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DEVELOPMENT

An atlas of embryogenesis

A transcriptomic atlas of human organogenesis has been recently published in *eLife*, providing a map of gene expression at organ-specific resolution during this crucial stage of development.

The authors used RNA sequencing (RNA-seq) to determine gene activity in human embryonic samples from 15 separate organs and tissues, including sites of mixed origin with regards to the three germ layers, such as palate and limbs, as these can be subject to major developmental disorders. "Many studies tend to focus on one organ system, when in fact understanding, for example, liver development is as much about deciphering why and how it differs from heart development," says senior author Neil Hanley (University of Manchester, UK). "Our approach provided an opportunity to obtain a global view of the processes at play in human embryogenesis."

Comparison of the embryonic RNA-seq data with previously published fetal RNA-seq data showed that the transcriptomes were distinct.

Hanley and co-workers then adapted the statistical principal components analysis (PCA), a mathematical algorithm that reduces data dimensionality while retaining most of the variation in a data set, by imposing a hierarchical developmental lineage on the different organs and tissues. When applied to the gene expression data, this approach, which the authors called lineage-guided PCA (LgPCA), revealed organ-specific signatures as well as unique patterns of gene expression across groups of related tissues.

On the basis of gene co-expression patterns across tissues or within individual organs, the team were able to determine key regulators of human organogenesis, including both previously established factors such as hepatocyte nuclear factor 4α (HNF4α) in the liver, as well as new candidate transcription factors.

LgPCA was also able to pinpoint the causes of human congenital disorders. For example, when applied to syndromes of unknown aetiology, LgPCA implicated the genes *DLX5*, *DLX6*, *LHX8* and *FOXF2* in the development of cleft palate.

Finally, the authors identified 6,251 novel transcripts during human organogenesis that are likely to be non-coding and that exhibit high tissue-specificity. Hanley and colleagues are currently expanding the atlas to incorporate more cell and organ types, across different developmental stages, and including epigenomic marks.

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ORIGINAL ARTICLE Gerrard, D. T., Berry, A. A., *et al.* An integrative transcriptomic atlas of organogenesis in human embryos. *eLife* **5**, e15657 (2016)