



'She's got a ticket to ride, but she don't care' (The Beatles, 1965)

The epidemiology of *Gyrodactylus salaris* in the best wild salmon river in the Baltic Sea basin

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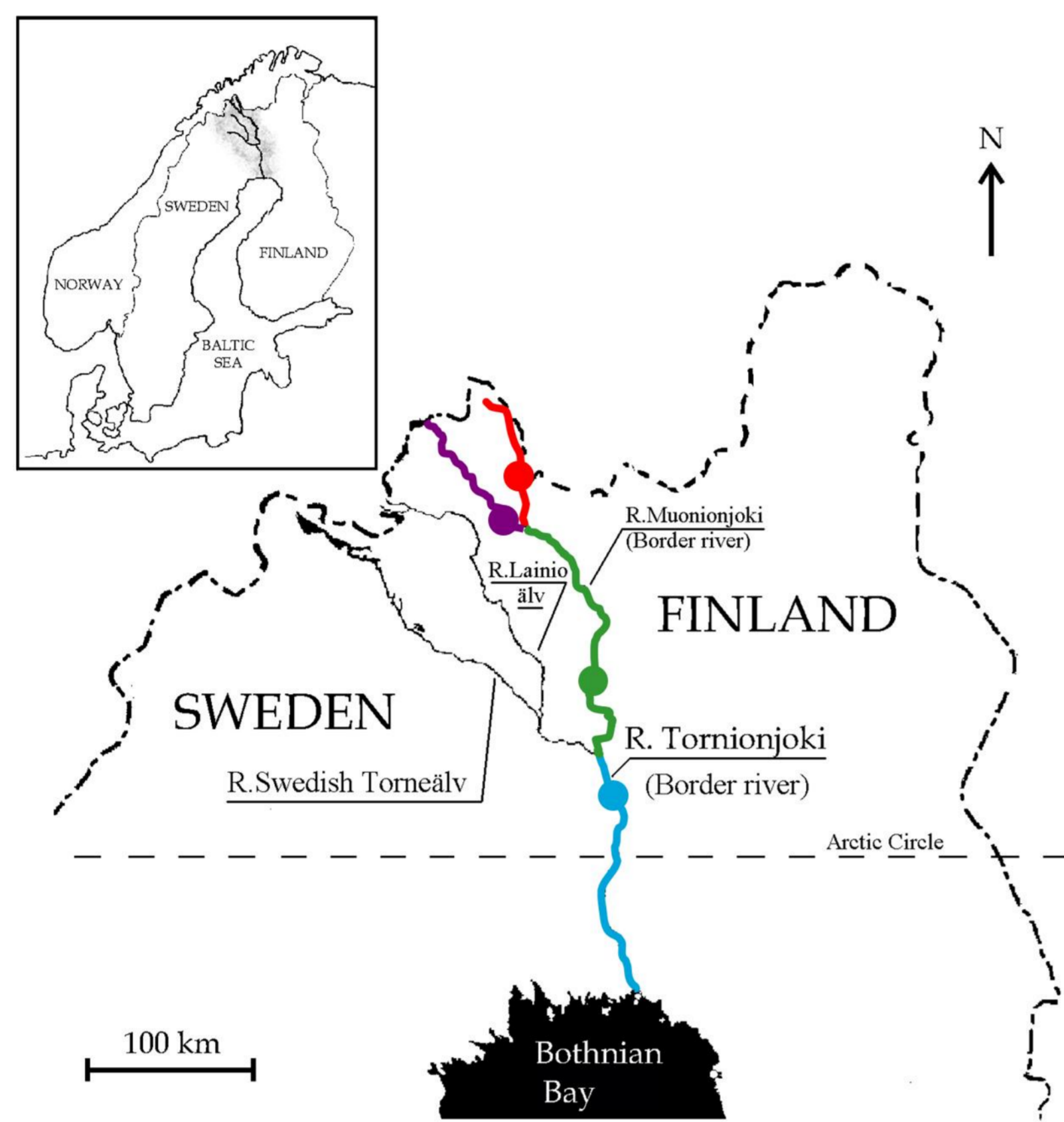


Fig. 1. The river sections of Tornionjoki water system studied here are indicated with colours: River Tornionjoki, River Muonionjoki, River Könkämäeno, River Lätäseno. The indicator rapids appear as circles.

Table 1. Prevalence of *Gyrodactylus salaris* infection in 2000-2012 in the indicator rapids. The P-value of the inclusion of the variable in the final logistic regression model and the adjusted odds ratio (Exp(B)) and its 95 % confidence interval estimate (C.I.E.) are reported in the last column. N = number of parr specimens.

Variable	N	Prevalence, %		Logistic regression P-value Exp(B) and (95.0% C.I.E. for Exp(B))
		<i>G. salaris</i> found	<i>G. salaris</i> not found	
(1) Watercourse section				
River Tornionjoki	651	9.4	90.6	< 0.001 1.0
River Muonionjoki	709	16.1	83.9	1.9 (1.4-2.7)
River Könkämäeno	527	22.4	77.6	2.4 (1.7-3.4)
River Lätäseno	684	38.6	61.4	6.7 (4.9-9.1)
(2) Age of the parr				
One-summer old	1155	10.1	89.9	< 0.001 1.0
2-summer old and older	1416	31.1	68.9	4.3 (3.4-5.5)
TOTAL	2571	21.7	78.3	

Table 2

The distribution of the nuclear marker ADNAM1 genotypes in *G. salaris* on the sedentary parr populations 2000-2009 in different river sections. Genetic differentiation among the sites $F_{ST}^a = 0.579$.

River section	ADNAM1 genotype (N)				
	S2	S6	S7	Others	Total
River Tornionjoki	1	50	8		59
River Muonionjoki	76	45		5	126
River Könkämäeno	74				74
River Lätäseno	143				143
Total	303	95	8	5	411

^a) Unbiased genotype / haplotype diversity estimate was calculated as $h = [N/(N-1)](1 - \Sigma p^2)$. The fixation index F_{ST} based on genotype / haplotype frequencies was calculated as $F_{ST} = (h_T - h_S) / h_T$, where h_T is the total diversity and h_S is the mean diversity in separate samples.

River Tornionjoki water system has an abundant and stable *G. salaris* infection

- River Tornionjoki water system is the best wild salmon river of the Baltic Sea catchment area. The salmon stock is on the rise with ca. 100 000 broodfish counted on their spawning migration in 2014 and 2016, ca. 60 000 in 2015, smolt run of 2016 ca. 2-3 million smolt.
- *G. salaris* infection most common in the upper tributaries (Fig. 1, Ref. 1). The occurrence pattern has remained like that for over a decade 2000-2012 (Table 1). There are no obstacles for the downstream spread of the parasites and smolt are heavily infected (Ref. 4). In spite of this, she (all *G. salaris* are females) is most prevalent in the north.
- Water quality parameters maybe explanatory (aqueous aluminium ion concentrations during floods?)

River Tornionjoki water system has two endemic and differentiated subpopulations of *G. salaris*

- Salmon parr in Rivers Lätäseno, Könkämäeno and upper Muonionjoki are mainly infected with genetical subpopulation (ADNAM1 type S2, mtDNA clades SalBa4, Ref. 2), which differs of that of the lower River Muonionjoki and Tornionjoki (Tables 2 and 3, Ref. 4).
- Again she is refusing the ticket to ride, the partition to the subpopulations remained same for ten years 2000-2009 (Ref 4).
- Possibility of local co-adaptation of the host-parasite subpopulations.

References

- 1) Anttila, P., Romakkaniemi, A., Kuusela, J. & Koski, P. (2008); Epidemiology of *Gyrodactylus salaris* (Monogenea) in the River Tornionjoki, a Baltic wild salmon river. *Journal of Fish Diseases* 31, 373-382.
- 2) Kuusela, J., Ziętara, M.S., Lumme, J., 2007. Hybrid origin of Baltic salmon-specific parasite *Gyrodactylus salaris*: a model for speciation by host switch for hemiclonal organisms. *Mol. Ecol.* 16, 5234-5245.
- 3) Kuusela, J., Holopainen, R., Meinilä, M., Anttila, P., Koski, P., Ziętara, M.S., Veselov, A., Primmer, C.R., Lumme, J., 2009. Clonal structure of salmon parasite *Gyrodactylus salaris* on a coevolutionary gradient on Fennoscandian salmon (*Salmo salar*). *Annales Zoologici Fennici* 46, 21-33.
- 4) Lumme, J., Anttila, P., Rintamäki, P., Koski, P. & Romakkaniemi, A. (2016); Genetic gradient of a host-parasite pair along a river persisted ten years against physical mobility: Baltic *Salmo salar* vs. *Gyrodactylus salaris*. *Infection, Genetics and Evolution* 45, 33-39 (<http://dx.doi.org/10.1016/j.meegid.2016.08.006>).

Table 3

Distribution of mtDNA haplotypes of *G. salaris* in sedentary parr samples 2000^a, 2004, 2006^a, 2008 and 2009 along the different river sections. Genetic differentiation between the sites $F_{ST} = 0.534$.

mtDNA haplotype	River Tornionjoki	River Muonionjoki	River Könkämäeno	River Lätäseno	Total
SalBa05	29	12		35	76
SalBa05/1257C		12 ^b			12
SalBa04		81	65	200	346
SalBa04/487Y		9 ^b			9
SalBa04/1460G				12 ^b	12
Total	29	114	65	247	455

^a) Data from Kuusela et al., 2009 (Ref. 3)

^b) Clones found on single or two fish.