Stem-cell genomics

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The surprising plasticity and trans-differentiation of transplanted stem-cells suggest that there may be a set of universal stem-cell genes that govern the undifferentiated proliferative state. In the July 3 Proceedings of the National Academy of Sciences, Terskikh *et al.* report attempts to define a common stem-cell gene profile by comparing hematopoietic and neural stem-cells (*Proc Natl Acad Sci USA* 2001, **98:**7934-7939). They isolated hematopoietic stem cells (HSC) from mouse bone marrow and created a subtracted cDNA library enriched in HSC genes. High-throughput sequencing identified 223 sequences representing known (40%) and novel genes. There were similarities and differences between these adult HSC genes and those characterized in fetal HSC. The HSC enrichment was demonstrated by PCR, northern and *in situ* hybridization experiments. The genes encode cell-surface proteins (notably two novel seven-transmembrane receptors), nuclear proteins and signalling molecules. Terskikh *et al.* compared their results with analysis of neural stem cellsand performed microarray analysis to define common stem-cell genes. Some of the HSC-enriched genes were expressed in the germinal zones of the brain, which contain neural progenitor cells. The authors suggest that identifying overlapping stem-cell gene profiles may indicate genes that regulate the common feature of stem cells, namely their capacity for self-renewal.

References

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