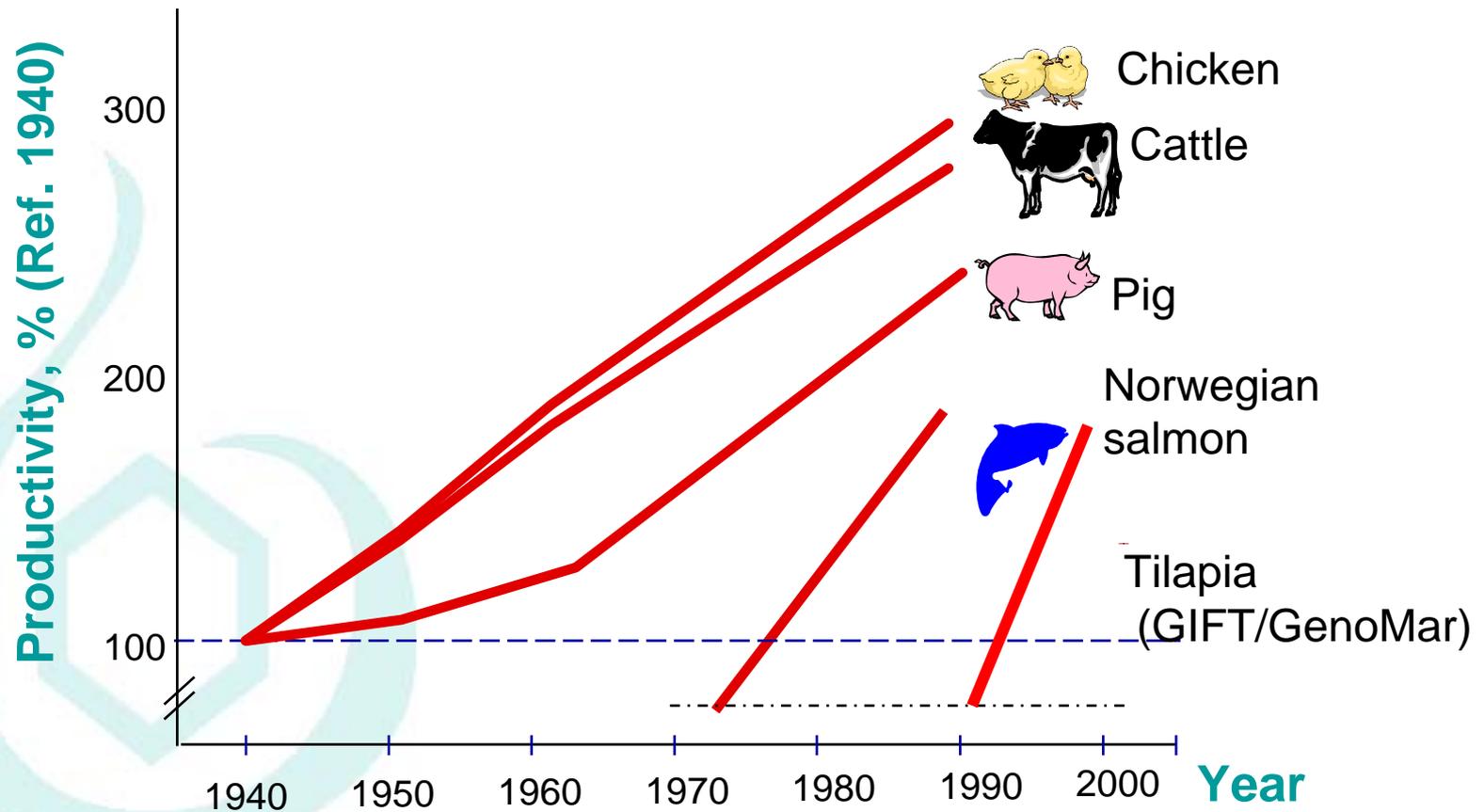


A new era:
The Merging of Quantitative and Molecular Genetics
– *Prospects for Tilapia Breeding Programs*

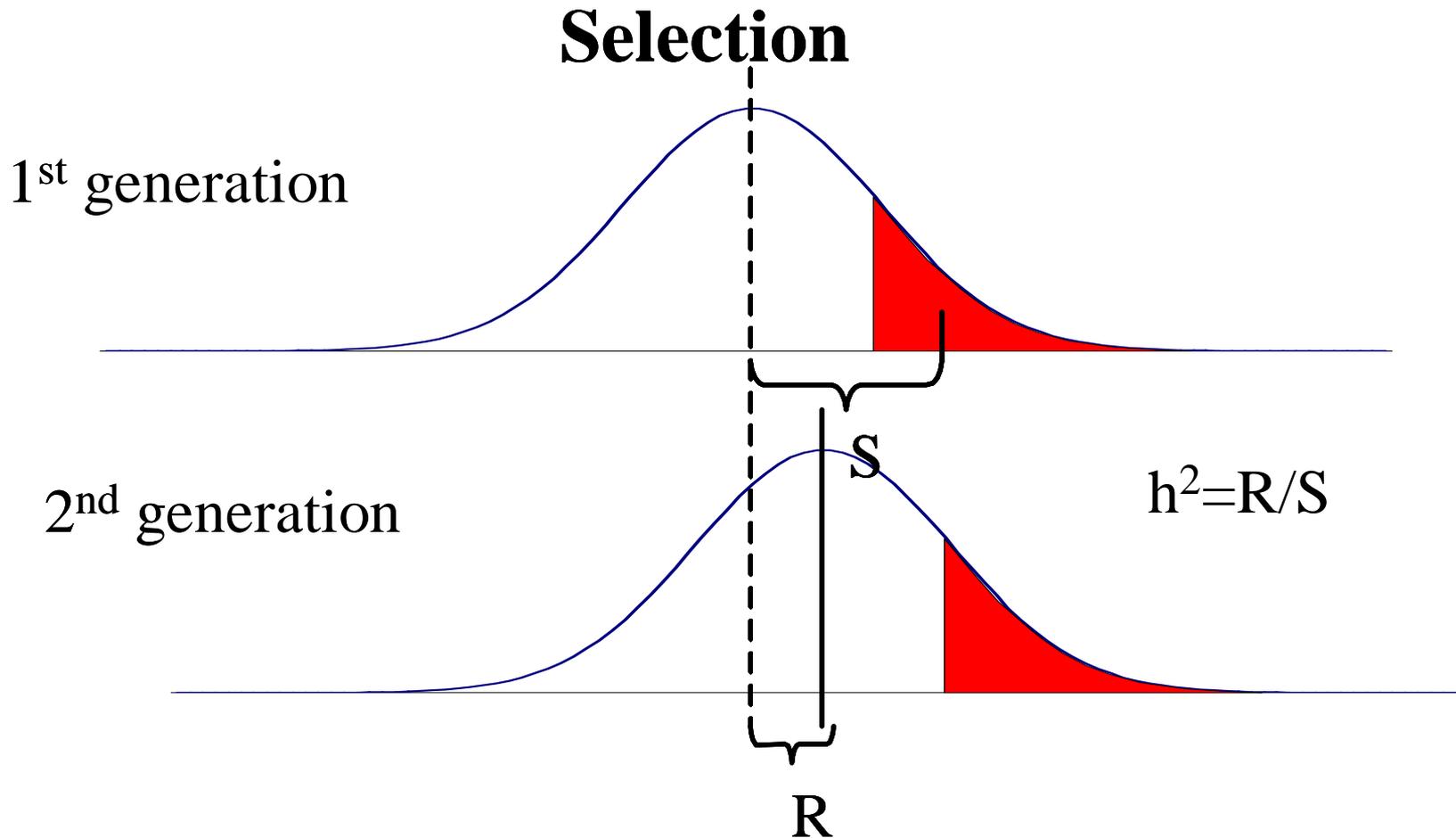
*Professor Hans Magnus Gjøen,
Department of Animal and Aquacultural Sciences
Agricultural University of Norway*



Traditional selective breeding works



(Modified after Eknath et al., 1997)



→ 10-20% genetic gain per generation for growth rate

How to find the optimal breeding scheme? -Simulation tools



- **Simulates well documented genetic systems/models**
(*"infinitesimal genetic model"*)
- **Long-term genetic effects** (15 generations)
- **Full track of inbreeding effects**
- **Optimises the use of any existing or planned facilities**



The simulation of "data-fish" (phenotypic values)

$$P = 0.5g_s + 0.5g_d \\ + v\sigma_a (0.5(1 - (F_s + F_d)/2))^{0.5} \\ + W\sigma_e$$

The goal: maximum genetic gain

Genetic gain expressed by:

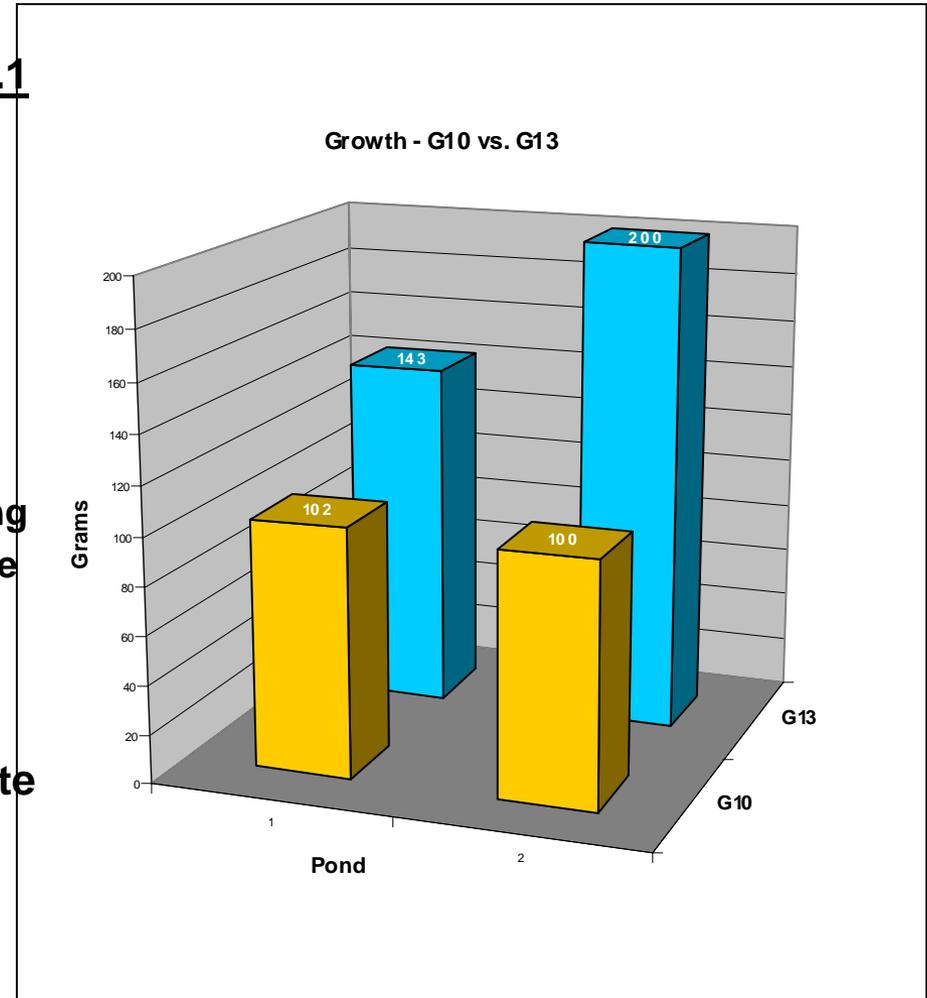
$$\Delta \mathbf{G} = i \sigma_G r_{GI}$$

- i is the selection intensity
- σ_G is the genetic variation
- r_{GI} is the accuracy of the BV

Some results from GenoMar

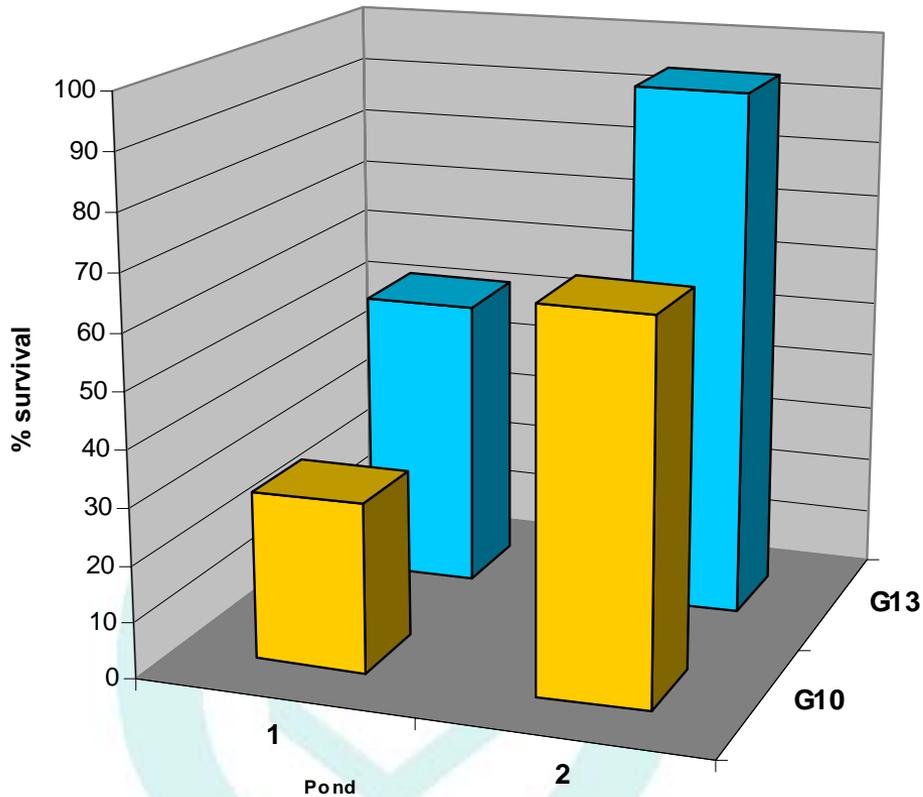
- Estimation of genetic gain – Exp.1
- Comparisons of Generation 10 (G10) and Generation 13
- Always difficult to compare different groups of fish:
 - Diff. behaviour
 - Diff. growth potential
 - Not easy to find ad libitum feeding
 - Overfeeding will severely damage the pond environment
- Tested in same ponds, divided by net
- Feeding adjusted close to appetite

Average growth rate improvement: 70%
i.e. About 19% per generation



Survival in experiment 1

Survival, G10 vs G13



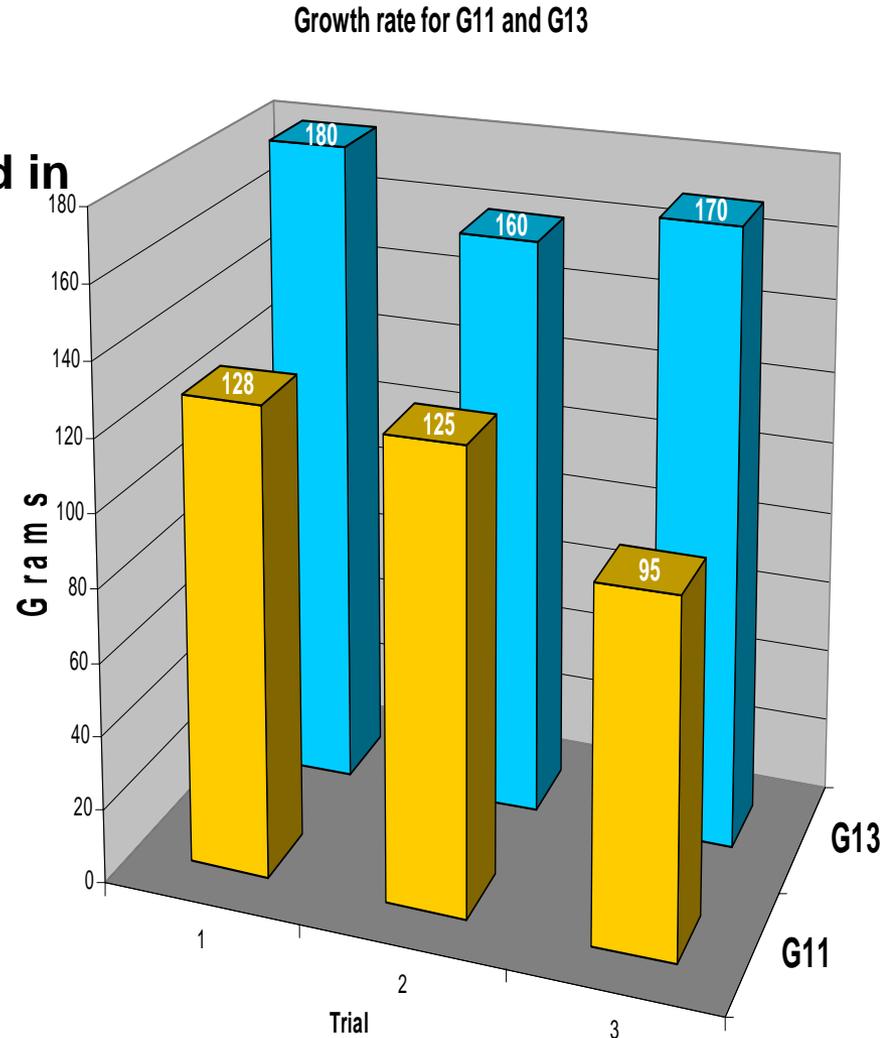
- In pond 1, there was a sudden plankton collapse on the 4th week, which continued for about 2 weeks.
- During this period very few fish were seen feeding in both G-10 and G-13.
- Survival rate has improved from an average survival rate of 48.5% (G-10) to 73.0% (G-13) → Total improvement of 50%, i.e. 14% per generation

FCR the same in all ponds: 1.0

Experiment 2 – G11 vs. G13

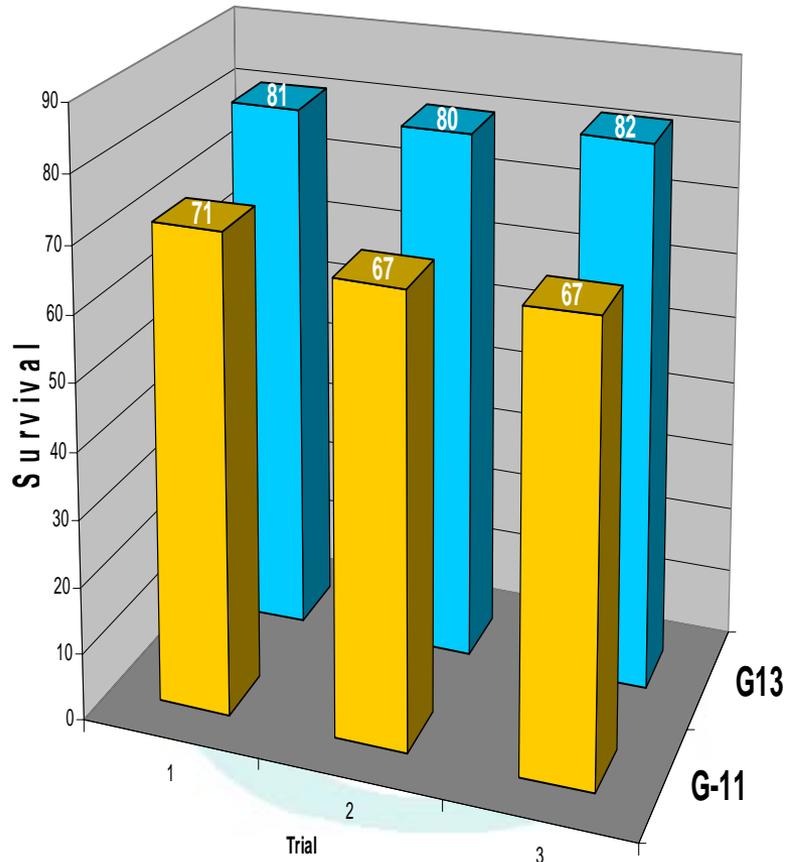
- Each generation is recorded in 3 ponds, i.e. 6 ponds in all
- More focus this time on optimisation of the pond environment and standard commercial conditions

Average growth improvement: 44%
i.e. 20% per generation
if poorest G11 is left out

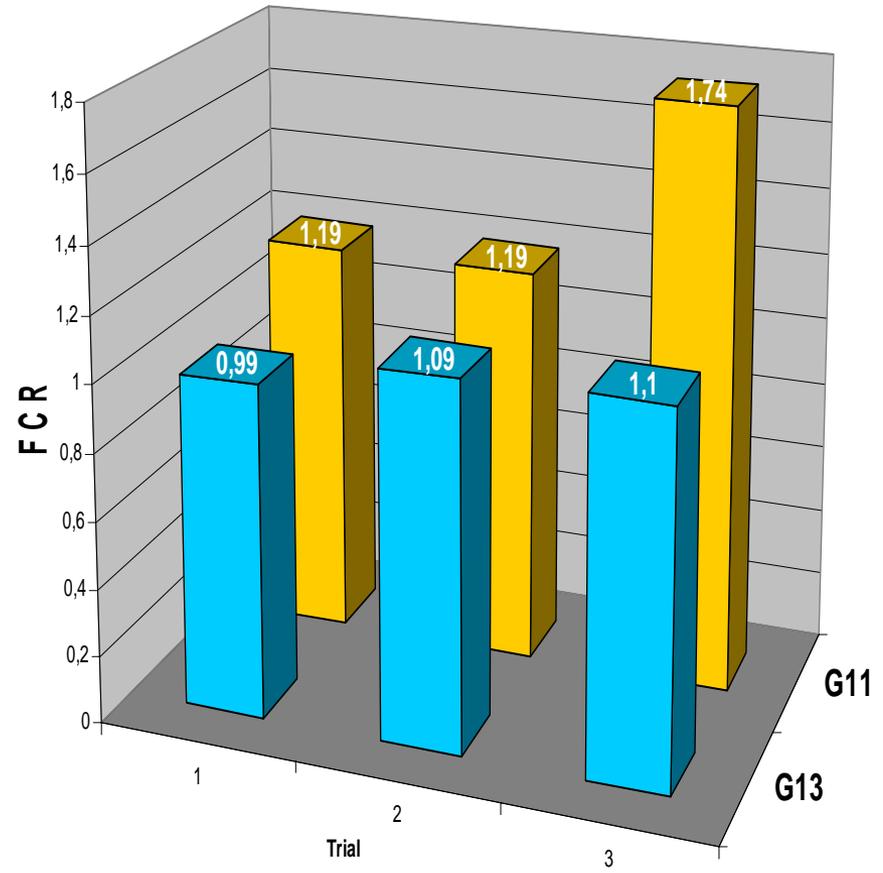


Exp. 2 – G11 vs. G13

Survival for G11 and G13



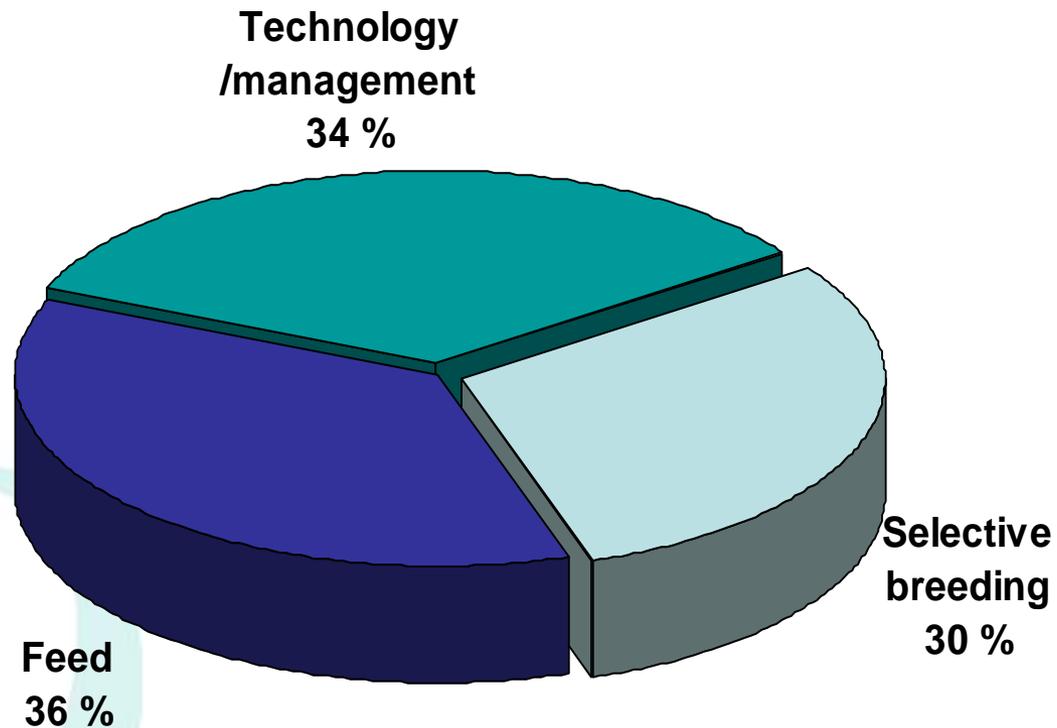
FCR for G11 and G13



Improvement: 8% per generation

Improvement: 6% per gen. without the worst G11 pond

Main contributions to Norwegian salmon success



(Source: Norsk fiskerinæring 8/1995)

So, traditional methods work well – why then bother with these new fancy stuff...?



- 1. Improvement of traditional methods**
- 2. Surpass "difficult traits"**
- 3. Opening the black box between phenotype and genotype**

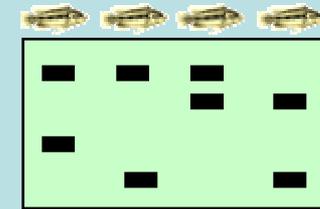


- Improvement of "conventional designs
- DNA as an ID

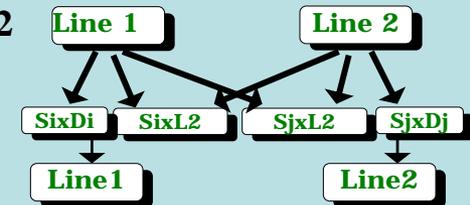
- Better breeding design

- Marker assisted selection

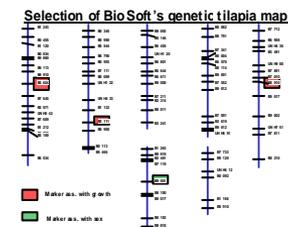
1



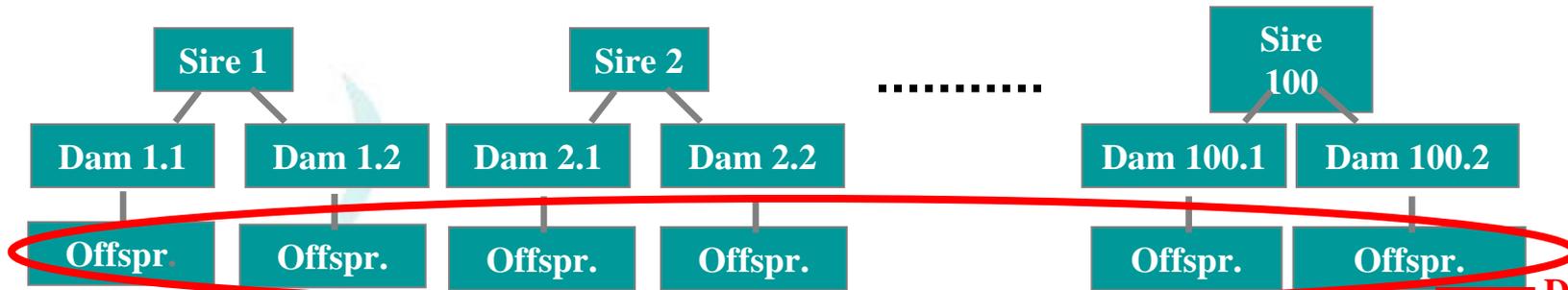
2



3



Disadvantages with conventional breeding designs



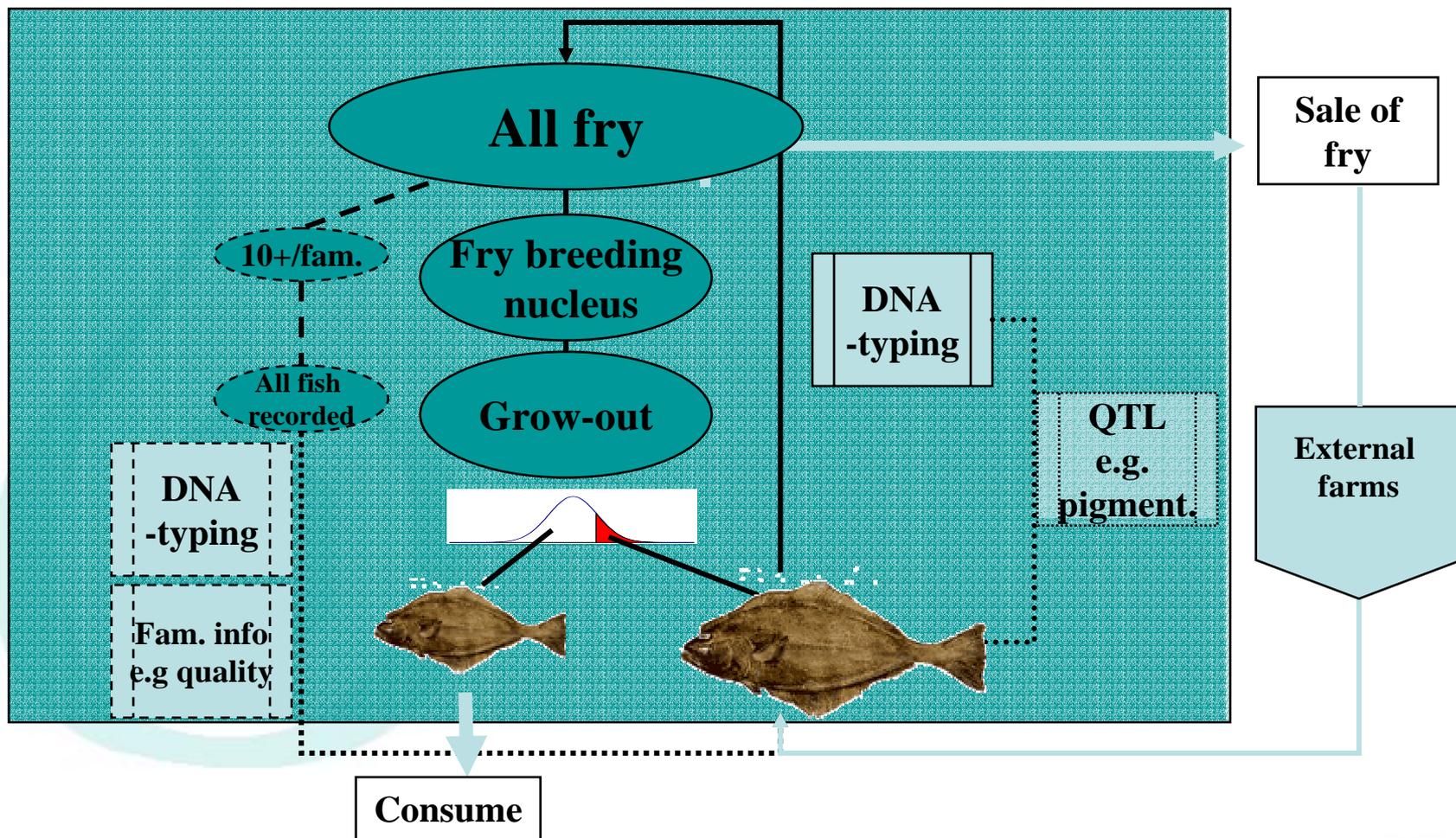
1. gen.

Drawbacks:

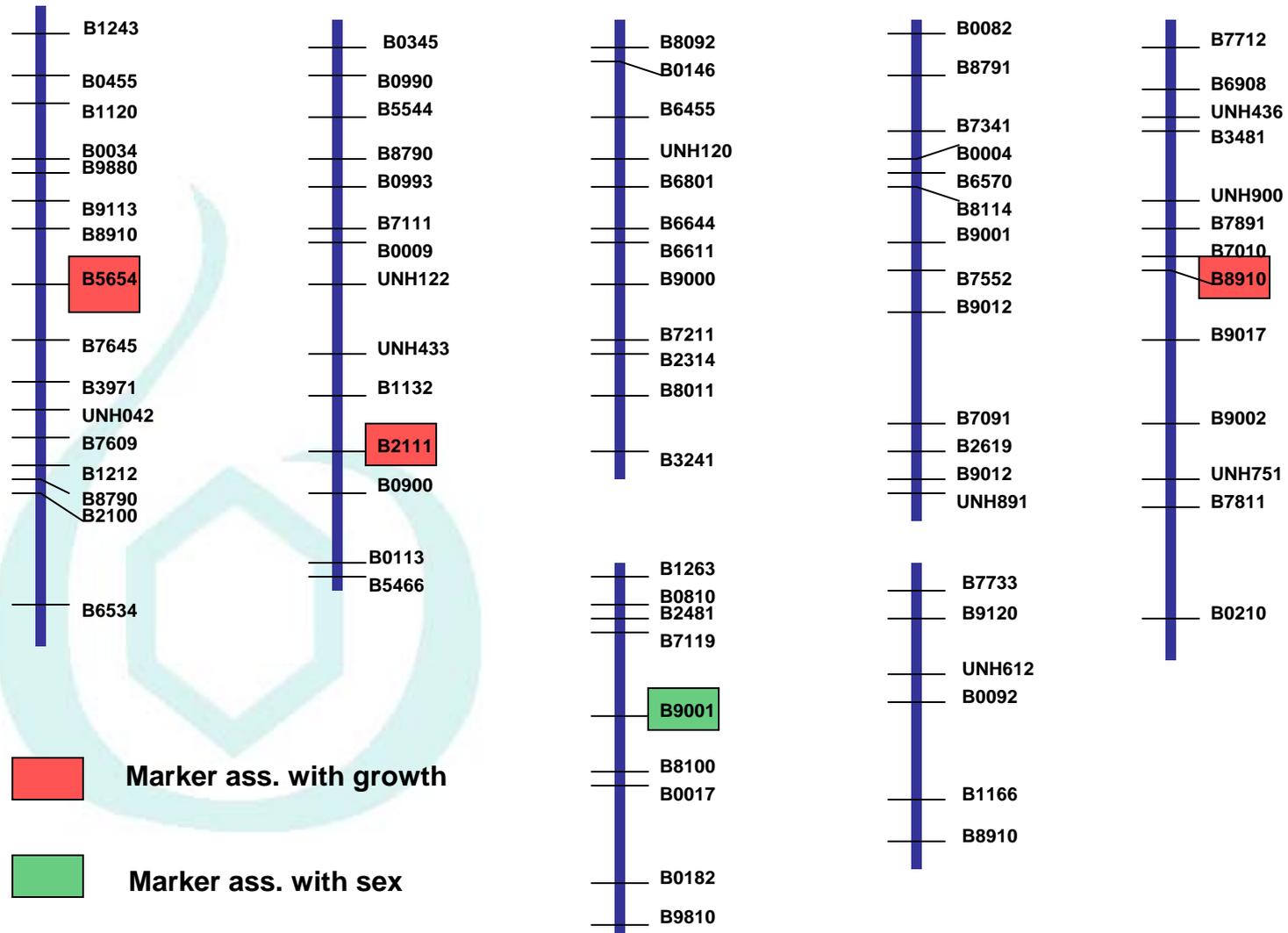
1. Common env. effekt
2. Low numbers
3. Cost

Communal rearing of all families

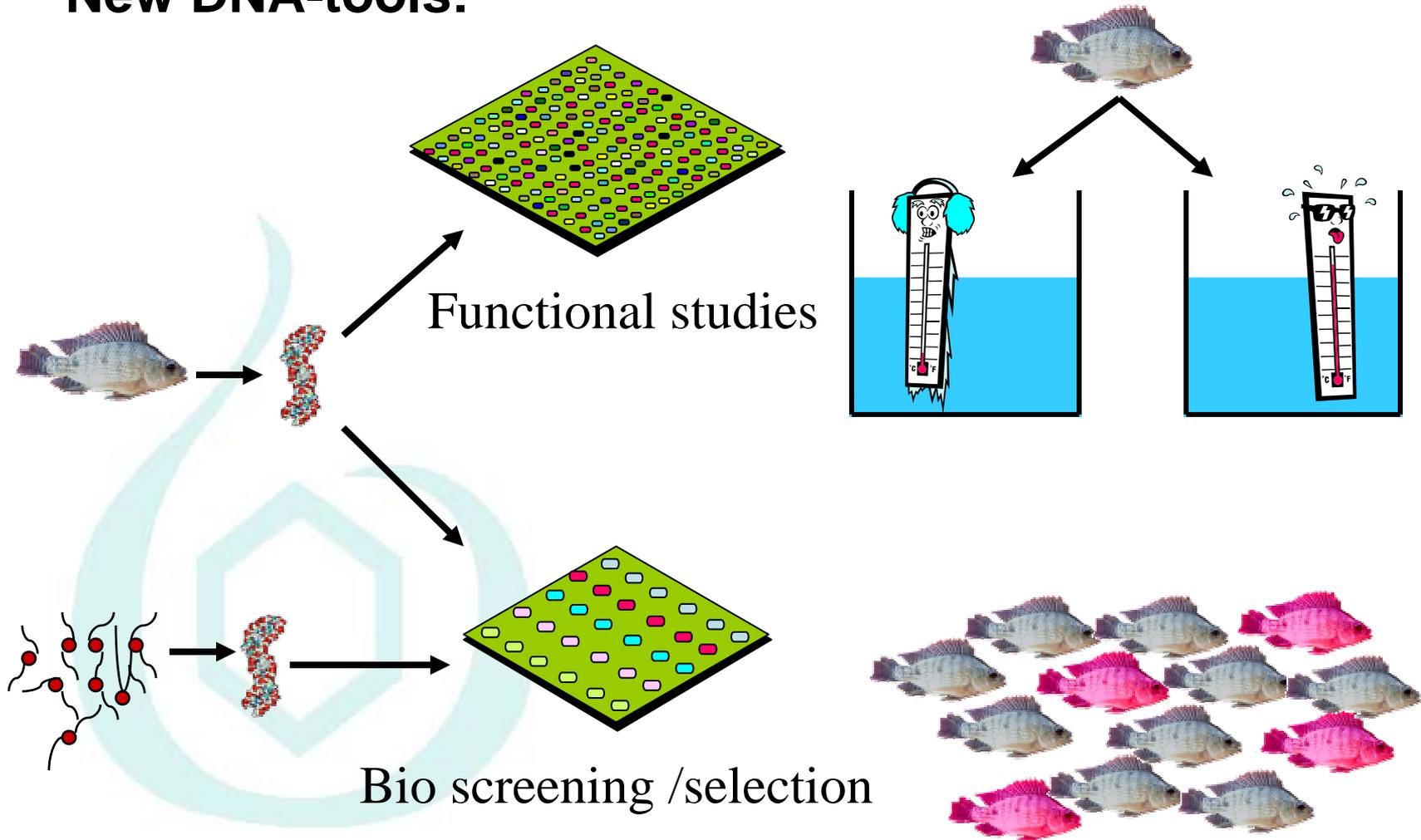
Breeding design with DNA-typing – an example



Gene map - an example



New DNA-tools:



A new era within biology



- **The ongoing revolution within experimental biology produces enormous amounts of data**
- **The sequencing of whole genomes has given new possibilities for collection of system wide biological data.**
- **Genes can be identified within a sequence and array technology makes it possible to measure genome wide expression levels simultaneously**
- **Furthermore, differences at single nucleotides between individual sequences, SNPs, are a new class of genetic markers.**
- **At present nearly 1.8 million SNPs have been detected in the human genome**
- **Analysing the amounts of information that can be produced from such experiments represents a huge challenge for modern biology.**
- **SNP data in itself can be analysed with the methods of genetics as genetic markers the SNPs can be arranged linearly in linkage groups and recombination fractions can be estimated to make dense genetic maps.**
- **These genetic maps can then be used in traditional genetic studies for example in a search for QTLs.**
- **But the traditional model of gene action, which is based on additivity is not well suited for handling data on the levels of mRNA or proteins as these are expressions of dynamic system of interacting genes rather than independent effects.**

P. Melamed et al. / Aquaculture 204 (2002) 255–269

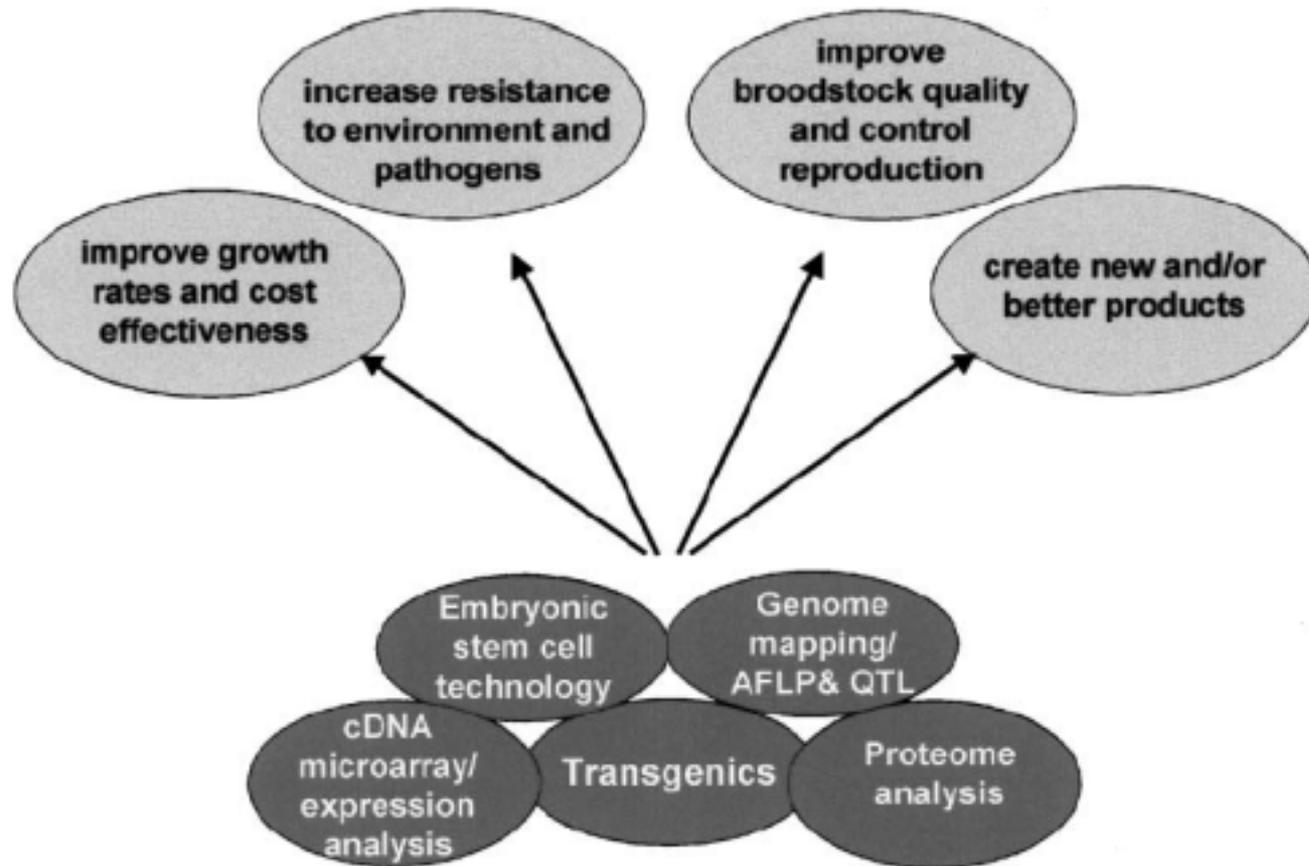


Fig. 1. An overview of some of the platform technologies (dark-shaded) in functional genomics, and their potential applications to aquaculture (light-shaded).

Effect of MAS – not always impressive

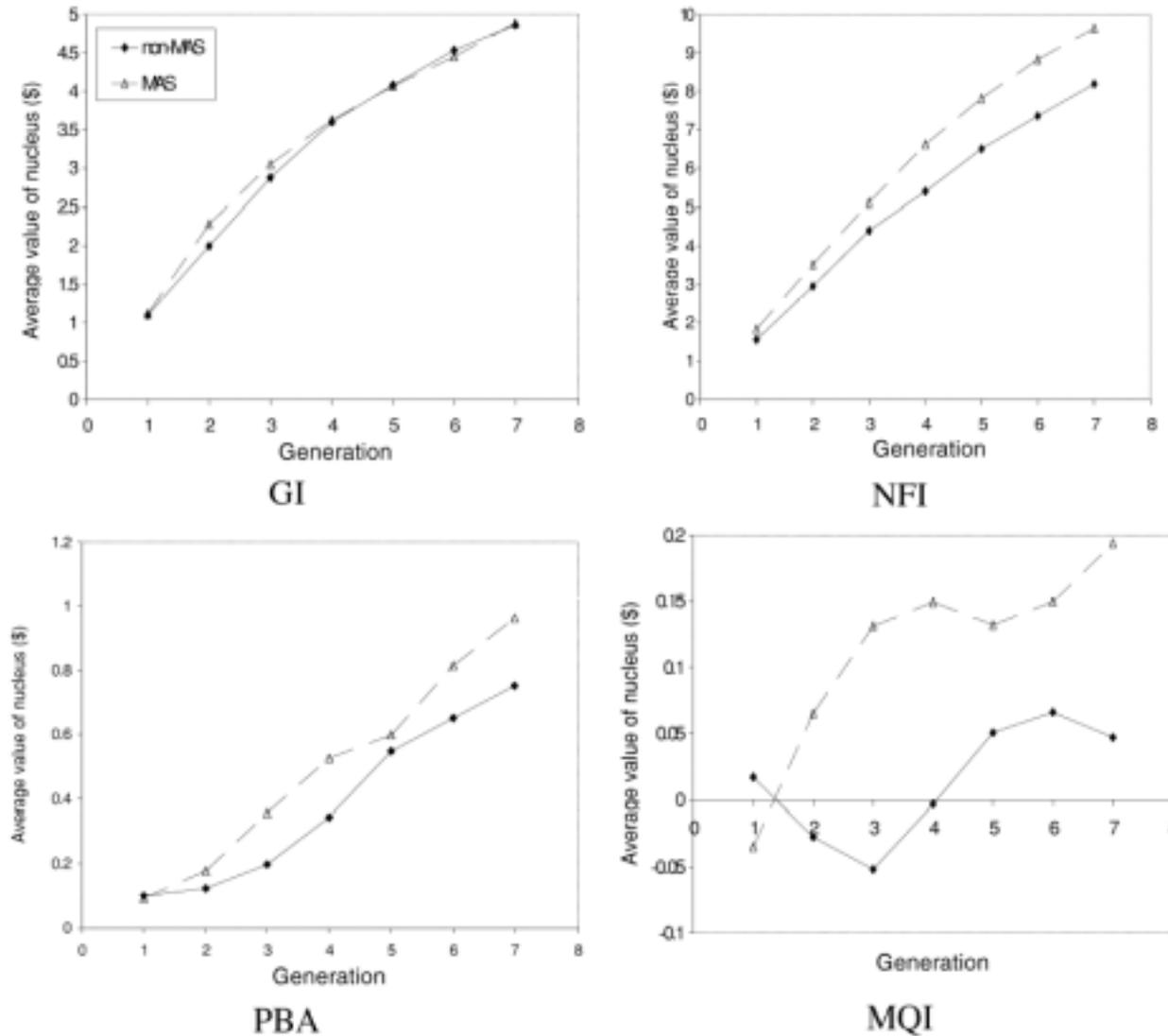


Fig. 3. Response in component traits of the index for non-MAS and MAS-LGW. Note the scale on the y-axis for each trait is different.

Can a biologist fix a radio?

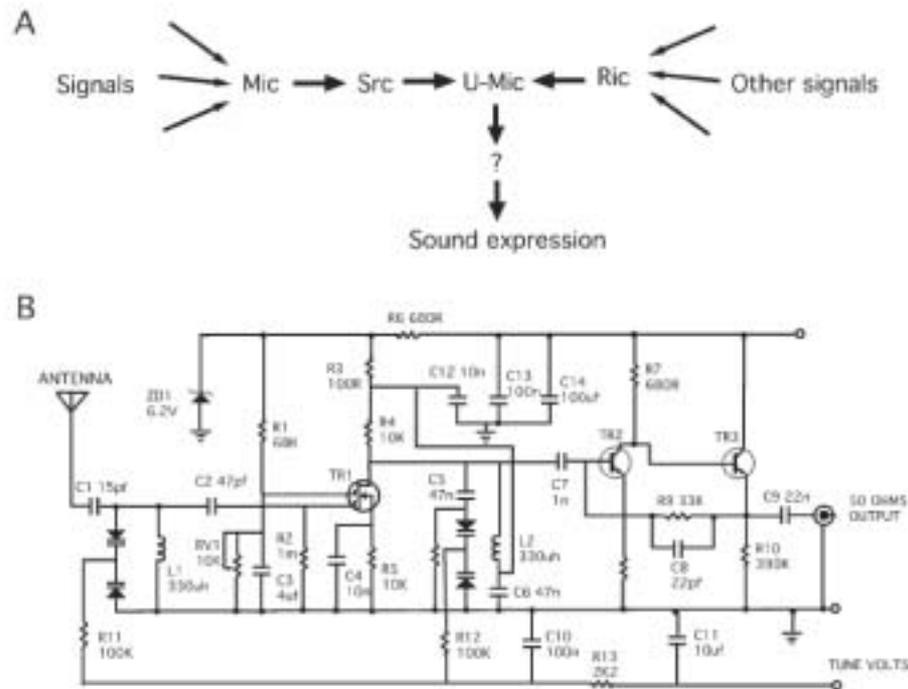


Figure 3. The tools used by biologists and engineers to describe processes of interest

A: The biologist's view of a radio. See Figure 2 and text for description of the indicated components. **B:** The engineer's view of a radio. (Please note that the circuit diagram presented is not that of the radio used in the study. The diagram of the radio was lost, which, in part, explains why the radio remains broken.)

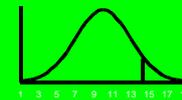
The merging of disciplines



Genomics



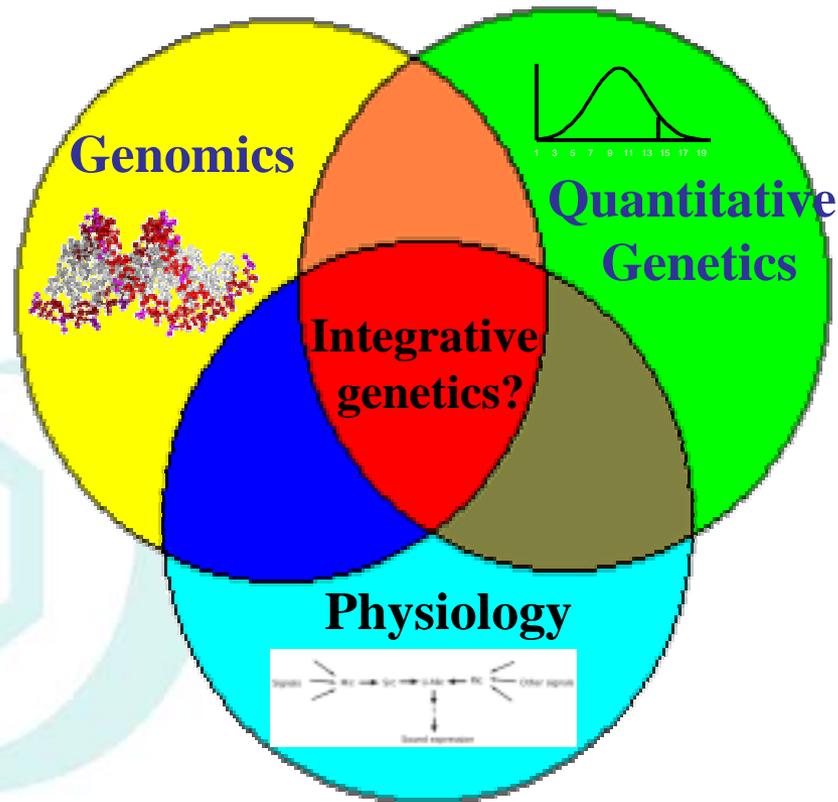
Quantitative Genetics



Physiology



The merging of disciplines



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What is integrative genetics?

[Stig Omholt](#)

The search for principles and methodologies that link the behaviours of molecules (i.e. genes) to system characteristics and functions (i.e. phenotypes) has been the prime occupation of genetics for the last 100 years. We do not think it is appropriate to introduce new terms like systems biology, bioinformatics or computational biology to describe this endeavour. To pay due credit to the immense efforts and achievements of the genetics community, while at the same time recognizing that genetics is undergoing a dramatic transition, we have coined the term integrative genetics.

Where is biology heading?

In this century genetic research will become almost synonymous with the efforts to understand the functional expression of genes within the context of integrated biological systems. We are finally in position to start revealing the causal links between genotype and phenotype in the wide sense. To achieve this, genetics will be forced to become much more inter-disciplinary and theoretically inclined. In this process its statistical, mathematical and computational tools will become substantially more sophisticated, and conceptual and methodological apparatuses, which are today almost totally separated, will become much more integrated.

Motivation for the term "integrative"

We make use of the term integrative because it quite accurately describes the transition genetics is currently undergoing, namely

- * Integration of experimental and theoretical approaches in concrete research programmes;
- * Integration of processes and mechanisms connecting genotypic data with phenotypic data (in the wide sense) in a coherent mechanistic explanatory structure;
- * Integration of the explanatory frameworks of nonlinear system dynamics and statistics.

- **National SNP service facility**
- **Bridging the gap between genotypes and phenotypes by:**
 - **Integration of experimental and theoretical approaches in concrete research programmes;**
 - **Integration of processes and mechanisms connecting genotypic data with phenotypic data in a coherent mechanistic explanatory structure, by applying the explanatory frameworks of non-linear system dynamics and statistics.**

Example of genotype-phenotype model

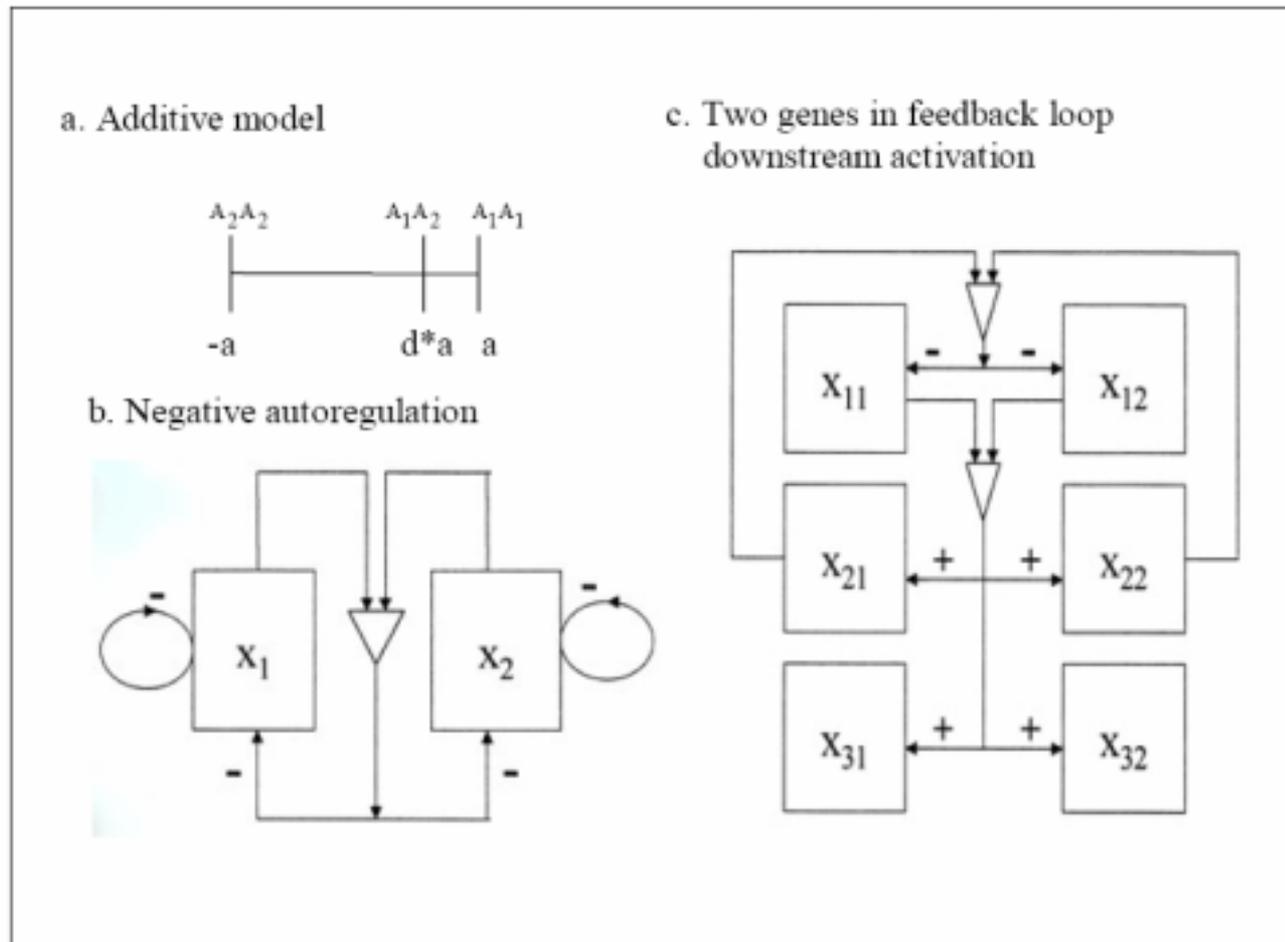


Figure 4: Graphical representations of the genotype-phenotype models used in the test simulations, model b. and c. are from Omholt et al.(2000). (a) The additive model of quantitative genetics, the parametrization is done such that $d=1$ means full dominance of A_1 . (b and c) A horizontal pair of boxes represents the two alleles of a gene. A triangle indicates that the concentrations of gene products from alleles pointing to it is added. Signed arrows means that the sum of gene products, from the triangle, regulates the production of the allele at which the arrow points. + means positive regulation and - means negative regulation.

Concluding remarks

- **Traditional selective breeding will remain a "main engine" in breeding program, incl. tilapia, in the foreseeable future**
- **Some immediate benefits should be harvested**
- **The enormous amount of new experimental data and new gene technological tools requires a whole new modelling concept**
- **Utilisation of this new gene-toolbox will require specific physiological, biological and hands-on knowledge for each species → networking**
- **Tilapia is likely to be a target species for much of this research and many of the news tools because of its high value production and short generation interval**