Australian National University

PUBLIC LECTURE

Is the genomic arrangment of the Zic genes crucial for their function?

Thursday 29 March 2012 1pm

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Gould Seminar Room Building 116, Daley Rd, ANU

The Arkell laboratory studies the genetic mechanisms that drive gastrulation of the mammalian embryo. Gastrulation is the process that converts a group of pluripotent cells (the inner cell mass of the blastocyst) into the three germ layers (ectoderm, endoderm and mesoderm) from which the entire adult organism is derived. In mammalian embryos gastrulation is concomitant with the establishment of the three embryonic axes (anterior-posterior, dorsal-ventral and left-right) that enables each embryonic cell to acquire a positional address without which differentiation and morphogenesis cannot take place.

One current focus of our research is the elucidation of the function of a family of highly related putative transcription factors encoded by the Zic gene family. The defining feature of these proteins is a zinc finger domain that is able to both bind DNA and other proteins. It seems likely that these proteins act both as classical transcription factors (to bind DNA and directly regulate transcription) and as co-factors (to bind other DNA binding proteins and indirectly regulate transcription). Our recent work suggests that post-translational modification of the Zic proteins by the small ubiquitin like modifier (SUMO protein) may influence whether a Zic protein acts as a transcription factor or co-factor. The genes that encode the Zic proteins have an unusual genome arrangement, generally existing as tightly linked tandem copies. Our work also suggests that this proximity between particular members of the Zic gene family may be essential for their functionality.

Presented by

Division of Evolution, Ecology & Genetics

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