fecal samples collected from wild foxes. Since the antigenicity did not decrease by heat and formalin treatment, all the fecal samples were treated by heat and formalin to sterilize Em eggs. The rAb / Em i / b-AntiM and rAb / b-EmA9 showed the same detection rate of positive samples. Feces of non-Em infected foxes showed low OD values in all of the three methods, even though the foxes were infected with variety of helminths excluding *Echinococcus* and *Taenia* species. Using the feces obtained from experimental infections with *T. hydatigena*, *E. granulosus* and *E. vogeli*, specificity of the methods were evaluated. Although rAb / b-EmA9 cross-reacted with *T. hydatigena* coproantigen at the onset of egg excretion, neither rAb / Em i / b-AntiM nor Em i / b-EmA9 reacted with *T. hydatigena* coproantigen. All methods detected coproantigens of *E. granulosus* and *E. vogeli*, suggesting genus specific diagnosis of *Echinococcus* infection can be feasible by the developed methods.

Morphological and molecular genetic analyses of jumbled spine and ribs (*Jsr*) mutant mouse

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Vertebral abnormality derived from genetic mutation has often been observed in many animals including human and mice. Since the vertebral development, beginning with somite formation, is associated with the expression of many genes, mutant mice have been contributed to understand these mechanisms. Jumbled spine and ribs (*Jsr*) mice, showing the irregular segmentation of axial skeleton was found as spontaneous mutation. The previous study revealed that the causal gene of *Jsr* related to the cell growth of somite and sclerotome, and that this abnormality was due to a single autosomal dominant gene. As a result of a high resolution map around *Jsr* with 1,026 backcross progeny generated by mating CKH and MOG, *Jsr* was mapped at the centromeric position with 0.2+/−0.14 cM (centi morgan) from *D5Mit24* and *D5Mit22* locating chromosome 5. In the present study, further morphological and genetic analyses were performed.

It was confirmed by histological observations that axial skeletons showed various abnormalities such as asymmetry, fusion and spina bifida. At 11.5 days of gestation, parasagittal sections of heterozygotes (*Jsr*/+) embryos revealed that the irregular arrangements of primitive vertebra and somite clefts were marked as well as the disappearance of boundary region between primitive vertebra. It was suggested that the causal gene was associated with the development of presomitic mesoderm.

The locus of candidate gene, *Lfng* (lunatic fringe), corresponded completely to that of *Jsr* according to genetic mapping. In the previous report, *Lfng* deficient mice was markedly similar to *Jsr* mutant, showing an phenotype, such as irregular segmentation in embryos at 9.0 days of gestation and entirely shortened and fused vertebrae, in adult mouse. These findings assumed that *Lfng* might be a strong possibility as causal gene of *Jsr*.

To analyze the chromosomal region around *Jsr*, the screening of the YAC library with *D5Mit22* and the BAC library with STS marker, 11MMHAP75FRD8. seq, locating in the same locus of *Jsr* was examined. The length of 380kb in BAC contig including *Jsr* was constructed; however, YAC clones were inappropriate because of deletion. It was expected that causal gene of *Jsr* was clarified by further analysis of BAC clones isolated in the present study.

Analysis of the relationship between antimicrocidal activity against *Salmonella typhimurium* and nitric oxide synthesis related with mouse natural resistant-associated macrophage protein1 gene (*Nramp1*)

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The ability of a host to resist infection with a wide range of viral, bacterial, and parasitic pathogens is strongly influenced by many genetic factors. The *Bcg/Ity/Lsh* gene on mouse chromosome 1 regulates priming/activation of macrophage for antimicrobial and tumoricidal activity. A candidate gene for *Bcg/Ity/Lsh* expressed in macrophages has been identified as the natural resistance-associated macrophage protein 1 (*Nramp1*). Macrophages are concerned with antimicrocidal activity by numerous cytokine-induced nitric oxide (NO) productions. In the present study, the relationships among *Nramp1*, antimicrocidal activity, NO production and tumor necrosis factor alpha (TNF-α) were analyzed with the experiments using peritoneal and splenic macrophages, isolated from *Nramp1* congenic and/or TNF-α knockout mice.

Peritoneal macrophage from *Nramp1* congenic, the resistant (*Nramp1*^{r}) and the susceptible (*Nramp1*^{s}) mice, infected with six strains of *S. typhimurium*, were analyzed to examine the relationship between antimicrocidal activity and NO production. Antimicrocidal activity of *Nramp1*^{r} macrophage was higher at 3hr after infection than that of *Nramp1*^{s}. Although NO production was very low in both types of macrophages within 3hr after infection, the significant levels of NO production were detected in *Nramp1*^{r} macrophage compared to that from *Nramp1*^{s} with four strains of infection.

Peritoneal macrophages from TNF-$\alpha^{-/-}$·*Nramp1*^{r} and TNF-$\alpha^{-/-}$·*Nramp1*^{s} infected with six strains of *S. typhimurium* were analyzed to examine the influence of antimicrocidal activity by TNF-α defiency. No significant effect of TNF-α was observed within 3 hrs after infection at all strain of *S. typhimurium*. At 24 hrs after infection, except for two strains of bacteria showing markedly weak antimicrocidal activity, *S. typhimurium* was proliferated remarkably in both types of TNF-$\alpha^{-/-}$ macrophages, compared to TNF-$\alpha^{+/-}$ macrophages. The production of NO was significantly low throughout the infection. In splenic macrophages, after stimulation with IFN-γ (10U/ml), LPS(10mg/ml) or with IFN-γ (10U/ml) + LPS(10mg/ml), NO production in *Nramp1*^{r} was higher than those in *Nramp1*^{s}, but not in TNF-$\alpha^{-/-}$ splenic macrophages, suggesting similar results as peritoneal macrophages.

It was suggested in both peritoneal and