

EVOLUNCH - Clai et al - Bristle # Variation in *D. melanogaster*  
presented by Kevin White

Variation

12:14 D. Ardell

① Determining loci

- QTL loci - need lots of markers; syngamy,
- eg. many crosses w/ relatives

② Candidate gene approach

- guess based on other data which genes might be involved

Bristles

How might they affect fitness?

12:20

- mean # of bristles ... certain ones have little variation in natural populations but seems to be a lot of genetic variation because selection can drive incr. or decr.

- if relax selection a good deal of ~~more~~ the new bristle # is maintained

- competition among strains suggests normal bristle # of is better



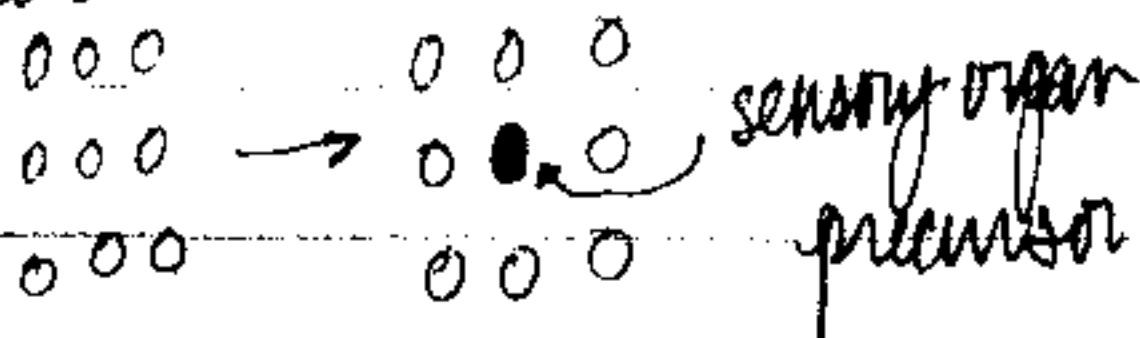
④ so... how really test this?

- LS
- neural retardation
- cancer
- mutation
- develop. slowdown

③ bristle development

- lots known
- achaete scute HLH proteins  $\rightarrow$  regulates scabrous expression

proventral cluster



- So... w/ QTL mapping frequently get 1-5 loci w/  $>15\%$

- Achaete Scute  $\approx 5\%$  (by candidate gene technique)

- Scabrous... on 2nd chromosome

- 47 2nd chromosomes

- mean variance

$$V_p = V_E + V_G + V_{G \times E}$$

$$\text{broad heritability} = h^2 = \frac{V_G}{V_P}$$

$$\text{narrow heritability} = \frac{V_A}{V_P}$$

QT



Steps

① QUANTIFY VARIANCE

② COMPARE w/ 47 LINES (w/ DIFF CHROM 2)

- RFLP } 27 total polymorphisms  
- SSCP }

- 1) show significant association w/ bristle #

- try and take into account linkage disequilibrium

47 lines

