cancer. That is, none of the documents described methods of early analysis of possible drugs useful in treating a known or unknown disease.

Hence, there is still an ongoing need for methods for enabling predictions of the survival rate of individuals within a predetermined time period or at a predetermined time end point, in particular, in case of healthy individuals prospective predictability of adverse events, in particular, death, is desired to allow preventive measures including pharmaceutical and physical interference.

Moreover, although UPP signatures to predict various outcomes in a predefined correlation, the prediction is not sufficient to identify suitable therapeutic regimen nor allow to predict treatment success based on treatment therapies. That is, although a large number of specific endogenous peptides can be detected in urine, an association with onset and progression of specific chronic diseases, like chronic kidney disease, coronary artery disease, heart failure or malignant tumors and also death may be allowed, the treatment success either prophylactically or therapeutically, cannot be predicted.

Further, the methods described so far allow to diagnose a specific disease, however, the methods described so far do not identify or predict suitability of a specific active agent beneficial for preventive or therapeutic treatment of a disease. In addition, the prior art is silent on methods analysing in advance the treatment success of active agents known for treating the disease. However, presently the decision on the selected therapy is based on general knowledge on therapeutic success in the past but not individualized allowing prediction of the optimal therapy.

Hence, it is required to provide improved methods allowing the same.

Thus, an object of the present invention is to provide a method allowing prediction of therapy success in treating an individual afflicted with a disease, disorder or condition or of individuals although not diagnosed for a specific disease but may develop a disease based on the UPP determined.

In particular, an object of the present invention is to provide a method allowing personalised treatment of individuals in need thereof.

Summary

In one aspect, the present disclosure refers to a method for determining the treatment success and/or the therapy regimen of a treatment of an individual, preferably said individual is afflicted with or is supposed to be afflicted with a vascular disease, like a cardiovascular disease or a renal disease, with a predetermined active

agent, comprising the steps of a) Determining the peptidome/proteome in a body fluid sample obtained from said individual; b) Calculating of a reference value based on processing information of a predetermined group of peptide/protein markers of the peptidome/proteome determined in step a); c) Determining a score for the predetermined group of peptide/protein markers of step b), whereby the score is calculated by processing information for each marker of the group obtained under the impact of the active agent, whereby the information is present in a database; d) Processing the value obtained in step b) with the score obtained in step c); e) Predicting the treatment success and/or determining the therapy regimen with the active agent based on the processing in step d), whereby if the score calculated from data reflecting the impact of the active agent is above the reference value, the treatment success is positive and/or the therapeutic regimen shall be applied and if the score calculated from data reflecting the impact of the active agent is below the reference value, the treatment success is negative and/or the therapeutic regimen shall not be applied.

In another aspect, the present disclosure refers to a method for the prediction of a very relevant health event for an individual, wherein the very relevant health event is selected from vascular disease including major cardiovascular events, kidney failure, tumor recurrence or death as a result of a disease and the determination of possible preventive treatment of said relevant health event in the individual with an active agent, comprising firstly, the steps for determining the probability of a very relevant health event by a) Determining the peptidome/proteome in a body fluid sample obtained from said individual; b) Comparing the information on the peptidome/proteome obtained in step a) with information on the peptidome/proteome present in a database; c) Determining the probability of a very relevant health event for an individual based on the comparison in step b); and, secondly, d) Calculating of a reference value based on processing information of a predetermined group of peptide/protein markers determined in step a); e) Determining a score for the predetermined group of peptide/protein markers used in step b), whereby the score is calculated by processing information for each marker of the group obtained under the impact of the active agent, whereby the information is present in a database; f) Processing the value obtained in step d) with the score obtained in step e); g) Determining a treatment regimen and/or predicting the clinical outcome and/or predicting the treatment success with the active agent based on the processing in step f), whereby if the score is above the reference

value, a treatment success is positive and/or a therapeutic regimen shall be applied, e.g. for prevention of said very relevant health event.

In another aspect, the present disclosure refers to a computer implemented method of prediction of a very relevant health event for an individual; for determining the therapeutic regimen; and/or for predicting the treatment success of a treatment for an individual with an active agent, respectively, comprising the steps of a) Obtaining information of the peptidome/proteome in a body fluid sample of the individual; b) Computing the information of step a) by i. Comparing the information on the peptidome/proteome obtained in step a) with information on the peptidome/proteome obtained from a database; or ii. by calculating of 1) a reference value based on the information of a predetermined group of peptide/protein markers and 2) computing a score for the predetermined group of peptide/protein markers, whereby the score is calculated from information for each marker of the group under the influence of the active agent, whereby the information is obtained from a database, and comparing the computed reference value with the computed score, c) Determining the probability of a very relevant health event of an individual; or determining a treatment regimen and/or predicting the treatment success with the active agent, respectively; d) Optionally further comprising the step of showing the data of prediction of a very relevant health event for an individual, treatment regimen, predicting the clinical outcome and/or predicting the treatment success with the active agent, respectively, on an output unit.

In yet another aspect, the present disclosure refers to a computer readable medium or computer program product having computer executable instructions for performing the steps as described herein.

Brief description of the present invention

In a first aspect, the present invention relates to a method for determining the treatment success and/or the therapy regimen of a treatment of an individual, preferably said individual is afflicted with or is supposed to be afflicted with a vascular

Claims

1. A method for determining the treatment success and/or the therapy regimen of a treatment of an individual, preferably said individual is afflicted with or is supposed to be afflicted with a vascular disease, like a cardiovascular disease or a renal disease, with a predetermined active agent, comprising the steps of
    a) Determining the peptidome/proteome in a body fluid sample obtained from said individual;
    b) Calculating of a reference value based on processing information of a predetermined group of peptide/protein markers of the peptidome/proteome determined in step a);
    c) Determining a score for the predetermined group of peptide/protein markers of step b), whereby the score is calculated by processing information for each marker of the group obtained under the impact of the active agent, whereby the information is present in a database;
    d) Processing the value obtained in step b) with the score obtained in step c);
    e) Predicting the treatment success and/or determining the therapy regimen with the active agent based on the processing in step d), whereby if the score calculated from data reflecting the impact of the active agent is above the reference value, the treatment success is positive and/or the therapeutic regimen shall be applied and if the score calculated from data reflecting the impact of the active agent is below the reference value, the treatment success is negative and/or the therapeutic regimen shall not be applied.

2. Method for the prediction of a very relevant health event for an individual, wherein the very relevant health event is selected from vascular disease including major cardiovascular events, kidney failure, tumor recurrence or death as a result of a disease and the determination of possible preventive treatment of said relevant health event in the individual with an active agent, comprising firstly, the steps for determining the probability of a very relevant health event by
    a) Determining the peptidome/proteome in a body fluid sample obtained from said individual;

b) Comparing the information on the peptidome/proteome obtained in step a) with information on the peptidome/proteome present in a database;

c) Determining the probability of a very relevant health event for an individual based on the comparison in step b); and, secondly,

d) Calculating of a reference value based on processing information of a predetermined group of peptide/protein markers determined in step a);

e) Determining a score for the predetermined group of peptide/protein markers used in step b), whereby the score is calculated by processing information for each marker of the group obtained under the impact of the active agent, whereby the information is present in a database;

f) Processing the value obtained in step d) with the score obtained in step e);

g) Determining a treatment regimen and/or predicting the clinical outcome and/or predicting the treatment success with the active agent based on the processing in step f), whereby if the score is above the reference value, a treatment success is positive and/or a therapeutic regimen shall be applied, e.g. for prevention of said very relevant health event.

3. The method according to claim 2, wherein the step of comparison according to step b) includes the application of a classifier, comprising at least three, like at least 5, at least 10, at least 20, at least 30, e.g. at least 50 of predetermined peptide/protein markers.

4. The method according to any one of the preceding claims, wherein at least one of steps b) to f) according to claim 2 or at least one of steps b) to d) according to claim 1 are conducted with an artificial intelligence routine including neural network, machine learning algorithm, in particular, support vector machine.

5. The method according to claim 2, wherein the individual is an apparently healthy individual or the individual is afflicted with a known disease.

6. The method according to any one of the preceding claims, wherein the comparison or calculation comprises an evaluation of the determined

presence or absence or amplitude of peptide/protein markers.

7. The method according to any one of the preceding claims, wherein said sample of the individual is a urine sample, in particular, a midstream urine sample.

8. The method according to any one of the preceding claims, wherein capillary electrophoresis, HPLC, gas-phase ion spectrometry and/or mass spectrometry is used for determining the peptide/protein, in particular, the peptide/protein markers present in the sample.

9. The method according to any one of the preceding claims, wherein the peptide/protein determined in the peptide/protein sample includes collagen derived peptides/proteins, in particular, collagen α-1 derived peptides/proteins.

10. The method according to any one of the preceding claims, wherein the method predicts a treatment success with a predetermined active agent *in silico* for stratification of the therapeutic regimen.

11. The method according to any one of the claims 2 to 9 for determining the therapy end with an active agent, wherein according to step e) when the score is below the reference value representing the classifier, the administration of the active agent does not have any additional therapeutic effects.

12. The method according to any one of the preceding claims, wherein the information of the peptidome/proteome, in particular, the predetermined group of peptide/protein markers include values for the molecular masses and migration times, in particular, obtained by CE-MS and/or the information includes an adjusted p-value for the association with the predefined outcome.

13. The method according to any one of the preceding claims wherein the information of the peptidome/proteome is obtained by CE-MS analysis.

14. The use of a test kit or kit of parts for the prediction of a very relevant health event for an individual; for determining the therapeutic regimen; and/or for

predicting the treatment success of a treatment for an individual, respectively, said kit comprising means for determining the peptidome/proteome present in a body fluid sample and, optionally, means for reprocessing of the body fluid sample before determining the peptidome/proteome and instructions on how to use said test kit or kit of parts for a method according to any one of claims 1 to 13.

15. A computer implemented method of prediction of a very relevant health event for an individual; for determining the therapeutic regimen; and/or for predicting the treatment success of a treatment for an individual with an active agent, respectively, comprising the steps of

a) Obtaining information of the peptidome/proteome in a body fluid sample of the individual;

b) Computing the information of step a) by

i. Comparing the information on the peptidome/proteome obtained in step a) with information on the peptidome/proteome obtained from a database; or

ii. by calculating of 1) a reference value based on the information of a predetermined group of peptide/protein markers and 2) computing a score for the predetermined group of peptide/protein markers, whereby the score is calculated from information for each marker of the group under the influence of the active agent, whereby the information is obtained from a database, and comparing the computed reference value with the computed score,

c) Determining the probability of a very relevant health event of an individual; or determining a treatment regimen and/or predicting the treatment success with the active agent, respectively;

d) Optionally further comprising the step of showing the data of prediction of a very relevant health event for an individual, treatment regimen, predicting the clinical outcome and/or predicting the treatment success with the active agent, respectively, on an output unit.

16. A computer readable medium or computer program product having computer executable instructions for performing the steps as identified in any one of the claims 1 to 13.