Temporal genetic variation of Fasciola hepatica from sheep in Galicia (NW Spain)

Vázquez-Prieto S.

Vilas R.

Ubeira F.M.

Paniagua E.

We found low genetic differentiation between two temporal samples of Fasciola hepatica (2006 and 2008) collected from nine sheep of the same flock that shared the same pasture for at least 2 years. However, each sample, represented by four and five infrapopulations respectively, showed strong heterozygote deficits regarding Hardy-Weinberg expectations and a high degree of genetic structure at infrapopulation level. This is an unexpected result since genetic drift should increase temporal variation among years. Our findings are most likely explained by the fact that the parasite can survive many years in the definitive host. Temporal gene flow favored by high longevity probably increases levels of genetic variability of the population but could also contribute to the observed heterozygote deficits within temporal samples and infrapopulations if it favors the Wahlund effect. Despite the homogenizing effect of gene flow, the high genetic divergence observed between infrapopulations is most likely a consequence of strong genetic drift associated to the complexity of the life cycle. © 2015 Elsevier B.V.

Allozymes

Fasciola hepatica

Microsatellites

Population genetic structure

Temporal variation

allele

Article

effective population size

Fasciola hepatica

- fascioliasis
- gene flow

gene frequency

genetic distance

genetic drift

genetic variability

heterozygote

host parasite interaction

longevity

nonhuman

parasite survival

population genetic structure

sheep

Spain

time

animal

Fasciola hepatica

fascioliasis

gene expression regulation

genetics

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Sheep Diseases

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- Ovis aries
- helminth protein
- Animals

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Gene Expression Regulation

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Helminth Proteins

Sheep

Sheep Diseases

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Time Factors