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(54) Title: DNA-METHYLATION BASED EVALUATION OF ANIMAL FEED

(57) Abstract: The present invention relates to a method of assessing the effect of at least one test component of animal feed on at least performance and/or general health of a test animal consuming the animal feed with the test component, the method comprising the steps of: (a) determining a test methylation profile of one or more pre-selected methylation sites within the DNA of the test animal; (b) comparing the test methylation profile obtained from (a) with at least one control methylation profile from a control animal of the same biological taxon as the test animal consuming animal feed without the test component; and wherein the results of (a) is used to determine the performance and/or general health of the test animal; and (c) comparing the test methylation profile obtained from (a) with (i) a first reference methylation profile obtained from a control animal of the same biological taxon as the test animal having good performance and/or general health; and/or (ii) a second reference methylation profile obtained from a control animal of the same biological taxon as the test animal having poor performance and/or general health; and wherein a significant similarity in the test methylation profile of (a) compared to the control methylation profile, is indicative of the test component not having an effect on the performance and/or general health of the test animal; and wherein a significant difference in the test methylation profile of (a) compared to the control methylation profile, is indicative of the test component having an effect on the performance and/or general health of the test animal; and wherein a significant similarity in the test methylation profile of (a) to the first reference methylation profile and/or a difference in the test methylation profile of (a) to the second reference methylation profile is indicative of the test animal having good performance and/or general health as the control cell; and/or wherein a difference in the test methylation profile of (a) compared to the first reference methylation profile and/or a significant similarity in the test methylation profile of (a) to the second reference methylation profile is indicative of the test animal having poor performance and/or general health as the control animal; and wherein the test animal is selected from livestock or poultry.

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