

## Biochemical Characterization of *Trichinella* in Greenland

In 1961 Madsen published detailed studies on the prevalence rates of *Trichinella* infections in sledge dogs and wild mammals in Greenland. The highest frequency was registered among sledge dogs with a prevalence rate of 61.9 % while the corresponding rate among polar bears was 24.2 %. Studies on polar bears carried out during the 80's have demonstrated a prevalence rate comparable to that reported by Madsen (1961) (Born & Henriksen, in preparation). In Greenland infections with *Trichinella* have also been observed in walrus (Madsen 1961, Thing *et al.* 1976, Born *et al.* 1982), in seals and arctic foxes (Madsen 1961), and in man (Thorborg *et al.* 1948, Bohm, cit. James 1989).

Considering the high genetic variability of the *Trichinella* genus (Dick 1983) studies on the identification of isolates of *Trichinella* from Greenland by enzyme system analyses have been carried out. Previous studies on *Trichinella* isolates originating from other regions of the world have demonstrated the presence of seven distinct gene pools designated T1 to T7 (Pozio *et al.* 1989a, La Rosa *et al.* 1989). All arctic isolates examined so far have been referring to the same gene pool (T2) assumed as *T. nativa*, characterized by e.g. resistance to freezing ( $-20^{\circ}\text{C}$ ) and a low infectivity to laboratory rats (Rausch 1970).

In the present investigation two *Trichinella* isolates from Greenland were studied, one obtained from a sledge dog (DOG, code MCAN/DK/81/ISS83) in the Qaanaaq district (Thule area) (Lat  $77^{\circ}\text{N}$ , Long  $69^{\circ}\text{W}$ ) and the other from a polar bear (BEAR, code MURS/DK/82/ISS84) shot in the Na-

nortalik district (Lat  $60^{\circ}\text{N}$ , Long  $45^{\circ}\text{W}$ ). The isolates have been maintained through 5 (DOG) and 4 (BEAR) passages in guinea pigs and subsequently through 11 (DOG) and 10 (BEAR) passages in Swiss mice prior to biochemical identification.

Twenty-seven enzyme systems were examined in using 12 % horizontal starch gel electrophoresis:  $\alpha$  PGD (1.1.1.8), LDH (1.1.1.27), MDH (1.1.1.37), ME (1.1.1.40), IDH (1.1. 1.42), 6PDG (1.1.1.44), G6PD (1.1.1.49), G3DP (1.2.1.12), GLDH (1.4.1.3), SOD (1.15.1.1), GOT (2.6.1.1), ALAT (2.6.1.2), AK (2.7.4.3), PGM (2.7.5.1), ES (3.1.1.1), ACPH (3.1.3.2), PEP1 (3.4.1.1), PEP2 (3.4.1.1), ADA (3.5.4.4), ALDO (4.1.2.13), CA (4.2.1.1), FUM (4.2.1.2), ACON (4.2.1.3), ENOL (4.2.1.11), TPI (5.3.1.1), MPI (5.3.1.8) and GPI (5.3.1.9).

The Greenland isolates were compared with the reference strains used by the *Trichinella* Reference Centre (Pozio *et al.* 1989b). The 2 isolates presented similar allozymic patterns with only GLDH enzyme different from one another: BEAR isolate showed one low band whereas DOG isolate showed 3 bands (Fig. 1). The average genetic similarity of Greenland parasites with respect to the reference strains was calculated according to Jaccard's similarity index (J): J = 27 % vs. T1 (*T. spiralis*), J = 98 % vs. T2 (*T. nativa*), J = 55 % vs. T3 (*Trichinella* type 3, present in Europe and Asia), J = 20 % vs. T4 (*T. pseudospiralis*) and J = 44 % vs. T7 (*T. nelsoni*). These results support the idea that gene flow is very low or absent among *Trichinella* gene pools. The factorial analyses of correspond-

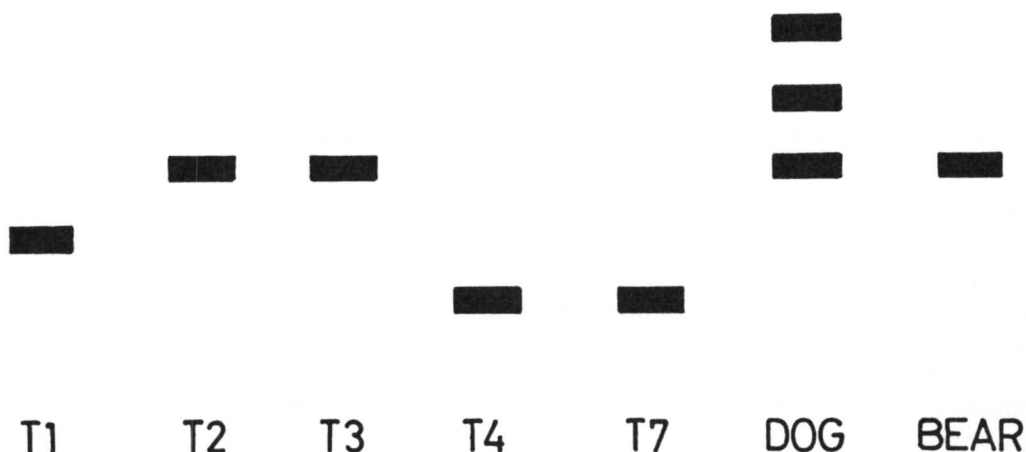


Figure 1. Isoenzyme pattern of GLDH (E.C.1.4.1.3). T1 = *Trichinella spiralis* s. str., T2 = *T. nativa*, T3 = *Trichinella* type 3, T4 = *T. pseudospiralis*, T7 = *T. nelsoni* (cf. Pozio et al. 1989b). DOG and BEAR = Greenland isolates.

ences (La Rosa et al. 1989) demonstrate that the Greenland genotypes were located within the range of the variation of the *T. nativa* gene pool.

A GLDH pattern comparable to the one observed in the DOG isolate has previously been observed in four *T. nativa* isolates originating from the Svalbard Islands, Norway, and from the Primorsk region, USSR. The results seem to indicate a gene flow among *T. nativa* isolates from places far apart, respectively that the GLDH variant pattern could be utilized as a genetic marker for the parasite and for host dispersion. Thus the biochemical analyses of a higher number of isolates, obtained from different places in Greenland, may explain the correlations between parasite (genetic variants), host, and distribution.

The presence of geographic boundaries is not to be expected as to a parasite like *Trichinella* which infects homeothermic animals. Therefore the arctic fauna has a potential contact through the icefield in the Polar Sea, and subsequently the ice could

help to spread out *Trichinella* gene variants in the arctic and subarctic areas. Finally it seems relevant to consider that factors related to climatic and host conditions may regulate the distribution and the evolution of *Trichinella* species, in particular considering *T. nativa*, which primarily seems confined to the arctic and subarctic regions of the world.

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