A comparison of classic selection and mating methods for aquaculture breeding programmes

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State of the art

- Fish species → 10% of the global production based on genetically improved stocks (Gjedrem et al 2012)

- High reproductive capacity → higher selection pressures

↓

higher genetic responses

AQUACULTURE HAS A TREMENDOUS POTENTIAL FOR GENETIC IMPROVEMENT

Aquaculture selection methods

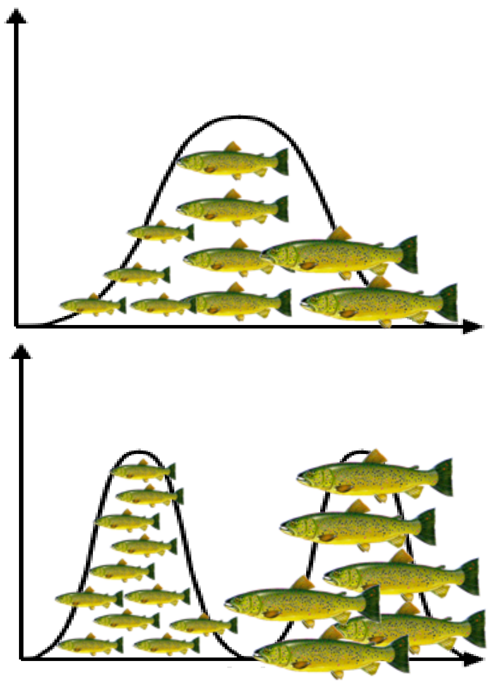
- **Individual selection**
  - Based on **phenotypic values** of the selection candidates
  - Simplest method to operate and rapid response (high h^2)
- **BLUP**
  - Combines information within and between families
  - **Higher accuracy**
- **Sib selection**
  - Based on phenotypic values recorded **on sibs of the selection candidates**
  - For traits that cannot be measured on the candidates (e.g. disease resistance)

Mating designs

- External fertilization → management of matings

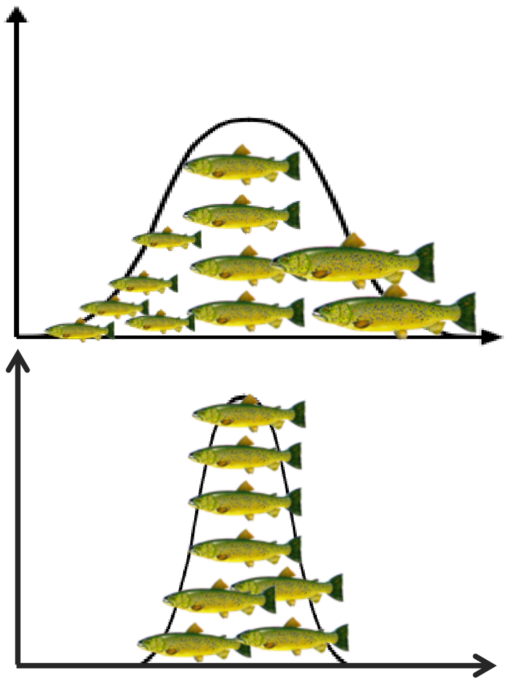
ASSORTATIVE MATING

- Between similar phenotypes



DISASSORTATIVE MATING

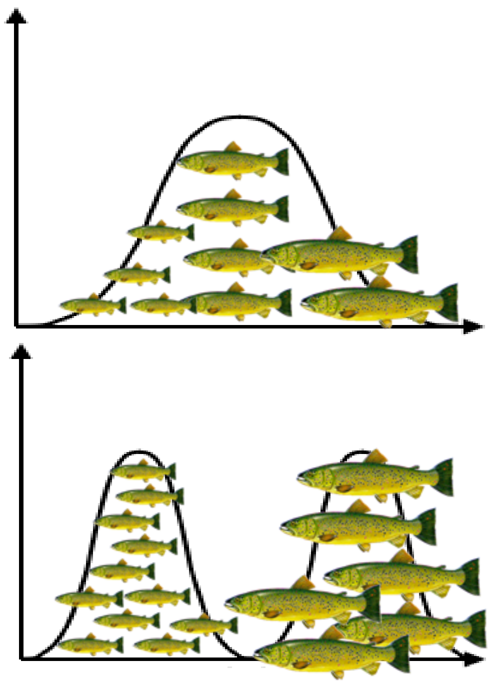
- Between dissimilar phenotypes



Mating designs

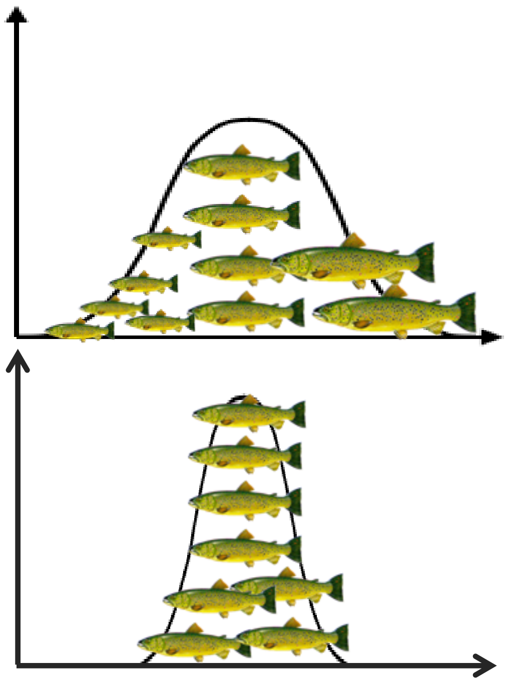
ASSORTATIVE MATING

- Between similar phenotypes
- ↑↑ Genetic variance



DISASSORTATIVE MATING

- Between dissimilar phenotypes
- ↓↓ Genetic variance



Mating designs

Not studied in an aquaculture context where **family sizes are large** and **common environmental effects** (tank) are usually present

Objective

*To explore the effect of the **mating design** on genetic gain under different selection methods (phenotype) in the context of **aquaculture breeding programmes***

-Family sizes are large

- Common environmental effects

Simulation of the population

50 families

50♂
50♀

100♂
100♀

Base population in global linkage equilibrium

10 chrom

1 Morgan

x100 biallelic markers/chro

x100 biallelic QTLs/chro

$p_0 = 0.5$

Mating schemes

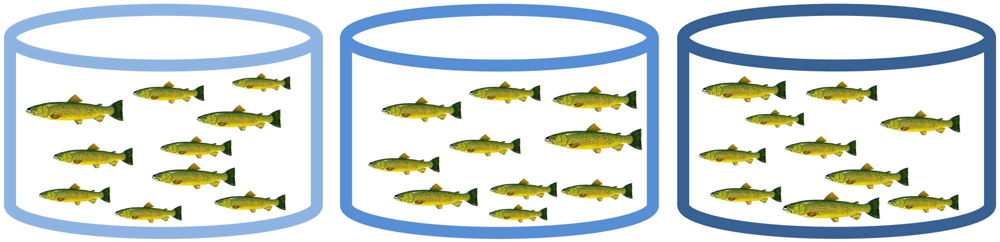
- Random mating (RM)
- Disassortative mating (DM)
- Assortative mating (AM)

$V_P = 1$
$V_A = h^2$

Simulation of the population

Scenarios

- $h^2 = 0.1, 0.4$
- $c^2 = 0.0, 0.4$



Selection methods

- Random
- Individual
- Optimum combined
- Sib → 1/50, 10/50, 25/50

10 generations of selection

100 replicates

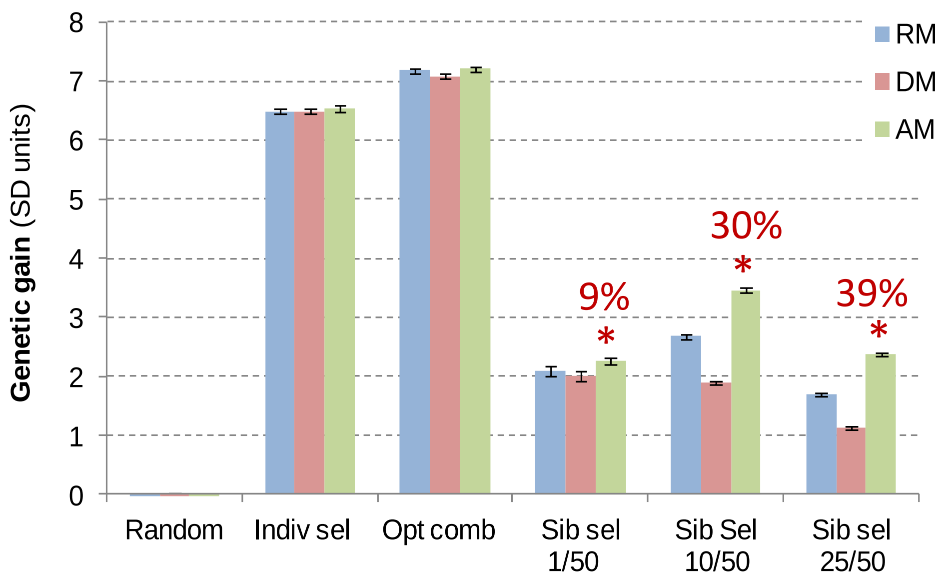
Results

Effect of mating scheme

- **Sib selection** → selection strategy with the highest differences among different mating designs → up to 39% increase in genetic gain with AM

Generation 10

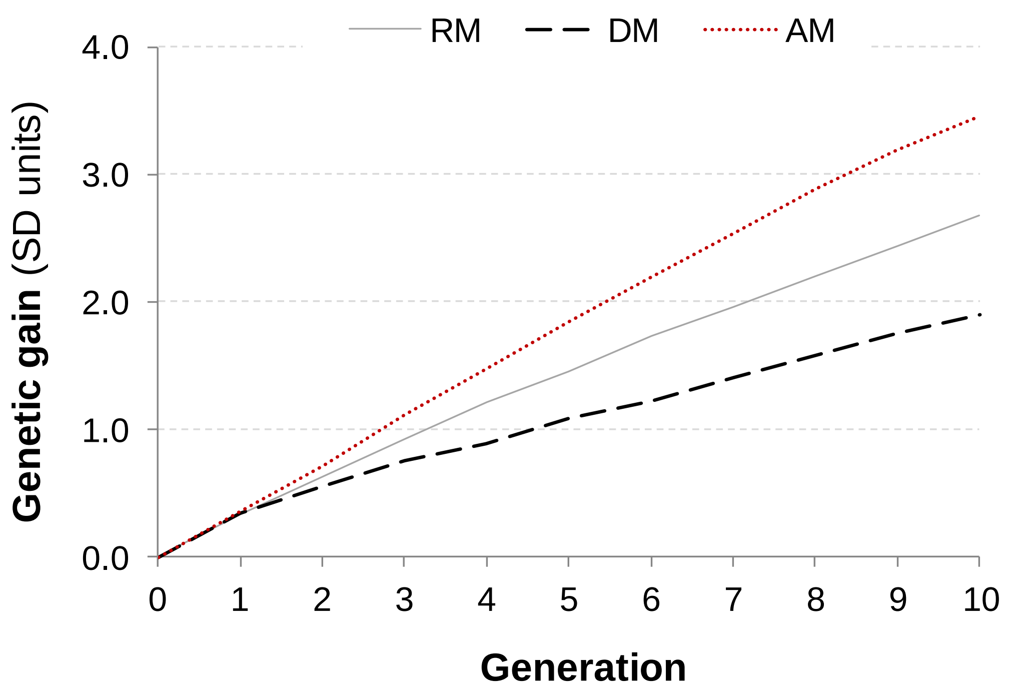
$h^2 = 0.4$ $c^2 = 0.4$



Results

Effect of mating scheme

- Differences among mating schemes increase across generations



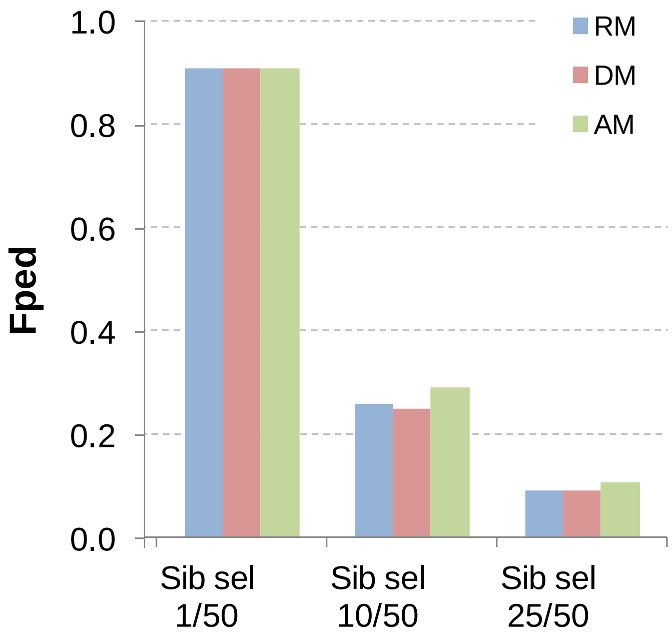
25/50 families

h^2 = 0.4
c^2 = 0.4

Results

Inbreeding

- Similar levels of inbreeding for all mating schemes



$h^2 = 0.4$

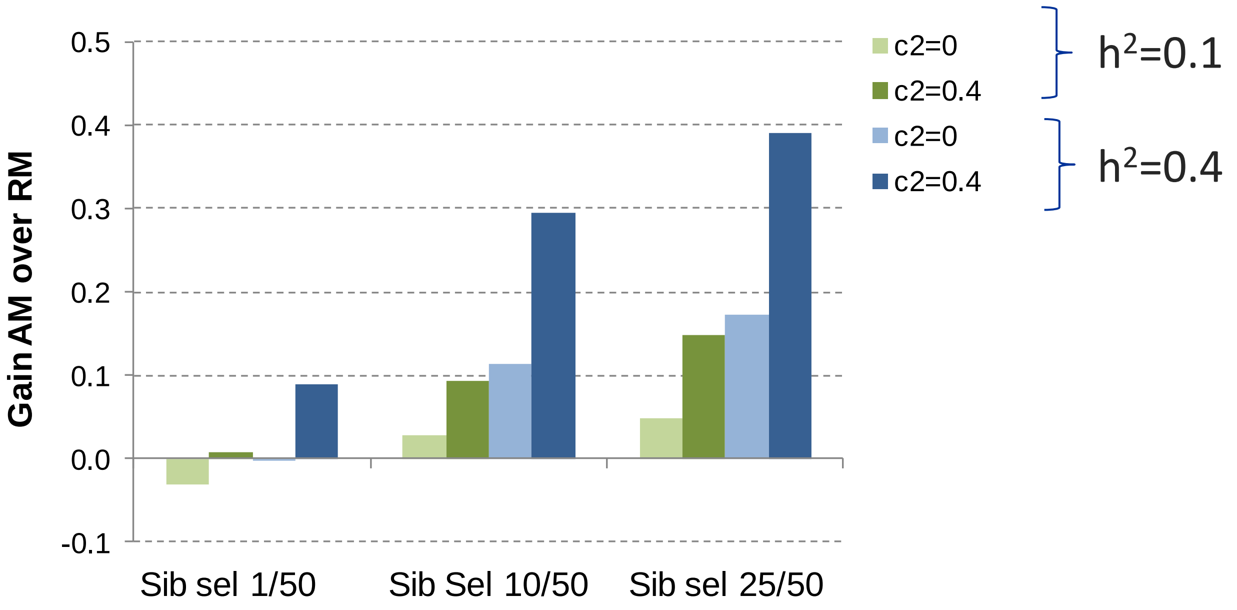
$c^2 = 0.4$

Gen = 10

Results

Effect of heritability & common environmental effect

- Higher effect of assortative mating on genetic gain when h^2 is higher
- Higher effect of assortative mating on genetic gain when c^2 is higher

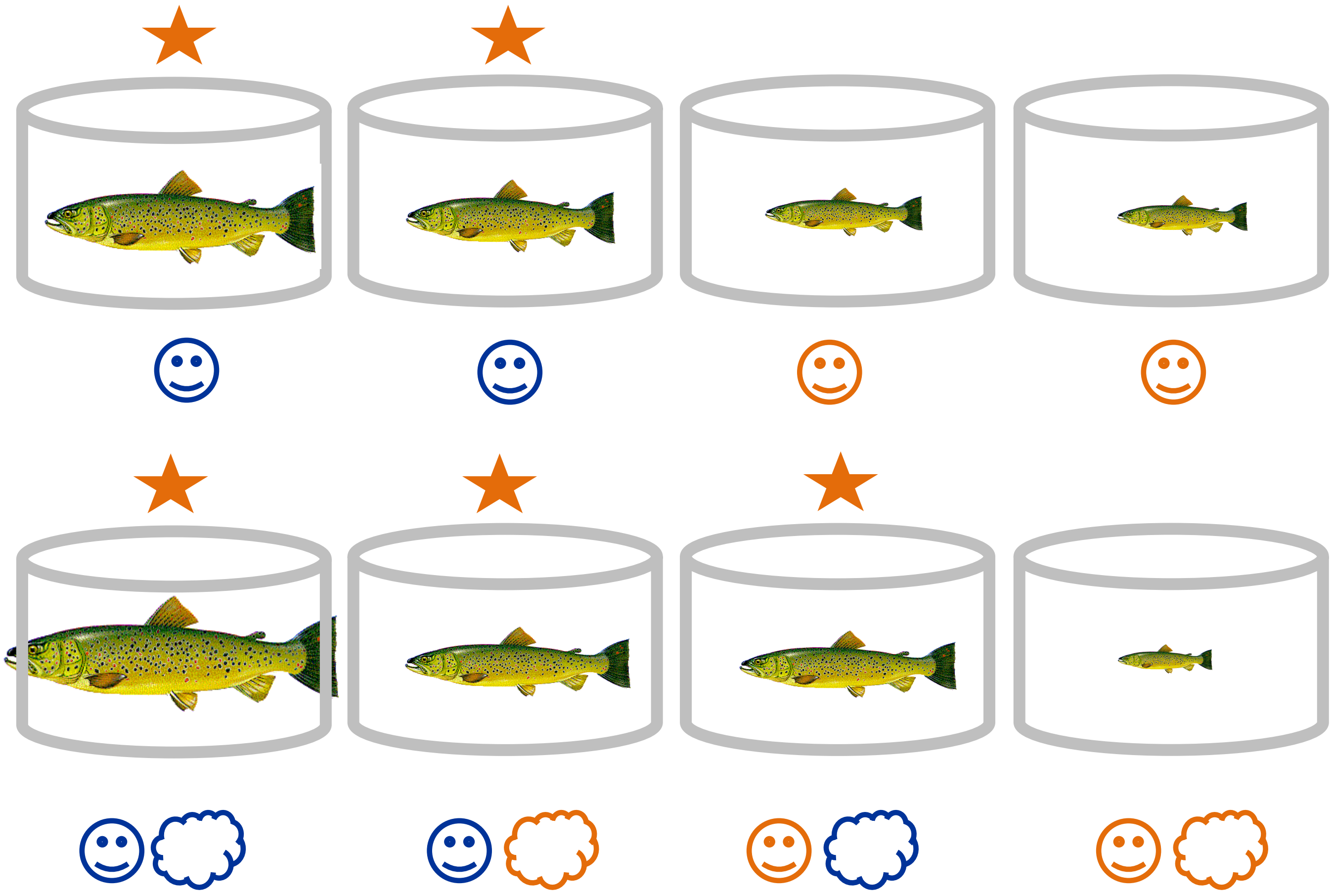


Results

Effect of heritability & common environmental effect

$c^2 = 0$

$c^2 = 0.4$



Conclusions

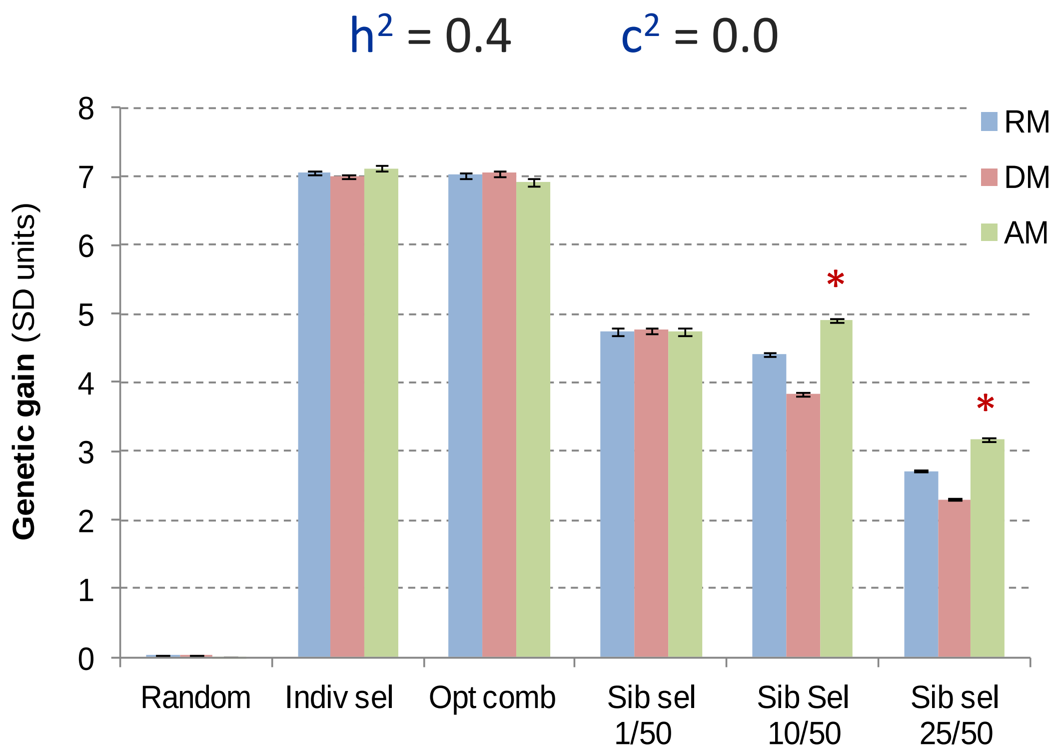
- The mating scheme affects significantly the genetic gain under sib-sel
  - Different scenarios of heritability and common environmental effect
  - Higher effect of AM when h^2 and c^2 are higher
- Assortative mating can produce a 39% increase in genetic gain when compared to RM while maintaining the same levels of inbreeding
- The common environmental effect seems to be an important factor that needs to be considered

An extension to genomics will be presented by Miguel Ángel Toro next Wednesday at the session GENOMIC SELECTION AND MAS

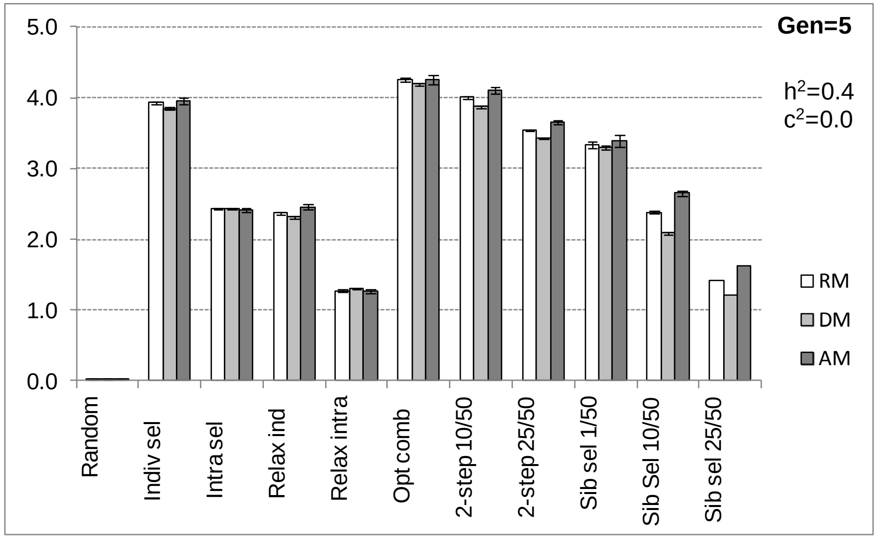
Within-family genomic selection in aquaculture breeding programmes

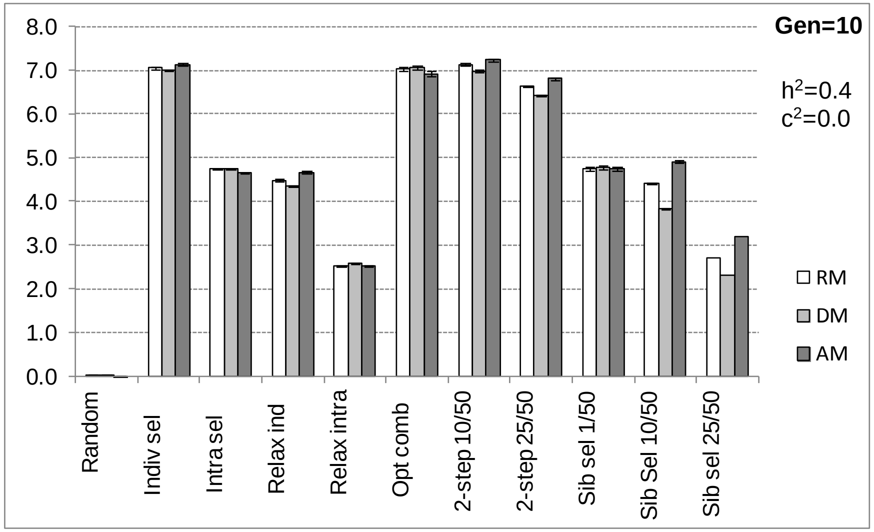
Aknowledgements

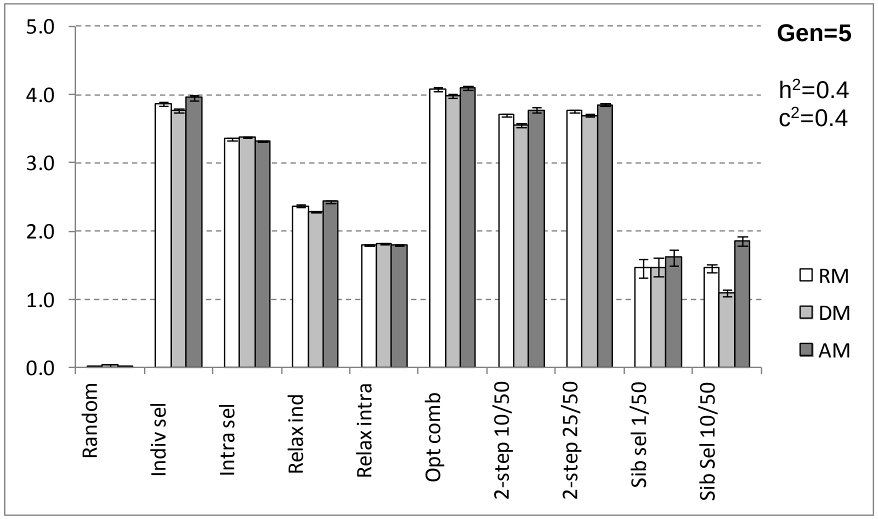
To the audience

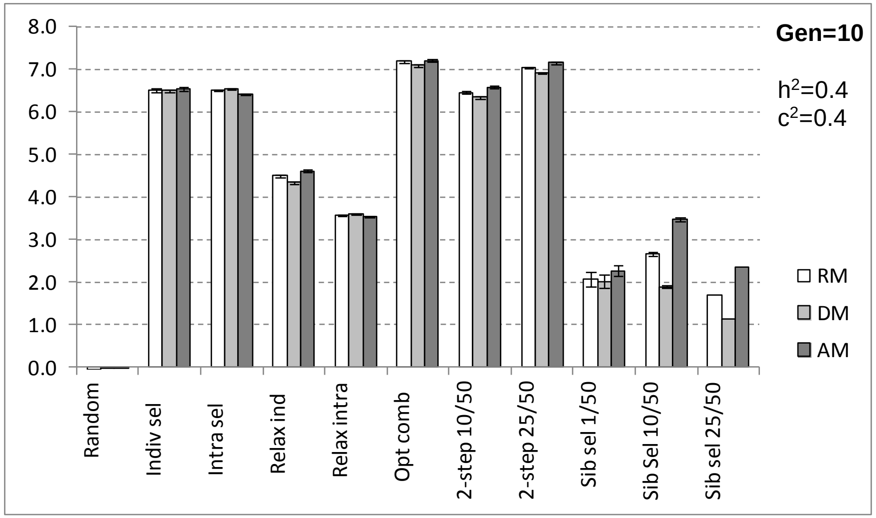

$h^2 = 0.4$ $c^2 = 0.0$
Genetic gain (SD units)
0
1
2
3
4
5
6
7
8
RM
DM
AM
*
*
Random
Indiv sel
Opt comb
Sib sel 1/50
Sib Sel 10/50
Sib sel 25/50

Genetic gain









Assortative mating (AM)

Common environment = 0

Gen	*CumP*	*Var*	Var_P	Var_{P_BTW}	Var_{P_WT}	r_P	Var_{G_BTW}	Var_{G_WT}	r_G	F_{ped}
0	0.0000	-0.0003	0.9919	0.1960	0.8006	0.1954	0.1962	0.1999	0.4899	0.0125
1	0.3452	0.0066	0.9769	0.1794	0.7995	0.1820	0.1795	0.1992	0.4690	0.0207
2	0.6711	0.0100	0.9703	0.1761	0.7969	0.1795	0.1760	0.1963	0.4670	0.0296
3	0.9872	0.0088	0.9659	0.1754	0.7919	0.1801	0.1759	0.1926	0.4723	0.0387
4	1.2970	0.0175	0.9636	0.1767	0.7899	0.1809	0.1776	0.1891	0.4767	0.0479
5	1.6200	0.0256	0.9487	0.1684	0.7866	0.1749	0.1686	0.1864	0.4690	0.0573
6	1.9345	0.0272	0.9465	0.1703	0.7810	0.1777	0.1696	0.1840	0.4740	0.0663
7	2.2521	0.0281	0.9439	0.1695	0.7811	0.1769	0.1700	0.1804	0.4797	0.0754
8	2.5686	0.0366	0.9411	0.1663	0.7785	0.1746	0.1660	0.1776	0.4773	0.0844
9	2.8744	0.0315	0.9300	0.1584	0.7740	0.1683	0.1577	0.1748	0.4675	0.0933
10	3.1755	0.0408	0.9268	0.1535	0.7722	0.1642	0.1537	0.1721	0.4641	0.1017

Assortative mating (AM)

Common environment = 0.4

Gen	*CumP*	*Var*	Var_P	Var_{P_BTW}	Var_{P_WT}	r_P	Var_{G_BTW}	Var_{G_WT}	r_G	F_{ped}
0	0.0000	0.0095	1.0014	0.6183	0.4002	0.5993	0.1962	0.1999	0.4899	0.0125
1	0.1957	0.0118	1.0273	0.6450	0.3990	0.6104	0.2345	0.1985	0.5347	0.0204
2	0.4221	0.0114	1.0242	0.6439	0.3942	0.6156	0.2559	0.1933	0.5628	0.0290
3	0.6657	0.0320	1.0529	0.6719	0.3916	0.6251	0.2593	0.1920	0.5678	0.0377
4	0.8945	0.0304	1.0232	0.6467	0.3891	0.6182	0.2622	0.1889	0.5735	0.0469
5	1.1685	0.0392	1.0290	0.6525	0.3857	0.6232	0.2631	0.1863	0.5765	0.0565
6	1.3898	0.0546	1.0456	0.6700	0.3851	0.6283	0.2512	0.1857	0.5670	0.0664
7	1.6406	0.0652	1.0069	0.6395	0.3822	0.6198	0.2417	0.1828	0.5610	0.0762
8	1.8812	0.0741	1.0132	0.6461	0.3798	0.6220	0.2447	0.1796	0.5667	0.0856
9	2.1287	0.0953	1.0077	0.6411	0.3777	0.6228	0.2503	0.1776	0.5754	0.0951
10	2.3612	0.0936	1.0106	0.6534	0.3750	0.6288	0.2488	0.1742	0.5774	0.1043