



Heritabilities and GxE interactions for growth in the European sea bass (*Dicentrarchus labrax* L.)

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Comparison of pressure or thermal treatments on triploid yields and malformations up to swim up stage in rainbow trout (*Oncorhynchus mykiss*)

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Effects of pressure or thermal treatment performed at fertilization to induce triploidy were assessed by monitoring survival rates at eyed, hatching and swim-up stages, and morphological anomalies in surviving fry. Pressure treatment (at 700 bars), thermal treatment (at 26.6 °C) and control fertilization were performed on the same 14 spawns of individual females of rainbow trout (INRA UR544 Génétique des Poissons, F-78350 Jouy en Josas, France). Fry ploidy was assessed by flow cytometry at yolk sac stage on 80 larvae per treatment. Fry triploid rates were not statistically different between pressure and thermal treatments ($97.5\% \pm 3.5$ and $92.9\% \pm 5.6$). However, survival was significantly better after pressure rather than thermal treatment, either at eyed stage (89.5% vs. 68.0%) or at hatching (96.8% vs. 92.3%), and was not different from diploid control. Nine different types of morphological anomalies were noticed at swim up stage. The global rate of anomalies was not different between pressure treatment and diploid control (2.8% vs. 1.9%), but was significantly higher in fry from thermal treatment (11.7%). The pressure treatment induced a final yield of fry similar to diploid control, but significantly higher than the thermal treatment (81.7% vs. 49.6%). Data analysis of morphological anomalies types and rates, recorded at swim up stage, displayed an interaction between individual spawns and triploidisation treatments. Finally, no difference in performances and morphological anomalies rates could be observed in this experiment, at hatchery stages, between triploid fry from pressure treatment and control diploids.

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Heritabilities and $G \times E$ interactions for quality traits in the European sea bass (*Dicentrarchus labrax* L.)

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253 families of the European sea bass *Dicentrarchus labrax* were pooled in the tank and reared communally from hatching, dispatched in 4 different farming systems (semi-intensive ponds, cages, race ways and closed recirculated system), slaughtered (338 to 487 g) and identified by genotyping of microsatellites. Indirect estimation of muscle fat content by microwaves (Torry Fish Fat Meter) was linearly related with the real content estimated by NMR ($R^2 = 0.70$, $n = 200$). Heritabilities of Fat Meter values were high in all sites and for all the positions ($n = 3$) of the meter (from 0.43 ± 0.05 to 0.77 ± 0.07). Genetic correlations between sites (used to estimate $G \times E$ interactions) varied from 0.70 ± 0.07 to 0.96 ± 0.02 . The genetic correlation between fat muscle fat and growth was intermediate (0.46 ± 0.09 to 0.65 ± 0.06). Selection for growth will induce the production of fatter fish when fish will be slaughtered at the same age, but this increase is mainly due to the positive phenotypic correlation between weight and fat content. However, if fish will be slaughtered at the same weight, different correlated responses are observed from the production of leaner to fatter fish depending on farms. Heritability of carcass yield was medium to high (0.58 to 0.74) and this trait was highly correlated with the fat deposited around the digestive tract (-0.98 ± 0.01) but independent with the fat deposited at the top of the belly cavity (-0.01 ± 0.10). It is concluded that improvement of quality traits in sea bass can be initiated and that rapid progress could be achieved in most traits recorded in this experiment.

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Identifying regions of the genome responsible for early maturation and associated traits in rainbow trout (*Oncorhynchus mykiss*)

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