ABECASIS: "PEDSTATS: descriptive statistics, graphics and quality assessment for gene mapping data", BIOINFORMATICS, vol. 21, no. 16, 9 June 2005, pages 3445-3447; and
D4: C. VAN OOSTERHOUT, W. HUTCHINSON, D.P.M. WILLS, P. SHIPLEY: "MICRO-CHECKER: software for identifying and correcting genotyping errors in microsatellite data", MOLECULAR ECOLOGY NOTES, vol. 4, 2004, pages 535-538.

II. The notice of appeal was received on 22 March 2010. The appeal fee was paid on the same day. The statement setting out the grounds of appeal was received on 7 June 2010. The appellant requested that the decision under appeal be set aside and that a patent be granted on the basis of the main request filed during the first-instance oral proceedings on 15 December 2009, or

subsidiarily on the basis of one of the auxiliary requests likewise filed during these oral proceedings on 15 December 2009. Oral proceedings were requested on an auxiliary basis.

III. With a communication dated 18 June 2014 the board summoned the appellant to oral proceedings on 21 October 2014, subsequently rescheduled to 14 April 2015. In an annex to the summons the board expressed its preliminary opinion that all requests lacked clarity (Article 84 EPC) and inventive step (Article 56 EPC). Furthermore, the following document was referred to by the board as evidence of the skilled person's general knowledge in relation to programs for genetic analysis and error checking in the context of such programs:

D5: Encyclopedia of Biostatistics, Wiley & Sons, ISBN: 9780470011812, DOI: 10.1002/0470011815, published online 15 July 2005, entries for "Genotyping and Error-checking", "Linkage Analysis, Model-based", "Linkage Disequilibrium".

Reference was additionally made to the following document related to D4:

D6: Micro-Checker User Guide, C. Van Oosterhout et al., University of Hull, Department of Biological Sciences and Department of Computer Sciences, 2005, this being a copy of the "User Manual" referred to in the concluding paragraph of D4 on p. 537. According to the Internet site of the University of Hull, http://www.microchecker.hull.ac.uk/, the last update of the Micro-Checker program was Version 2.2.3 on 27 February 2005. The file containing the User Guide

downloaded from http://www.microchecker.hull.ac.uk/Updates.html bears the date-stamp 21 February 2005.

On this basis, the board took the view that the User Guide was publicly available before the claimed priority date of the present application (i.e. 8 November 2005).

IV. By letter dated 11 November 2014 the appellant submitted an amended main request, amended first and second auxiliary requests and a new third auxiliary request supported by arguments in favour of clarity and inventive step.

V. The appellant requested that the decision under appeal be set aside and that a patent be granted on the basis of the claims of the main request submitted with the letter dated 11 November 2014, or on those of the first auxiliary request submitted during the oral proceedings before the board, or of the second or the third auxiliary request submitted with the letter dated 11 November 2014.

The further documents on which the appeal was based corresponded to those underlying the impugned decision, viz.:
Description, pages: 1-5, 7-11, 13-37 as originally filed; 6, 6a, 12 as filed with letter of 29 July 2008.
Drawings, sheets: 1/20 - 20/20 as originally filed.

VI. Independent claim 1 according to the main request reads as follows:

"1. A data input support system for inspecting genotype data input into a program for linkage disequilibrium analysis, wherein the genotype data is described in the

IUB code description format, wherein the system comprises:
a storage section for retaining error types for genotype data corresponding to the program for linkage disequilibrium analysis,
said error types corresponding to false descriptions of genotype data,
an error detection section checking the input genotype data for the error types and detecting errors;
means for displaying the report of the detected errors as well as a proposal what the correction to the input data could be; and
error correction means which accepts a user input confirming to correct the reported error in the input genotype data according to the proposed correction and corrects the genotype data according to the proposed correction."

Independent claim 1 according to the first auxiliary request reads as follows:

"1. A data input support system for inspecting genotype data input into a program for linkage disequilibrium analysis, wherein the genotype data is described in the IUB code description format, wherein the system comprises:
a storage section for retaining error types for genotype data corresponding to the program for linkage disequilibrium analysis,
said error types corresponding to false descriptions of genotype data,
an error detection section checking the input genotype data for the error types and detecting errors;
means for displaying the report of the detected errors as well as a proposal what the correction to the input data could be; and

error correction means which accepts a user input confirming to correct the reported error in the input genotype data according to the proposed correction and corrects the genotype data according to the proposed correction,
wherein one of said error types is the occurrence of three or more alleles at a locus,
and wherein the error detection section checks for one or more of the following conditions:
(i) missing data is accidentally described as a one-byte blank character or tab,
(ii) a heterozygous genotype is accidentally described as two alleles separated by a one-byte blank character,
(iii) a heterozygous genotype is falsely described at each locus."

VII. Oral proceedings were held on 14 April 2015. After due consideration of the appellant's arguments the chair announced the decision.

Reasons for the Decision

1. Admissibility

The appeal complies with Articles 106 to 108 EPC (see Facts and Submissions, point II above). It is therefore admissible.

Main request

2. In the decision under appeal the term "false descriptions" in the expression "error types corresponding to false descriptions of genotype data" of claim 1 was considered to be vague and unclear as it lacked an established technical meaning in the art.

According to the decision under appeal the term appeared to designate a data format different from that expected by the program for linkage disequilibrium analysis, i.e. the error types appeared to refer to syntax incompatibilities in the input data compared to an expected input data format. On the basis of the foregoing interpretation, it was found that the subject-matter of claim 1 of the main request did not involve an inventive step in the light of D1.

3. Article 123(2) EPC - Amendments

In reaction to this objection, claim 1 has been further defined by the "genotype data is described in the IUB code description format".

This amendment is supported by figure 34 in combination with the first sentence of paragraph [0017] of the published application.

4. Article 84 EPC - Clarity

4.1 By specifying that the genotype data in independent claim 1 is described in the IUB code description format, i.e. oligonucleotide codes according to the International Union of Biochemistry, it is considered to be sufficiently clear that the term "false descriptions of genotype data" in claim 1 refers to such IUB codes and not to the content or the meaning of the genotype data. It is therefore considered to be clear that when claim 1 refers to the error codes which correspond to false descriptions of genotype data, it is referring not to errors in the content of the genotype data but to errors in the description format, i.e. the IUB codes as shown in figure 34 of the application.

4.2 The objection raised in point III.1.1 of the decision under appeal is therefore regarded as overcome by amendment.

5. Articles 54(2) and 56 EPC - Novelty and inventive step

5.1 Interpretation of claim 1

According to the most general embodiment of the invention described in the disclosure (cf. published application: [0089], [0120], Fig. 4), input data are loaded (step 401), errors in the input data are detected and reported and user input is accepted to produce a modified version of the input data (step 402).

Various types of errors are listed in paragraphs [0022] to [0046] of the published application and corresponding error correction functions are disclosed in [0047] to [0089]. Likewise, figure 5 and the associated passages of the description disclose specific examples of detecting and reporting errors (cf. published application, paragraphs [0121] to [0135]).

In view of the afore-mentioned passages of the description, the "errors" which it is envisaged to correct include *inter alia* items of the genotype data such as the arrangement of loci or alleles (cf. [0049], [0068]) as well as data entry errors such as wrongly specified or erroneously spelled names (cf. [0060]), unexpected character strings (cf. [0058], [0062]) and formatting errors such as the incorrect use of symbols such as "*" (asterisk) or the irregular use of blank characters (cf. [0072]-[0073]).

5.2 Since no concrete error types are specified in claim 1 and in the light of the description, these terms cover a wide range of irregularities or deficiencies in the input data. In view of this the board interprets the terms "error" and "error type" as used in claim 1 in a broad manner, including typographical errors.

5.3 The appellant disputed the argument in the decision under appeal (see point III.1.2.4) that discarding erroneous data was also a way of "correcting input data" and submitted that there was clearly a difference whether input data was corrected, i.e. repaired, as was the case in the input support system of claim 1, or whether experimentally wrong and therefore inconsistent data was simply discarded. With respect to the embodiments of figures 19 and 20 of the present application, the appellant submitted in this regard that there was clearly a proposal to correct the data in addition to giving the users the possibility to delete the locus altogether. The appellant argued that, in the context of the present invention, the concept of a "correction" involved the replacement a "false description" by a "correct description" of the content of the genotype data and was thus inherently different from the deleting or discarding of data determined to be erroneous.

5.4 A significant number of passages of the description which relate to particular types of errors being "reported and corrected" disclose the presentation of a sole option for deletion or discarding of allegedly erroneous data which can be selected by a user "to produce a modified version of the input data" (see the published application, paragraphs [0128] to [0130]; [0132] to [0134]; figures 24 to 26 and 28 to 30).

In the further embodiments shown in figures 19 and 20, in the context of errors being "reported and corrected" a user is presented with options for deletion or replacement of the allegedly erroneous data and the user may select either of these mutually exclusive options "to produce a modified version of the input data" (see the published application, paragraphs [0144] and [0145]).

5.5 In view of the lack of a concrete specification of error types in claim 1, from which the skilled person could conclude that false description data has actually been corrected, the production of "a modified version of the input data" expresses essentially the same idea as a "correction" of the input data and the application discloses that such a "correction" may involve the deletion or discarding of allegedly erroneous data as an alternative option to a replacement or "repair" of such data. The board therefore concurs with the decision under appeal (see point III.1.2.4) that a proposal for discarding erroneous data falls within the scope of a correction of errors in claim 1 according to the main request.

5.6 Closest prior art

Claim 1 is directed to a data input support system for inspecting genotype data input into a program for linkage disequilibrium analysis. While publication D1 deals with classical linkage analysis studying the segregation of certain alleles in a pedigree-based pool of individuals with blood relationship (see program "PedCheck" referring to pedigree analysis), further prior-art publication D4 is directed to software-based tests of population-based genetic analyses. D4 hence discloses a system suitable for linkage disequilibrium

analysis (see abstract and page 535, right-hand column, second paragraph). For this reason D4 is considered to be closer to the claimed invention and is therefore regarded as the closest prior art.

5.7 D4 discloses a software program called "Micro-Checker" details of which are found in the user manual according to D6, the information of which is therefore regarded as implicitly disclosed in publication D4.

5.8 By disclosing the micro-checker software program run on a computer system (see e.g. figure 1) D4 discloses a data input support system for inspecting genotype data input into a program for linkage disequilibrium analysis.

D4 further discloses carrying out a check for typographical errors while a variety of formats are accepted (see D4, page 536, right-hand column, second paragraph; see also figure 1, Typographic error test). Following the afore-mentioned broad interpretation of the expression "error types", D4 hence discloses a storage section for retaining error types for genotype data corresponding to the program for linkage disequilibrium analysis, while those typographical errors correspond to false descriptions of genotype data. D4 further discloses suggestions on how to correct for errors (see D4, page 537, left-hand column, second paragraph), which inherently requires an error detection section checking the input genotype data for the error types and detecting errors. By providing such suggestions, means for displaying detected errors as well as a proposal as to what the correction to the input data could be have to be foreseen.

5.9 Reference is also made to D6 (see bottom of page 13) where it is disclosed that details of faults are displayed. Following the board's view that a proposal for discarding erroneous data falls within the scope of a correction of errors in claim 1 (see above) which is disclosed in D6 (see e.g. figure 15 of D6 "Omit the suspect data from analysis" and bottom of page 13), D6 hence further discloses error correction means which accepts a user input confirming that the reported error in the input genotype data is to be corrected as proposed, and corrects the genotype data accordingly, as claimed in claim 1.

5.10 D4 with the implicit knowledge of the user manual according to D6 therefore discloses all the features of claim 1 except for the genotype data being described in the IUB code description format. The subject-matter of claim 1 is therefore novel with regard to the disclosure of D4 (Articles 52(1) and 54(2) EPC).

5.11 The IUB code description format, i.e. oligonucleotide codes according to the International Union of Biochemistry, is an industry standard that was well known in the art before the priority date of the present application. That is reflected by the reference in paragraph [0017] of the present application to IUB codes having been known, which was not disputed by the appellant during the oral proceedings.

In view of the disclosure in D4 that a check for typographical errors can be applied to a variety of formats (see D4, page 536, right-hand column, second paragraph), the skilled person looking for a solution to the underlying problem of inspecting genotype input data for errors including typographical errors would realise from D4 without the need for inventive skills

that the corresponding teaching of D4 can be applied to the IUB codes as input format without technical hurdles to be overcome or any surprising technical effect achieved.

5.12 The skilled person for solving this problem is regarded as a software engineer with skills in implementing abstract information models and description formats without need of further skills in genetic engineering.

Having been provided with the known IUB code description format, the skilled person would be able to derive possible typographical errors from the formatting specifications as shown in figure 34 of the present application without inventive skills. In particular, no knowledge about the underlying genetic data and analysis procedure would be required for this purpose.

The board therefore does not see any specific requirements related to the IUB code description which would prevent the skilled person from applying the teaching of D4 to the correction of typographical errors in genotype data described according to IUB code description format.

5.13 Thus, the board judges that the subject-matter of claim 1 according to the main request does not involve an inventive step over the disclosure of D4 with regard to the common general knowledge of the skilled person (Article 56 EPC).

First auxiliary request

6. Claim 1 according to this request is further specified

in that one of said error types is the occurrence of three or more alleles at a locus, and that the error detection section checks for one or more of the following conditions:
(i) missing data is accidentally described as a one-byte blank character or tab,
(ii) a heterozygous genotype is accidentally described as two alleles separated by a one-byte blank character,
(iii) a heterozygous genotype is falsely described at each locus.

7. Article 123(2) EPC - Amendments

Those features added by amendment are disclosed in figures 19 to 21 and in paragraphs [0029] to [0034] with regard to error type 7 in the published application.

8. Interpretation of claim 1

8.1 In view of the more concrete specification, the expression "error types" in amended claim 1 can no longer be interpreted to be limited to typographical errors, but involves false descriptions of IUB codes which do not appear to correctly describe the underlying genotype data.

8.2 For this purpose the term "genotype" is interpreted in the light of the description in order to correctly interpret the added features, in particular with regard to the occurrence of three or more alleles at a locus.

According to the specification of the present application, the term "genotype" refers to the sum of allelic information at a certain site on both of the two homologue chromosomes of a diploid organism (see

paragraph [0005], "Genes present at sites corresponding to one another in the pair of genomes are called alleles to one another, and a pair of these alleles is called a genotype. The two alleles may be the same or different since there are different nucleotide sequence portions among individuals in genome. When genes at a particular genomic site are paid attention to, the presence of the same two alleles is called homozygotes, while the presence of different two alleles is called heterozygotes"). The expression "genotype data" in claim 1, hence, encompasses the sum of the allelic information at a certain locus/certain loci, not just on one but on both of the two corresponding chromosomes of a diploid organism.

According to the wording of claim 1 such genotype information is described by IUB codes as shown in figure 34, i.e. by a one-letter code in which a single letter indicates, jointly, the identity of the alleles at a certain locus on both corresponding chromosomes. Thus, by referring to the "IUB code description format" for the description of "genotype data", amended claim 1 specifies that the genotype data used is represented by a data format in which the one-letter IUB code specifies with a single letter simultaneously which base is present at a specific base position on both of the two corresponding chromosomes, and thus inherently also provides the information whether the chromosomes are homozygous or heterozygous at this locus.

9. Articles 54(2) and 56 EPC - Novelty and inventive step

9.1 The board concurs with the decision under appeal (see point III.2.2.1) that prior-art publication D4 fails to disclose the specific error types according to the

features added to claim 1, which are therefore considered to be distinguishing features.

9.2 In contrast to the decision under appeal (see point III.2.2.2) the board agrees with the appellant's argument that the definition of the specific error rules (i) to (iii) in combination with the occurrence of three or more alleles at a locus according to the added features provides for a technical contribution which goes beyond mere user requirements regarding the input format of the data imposed by the specific program and the syntax required.

The error codes defined in claim 1 according to this request are related to the detection and correction of a specific error type in which three or more alleles occur at a locus (see error 7 described on page 7, last line to page 9, second paragraph of the specification and figure 8 with corresponding description on page 33, paragraph 3 to page 35, paragraph 2). The board concurs with the appellant that if such an error remains unnoticed, the content of the genotype data will be misinterpreted due to a wrong description and will lead to an erroneous result of the linkage disequilibrium analysis. Apart from providing for a data input support system allowing the detection of description errors of genotype data in a program for linkage disequilibrium analysis, by identifying a respective error condition (i) to (iii) the claimed system allows correction of input data, i.e. repair of a genotype data set which contains correct biological measurement content but description errors.

In contrast to the situation when a cause for the error cannot be found and the genotype data set as a whole has to be discarded, though its biological content may

be perfectly correct and the problems are due only to description errors, the claimed system allows correction of the description errors under certain circumstances (see e.g. figures 19 to 21 of the application), which is considered to be a technical effect.

9.3 In contrast to point III.2.2.2 of the decision under appeal, the specified error type rules according to the additional features are therefore technical means in that functional data structures of the error correction means are thereby defined (see T 1194/97 - Data structure product/Philips; OJ EPO 2000, 525) in order to enhance correction of input data by allowing repair of a genotype data set which contains correct biological measurement content but description errors. Those functional data structures each contribute to the technical character of the claimed invention according to claim 1 of this request.

9.4 The board agrees with the appellant (see also point III.1.2.5 of the decision under appeal) that the technical problem underlying the added features is that to identify and correct errors in genotype data which are based on a false description and can therefore be anticipated.

9.5 The solution to this problem requires the design of error detection rules which involve, apart from knowledge of the IUB code description format, knowledge in analysing genotype data for designing criteria for identifying potential errors caused by false description of genotype data and for providing a proposed correction (see e.g. figures 19 to 21 of the application). This involves technical considerations of a genetic engineer (e.g. whether data is missing or

what data might be expected at a certain locus in a population and when a shift might have occurred in a genotype data set resulting in an erroneous interpretation; see paragraphs [0031] to [0033] of the published application and figures 21, 22 and 36). Those technical considerations have to be taken into consideration when assessing inventive step.

The definition of the specific error rules (i) to (iii) in combination with the occurrence of three or more alleles at a locus according to the added features of claim 1 therefore go beyond mere rules according to Article 52(2)(c) EPC or a mere automation of non-technical preconditions.

9.6 The skilled person for solving the above-mentioned objective technical problem, in contrast to the main request, now requires knowledge in genetic engineering and is therefore considered to be a team of experts in software engineering and genetic engineering.

9.7 The closest prior-art document D4 considered with the content of D6 merely involves checking for formal errors like wrong data types (see above with regard to the main request), but neither discloses the use of IUB codes nor discloses or renders obvious one of the specific error types and rules for detecting them according to the distinguishing features (i) to (iii) of claim 1.

The board agrees with the appellant's argument (see e.g. page 11, third paragraph of the letter dated 11 November 2014) that D4 and D6 use data formats that do not allow representation of the kind of information that claim 1 is concerned with, i.e. genotype data described by IUB code representation defining the

specific base present at a certain locus present on both chromosomes.

9.8 Documents D4 and D6 are concerned with genotyping errors in microsatellite data. The essential feature for the analysis of microsatellite data is the length of the product obtained during PCR amplification. Microsatellite data for genotyping suffer from specific problems, in particular the loss of large alleles during amplification or the amplification of an allele that is too short. Thus, error checking in D4 and D6 is based on the specific features and potential errors of microsatellite data. Such an approach for error checking disclosed in D4 can, however, not be properly performed with non-microsatellite DNA such as the kind of genotype data to which claim 1 of the present invention relates.

Documents D4 and D6 use a data format that only includes information about the length of the microsatellite allele (Genepop and Excel formats, see e.g. D6, pages 5 and 6). Each entry of D4 and D6 consists of a single item in number format, see e.g. D6, page 6, figure 2). For this reason it does not make sense to check for undesired blank characters within the data of D4 or D6 according to error rule (i) of claim 1.

The data format in D4 and D6 furthermore does not contain information about the identity of the bases at the locus and information about the bases at the corresponding site of both corresponding chromosomes. Similarly, the microsatellite data used in the program of D4 only specifies the size of the microsatellite allele. D4 states that "Genepop [...], Microsoft Excel and textfile formats (ASCII)" can be used (see D4, page

536, right-hand column, second paragraph). The Genepop format only includes the length of the allele (see D6, page 5). The specific problems addressed by claim 1 therefore cannot arise in the case of document D4 or D6. D4 and D6 therefore do not hint the skilled person to the design of one of the error rules according to (ii) and (iii) of claim 1.

9.9 The board therefore judges that D4 and D6 both deal with microsatellite data and, hence, with a different type of data than the claimed invention, and do not point the skilled person towards come up with one of the error types according to the distinguishing features of claim 1 and therefore do not render the claimed solution according to claim 1 of this request obvious.

9.10 D1, on which the decision under appeal was based as most pertinent prior art, does not only relate to a different type of analysis (linkage analysis of pedigree data rather than linkage disequilibrium analysis, see above), but it also uses a data format that is incompatible with the IUB format (the different alleles at a locus are only referred to by numbers, see e.g. figure 1 of D1 "2/1", "4/3", "5/1" etc.). D1 thus does not contain the information as to which base (A, T, G or C) is present at the locus at the two corresponding chromosomes of a diploid organism. Thus, the board concurs with the appellant (see essentially page 9 of the letter dated 11 November 2014) that the error types addressed by the claimed data input system cannot possibly occur in the data format used in D1. Checking for errors in D1 is based on the premise that a plurality of pedigree data are used as genetic data and errors are checked for in the form of Mendelian inconsistencies which do not occur in linkage

disequilibrium analysis according to claim 1. D1 does not provide any information about the identification of genotype errors in non-pedigree data as used in claim 1 according to this request.

D1 therefore does not disclose or suggest the claimed solution, either alone or in combination with D4.

10. The board agrees with the decision under appeal that none of the further prior-art publications on file discloses the added distinguishing features of claim 1 (see point III.2.2.1). In view of D4 as the closest prior art dealing with microsatellite data and D1 as the most pertinent document dealt with in the decision under appeal directed to "traditional" linkage analysis (see above) disclosing rules in order to eliminate Mendelian errors in genotype data (that cannot even occur in linkage disequilibrium analysis according to claim 1), the specific error rules (i) to (iii) furthermore cannot be considered to be suggested by the most pertinent prior-art publications. With the prior art on file, the board does not see how the skilled person could have been prompted or motivated to come up with those specific error rules (i) to (iii) in combination with the occurrence of three or more alleles at a locus in order to solve the problem posed.

10.1 The board also does not have any evidence that such a solution was notorious knowledge in the field of genetic engineering, either in general or related to the use of the IUB code description format.

10.2 The claimed solution according to claim 1 of this request with the specific error rules (i) to (iii) in combination with the occurrence of three or more

alleles at a locus therefore has to be considered to involve an inventive step over the prior art on file.

10.3 The dependent claims, because of their reference to independent claim 1, also involve an inventive step for the same reasons.

11. Since the first auxiliary request fulfils the requirements of the EPC, the board did not have to deal with the second and third auxiliary requests.

Order

For these reasons it is decided that:

1. The decision under appeal is set aside.

2. The case is remitted to the department of first instance with the order to grant a patent on the basis of claims 1 to 3 of the first auxiliary request submitted during the oral proceedings before the board, and a description and the figures to be adapted.

The Registrar: The Chair:

K. Götz-Wein A. Ritzka

Decision electronically authenticated