CLAIMS

1. A method for the identification of the geographic origin of an individual test subject or of an individual group of test subjects, the method comprising
   - the comparison of a test methylation profile obtained from genomic material of the individual test subject or of the individual group of test subjects with one or more predetermined reference methylation profiles each being specific for a distinct geographic origin.

2. The method of claim 1, comprising the steps of:
   a. determining the methylation status of one or more pre-selected methylation sites within the genomic material contained in a biological sample obtained from the individual test subject, or of the individual group of test subjects;
   b. determining from the methylation status determined in (a) a test methylation profile of the individual test subject, or of the individual group of test subjects; and
   c. comparing the test methylation profile determined in (b) with one or more predetermined reference methylation profiles, wherein each of the one or more predetermined reference methylation profiles is specific for a distinct geographic origin of subjects or group of subjects which are of the same biological taxon of the individual test subject or individual group of test subjects;

   wherein if the test methylation profile is significantly similar to one of the one or more predetermined reference methylation profiles, the individual test subject or the individual group of test subjects has a geographical origin similar to the subjects or group of subjects of the one or more predetermined reference methylation profiles.

3. The method of claim 1 or of claim 2, wherein the individual test subject or individual group of test subjects is any biological entity having a DNA genome and DNA genome methylation, preferably the methylation site being a CpG site.

4. The method of any one of the preceding claims, wherein the individual test subject or individual group of test subjects are selected from a prokaryote, or a eukaryote.

5. The method of any one of the claims 2 to 4, wherein the one or more pre-selected methylation sites in (a) are methylation sites associated with tissue specific gene expression, preferably wherein the pre-selected methylation sites are associated with gene expression of one distinct tissue.

6. The method of claim 5, wherein the tissue is selected from the group consisting of
   (i) metabolic tissue preferably being gut tissue,

(ii) muscular tissue,
(iii) skin or feather tissue, and
(iv) organ tissue, said organ tissue preferably being hepatic and/or pancreatic tissue.

7. The method of any one of the preceding claims, wherein the individual test subject, or the individual group of test subjects, are animals.

8. The method of any one of the preceding claims, wherein the distinct geographic origin is a geographic location that is considered to be the habitat, wherein the individual test subject, or individual group of test subjects, were spawned and/or cultured, or at least cultured for a significant time during their lifetime.

9. The method according to any one of the preceding claims, wherein the one or more pre-selected methylation sites are within the 20% most differentially methylated genes of the genome of the individual test subject, or individual group of test subjects.

10. A method for quality controlling a suspected geographic origin of an individual test subject, or of an individual group of test subjects, the method comprising the steps of
    a. determining the methylation status of one or more pre-selected methylation sites within genomic material contained in a biological sample obtained from the individual test subject, or of the individual group of test subjects;
    b. determining from the methylation status determined in (a) a test methylation profile of the individual test subject, or of the individual group of test subjects; and
    c. comparing the test methylation profile determined in (b) with a predetermined reference methylation profile, wherein the predetermined reference methylation profile is specific for individual subjects, or individual groups of subjects, of the same biological taxon of the individual test subject or individual group of test subjects, and which were obtained from the suspected geographic origin;

    wherein if the test methylation profile is significantly similar to the predetermined reference methylation profile, the individual test subject or the individual group of test subjects passes the quality control and the suspected geographical origin is indicated as true geographical origin.

11. A method for assessing one or more environmental parameters of a habitat of an individual test subject, or of an individual group of test subjects, the method comprising the steps of
    a. determining the methylation status of one or more pre-selected methylation sites within the genomic material contained in a biological sample obtained from the individual test subject, or of the individual group of test subjects;

b. determining from the methylation status determined in (a) a test methylation profile of the individual test subject, or individual group of test subjects; and

c. comparing the test methylation profile determined in (b) with one or more predetermined reference methylation profiles, wherein the one or more predetermined reference methylation profiles are each specific for individual subjects, or individual groups of subjects, of the same biological taxon of the individual test subject or individual group of test subjects, and which were each obtained from distinct geographic origins; and wherein the distinct geographic origin is distinguished from other distinct geographic origins by one or more environmental parameters;

wherein if the test methylation profile is significantly similar to one of the one or more predetermined reference methylation profiles, the individual test subject or the individual group of test subjects is derived from a geographical origin having similar, or preferably equal, environmental parameters to the geographical origin of the individual test subjects or individual group of test subjects of the one of the one or more predetermined reference methylation profiles.

12. A method for confirming or declining an assumed geographic origin of an individual test subject or of an individual group of test subjects, the method comprising

- the comparison of a test methylation profile obtained from genomic material of the individual test subject or of the individual group of test subjects with one or more predetermined reference methylation profiles each being specific for a distinct geographic origin.

13. A method for developing a test system for confirming an assumed geographic origin of an individual test subject or of an individual group of test subjects, the method comprising the steps of:

a. determining the methylation status of one or more methylation sites within genomic material contained in a biological sample obtained from the individual test subject, or of the individual group of test subjects;

b. selecting from the one or more methylation sites a reference panel of methylation sites which is characterized by a specific and distinct differential methylation profile for each of the known geographic origins;

c. obtaining a test system by assigning a reference methylation profile for each of the known geographic origins; and

wherein a comparison of a test methylation profile obtained from a test sample with the reference methylation profiles obtained in (c) allows for confirming the assumed geographic origin of the individual test subject or of the individual group of test subjects from which the test sample was obtained.

14. The method of any one of the preceding claims, wherein the individual test subject, or the individual group of test subjects is marbled crayfish and/or wherein the distinct geographic origins are geographically distinct waters, these waters preferably being selected from the group consisting of lake(s), river(s) and aquaculture farms.

15. The method of claim 14, wherein the geographically distinct waters are made distinct by one or more environmental parameters selected from the group consisting of pH, water hardness, manganese content, iron content, and aluminum content.

16. The method of any one of claim 14 or claim 15, wherein the method comprises a genome wide methylation analysis or a methylation analysis of a pre-selected panel of methylation sites, the pre-selected panel of methylation sites preferably containing methylation sites within 500 to 1000, and preferably about 700 genes.

17. The method of claim 16, wherein the panel of methylation sites does not comprise consistently methylated or unmethylated methylation sites.