METHOD FOR ANALYSING THE DEGREE OF SIMILARITY OF AT LEAST TWO SAMPLES USING DETERMINISTIC RESTRICTION-SITE WHOLE GENOME AMPLIFICATION (DRS-WGA)

ABSTRACT

The present disclosure relates to a method for analyzing the degree of similarity of at least two samples in a plurality of samples comprising genomic DNA. The method comprises the following steps. a) Providing a plurality of samples comprising genomic DNA. b) Carrying out, separately on each sample, a deterministic restriction-site whole genome amplification (DRS-WGA) of said genomic DNA, c) Preparing a massively parallel sequencing library using a fragmentation-free, sequencing-adaptor/WGA fusion-primer PCR reaction from each product of said DRS-WGA. d) Carrying out low-pass whole genome sequencing at a mean coverage depth of < 1x on said massively parallel sequencing library. e) Aligning for each sample the reads obtained in step d) on a reference genome. f) Extracting for each sample the allelic content at a plurality of polymorphic loci. g) Calculating a pair-wise similarity score for the at least two samples as a function of the allelic content measured at said plurality of loci. h) Determining the degree of similarity of the at least two samples on the basis of the similarity score.

[Figure 1]