markable increase of parasite specific intestinal IgA secretion was observed in reinfection groups, but no obvious responses in oral immunization groups. All hamsters showing increased intestinal IgA secretion harbored low numbers of worms. Western blot analysis with serum IgG and IgA in intestinal flush showed strong reaction with 38kDa band of adult somatic antigen. The same band was also detected in protoscolex somatic antigen. Common band was detected in adult somatic antigen and adult ES antigen at 51kDa. These results suggested that acquired resistance to *E. multilocularis* infection may be associated with systemic recognition of protoscolices and adult somatic antigens, and with local specific intestinal IgA secretion.

Studies on the parasite fauna of raccoon (*Procyon lotor*) naturalized in Hokkaido, Japan

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From July 1998 through October 1999, 128 naturalized raccoons (*Procyon lotor*), captured in Eniwa, Sapporo, Kitahiroshima, Naganuma, Chitose and Nopporo, in Hokkaido were examined for gastrointestinal helminths and ectoparasites. Nine species of helminths were recognized; Trematoda: *Euparyphium* sp. (prevalence: 27.3%), *Metagonimus takahashii* and *Metagonimus miyatai* (21.9%), *Brachylaima* sp. (6.3%), *Plagiorchis muris* (7.8%), Nemadoda: *Molineus legerae* (7.0%), *Ancylostoma kusimaense* (0.8%), *Capillaria putorii* (3.9%), larvae of nematoda possibly *Porrocaecum* sp. (1.6%). And three species of ticks were collected; *Ixodes ovatus, I. persulcatus*, and *I. tanuki*.

Seven of the nine helminth species (*M. miyatai, Brachylaima* sp., *P. muris, M. legerae, A. kusimaense, C. putorii, Porrocaecum* sp.) were new parasite records for raccoon in Japan.

The diversity of gastrointestinal helminth fauna of the raccoons in Hokkaido, determined by the Simpson index, were poorer than that of red foxes captured at the same area and that of raccoons in North America which is their natural habitat. The gastrointestinal helminth fauna of the raccoon was found similar to that of raccoon dogs rather than that of foxes or weasels. The result suggests that the behavioral pattern of the raccoons resemble that of raccoon dogs in Hokkaido, and that invasion of raccoon may influence the population of raccoon dogs.

In this survey, *Echinococcus multilocularis* and *Baylisascaris procyonis* causing fatal zoonosis were not found. However *E. multilocularis* is now endemic all over Hokkaido Island and the role of raccoon in its life cycle is one of the public health concerns. Accordingly, protoscoleces of *E. multilocularis* were experimentally inoculated to a juvenile raccoon. The raccoon was autopsied at fifteen days post-infection, however, no parasites

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.