develops to adult at the same site where it initially attaches to the host intestine. In 3 pups with about 17–26 days of age, most of the parasites were found in the lower part of the small intestine and also in the large intestine. This finding suggests that the expulsion of the parasite could occur as early as 14 days of infection. Density effect was observed on number and size of the parasites. The size of the parasites in the same site of the intestine of the different hosts decreased as the total number of the parasites in one host increased. Moreover, the size of the parasites was differed among the different sites of the intestine in the same host. The comparison of the age of the pups and the development of the parasite revealed that the parasites can develop into adult in 14 days old hosts. The color test of feces in the rectum was carried out as an indicator of the amount of blood in the feces. Pups which showed high level of red color in their feces ranked to heavy infection of the parasites. Further studies are required for investigating a correlation of the rectum color, blood contents and parasite burden. In this survey, the mean number of the parasites in a dead pup (X) was 1,200 and standard deviation (S) was 1,005. Therefore, $S^2/X \gg 1$. This indicates over dispersion in the distribution of *U. lucasi* in their hosts.

It is concluded that transmammal infection with *U. lucasi* in the northern fur seals occurs only during the first week after birth and this period is critical for *U. lucasi* to complete its life cycle. *Uncinaria* infection is common in the seals of Bering island, and the population of fur seal is exposed to *U. lucasi* with high mortality risk.

Analysis of a mouse cDNA which can complement the first meiotic-deficient mutant of the fission yeast *Schizosacchromuces pombe*

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Meiosis is a key step of sexual reproduction in all eukaryotic organisms. The molecular controls of meiosis, however, are poorly understood compared with those over of mitosis. Meiotic cells undergo premeiotic DNA synthesis which is followed by the first and second meiotic divisions to yield haploid cells. This process is highly conserved among a variety of species from yeast to mammals. Total testis cDNA library from mouse was constructed in a fission yeast expression vector. Using the genetic functional complementation method, a mouse cDNA clone which can rescue *sme2* mutation has been identified. This mutant was arrested before the first meiotic phase I. A 1.2-kb cDNA clone was obtained, named poly (A) binding protein 3 (*Pabp3*), which contains an open reading of 906 nucleotides encoding a predicted 32-kD protein. The amino acid sequence includes a clear match to the RNA-recognition motif (RRM). Furthermore, a search of the Genebank database revealed that the *Pabp3* protein has 95.8% amino acid identity with the bovine poly (A) binding protein II (PABII). These results strongly suggest that *Pabp3* is the mouse homolog of PABII, which stimulates poly (A) polymerase. Poly (A) polymerase synthesizes poly (A) tails rapidly only when the substrate RNA is bound simultaneously

by two stimulatory proteins, the cleavage and polyadenylation specificity factor (CPSF) and PABII. Northern blot analysis of *Pabp3* revealed a single transcript of approximately 1.2kb only in testis. To determine if *Pabp3* is differentially expressed in specific testicular cell lineages, northern blot analysis was performed in testis from normal and germ cell-defficient W/W^V mutant mice, and also the different stages of post-natal development in normal mice. As a result, *Pabp3* was expressed only in the adult testis. *Pabp3* protein was detected in the nucleus in a specific period (from late pachyten spermatocytes to step 9 round spermatid) by immunohistochemistry. *Pabp3* function is unclear in the mouse testis, but these results suggest that *Pabp3* is involved in specific spermatogenetic cell differentiation.

It was demonstrated in this study that *Pabp3* locus mapped at centromeric position with 4.2 ± 2.9cM apart from *Ctla1* on mouse chromosome 14.

Functional analysis of natural resistance-associated macrophage protein (Nramp) in the pathway of nitric oxide synthesis in mice

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The ability of a host to resist infection with a wide range of viral, bacteria, and parasitic pathogens is strongly influenced by a lot of genetic factors. The Bcg/Ity/Lsh gene on mouse Chromosome 1 regulates priming/activation of macrophage for antimicrobial and tumoricidal activity. A candidate gene expressed in macrophages has been identified as the natural resistance-associated macrophage protein (Nramp) by positional cloning and full-length sequence analysis. Macrophages are concerned with antimicrocidal activity by numerous cytokine-induced nitric oxide productions.

In this study, the following experiments were performed to reveal the relationship between Nramp and NO production by macrophages. The production of NO by macrophages from $Nramp^r$ mice ($Nramp^r$ macrophage) was much larger than that from $Nramp^s$ mice ($Nramp^s$ macrophage), in the case of activations with IFN-γ, LPS+IFN-γ, IL-1β, TNF-α and L-Mannose. No significant difference between the expressions of Nramp mRNA in the cytokine-activated $Nramp^r$ and $Nramp^s$ macrophages was determined by Northern blot analysis. In order to examine the cause of different NO production between $Nramp^r$ and $Nramp^s$ macrophages, both $Nramp^r$ and $Nramp^s$ macrophages were activated by LPS, IFN-γ, LPS+IFN-γ. After activation, the levels of iNOS mRNA were detected by Northern blot analysis. It was noted that high levels of iNOS mRNA were found in the $Nramp^r$ macrophages activated by IFN-γ, LPS+IFN-γ. Under these same conditions, high levels of iNOS mRNA were not seen in the $Nramp^s$ macrophages. In the analysis of uptake of L-arginine by $Nramp^r$ and $Nramp^s$ macrophages, no significant relationship between the uptake of L-arginine and the NO production was observed in both macrophage types.

These results suggested that the antimycobacterial activity controlled by Nramp was depen-