The Microorganism Community in Subcutaneous Abscess of Goat

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Abstract

Background: Subcutaneous abscess is a common disease, which seriously affects the quality and yield of goatPhe

The abscess like egg size; 2) The abscess larger than the first; 3) The scabby abscess after rupture.

Materials and Methods

Sample collection

In August 2021, five pus samples were collected from 5 different goat farms (4 farms are house feeding and another one is grazing locally) in Jiangsu Province, China. The number of goats in each farm is about 2000, and the incidence of subcutaneous abscess is 1% to 5%. The diseased goats with large swelling (Figure 2) were picked out and the swollen area were disinfected with iodophor diluent and alcohol (75%) after fixation. Following the abscess was cut open with a sterilized scalpel (Figure 3); about 2 ml of pus was sampled with a sterilized pipette and store in a 5 ml EP tube.



Figure 2: The diseased goats for sampling.

A) An abscess located in the ventral side; B) An abscess located in the front of the forelimb.



Figure 3: The pus that flows out after the abscess was cut open.

Metagenomics sequencing and bio-information analysis

Following the EP tubes which contained pus were stored in the biosafety transport box (UN3373), all the samples were sent to Suzhou Genomics Biotech Co., Ltd. (China) for metagenomics sequencing and bioinformatics analysis. To investigate into the microbial species contained in the samples, all the tested sequences were blasted to the NCBI's nucleic acid database, including bacteria, fungi, archaea, viruses and parasites. The microbial abundance information in the samples was calculated based on the unigene. The samples for this research were analyzed without removal of the host genome, so some genes could be annotated to the host animal or closely related species.

Results

Validity of samples

The quality of the sequencing is not only affected by the sequencer itself and the sequencing reagent, etc., but also by the amount of the sample. So each pus sample in this research was provided more than 2 g, which was referred to the requirements for feces samples. The DNA extraction of the samples carried out by the company is valid for testing. The extracted DNA has obvious main band, no degradation, no impurities such as RNA and protein (OD260/280 1.5, OD260/230 1.0).

Diversity of microorganism in subcutaneous abscess of e

Interestingly, each sample contained similar microbial species, including 53-59 species of bacteria, 5-6 fungi, 3 viruses and 16-18 parasites. The top 5 dominant bacteria are *Staphylococcus aureus*,

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