ALLERGY, GENETICS

HUBS AND SUPERHUBS IN ASTHMA: LOW ACTIVITY

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Here comes the reference to a first molecular system biology paper on asthma – something on my to-do list for 3 years. The authors constructed a biological interaction network using a database of curated molecular interactions.In a next step they mapped differentially expressed genes from microarray data and analyzed the correlation between the topology and biological function using gene ontologies.
Hubs are defined as nodes with a connectivity greater than 5 (they found 88 hubs, mostly evolutionary late genes, seven were significantly modulated but I couldnÂ´t find out which genes). Superhubs are those with a connectivity of >5 in the shortest path connecting hubs (16 found, mainly evolutionary ancient processes, all with a small dynamic range).
So far, the model comprises only BALB/c and RAG KO mice – I am sure that this exercise will soon be repeated for human lungs.
I wonder why they haven't identified more transcription factors – is the rather unorthodox definition of hubs responsible for that? An alternative option could take into account the hierarchical (or temporal?) relationship of nodes. Even then might be only a small overlap between affected genes and binding targets as noticed in a recent yeast paper.

First, a transcription factor can regulate secondary targets via regulatory cascades. Therefore, the unrefined knockout targets are likely to include both direct and indirect targets. Second, different transcription factors occupying a promoter could compensate for each other's loss, masking the deletion effect. Finally, a transcription factor could bind a promoter under normal growth conditions but function only under specific environmental conditions…

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