



Corrigendum: The Resistome of Farmed Fish Feces Contributes to the Enrichment of Antibiotic Resistance Genes in Sediments below Baltic Sea Fish Farms

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A corrigendum on

The Resistome of Farmed Fish Feces Contributes to the Enrichment of Antibiotic Resistance Genes in Sediments below Baltic Sea Fish Farms

by Muziasari, W. I., Pitkänen, L. K., Sørum, H., Stedtfeld, R. D., Tiedje, J. M., and Virta, M. (2017).
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In the original article, there was a mistake in **Table 2**. Twenty of the 28 genes detected in the farmed fish intestinal contents as published. In the **Table 2**, the numbers of average relative abundance of the 20 genes to the 16S rRNA gene were not correct. The corrected numbers of the gene abundances appears below. We apologize for this error and the error does not change the scientific conclusions of the article in any way.

Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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TABLE 2 | Twenty of the 28 genes detected in the farmed fish intestinal contents.

Classification of the antibiotics the genes confer resistance to	qPCR assay	Average relative abundance to the 16S rRNA gene	
		Fish intestinal contents (sampled in 2014)	Fish farm sediments (sampled in 2006–2012)
Aminoglycoside	aadA1	2×10^{-2}	$a_3 \times 10^{-4}$
Aminoglycoside	aadA2-01	2×10^{-2}	$a_2 \times 10^{-4}$
Aminoglycoside	aadA2-02	2×10^{-2}	$a_4 \times 10^{-4}$
Aminoglycoside	aadA2-03	4×10^{-2}	$a_8 \times 10^{-4}$
Trimethoprim	dfrA1	6×10^{-2}	$a_3 \times 10^{-3}$
Trimethoprim	dfrA1-02	4×10^{-2}	$b_1 \times 10^{-3}$
Class 1 integron	intl1	6×10^{-2}	$b_3 \times 10^{-3}$
Other (Antiseptic)	qacEΔ1-01	1×10^{-2}	$a_5 \times 10^{-3}$
Other (Antiseptic)	qacEΔ1-02	1×10^{-1}	$a_3 \times 10^{-3}$
Sulfonamide	sul1	7×10^{-2}	$b_4 \times 10^{-3}$
Tetracycline	tet(32)	3×10^{-2}	$a_1 \times 10^{-3}$
Tetracycline	tetM-01	1×10^{-1}	$a_3 \times 10^{-3}$
Tetracycline	tetM-02	9×10^{-2}	$a_2 \times 10^{-3}$
Tetracycline	tetM-03	4×10^{-2}	$c_1 \times 10^{-3}$
Tetracycline	tetO-01	2×10^{-2}	$a_2 \times 10^{-3}$
Tetracycline	tetW-01	4×10^{-2}	$a_4 \times 10^{-4}$
Transposon	tnpA-01	3×10^{-2}	$a_6 \times 10^{-4}$
Transposon	tnpA-04	4×10^{-2}	$a_2 \times 10^{-4}$
Transposon	tnpA-06	5×10^{-1}	$a_1 \times 10^{-3}$
Transposon	tnpA-07	4×10^{-2}	$a_4 \times 10^{-3}$

^aMuziasari et al., 2016.

^bMuziasari et al., 2014.

^cTamminen et al., 2011.

^{b,c}The quantification of the genes used standard qPCR.

The 20 genes were the same genes found to be enriched in the sediments below fish farms in the Northern Baltic Sea, Finland. The table also shows the average relative abundance of the genes to the 16S rRNA gene in the intestinal contents and in the farm sediments. The gene assays of the qPCR array grouped by classification of the antibiotics the genes confer resistance to, class 1 integron and transposon.