# Case study development of a challenge test against Edwardsiella ictaluri in Mekong striped catfish (Pangasianodon hypophthalmus), for use in breeding: Estimates of the genetic correlation between susceptibility in replicated tanks 

## Running title: Challenge testing striped catfish

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[^0]numerous white spots in swelled liver, kidney and spleen. An alternative to antibiotic treatment and vaccine is to select for improved genetic resistance to the disease that require to establish a proper challenge test. Here, four challenge tests of Mekong striped catfish against E. ictaluri are reported proposing three days acclimatization of test fish prior to the challenge, with restricted water level in the test, keeping a temperature of $26^{\circ} \mathrm{C}$. In the challenge, cohabitant shedders should be released directly into the test tank and make up around $1 / 3$ of the fish, and bacteria should be added directly to water. The last two experiments, with the highest mortality, suggest that any factor involving the dead cohabitants should be removed, and that additional experimentation should focus on bacteria (density) and timing for addition of bacteria to water. Genetic analyses revealed that resistance to bacillary necrosis tested in replicated tanks in the same experiment can be considered the same genetic trait.

Keywords: Bacillary necrosis; test environment.

## 1. Introduction

The Mekong striped catfish (Pangasianodon hypophthalmus) farming in Vietnam has faced increasing disease problems, particularly bacillary necrosis (BN). Clinical signs are internal numerous white spots of different sizes in swelled liver, kidney and spleen (Crumlish, Dung, Turnbull, Ngoc \& Ferguson 2002). These authors described the histopathological lesions as acute to sub-acute multifocal areas of necrosis and pyogranulomatous inflammation, with several species of parasites associating with these lesions. Specifically, a variable number of large bacilli are usually seen at the margins of lesions. BN belongs to Edwardsiellosis and is caused by the Edwardsiella ictaluri (E. ictaluri) bacteria, first observed in 1998, with its cause identified in 2002 (Crumlish, Dung, Turnbull, Ngoc \& Ferguson 2002). The disease has been found in the whole Mekong Delta, in all life stages of catfish, but is especially frequent in the
fingerling period. Unless antibiotic treatment is timely applied, fish mortality may rise as high as $90 \%$ (Dong \& Hoa 2008). In 2010, the first BN vaccine trial was conducted by Pharmaq Ltd. Vietnam (Thanh \& Berntsen 2012). The trial was successful with significant lower mortality of vaccinated than non-vaccinated groups. The Alpha Ject ${ }^{\circledR}$ Panga 1 vaccine was licensed in 2013 (https://www.pharmaq.no/sfiles/8/66/4/file/2013_08-cty-pharmaq-vn_thuy-san-nam-14-so164.pdf). However, improved resistance to BN using vaccination is often costly and impractical since it must be repeated for each fish, and in each generation. At current, to treat BN, antibiotics is used which may lead to resistance and potential contamination of the final product (Chuah, Effarizah, Goni \& Rusul 2016). Moreover, reduction of mortality through drug application is costly and does not solve the problem permanently (van Muiswinkel, Wiegertjes \& Stet 1999). Besides development of vaccines, improvement of resistance to BN through selective breeding can be used as a tool for sustainable disease control. This is aimed at in the Mekong striped catfish breeding program initiated by the Research Institute for Aquaculture No. 2 (RIA2), Vietnam. Initially in this program, three base sub-populations were created from fish being domesticated in three hatcheries, making up year-classes 2001, 2002 and 2003, respectively (Sang, Klemetsdal, Ødegård \& Gjøen 2012). So far, selection has been carried out for final body weight and fillet yield. Heritability estimates have been found moderate for body weight ( $0.21-0.34$ ), while low estimates have been obtained for fillet yield (0.03-0.05) (Sang, Klemetsdal, Ødegård \& Gjøen 2012). Recently, Vu, Sang, Phuc, Vuong \& Nguyen (2019) reported on the genetic response achieved in the program.

Development of a challenge-test for BN was initiated in 2009. The objective was to rank individuals with respect to disease resistance towards $E$. ictaluri. The developments were based on the cohabitation method, known a priori to be difficult to standardize (Nordmo, Sevatdal \& Ramstad 1997) and even not always successful (Mahapatra, Gjerde, Sahoo, Saha, Barat, Sahoo,

Mohanty, Ødegård, Rye \& Salte 2008). However, Gjøen, Refstie, Ulla \& Gjerde (1997) have shown that the cohabitation method mimics a natural infection well.

Here, findings in four experiments with family materials of Mekong striped catfish challenged with E. ictaluri are summarized. The aim was to establish a challenge-test applicable in the breeding program including to examine the genetic correlation of resistance to BN between two replicated test-tanks within the same experiment.

## 2. Materials and methods

By granting the research, the Vietnamese Ministry of Agriculture and Rural Development preapproved the experiments carried out.

### 2.1 Inoculums

A strain of E. ictaluri Gly09M (Southern Monitoring Centre for Aquaculture Environment \& Epidemic, RIA2, Ho Chi Minh City, Vietnam) was used in all experiments. The strain was isolated from diseased fish sampled in commercial striped catfish farms in the Mekong Delta in 2009. Each year, reference stocks were sub-cultured and stored in a solution of Brain Heart Infusion Broth (BHIB) and 20\% glycerine supplementation, at $-20^{\circ} \mathrm{C}$. Working seed was cultured in Sheep Blood Agar (SBA) and incubated for 24 hours at $30^{\circ} \mathrm{C}$. Bacterial biomass was suspended into a flask containing 500 ml BHIB, incubated with shaking for 18 hours. The liquid culture was transferred into a 5 litter BHIB medium contained in a 10 liter fermenter, cultured for $18-20$ hours, stirred at 150 rounds/minute, and air supplied 5 vvm (in 1 minute, 5 liters of air are passing through 1 liter of medium). The density of bacteria was measured at 550 $\mathrm{nm}\left(\mathrm{OD}_{550}\right)$ to calibrate the bacterial doses.

### 2.2 Cohabitant shedders

Cohabitant shedders were randomly sampled from the hapas with the highest survival among fish to be challenged, just prior to tagging of the latter fish. Cohabitants were not tagged while test fish were, for discrimination. Shedders were acclimated in a separate tank and were intraperitoneally injected at experimental day 0 .

### 2.3 General test-environment: Tanks, water quality and feeding

Experiment 1 was conducted in one outdoor fiber-glass tank at the National Breeding Centre for Southern Freshwater Aquaculture (NABRECSOFA, in the Tien Giang province) in 2009 (Table 1). The tank was partly covered by net to prevent eutrophication. Experiments 2,3 and 4 were carried out indoor in the Govap Experimental Centre (GEC), RIA2, in 2010, 2011 and 2012, respectively (Table 1). GEC is located 125 km away from NABRECSOFA, and the fish were transported there by a lorry. In these three latter experiments, two replicated tanks were used (Table 1). In all experiments, tagging was done when the fish were netted out of the original hapas. In the last three experiments an equal number of randomly tagged fish from each hapa were transferred to either of two tanks at NABRECSOFA, before transfer to GEC. In the first experiment, tagged fish were kept in separate hapas for seven days prior to transfer to the test tank.

The test tanks were of circular shape; diameter 4.0 m , depth 1.8 m , and water volume of $20 \mathrm{~m}^{3}$. Water was not exchanged unless considered necessary. Daily, the water quality was monitored by the use of Sera Test Kits (Germany): Water oxygen levels were kept higher than 1.0 ppm , using aeration to avoid losing energy on air-breathing behaviour (Lefevre, Jensen, Huong, Wang, Phuong \& Bayley 2011). Across experiments, water-pH levels varied from 6.5 to 7.5. Fish were daily fed a standard commercial fingerling feed, $1 \%$ of total biomass.

### 2.4 Specific test-environment: Acclimatization, water temperature and level

In experiment 1, fish to be challenged were transferred from the hapas to the test tank 22 days prior to the experiment (Table 1). In experiment 2, tagged fish in the two tanks at NABRECSOFA were transported separately to GEC in oxygenated containers and transferred to the two replicated test tanks 14 days prior to the experiment. In experiments 3 and 4, transportation was as in experiment 2, but just 3 days prior to challenge. Thus, in experiments 1 and 2 fish were more adapted to the new environment than in experiments 3 and 4 where, in fact, a shortened acclimation period was used as a stressor.

Since experiment 1 was conducted outdoor, water temperature was $29.5^{\circ} \mathrm{C}$ (standard deviation $=1.0^{\circ} \mathrm{C}$ ), i.e., it followed the surrounding temperature (Table 1). In experiment 2, water temperature was partly controlled using air conditioner; $29.0^{\circ} \mathrm{C}$ during the first 10 days postcohabitation and thereafter $26^{\circ} \mathrm{C}$, until termination. In experiments 3 and 4, temperature was set at $26^{\circ} \mathrm{C}$ because this temperature has been widely used in Enteric Septicaemia of Catfish (ESC) studies with channel catfish (Camp, Wolters \& Rice 2000; Lim \& Klesius 1997; PatrieHanson \& Jerald Ainsworth 1999).

In experiment 1 , the water level was kept constant during acclimatization and the entire testing period (Table 1). In experiments 2, 3 and 4, water levels were halved 1 day prior to challenge and kept at this level throughout the entire experimental period. This resulted in increased density and posed additional stress to the fish.

### 2.5 Specific test-environment: Cohabitant shedder density, dose and placement, and addition of bacteria to water

In experiment 1 , the ratio of cohabitant shedders to test fish (for number of cohabitants and test fish, see Tables 1 and 2, respectively) was 1:7, whereas in the other three experiments this ratio was approximately 1:3 (Table 1 ).

Injected doses are given in Table 1. Throughout the experiments, the doses for shedders were reduced from $2.5 \times 10^{6}$ to $1.0 \times 10^{5}$ (in experiment 2 , two doses were used), with the intention to prolong the survival time and thus the time for pathogen dispersion.

In experiment 1 , cohabitants were released into a $1 \times 1 \times 1 \mathrm{~m}^{3}$ hapa located to the centre of the tank, whereas they were released directly into the tanks in the other experiments (Table 1). Release was done directly after injection.

In experiment 1, dead cohabitants were removed when they were observed lifeless on the bottom of the hapa (Table 1), while in experiment 2 only floating dead fish (note that all dead fish float for some time, before sinking and then floating again) were removed to mimic the practice used by the industry. Additionally, in experiments 3 and 4 dead and floating cohabitants were collected into plastic baskets, which were hung down into the water for another 2 days. No pathogen was added directly to water in experiments 1 and 2 . However, in experiment 3 external pathogen was added to the tanks after complete mortality of cohabitants, which occurred at day 6 post-challenge. The density aimed at was $2.5 \times 10^{6}$ bacteria/ml water (Table 1), which was kept for another 8 days. In experiment 4, pathogen addition to water was started earlier, at day 3 post-challenge and stopped at day 6 . At day 3 , cohabitant mortality was $30 \%$, while it peaked at day 6 .

### 2.6 Test fish

In all four experiments, spawning, incubation and nursing until tagging were done as described by Pham, Ødegård, Sang, Gjøen \& Klemetsdal (2020).

Experiment 1: Challenge started April 30, 2009, with year-class 2008

Year-class 2008 was the third generation of the first sub-population in the breeding program. The fish were produced in June and July 2008 by use of a nested mating design, i.e. one male mated to two females. A total of 156 full-sib families were made. These were from 93 sires and 156 dams (Sang, Klemetsdal, Ødegård \& Gjøen 2012). Due to high mortality in some families during nursing, only a total of 2,155 fish from 81 families could be included in the challenge test (Table 2). Mean weight of test-fish at the start of the experiment was 47.6 g .

## Experiment 2: Challenge started February 23, 2010, with year-class 2009

Year-class 2009 was the third generation of the second sub-population. Using a nested mating design, as before, a total of 196 full-sib families (103 sires and 196 dams) were produced in July and August 2009. As in experiment 1, one hapa per family was used for nursing. High mortality after nursing resulted in only 64 full-sib families available for challenge (Table 2). All families were represented in tank 1 (1,019 fish), whereas only 60 families were represented in tank 2 ( 969 fish). Mean fish weight at the start of the experiment was 22.6 g in tank 1 and 22.4 g in $\operatorname{tank} 2$.

## Experiment 3: Challenge started January 14, 2011, with year-class 2010

Year-class 2010 was again the third generation, with parents mainly from the third subpopulation. Families were produced from July to September 2010, by use of a nested mating design. A total of 233 families were made from 137 sires and 230 dams. Parents were mainly from year-class 2007 ( 88 sires and 151 dams), but parents from the two preceding year-classes were also used; 2005 (second generation of first sub-population: 21 sires and 32 dams) and 2006 (second generation of second sub-population: 12 sires and 18 dams) as well as some parents of wild type ( 16 sires and 29 dams). Each family was nursed in a separate hapa until tagging. A total of 187 full-sib families took part in the challenge (Table 2). The numbers of
fish were 2,944 and 2,745 in the two replicated tanks, respectively, and mean fish weight at the start of test was 20.4 and 19.5 g .

## Experiment 4: Challenge started January 3, 2012, with year-class 2011

Year-class 2011 was the fourth generation of the first sub-population. Fish were produced in June and July 2011 with a nested mating design. Most parents came from year-class 2008 (93 sires and 154 dams), but parents from the other three preceding year-classes were also included: 2005 ( 3 sires), 2006 ( 16 sires and 37 dams), 2007 ( 20 sires and 43 dams) as well as parents of wild type ( 8 sires, 13 dams). The 250 families (from the 140 sires and 247 dams) produced were raised in a total of 269 hapas, meaning that some families were represented in more than one. Of these, 233 families were utilized in the challenge test (Table 2). A total of 3,246 and 2,931 fish were tested in the two replicated tanks, respectively. Mean fish weight at the start of test was 20.0 and 20.2 g , for tanks 1 and 2 , respectively.

### 2.7 Recoding of data

Collection of dead fish was carried out twice daily, either at 8:00 or 14:00, throughout the test period. PIT-tag (Passive Integrated Transponder) identity was recorded for tested fish as well as weight, day and time of death. Moreover, time of death of cohabitants was recorded.

Mortality was observed for 22-23 days in experiments 1 and 2 and for 18-19 days in experiments 3 and 4, respectively. In the period with high daily mortality, random samples of dead fish were examined for presence of typical colonies of E. ictaluri, by having kidney samples grown on sheep blood agar plates, incubated at $30^{\circ} \mathrm{C}$ for 24 hours (Crumlish, Dung, Turnbull, Ngoc \& Ferguson 2002). In experiment 2, with low daily mortality, one awaited it to increase implying that sampling was postponed, and in the end, it was not carried out. The sample sizes were 40,100 and 100 in experiments 1,3 and 4, respectively. After the challenge,
survivors were biosecure-buried, following the national veterinary regulations (Department of Animal Health, Vietnam).

### 2.8 Statistical analysis

In experiments 3 and 4 , dead or alive $(=0 / 1)$ at the end of the test in the two replicated tanks defined traits 1 and 2, respectively. Bivariate analyses across tanks were performed by a crosssectional linear sire-dam model.

In matrix notation, the bivariate model can be written:

$$
\left[\begin{array}{l}
y_{1} \\
y_{2}
\end{array}\right]=\left[\begin{array}{cc}
X_{1} & 0 \\
0 & X_{2}
\end{array}\right]\left[\begin{array}{l}
b_{1} \\
b_{2}
\end{array}\right]+\left[\begin{array}{cc}
Z_{1} & 0 \\
0 & Z_{2}
\end{array}\right]\left[\begin{array}{l}
a_{1} \\
a_{2}
\end{array}\right]+\left[\begin{array}{cc}
W_{1} & 0 \\
0 & W_{2}
\end{array}\right]\left[\begin{array}{l}
c_{1} \\
c_{2}
\end{array}\right]+\left[\begin{array}{l}
e_{1} \\
e_{2}
\end{array}\right]
$$

where $\boldsymbol{y}_{\boldsymbol{1}}$ and $\boldsymbol{y}_{2}$ are vectors of the observed survival to BN in tanks 1 and 2, respectively; the vectors $\boldsymbol{b}_{\boldsymbol{i}}$ both contain the intercept $\left(b_{o}\right)$, fixed regression coefficient on number of days from spawning until tagging $\left(b_{1}\right)$ and the fixed regression coefficient on number of days from tagging to start of experiment $\left(b_{2}\right) ; \boldsymbol{a}_{i}$ is a vector that for each trait contains the random additive genetic effect of sire $1\left(s_{1}\right)$, and the random additive genetic effect of dam $m\left(d_{\mathrm{m}}\right) ; \boldsymbol{c}_{\boldsymbol{i}}$ is a vector that for a trait contains the random common environmental effect of full-sib family $\operatorname{lm}\left(c_{\mathrm{lm}}\right)$, and $\boldsymbol{e}_{\boldsymbol{i}}$ is a residual vector for a trait with the random error term for fish $\mathrm{n}\left(e_{\mathrm{Imn}}\right) \sim \mathrm{N}\left(0, \mathbf{I} \sigma^{2} \mathrm{e}\right)$, with $\sigma^{2}{ }_{e}$ being the error variance. This assumes that the residual covariances were zero which is appropriate since a fish could only be represented in one tank. The design matrices for $\boldsymbol{b}_{i}, \boldsymbol{a}_{i}$ and $\boldsymbol{c}_{\boldsymbol{i}}$ are denoted $\boldsymbol{X}_{\boldsymbol{i}}, \boldsymbol{Z}_{\boldsymbol{i}}$ and $\boldsymbol{W}_{\boldsymbol{i}}$, respectively. The $\boldsymbol{a}_{\boldsymbol{i}}, \boldsymbol{c}_{\boldsymbol{i}}$ and $\boldsymbol{e}_{\boldsymbol{i}}$ effects were distributed as follows: $\left[\begin{array}{l}\boldsymbol{a}_{\mathbf{1}} \\ \boldsymbol{a}_{\mathbf{2}}\end{array}\right] \sim \boldsymbol{N}\left(\mathbf{0}, \boldsymbol{A} \otimes\left[\begin{array}{cc}\sigma_{s d_{1}}^{2} & \sigma_{s d_{1}, s d_{2}} \\ \sigma_{s d_{1}, s d_{2}} & \sigma_{s d_{2}}^{2}\end{array}\right]\right)$, $\left[\begin{array}{l}\boldsymbol{c}_{\mathbf{1}} \\ \boldsymbol{c}_{\mathbf{2}}\end{array}\right] \sim \boldsymbol{N}\left(\mathbf{0}, \boldsymbol{I} \otimes\left[\begin{array}{cc}\sigma_{c_{1}}^{2} & \sigma_{c_{1}, c_{2}} \\ \sigma_{c_{1}, c_{2}} & \sigma_{c_{2}}^{2}\end{array}\right]\right)$, and
$\left[\begin{array}{l}\boldsymbol{e}_{1} \\ \boldsymbol{e}_{2}\end{array}\right] \sim \boldsymbol{N}\left(\mathbf{0},\left[\begin{array}{cc}\boldsymbol{I} \sigma^{2}{ }_{e_{1}} & \mathbf{0} \\ \mathbf{0} & \boldsymbol{I} \sigma^{2}{ }_{e_{2}}\end{array}\right]\right)$,
where $\boldsymbol{A}$ is the additive genetic relationship matrix, and $\boldsymbol{I}$ are an identity matrices of appropriate sizes, while $\left[\begin{array}{cc}\sigma^{2}{ }_{s d_{1}} & \sigma_{s d_{1}, s d_{2}} \\ \sigma_{s d_{1}}, s d_{2} & \sigma^{2}{ }_{s d_{2}}\end{array}\right]$ and $\left[\begin{array}{cc}\sigma_{c_{1}} & \sigma_{c_{1}, c_{2}} \\ \sigma_{c_{1}, c_{2}} & \sigma_{c_{2}}^{2}\end{array}\right]$ are the sire-dam and common environmental (co)variance matrices, respectively, and $\sigma^{2}{ }_{e_{1}}$ and $\sigma^{2}{ }_{e_{2}}$ are the residual variances of the two traits. The relationships were traced back to the base. In experiments 3 and $4, \boldsymbol{A}$ contained 6239 and 6896 animals, respectively.

The estimated heritability for each trait was calculated as:
$h^{2}=\frac{4 \sigma_{s d}^{2}}{2 \sigma_{s d}^{2}+\sigma_{c}^{2}+\sigma_{e}^{2}}$

Additive genetic ( $r_{a 1, a 2}$ ) and common environmental correlations ( $r_{c 1, c 2}$ ) between traits were estimated as:
$r_{a 1, a 2}=\frac{\sigma_{s d 1, s d 2}}{\sigma_{s d 1} \sigma_{s d 2}}$
and
$r_{c 1, c 2}=\frac{\sigma_{c 1}, c 2}{\sigma_{c 1} \sigma_{c 2}}$

The ASREML software (Gilmour, Gogel, Cullis, Welham \& Thompson 2015) was used to estimate (co)variance components and genetic parameters.

## 3. Results

In experiment 1, the overall cumulative mortality of test fish approached 25\% (Figure 1). First mortality of cohabitants was recorded 2 days post-challenge and reached $100 \%$ on day 3 (Table
3). First mortality of test-fish was recorded on day 8 , while daily mortality peaked at day 11 , at $7.6 \%$ dead/day, and remained low until the end of challenge (Figure 2).

In experiment 2, cumulative mortality was only $3.0 \%$ and $5.7 \%$ for tanks 1 and 2 , respectively (Figure 1). In both tanks, mortality among cohabitants started 2 days post-challenge and reached $100 \%$ on day 8 (Table 3). In tanks 1 and 2, first mortality of fish was at days 11 and 9 , respectively, while daily peak mortality was reached on day 12 , in both tanks $(0.7 \%$ and $1.6 \%$, respectively) (Figure 2).

In experiment 3, cumulative mortality was considerable in both tanks: $84.0 \%$ and $83.1 \%$, respectively (Figure 1). Cohabitants in both tanks started to die 2 days post-challenge, and all were dead (both tanks) on day 6 (Table 3). In both tanks, first mortality of fish was at day 3 but with a much-delayed development of daily mortality in tank 2 compared to tank 1 (Figure 2). In the fourth experiment, cumulative mortality was $87.1 \%$ and $87.7 \%$ in tanks 1 and 2, respectively (Figure 1). In both tanks, first mortality of cohabitants occurred at day 2 and reached $100 \%$ on day 8 (Table 3). Moreover, in both tanks, fish started to die at day 6 , with similar daily mortality patterns, peaking at days 12 and 11, respectively (Figure 2).

Test-fish that died during the challenge showed typical signs of BN; bugged-eyes, less reactive to sound, and with jumping and spinning before death. Internal clinical signs were numerous white spots of different sizes ( $0.3-3 \mathrm{~mm}$ ) in swelled liver, kidney and spleen. The white spots appeared primarily on the kidney, making them swollen, but could also in critical cases be found in liver and spleen. In all samples, E. ictaluri was identified.

Estimated variance components and heritabilities of the traits (tank) as well as additive genetic and common environmental correlations between the traits (tank), using the cross-sectional linear sire-dam model, are presented in Table 4. In experiment 3, heritabilities were similar in
the two tanks ( $0.09 \pm 0.05$ and $0.08 \pm 0.04$, respectively), and the genetic correlation between tanks was close to unity (fixed at boundary). Moreover, the estimated correlation between common environmental effects in the two tanks was negative ( -0.29 ), with a large standard error (0.78). In experiment 4, the estimated heritabilities were also low ( $0.08 \pm 0.04$ for tank 1 and $0.04 \pm 0.03$ for tank 2, Table 4). Again, the estimated additive genetic correlation was high ( $0.95 \pm 0.19$ ), while the common environmental correlation was fixed at boundary ( 0.99 ).

## 4. Discussion

In challenge testing of fish, a natural reference is a mortality of $50 \%$ because it maximizes the phenotypic variance for a binary trait (Gjøen, Refstie, Ulla \& Gjerde 1997). This reasoning is as follows: If the infection load becomes too low/massive, all the fish will eventually live/die, and any phenotypic variance will not exist when analysing endpoint data (at least as dead/alive). More recently, Ødegård, Baranski, Gjerde \& Gjedrem (2011) have argued that mortality should naturally cease in the endpoint because surviving fish then are more likely to be non-susceptible to the disease. Establishing such a testing practice will have implications not only for genetic analysis, but also when examining effects of treatments, for example effects of vaccines (Drangsholt, Gjerde, Ødegård, Finne-Fridell, Evensen \& Bentsen 2012; Fredriksen, Olsen, Furevik, Souhoka, Gauthier \& Brudeseth 2013) or effects of feed ingredients/feed additives (Ward, Bengtson, Lee \& Gomez-Chiarri 2016).

In the first experiment, mortality was only $25 \%$. To increase mortality in the second experiment, several of the environmental factors were made more extreme: Acclimatization shortened, temperature more stressful, water level reduced, direct contact between the test fish and the cohabitants, a larger fraction of cohabitants per test fish, and cohabitant shedders expected to contaminate over a longer time-period (half the cohabitants given a reduced dose) (Table 1).

However, the temperature was first changed from $29^{\circ} \mathrm{C}$ to $26^{\circ} \mathrm{C}$, at day 10 of the experiment (Table 1), when realizing that mortality would be low, but this change probably occurred too late to have any effect since the cohabitants had already died out at day 8 (Table 3). The experience in the Mekong Delta is that outbreak of BN is highly affected by the temperature, since it is mostly found in the winter when water temperature is low and fluctuating. Moreover, in channel catfish, a temperature range of $22-28^{\circ} \mathrm{C}$ has been found to stimulate outbreaks of ESC, a disease also caused by E. ictaluri (Hawke, Durborow, Thune \& Camus 1998; PatrieHanson \& Jerald Ainsworth 1999; Thune, Fernandez, Benoit, Kelly-Smith, Rogge, Booth, Landry \& Bologna 2007). Mortality in cohabitation challenge with Aeromonas salmonicida in Atlantic salmon can also to a large degree be adjusted by varying the water temperature (Nordmo \& Ramstad 1999) and led us to choose a temperature of $26^{\circ} \mathrm{C}$ in the challenge test with Mekong striped catfish. Changes of the remaining environmental factors in experiment 2 were, however, decided a priori to carrying out the experiment. It was assumed that a shortened acclimatisation time, i.e., the time from arriving GEC (test station) to the release of the cohabitants (day 0 ), would pose stress to the fish. The same was assumed for halving the water level, despite Mekong striped catfish being an air breather. Regarding cohabitants, they were released directly into the test tanks with direct exposure of cohabitants to test fish, expected to increase the infectious pressure. So was the increased density of cohabitants (from 1:7 to 1:3) and the reduced dose applied for half the number of cohabitants, expected to increase the time for pathogen dispersion because those given the lowest dose should live longer. Despite all these environmental factors being more extreme in experiment 2 than in experiment 1 , still one factor was less extreme, the earlier removal of the dead fish, and mortality became very low (< 5.7\%).

The results of experiments 1 and 2 proposed that the practise around removal of the dead cohabitants affected mortality, meaning that the infectious load of the water could be instrumental to regulation of the disease frequency. Thus, in experiment 3 the load was increased by adding bacteria directly to water (from day 6 to day 13) but also from collecting dead cohabitants into plastic baskets that were hung down into the water for another 2 days. Additionally, smaller modifications were done to the experimental factors applied in experiment 2 ; the acclimatisation time was shortened from 14 to 3 days, and the lowest dose for the cohabitants was kept ( $10^{5}$ bacteria). Now, the mortality increased considerably relative to the first two experiments, reaching $83-84 \%$ in the two test tanks at termination.

In order to reduce the high disease frequency obtained in experiment 3, addition of bacteria to water was done earlier in experiment 4 and for a shorter time (days 3 to 6 ), otherwise for the same environmental factors as in experiment 3 . Despite the change, mortality was still high and approached $87 \%$ in the two test tanks at termination. However, mortality curves were more similar in experiment 4 than in experiment 3 suggesting that the bacteria need to be added to the water already in the initial phase of the challenge test.

An experiment 5 was reported by Vu, Sang, Trong, Duy, Dang \& Nguyen (2019), also in replicated tanks with fish of size $\sim 20 \mathrm{~g}$. To reduce the pathogen load of experiments 3 and 4 , the factor involving the dead cohabitants was removed from the experiment. Relative to the first four experiments, one awaited 2 days from cohabitant injection to release to the test tanks (released at day 0 in experiments $1-4$ ). The bacterium used was now the most virulent (determined by lethal dose $50, \mathrm{LD}_{50}$, i.e. the dose needed for $50 \%$ of fish to die) of four serotypes (found by use of biochemical tests and polymerase chain reaction, PCR), as tested prior to the experiment. Cohabitant dose was $10^{6}$ bacteria, and bacteria were added to water only once, 4 days after cohabitant injection ( $10^{5}$ bacteria/ml). Otherwise the same
environmental factors were as established; acclimatisation time of 4 days, water temperature $26^{\circ} \mathrm{C}$, restricted water level (2/3) and cohabitant density $1: 3$, with direct release into the test tanks. The reported average mortality across the two test tanks in experiment 5 became $39 \%$, close to the desired frequency of $50 \%$. This disease frequency is considered highly acceptable because the phenotypic variance is not much affected by frequencies deviating slightly from $50 \%$ ( $=2 p q$, where $p$ and $q$ are the frequencies of dead and alive, respectively). In a longer time perspective, however, one should take into account that resistance due to selection will increase over time, meaning that a higher BN dose will likely be required to obtain the desired frequency.

A linear cross-sectional sire-dam model was applied to the data in experiment 3 and 4, and the estimates of the heritability were limited since they are frequency dependent (Gianola \& Foulley 1983). Moreover, the estimated genetic correlations were consistently high, while the common environmental correlations were imprecisely estimated. The precision of the estimate is highly affected by the many parameters determined and from the nested mating design, known to weakly separate the common environmental and additive genetic effects (Berg \& Henryon 1998). Genetic analyses revealed that resistance to bacillary necrosis tested in replicated tanks (in the same experiment) can be considered the same genetic trait.

In these experiments, no outbreak of disease was observed during the nursing period. However, note that the water supply during the hapa period was from the Mekong river, such that the fish might have been exposed to the pathogen a priori to the challenge.

## 5. Conclusions

The four challenge tests of Mekong striped catfish against E. ictaluri propose three days acclimatization of test fish prior to the challenge, with restricted water level in the test, keeping a temperature of $26^{\circ} \mathrm{C}$. In the challenge, cohabitant shedders should be released directly into
the test tank and make up around $1 / 3$ of the fish, and bacteria should be added directly to water. The last two experiments, with the highest mortality, suggest that any factor involving the dead cohabitants should be removed, and that additional experimentation should focus on bacteria (density) and timing for addition of bacteria to water. Genetic analyses revealed that resistance to bacillary necrosis tested in replicated tanks (in the same experiment) can be considered the same genetic trait.

## Conflict of interest statement

There is no conflict of interest.

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Table 1. Environmental factors varied across the four challenge-test experiments (Exp) with Mekong striped catfish.

| Factor | Exp1 | Exp2 | Exp3 | Exp4 |
| :---: | :---: | :---: | :---: | :---: |
| Year | 2009 | 2010 | 2011 | 2012 |
| Test-tank location | Outdoor at | Indoor at | Indoor at | Indoor at |
|  | NABRECSOFA | GEC | GEC | GEC |
| No. of replicated tanks | 1 | 2 | 2 | 2 |
| No. of days of acclimatization prior | 22 | 14 | 3 | 3 |
| to experiment |  |  |  |  |
| Water temperature, ${ }^{\circ} \mathrm{C}$ | 29.5 | 29 (the first 10 days postcohabitation) and 26 (until termination) | 26 | 26 |
| Reduction of water level | No | Halved 1 day prior to test | Halved 1 day prior to test | Halved 1 day prior to test |
| No. of cohabitants | 323 | 340 in tank 1 | 1,000 in tank 1 | 1,280 in tank 1 |
|  |  | 320 in tank 2 | 1,000 in tank 2 |  |
| Ratio of cohabitant: test fish | $\sim 1: 7$ | $\sim 1: 3$ | $\sim 1: 3$ | $\sim 1: 3$ |
| No. of bacteria in cohabitant-dose | $2.5 \times 10^{6}$ | $2.5 \times 10^{6}$ for half the cohabitants, and $2.5 \times 10^{5}$ for the rest | $1 \times 10^{5}$ | $1 \times 10^{5}$ |
| Placement of cohabitants | In hapa, located central in tank | Direct into tank | Direct into tank | Direct into tank |
| Dead cohabitant removal | When dead and sunk down to bottom of hapa | When dead and floating | Dead and floating fish collected into plastic baskets hung down into water for another 2 days | Dead and floating fish collected into plastic baskets hung down into water for another 2 days |
| Addition of pathogen to water | No | No | Post-exposure to cohabitants: From day 6 to day 13 , to reach a density of $2.5 \times 10^{6}$ bacteria/ml | Post exposure to cohabitants: From day 3 to day 6 , to reach a density of $2.5 \times 10^{6}$ bacteria/ml |

Table 2. Numbers of families and fish per tank in the four challenge-test experiments (Exp) with E. ictaluri in Mekong striped catfish: Experiment 1 had one tank ( t 1 ), while the other experiments had two replicated tanks.

| No. of families and <br> fish | Tank | Exp1 | Exp2 | Exp3 | Exp4 |
| :--- | :---: | :---: | :---: | :---: | :---: |
| No. of families | t 1 | 81 | 64 | 187 | 233 |
|  | t 2 | - | 60 | 187 | 233 |
| No. of fish | t 1 | 2,155 | 1,019 | 2,944 | 3,246 |
|  | t 2 | - | 969 | 2,745 | 2,931 |

Table 3. Number of days from injection (experimental day 0 ) to first and complete death of cohabitants in four challenge-test experiments with E. ictaluri in Mekong striped catfish: Experiment (Exp) 1 had one tank ( t 1 ), while the other experiments had two replicated tanks.

|  | No. of days to |  |
| :--- | :---: | :---: |
| Experiment | First mortality of cohabitants | Complete mortality of cohabitants |
| Exp1-t1 | 2 | 3 |
| Exp2-t1 | 2 | 8 |
| Exp2-t2 | 2 | 8 |
| Exp3-t1 | 2 | 6 |
| Exp3-t2 | 2 | 8 |
| Exp4-t | 2 | 8 |
| Exp4-t2 | 2 | 8 |

Table 4. Estimates (linear model) of genetic sire-dam variance ( $\sigma^{2}$ sd), common environmental variance $\left(\sigma^{2} \mathrm{c}\right.$ ), heritability $\left(\mathrm{h}^{2}\right)$, and additive $\left(r_{a 1}, a 2\right)$ and common environmental correlations $\left(r_{c 1, c 2}\right)$ between survival ( dead $=0 /$ alive $=1$ ) in the endpoint of two replicated tanks, defining traits 1 and 2, in two experiments (Exp) of Mekong striped catfish with E. ictaluri.

|  | Trait | Exp3 | Exp4 |
| :--- | :--- | :--- | :--- |
| $\sigma_{\text {sd }}^{2}$ | Trait 1 | 0.0030 | 0.0020 |
|  | Trait 2 | 0.0029 | 0.0010 |
| $\sigma^{2}{ }_{c}$ | Trait 1 | 0.0048 | 0.0037 |
|  | Trait 2 | 0.0020 | 0.0020 |
|  | Trait 1 | $0.09 \pm 0.05$ | $0.08 \pm 0.04$ |
| $\mathrm{~h}^{2 \dagger} \pm \mathrm{SE}$ | Trait 2 | $0.08 \pm 0.04$ | $0.04 \pm 0.03$ |
|  |  | $0.99 \ddagger)$ | $0.95 \pm 0.19$ |
| $r_{a 1, a 2} \pm \mathrm{SE}$ |  | $-0.29 \pm 0.78$ | $0.99 \ddagger)$ |
| $r_{c 1, c 2} \pm \mathrm{SE}$ |  |  |  |

${ }^{\dagger)} \mathrm{h}^{2}=\frac{4 \sigma^{2}{ }_{\mathrm{sd}}}{2 \sigma_{\mathrm{sd}}^{2}+\sigma_{\mathrm{c}}^{2}+\sigma_{\mathrm{e}}^{2}}$.
${ }^{\ddagger}$ ) Fixed at boundary.


Figure 1. Cumulative mortality observed in four challenge-test experiments with E. ictaluri in Mekong striped catfish: Experiment (Exp) 1 had one tank ( t 1 ), while the other experiments had two replicated tanks.


Figure 2. Daily mortality in four challenge-test experiments with E. ictaluri in Mekong striped catfish: Experiment (Exp) 1 had one tank ( t 1 ), while the other experiments had two replicated tanks.


[^0]:    Abstract

    Bacillary necrosis is a problematic disease in farming of Mekong striped catfish (Pangasianodon hypophthalmus). The pathogenic bacterium is Edwardsiella ictaluri, causing

