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"Stemness"

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The recent isolation of human embryonic [stem cells](#) and the demonstration of their remarkable pluripotency have focused attention on the properties of stem cells. Two studies published in the September 12 [Scienceexpress](#), use functional genomics to investigate common features of stem-cell populations of different origins. Both groups used Affymetrix oligonucleotide microarrays covering around 12,000 genes to investigate the stem-cell transcriptome. Ramalho-Santos *et al.* carried out [transcription profiling](#) of embryonic, neural and hematopoietic stem cells from mice, in the same experiment (*Scienceexpress* DOI:10.1126/science.1072530). Each stem-cell population had its own set of highly enriched genes, and 216 genes were enriched in all three stem-cell groups, revealing the core set required for "stemness" attributes. In the same issue, Ivanova *et al.* report their comparison of the gene expression profiles of either human or murine hematopoietic stem cells, compared with the non-hematopoietic embryonic and neural stem cells (*Scienceexpress* DOI:10.1126/science.1073823). The two types of hematopoietic stem cells shared a considerable number of genes, including those involved in signal transduction pathways, cell-cycle regulation and gene transcription. The challenge remains to link 'stemness' signatures to distinct biological features of stem cells.

References

1. The evolving concept of a stem cell: entity or function?
2. *Scienceexpress*, [<http://www.scienceexpress.org>]
3. Melton Lab of Molecular Embryology, [<http://mcb.harvard.edu/melton/index.html>]