were found in the small intestine nor coproantigen increased at the course of the infection.

Cloning and histological analysis of the mouse testis specific gene, Sperm tail associated protein (*Stap*)

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A serious problem nowadays is that about 1 of 10 couples are sterile. Male sterility can be classified by a decrease in number of sperms or by abnormalities in sperm motility. Over 60% of the mechanism for male sterility remains unclear. To analyse the genetic factor related to spermatogenesis, the author used cDNA subtractive hybridization method from mouse testis between normal and sterile mice, which both have C57BL/6 congenic background, and isolated a novel gene *Stap*. The transcript of *Stap* cDNA was expressed only in testis and in the germ cells. The aim of this study was to clone the full length of *Stap* cDNA and to carry out histological analysis of the gene product.

Full length of *Stap* cDNA was 3429bp containing a 33bp poly (A) tail. A protein with 1022 amino acids was predicted by the nucleotide sequence. Three leucine zipper motifs and four N-glycosylation sites were found in the protein using a motif search program. The *Stap* cDNA was mapped at the intermediate position between two microsatellite markers of *D8Mit198* (51.0) and *D8Mit138* (53.0) on mouse chromosome8, where no candidate gene was detected to be related to its nucleotide sequence. Northern blot analysis and in situ hybridization method revealed that *Stap* mRNA appeared only from step 2 round-spermatids up to step 12 in the normal seminiferous tubules. Western blot analysis showed the molecular weight of *Stap* protein was about 140kDa. The protein expression was observed initially at the perinuclear region in the cytoplasm of step 6 spermatid and extended caudally accompanied with the sperm tail development.

This study suggested that novel gene *Stap* could be concerned with the sperm tail structure and its function. It is expected that the function of *Stap* will be clarified by further analysis.