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10.1038/nrm1931

# IN BRIEF

## STEM CELLS

### *In vitro* germline potential of stem cells derived from fetal porcine skin.

Dyce, P. W. *et al. Nature Cell Biol.* **8**, 384–390 (2006)

The authors isolated stem cells from fetal porcine skin, induced them to differentiate, and identified a subpopulation of cells that expressed several specific germ-cell markers, including the growth differentiation factor 9b (*GDF9b*) and deleted in azoospermia-like (*DAZL*) genes. Further differentiation caused follicle-like cell aggregates that secreted the steroid hormones oestradiol and progesterone and that responded to stimulation by gonadotropin. Some aggregates extruded large oocyte-like cells that expressed oocyte and meiosis markers and that, eventually, developed structures that resembled pre-implantation embryos. Together, these findings indicate that somatic stem cells that are derived from the later stages of fetal development can develop into germ cells *in vitro*.

## TECHNOLOGY

### 3′ UTR seed matches, but not overall identity, are associated with RNAi off-targets.

Birmingham, A. *et al. Nature Methods* **3**, 199–204 (2006)

RNA interference is a powerful tool in research and therapeutic applications provided that the small interfering RNA (siRNA) that is used is potent and specific — that is, it does not cause 'off-target' gene silencing. Birmingham *et al.* applied an algorithm that is well suited for detailed alignment analysis of short sequences to a database of experimentally identified off-target genes, and found that the overall gene identity provides little insight into whether a gene will be affected by a given siRNA or not (except in the case of near identity). Instead, perfect matches between the hexamer or heptamer seed (positions 2–7 or 2–8 of the antisense strand) of an siRNA and the 3′ untranslated region (3′ UTR), but not the 5′ UTR or the open reading frame, were associated with off-target effects.

## CELL MIGRATION

### Analysis of cell migration using whole-genome expression profiling of migratory cells in the *Drosophila* ovary.

Wang, X. *et al. Dev. Cell* **10**, 483–495 (2006)

### Systematic analysis of the transcriptional switch inducing migration of border cells.

Borghese, L. *et al. Dev. Cell* **10**, 497–508 (2006)

To identify new genes that are involved in cell migration, two groups carried out genome-wide expression profiling on purified border cells — a type of migratory cell that is present in the *Drosophila melanogaster* ovary. The transcription factor Slbo is required for these cells to become migratory, and this switch is poorly understood. So both groups compared the expression profiles of wild-type border cells with *slbo* mutants. Wang *et al.* identified 413 genes that were enriched in migratory cells, and 149 that were Slbo dependent. Many of the isolated genes are involved in cytoskeletal regulation and the secretory pathway. Borghese *et al.* found almost 300 genes that were significantly enriched in border cells; 28% were regulated by Slbo. As well as cytoskeletal regulators, they identified a group of 'muscle-like' genes that might enable cells to acquire muscle-like properties to invade neighbouring tissue.