

CORRECTION

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# Correction to: Quantitative trait loci for resistance to *Flavobacterium psychrophilum* in rainbow trout: effect of the mode of infection and evidence of epistatic interactions

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**Correction to:** Fraslin et al. *Genet Sel Evol* (2018) 50:60  
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After publication of this work [1], we noted that there was an error in Table 3 Line 4: <sup>b</sup>Omy2<sub>Omy3</sub> should be <sup>b</sup>Omy21<sub>Omy3</sub>.

The correct Table 3 is included here.

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**Table 3 Results of QTL analysis using the model M2 for resistance trait following injection or immersion challenges**

| Infection route           | QTL                                  | LRTmax   | Position (cM) | CI (95%) | Increase in survival rate |             | Resistance origin |         | P value fixed effect | P value interaction |
|---------------------------|--------------------------------------|----------|---------------|----------|---------------------------|-------------|-------------------|---------|----------------------|---------------------|
|                           |                                      |          |               |          | Fixed_R (%)               | Fixed_S (%) | Fixed_R           | Fixed_S |                      |                     |
| IMMERSION                 | Omy17 <sub>Omy3</sub>                | 13.97*   | 61            | 0–92     | 38                        | 7           | AP2               | AP2     | ***                  | NS                  |
|                           | Omy25a <sub>Omy3</sub>               | 10.41*   | 4             | 0–35     | 10                        | 18          | B57               | B57     | ***                  | NS                  |
| <i>Type 1 interaction</i> |                                      |          |               |          |                           |             |                   |         |                      |                     |
| INJECTION                 | <sup>a</sup> Omy3 <sub>Omy29</sub>   | 15.27**  | 89            | 46–105   | 16                        | 47          | AP2               | AP2     | ***                  | ***                 |
| IMMERSION                 | <sup>b</sup> Omy21 <sub>Omy3</sub>   | 15.35**  | 97            | 63–104   | 4                         | 39          | B57               | B57     | ***                  | ***                 |
|                           | <sup>b</sup> Omy3 <sub>Omy21</sub>   | 40.73*** | 87            | 82–93    | 20                        | 55          | AP2               | AP2     | ***                  | ***                 |
|                           | <sup>c</sup> Omy3 <sub>Omy2</sub>    | 35.66*** | 87            | 81–94    | 17                        | 44          | AP2               | AP2     | ***                  | ***                 |
| INJECTION                 | <sup>a</sup> Omy29.2 <sub>Omy3</sub> | 14.85*   | 23            | 8–49     | 5                         | 48          | B57               | AP2     | ***                  | *                   |
|                           | Omy17 <sub>Omy25a</sub>              | 15.85**  | 73            | 53–79    | 11                        | 53          | AP2               | B57     | ***                  | ***                 |
| IMMERSION                 | Omy7.2 <sub>Omy21</sub>              | 11.48*   | 7             | 0–103    | 5                         | 31          | AP2               | B57     | ***                  | ***                 |
| <i>Type 2 interaction</i> |                                      |          |               |          |                           |             |                   |         |                      |                     |
| INJECTION                 | <sup>d</sup> Omy25a <sub>Omy3</sub>  | 25.49*** | 14            | 10–18    | 53                        | 16          | B57               | B57     | ***                  | *                   |
|                           | <sup>d</sup> Omy3 <sub>Omy25a</sub>  | 35.35*** | 89            | 86–92    | 59                        | 22          | AP2               | AP2     | ***                  | ***                 |
|                           | Omy26 <sub>Omy29</sub>               | 11.75*   | 18            | 0–34     | 30                        | 26          | AP2               | AP2     | ***                  | ***                 |
| INJECTION                 | Omy17 <sub>Omy29</sub>               | 18.29*** | 74            | 58–92    | 47                        | 11          | AP2               | B57     | ***                  | ***                 |
| IMMERSION                 | Omy24 <sub>Omy2</sub>                | 12.71*   | 4             | 0–19     | 20                        | 1           | B57               | AP2     | ***                  | ***                 |
| <i>Type 3 interaction</i> |                                      |          |               |          |                           |             |                   |         |                      |                     |
| IMMERSION                 | Omy7.1 <sub>Omy2</sub>               | 16.42**  | 61            | 32–87    | 19                        | 19          | B57               | AP2     | ***                  | ***                 |

The table presents chromosome-wide or genome-wide significant QTL detected for STATUS using model M2; Reciprocal interactions could be tested only for QTL detected in the first STATUS analysis (model M1); LRTmax = maximum of likelihood ratio test; Position in the genetic map in centimorgans (cM); CI = confidence interval; Chromosome-wide significant = \* $P \leq 0.01$ ; Genome-wide significant = \*\* $P \leq 0.05$  or \*\*\* $P \leq 0.01$ ; P values for fixed effect and interaction corrected with Benjamini–Hochberg method; Non-significant = NS; \*P value  $\leq 0.05$ ; \*\*\*P value  $\leq 0.001$

<sup>a</sup> The reciprocal interaction could not be tested as a new QTL (Omy29.2<sub>Omy3</sub>-QTL) was detected with the reciprocal model

<sup>b,d</sup> Reciprocal models for QTL pairs

<sup>c</sup> The QTL in the reciprocal model (Omy2<sub>Omy3</sub>-QTL) was only suggestive ( $P \leq 0.05$ ) at the chromosome-wide level

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