



Mesa 2

The Influence Of Stable State Eosinophil Count And Acute Exacerbations On The Airway Microbiome In COPD (ATS)

R. Singh, Z. Wang, J. R. Brown, B. E. Miller, R. Tal-Singer, S. Van Horn, L. Tomsho, B. Barker, U. Kolsum, D. Singh, C. E. Brightling, P. J. Barnes, G. C. Donaldson, J. A. Wedzicha.



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16S ribosomal DNA



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Methods

As part of the MRC COPD-MAP consortium, sputum samples from 285 COPD patients were collected at three UK centres (Imperial College London, Manchester and Leicester) at both stable and exacerbation states. Whole blood was collected for differential leukocyte at the first stable visit. Stable state was defined as no symptom-defined exacerbations or systemic treatment with antibiotics and/or steroids in the preceding four weeks. All exacerbation samples were collected prior to any systemic therapy.

16S rRNA sequencing was performed on 755 DNA samples extracted from sputum (483 stable and 272 exacerbation samples), using primers to the V4 region (Illumina Miseq NGS platform).



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Microbiota estable

Proteobacteria

Firmicutes

Bacteroidetes phyla

Microbioma

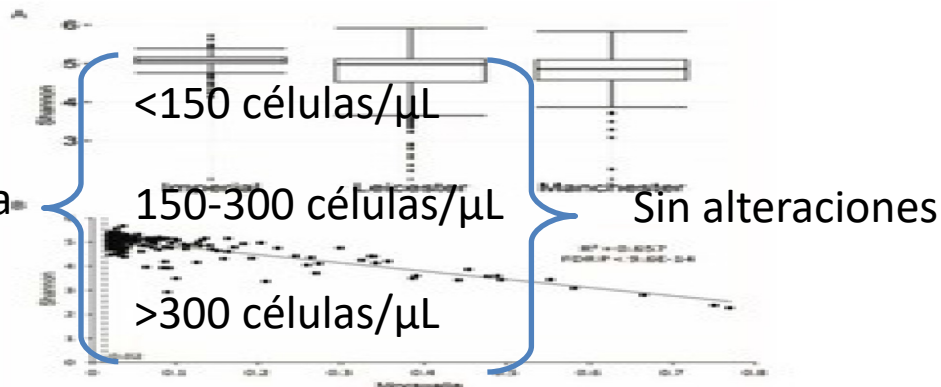


Figure 1A. Comparison of the airway microbial alpha diversity, as measured by Shannon index, between the three clinical sites.

Figure 1B. Relationship between *Moraxella* sp. and microbiome diversity.

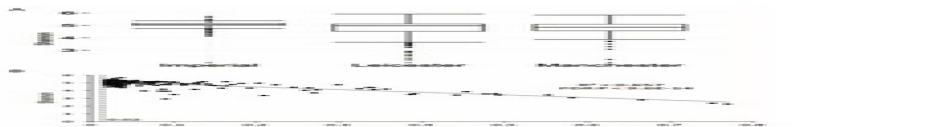


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Conclusiones:

- El pulmón no es estéril, posee una microbiota que parece estable
- En las exacerbaciones la composición de esa microbiota cambia y puede ser la responsable de las mismas
- El estudio de la microbiota con nuevas técnicas puede abrir un campo muy importante en las exacerbaciones