POWER CALCULATIONS FOR OPTIMISATION OF THE EXPERIMENTAL DESIGN TO DETECT G X E: SALMON EXPERIMENTS IN FUTUREEUAQUA

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Introduction

The objective of the WP1 in FutureEUAqua is to assess how the current breeding programmes for salmon, seabass, seabream and rainbow trout can respond to future demands for novel feed compositions, and to make further improvements to disease resistance, climate resilience and animal welfare. For Atlantic salmon (*Salmo salar*) we estimate the genotype by diet/climate interactions (GxE) in semi-commercial salmon production system and validate best selection methods in salmon breeding programs by comparing traditional BLUP selection with GS/MAS for production and robustness traits. Estimated correlations will be taken as indicators of the magnitude of re-ranking of genotypes across diets/environments.

Power calculations are elementary part of the experimental design but unfortunately often de-prioritized, compromising the critical interpretation of the results. *A priori* power calculations of genetic studies are characterized with multiple uncertainties, such as true relationship structure, number of families and individuals at the time of registration and unknown heritability of the traits of interest. This said, we argue that by performing a range of power calculations it is possible to frame the true power of the experiment and improve the probability of executing scientifically solid experiments with given restrictions of resources. We demonstrate the optimisation of the experimental design in order to have adequate power to detect significant GxE (diet/climate aggregate) given FutureEUAqua WP1 resources.

Material and methods

WP1 experiments will be run on two geographical locations in order to study both genotype by feed and genotype by climate interactions. Given the WP1 resources each treatment will be run in two parallels. We assessed the power of detecting heritability (0.05-0.35) in experiments using different number of families utilizing the maximum cage capacity of 750 fish. Same range of true trait heritability and true genetic correlation ranging from 0.1 to 0.9 was used to estimate power detecting genetic correlation (r_g) different from 1 (one). Standard error of heritability was calculated assuming full-sib family structure, thus multiplying the standard error of the intraclass correlation by two: $\sigma_{h^2} = 2\sigma_t = 2\sqrt{\frac{2[1+(n-1)t]^2(1-t)^2}{n(n-1)(N-1)}}$ $\sigma_{h^2} = 2\sigma_t = 2\sqrt{\frac{2[1+(n-1)t]^2(1-t)^2}{n(n-1)(N-1)}}$ (Falconer 1989, p182). Standard error of the genetic correlation is dependent on the heritability of the traits (assumed identical), the standard error of the heritability and the genetic correlation: $\sigma_{(r_A)} = \frac{1-r_A^2}{\sqrt{2}}\sqrt{\frac{\sigma_{(h_x^2)}\sigma_{(h_y^2)}}{h_x^2 h_y^2}}\sigma_{(r_A)} = \frac{1-r_A^2}{\sqrt{2}}\sqrt{\frac{\sigma_{(h_x^2)}\sigma_{(h_y^2)}}{h_x^2 h_y^2}}$ (Falconer 1989, p317). Power was calculated in the context of one-tailed test and 0.95 cumulative probability.

Results

Assuming equal full-sib family size, power of 0.8 to detect true heritability of 0.15 or above was achieved with 20 or more families. To obtain similar power to detect significant GxE ($r_g \leq 0.8$) a minimum of 35 families was required when both traits have true heritability of 0.2 or larger, (figure 1). For genetic parameter estimation it is common to choose the design aiming at 10 fish/famil at registration. With this design and 0.2 heritability, we would be able to detect significant GxE for $r_g \leq 0.9$ or below with power of 0.80, whereas for heritability 0.15 true genetic correlation of 0.6 is needed to detect significant re-ranking of genotypes with identical power.

If the available capacity is only 500 fish, the power of detection of 0.15 heritability would drop down to 0.75. Alike, the maximum probability of detecting significant GxE ($r_g \leq 0.8$) for trait heritability 0.2 reduces to 0.7. For 10 fish/family design, $r_g \leq 0.55$ or $r_g \leq 0.30$ would allow to conclude re-ranking of genotypes with 80% power for traits with trait heritability of 0.2 and 0.15, respectively.

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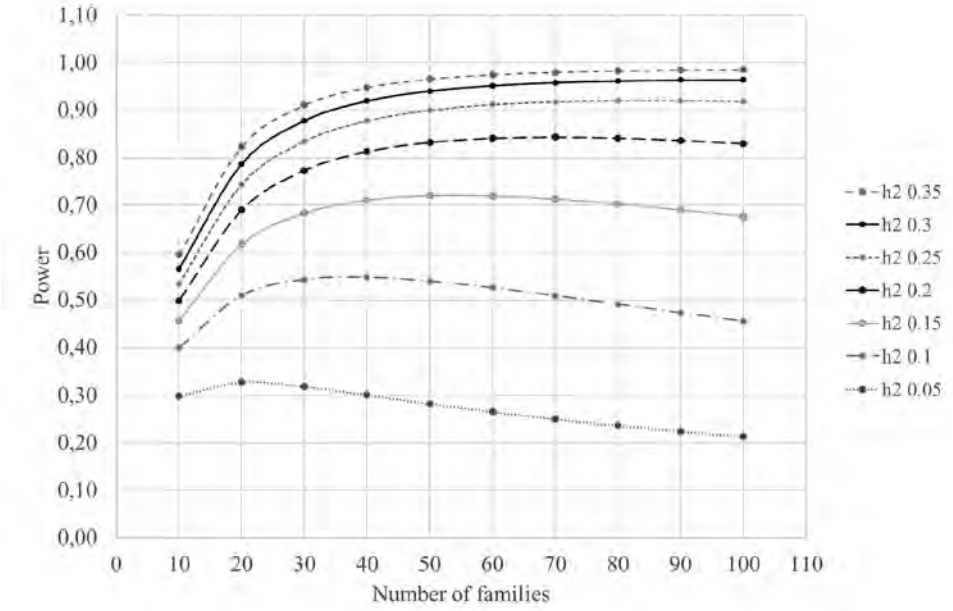

Fig. 1. Power to detect significant GxE, defined as r_g=0.8 (and below), with different number of families and true trait heritability given total capacity of 750 fish.

Discussion

Power calculations, demonstrated here, will allow appropriate reflections of the magnitude of r_g relative to the existence of GxE. The estimates presented here are based on full-sib family structure. In practical breeding programs the genetic material includes half-sib groups and/or related parents. Additionally, relationships are increasingly based on genomic information. Half-sib family structure will reduce the power, counteracted by the genomic relationship information. The true experimental design includes parallel cages to be able to detect treatment effects, whereas we have presented conservative calculations based on one cage only. Despite uncertainties, by performing a range of power calculations it is possible to frame the true power of the experiment with given restrictions of resources. Magnitude of power considered acceptable should be reflected and aligned with the overall objectives and resources of the project

References

Falconer, D. S. 1989. Introduction to quantitative genetics. Longman Scientific & Technical, Essex, England. 438pp.

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