

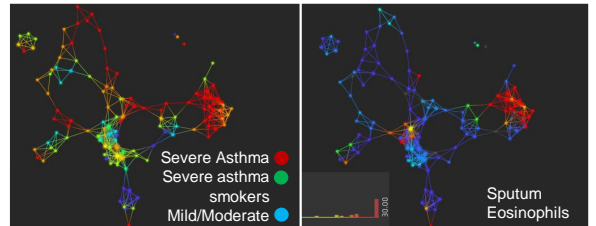
Data analytics and bioinformatics to successfully define asthma subphenotypes

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Facts & Figures

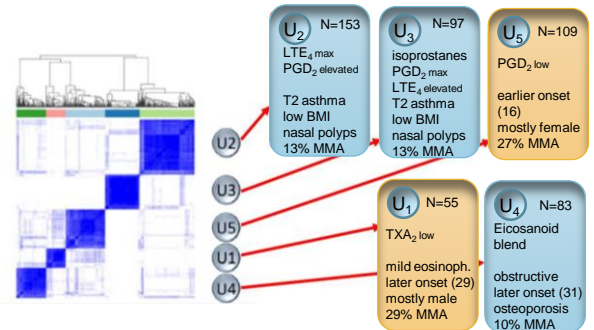
Start date:	01/10/2009
End date:	30/09/2015
Contributions	
IMI funding:	9 935 501 €
EFPIA in kind:	14 574 652 €
Other:	2 415 549 €
Total Cost:	26 925 702 €
Project website:	www.europeanlung.org/projects-and-research/projects/u-biopred/home
Social media:	@ubiopred

Topological data analysis of U-BIOPRED proteomics data



Exploring features of complex data from multiple sources. Dataset from 80 asthmatic participants. U-BIOPRED cohorts exhibit alignment with obtained network.

Sub-phenotypes defined by clustering of main lipid metabolites (urine)



Distinct pathways linked to highly symptomatic adult-onset severe asthma

Adult-onset severe asthma is characterized by inflammatory pathways involving eosinophils, mast cells, and group 3 innate lymphoid cells. Potential targets for adult-onset severe asthma treatment.

Value of IMI collaboration

Resources from Seventh Framework Programme (FP7) of the EU.

'In-kind' contributions from European Federation of Pharmaceutical Industries and Associations (EFPIA) member companies.

Collaboration: Partners from industry, academia, small- and medium-sized enterprises (SMEs), patient groups, and regulators worked alongside each other, each one bringing their expertise.

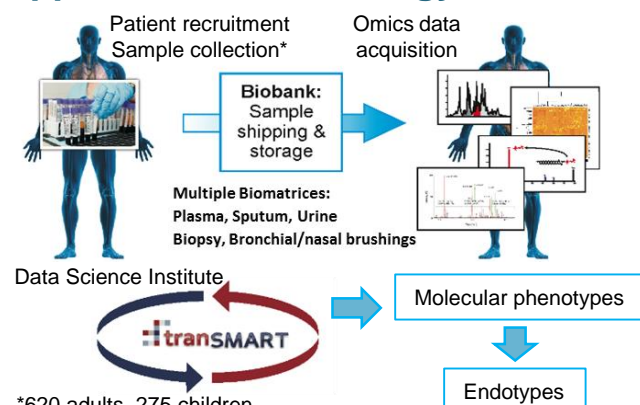
Impact & take home message

- U-BIOPRED legacy is its contribution to our understanding of asthma, which, in turn, contributes to the development of new drugs, enabling improved treatments of severe asthma patients.
- The multi-'omics integration handprints that are being produced entirely novel and will contribute to target discovery
- Close collaborative network that has been built in a team with diverse backgrounds
- Patients involvement U-BIOPRED had a positive impact on the passion and motivation
- The transSMART platform was invaluable for managing the data.

Challenge

Severe asthma is notoriously difficult to treat, with substantial number of patients exhibiting uncontrolled symptoms and steroid insensitivity. U-BIOPRED was an ambitious plan to tackle the understanding of asthma through an integration of clinical and multi-'omics approaches, to identify patient subpopulations with distinct underlying molecular pathology and improve patient care.

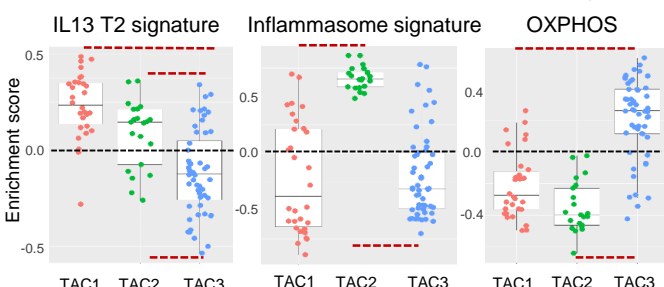
Approach & Methodology



*620 adults, 275 children, transcriptomics, proteomics, genomics, metabolomics, metagenomics

Results

Identification of patient sputum transcriptomics associated clusters (TAC) – novel patient phenotypes



Gene set variation analysis implies distinct underlying molecular pathology in the 3 groups, with TAC1 enriched for T2 high asthma, TAC2 for inflammasome activation and TAC3 for oxidative phosphorylation gene signatures.