Pi – A genetics-led system enabling drug target discovery in immune diseases

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Facts & Figures

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Contributions	
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EFPIA in kind:	21 664 981 €
Other:	7 204 092 €
Total Cost:	50 069 073 €
Project website:	www.ultra-dd.org

Challenge

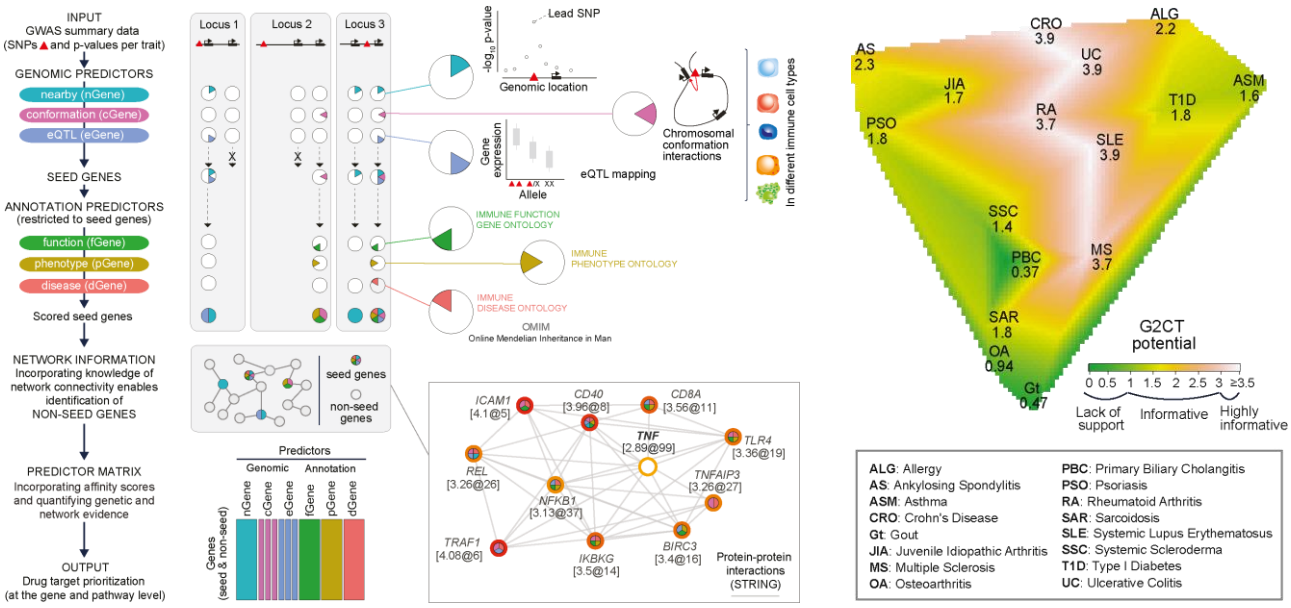
Most candidate drugs currently fail later-stage clinical trials, largely due to poor prediction of efficacy on target selection. Genetics can inform drug discovery but validated approaches that maximise the informativeness of genetic associations for early target validation at genome-scale are much needed.

Approach & Methodology

We integrate functional genomic predictors, knowledge of network connectivity and immune ontologies to maximise the informativeness of genetics for target validation, defining the target prioritisation landscape for 30 immune traits at the gene and pathway level.

Results

- Integrated, genetics-led rating system for drug targets at the gene and pathway level
- Captures current therapeutics and delineates druggable landscape of immune traits
- Pre-clinical utility illustrated using patient-derived cell assays and L1000 data
- Open access resource to advance early target selection and validation



Value of IMI collaboration

A key component of the success of our work has been the ability to do high quality science in an open source partnership between academia and pharma through IMI collaboration, collectively forming the ULTRA-DD Consortium to advance drug target development.

Impact & take home message

Pi is an open access, scalable system providing new insights into early-stage target prioritisation for immune-mediated diseases. Pi can be used with customised and user-defined genetic datasets through an R/Bioconductor package (http://bioconductor.org/packages/Pi).

imi innovative medicines initiative efpia

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