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O0593 Potential microbial biomarkers of lung cancer

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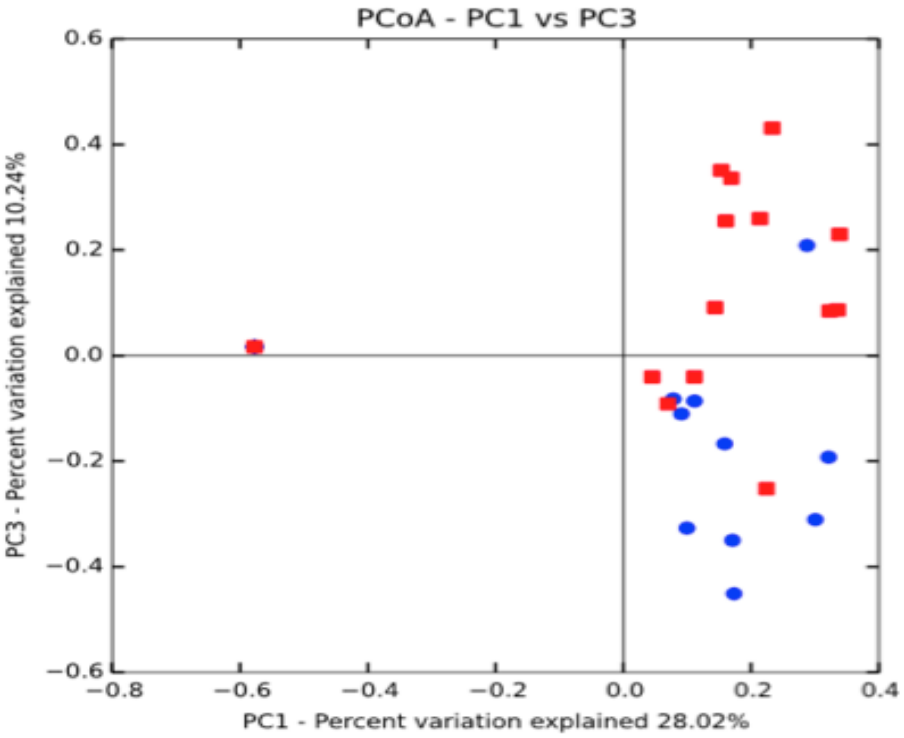
Background: It has been recognized that the respiratory microbiota is associated with respiratory diseases, and the re assemblage or dysbiosis of microbial communities exhibit characteristic compositional signatures in case of certain diseases. The microbial markers have an important potential as diagnostic markers, theuropathic targets or for a better understanding of pathogenesis, however the comparison is typically performed between a certain disease type and a healthy control group. It is poorly understood whether the dysbiotic microbiome has distinctive characteristics for different respiratory disorders that would enable the discovery of discriminatory biomarkers for a specific type of disease. Being the most prevalent cancer type worldwide, we selected lung cancer as our disease objective and investigated the potential microbial biomarkers of lung cancer from the bronchoalveolar microbiome of cancer cases and other scenarios of respiratory disorders.

Materials/methods: The bronchoalveolar fluid from 17 lung cancer cases and 15 controls with different respiratory situations (cases of pneumonia, pleurisy, granulomatous inflammation, bronchial dilatation, sarcoidosis, hydatid cyst, fibrinous inflammation, and healthy controls) were collected. After total DNA isolation from the samples using commercial kits, 16S rRNA gene regions V3-V4 were amplified by PCR. High-throughput DNA sequencing was performed using Illumina-MiSeq technology. The sequenced reads were assigned to taxonomic units at genus level using QIIME pipeline. Correlation based feature selection with a greedy stepwise algorithm was employed for biomarker discovery at genus level. Naive Bayes Classifier was used to evaluate the discriminatory performance of the selected biomarkers.

Results:A total of 325 genera (belonging to 20 bacterial phyla) were detected from the cohort microbiota. Performing biomarker selection using 5-fold cross validation, Microbacterium, Bifidobacterium, Coriobacteriaceae genera, and Rhizobiales genera were detected to be reduced in lung cancer cases while Moraxella found to be enriched. The combination of these taxa resulted in an area under ROC curve detection score of 0.931 ($p < 0.01$), and an F-score of 0.801 by 10-fold cross validation.

Conclusions: Our results suggest that bronchoalveolar microbiome carries strong biomarkers of lung cancer which is specific to cancer microbiome that can distinguish it from other respiratory disorder microbiota. This is an implication of potential diagnostic or therapeutic microbial markers for lung cancer.



PcoA plot of cancer (red) and control cases (blue) based on selected biomarkers