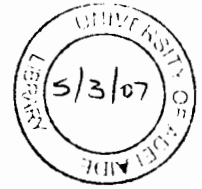


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**EXPRESSION AND FUNCTION OF GENES IDENTIFYING
PLURIPOTENT CELL SUB-POPULATIONS
IN THE EARLY MOUSE EMBRYO**

A Thesis Submitted To The University Of
Adelaide For The Degree Of Doctor Of Philosophy

by

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SUMMARY

The coordinated regulation of pluripotent cell developmental progression during early mouse development is critical for formation of the three primary germ layers of the embryo. Accumulating evidence suggested the existence of transient pluripotent cell sub-populations in the early mouse embryo, which could not be recognised at the molecular level. Marker genes generated by dd-PCR analysis of the ES to EPL cell transition *in vitro*, a model of the ICM to primitive ectoderm transition *in vivo* (Rathjen *et al.*, 1999; Lake *et al.*, 2000), potentially provided a means to distinguish these transient pluripotent cell sub-populations.

Wholemout *in situ* hybridisation analysis of the reported marker genes, *Oct4*, *Rex1* and *Fgf5* (Haub and Goldfaub, 1991; Hébert *et al.*, 1991; Rogers *et al.*, 1991; Rosner *et al.*, 1990, Schöler *et al.*, 1990a and b) in conjunction with markers identified and isolated from the dd-PCR screen of ES and EPL cell RNA, *L17*, *Psc1* and *K7* (Schulz, 1996; S. Sharma, unpublished) provided a molecular description of pluripotent cell developmental progression during peri-implantation mouse development. Expression of *Rex1* and *L17* was observed in the ICM and early epiblast populations of the developing blastocyst, and downregulated at approximately 4.75 d.p.c.. *Psc1* expression was detected in the pluripotent cells of the developing blastocyst and epiblast bud, and downregulated following proamniotic cavitation at 5.25 d.p.c.. *K7* was not expressed in the early blastocyst, but was expressed by pluripotent cells between 4.75 and 5.25 d.p.c., following the formation of the late stage blastocyst to immediately prior to primitive ectoderm organisation into a pseudostratified epithelial sheet. *Fgf5* expression was not detected during blastocyst development, but was detected in the primitive ectoderm following proamniotic cavitation at 5.25 d.p.c.. Compilation of gene expression data indicated the existence of at least four distinct pluripotent cell sub-populations within the *Oct4*⁺ pool. Comparison of pluripotent cell sub-populations with embryonic development indicated that the transient sub-populations correlated with embryonic events, including increased pluripotent cell proliferation, proamniotic cavitation and formation of a primitive ectoderm monolayer. Furthermore, gradual progression of pluripotent cells *in vivo* correlated closely with marker gene expression *in vitro* during the ES to EPL cell transition, validating the conversion of ES cells to EPL cells as an *in vitro* model of the ICM to primitive ectoderm transition and allowing more precise definition of ES and EPL cell embryonic equivalents.

K7 was selected for further analysis, based on its tight expression window during early development. cDNA clones spanning a 6.6 kb *K7* sequence were isolated and the complete *K7* cDNA was shown to be 79.3% identical to a human gene of unknown function, termed KIAA0165. This human gene was expressed in similar tissues to *K7*, including the testis, haematopoietic system and gastrointestinal tract, suggesting that these two genes were homologues. The C-terminal putative protein sequence of *K7* and KIAA0165 demonstrated similarity to three fungal proteins, *cut1* (*S. pombe*), *ESP1* (*S. cerevisiae*) and *bimB* (*A. nidulans*). Sequence similarity of the conserved C-terminal region of *K7* with Cut1 and Esp1 C-terminal protein sequence implicated *K7* in the control of cell division in mammals. A mitotic role for *K7* was consistent with the *in vivo* expression pattern of *K7* in the adult, which was confined to tissues containing rapidly proliferating cells for tissue and cellular regeneration. Functional investigation of *K7* in mammalian cells using overexpression studies demonstrated that like KIAA0165, *K7* interacted with a known cell cycle regulator encoded by the *pituitary transforming tumour gene* (*PTTG*). Furthermore, overexpression of mPTTG in Cos-1 cells increased the proportion of cells in the G2/M phase of the cell cycle, consistent with a role for this complex in cell cycle progression through G2/M. *K7* was also shown to localise to the centrosome, the microtubule organising centre from which the mitotic spindle emanates. Taken together these results suggested that the *K7*/mPTTG interaction shared similarities with the Cut1/Cut2 and Esp1/Pds1 complexes of budding yeast and fission yeast respectively, suggesting that aspects of the chromosome segregation mechanism may be conserved between yeast and mammals.