Variation in submergence tolerance

Linkage mapping (quantitative)

Fine-mapping

Finding the causative variant

Transgenic test
Coding variants

**Single-locus:**

AA x BB

↓

AB

(F1)

AB x AB

↓

AA

AB

BA

BB

(F2)

1 locus, incomplete dominance

Two loci

Parent A

Two loci

Parent B
Two loci

Parent A: AA/AA x BB/BB
Parent B: AB/AB

(F1)

Locus 1/Locus 2

Two loci, incomplete dominance

Epistasis is often neglected in complex trait studies.
Two loci, incomplete dominance

How many squares of the Punnett square are represented here?

What is the genotype?
A. AA/AA
B. AB/AA
C. BB/AA
D. AA/AB
Phenotype

What is the genotype?
A. AA/AB
B. BB/AB
C. AB/AB
D. AA/BB

Two loci, incomplete dominance

How many F2’s have this genotype?
A. 1/16
B. 2/16
C. 3/16
D. 4/16

Two loci, incomplete dominance

Fig. 3.17

Notation is different, trait is qualitative; math is the same.

2-locus interaction

2-locus interaction

http://www.projects.roslin.ac.uk/chickmap/organism.html

Leghorn
Junglefowl

Parent J

JL/JL x JL/JL

(F2)

16 possibilities

Parent L

JL/JL

16 possibilities
Effect of variation at locus 2 depends on genotype at locus 1: non-additive

Locus 2 is epistatic to locus 1: effects of locus 1 are masked in individuals with JJ or JL,LJ at locus 2
Locus 2 follows a dominance model: JJ and JL,LJ have the same phenotype, LL differs
“The dominant allele of locus 2 does the masking”
How did YJM145 gain the ability to grow at body temperature?
NO progeny as extreme as diploid hybrid

Did the mapping…
Significant linkage to yeast chrom XIV and chrom XVI.

Did the fine-mapping…

Which gene is causative?
Tested in hybrid diploids

Tested in hybrid diploids

Tested in hybrid diploids

Tested in hybrid diploids

Different in sequence

One mutant gene...

One mutant gene...
One mutant gene...

So diploid with this gene from the pathogenic strain grows BETTER at high T.

Two mutant genes...

Again, diploid with this gene from the pathogenic strain grows BETTER at high T.

Three mutant genes...

Diploid with this gene from the pathogenic strain grows WORSE at high T!
Three mutant genes

Alleles from the same strain at different genes/loci can have different effects.

No common coding alleles across strains

And no expression differences of >3-fold...

Three mutant genes in same “locus”

So why did 0/900 haploid progeny have a phenotype as extreme as the diploid hybrid?
NO progeny as extreme as diploid hybrid

Linked mutations of opposite effect

Linked mutations of opposite effect

Linked mutations of opposite effect

“Multiple linked loci”