

# BIOL2007 – QUANTITATIVE GENETICS:

## ADVANCED TOPIC: PHENOTYPIC PLASTICITY

### Summary

Quantitative traits are expressed differently in different environments. If genotypes differ in level or direction of plasticity expressed, genotype-by-environment interaction exists.

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### Quantitative traits and multiple environments

**Phenotypic plasticity (PP)** = when same genotype produces different phenotypes in different environments. How to analyse this?

**Reaction norms** are a useful way to visualise a complex situation. These depict the phenotypes produced by different genotypes within a population in 2 or more environments. See Figure 5.1 (handout). This group of hypothetical reaction norms aid understanding of phenotypic plasticity and **genotype-by-environment interaction** (“G by E”).

Figure 5.1 shows the key elements of reaction norms for a case of two different environments: **X-axis** = environments, **Y-axis** = mean phenotypic values for each genotype. Each solid line connects the genotypic values in one environment to those in the other environment.

The key to the experimental approach is that these genotypic values are typically obtained for a “**half-sib breeding design**”. In a half-sib breeding design, the data that is analysed comes from measurements on members of pairs of families. The pairs have one parent (father) in common. So the progeny have a known average degree of relatedness and this can be exploited to study **PP**.

**Family members are reared in each environment.** So slope of each line for each family is an estimate of the amount of plasticity for that family.

If the pattern of data for a population resembles that seen in **Figure 5.1A**: where the families are displayed as a series of parallel lines”, then the population has **no plasticity**. The phenotypic mean of each family is same in each environment. There is **variance between families** – a spread of genetic values within environments – the amount of this variance is similar across the 2 environments.

If a population resembles **Figure 5.1B** with steep gradients of lines joining means in the pair of environments, then it indicates **high amount of plasticity**. The phenotypic means are very different between environments.

Still see genetic variance (**between families**) within each environment.

\*Also - all families respond to 2 environments in exactly same way, decreasing by same amount (**slopes are parallel**) – so there is **no genetic variation in plasticity**

If a population resembles **Figure 5.1C** – Now there are large differences among families in plasticity (different slopes of reaction norms). Note that lines cross (no longer parallel), so the phenotypic rank of the families is different in the 2

environments. The families respond differently to the environments. = genotype-by-environment interaction (G x E).

**Fig. 5.1D** – here the reaction norms rarely cross. High variance in env2 and low in env1.

Many individuals = plastic (sloped reaction norms) but approx equal number of families increase and decrease their phenotype – hence means across all families don't differ between environments

Appropriate to analyse reaction norms via 2-way ANOVA where the 2 main factors are genotype (sire/family) and environment. Individuals at each level of each factor are represented at each level of the other factor. Thus there are members of each half-sib family in each of the 2 environments.

To summarise the various outcomes:

**Significant sire/family effect (Genotype, G) observed** – then have evidence for overall additive genetic variance for the trait.

**Significant environment (E) effect observed** = evidence for overall plasticity

**Significant G-by-E interaction observed** = evidence for additive variance for plasticity.

**Lots of evidence that significant G\*E interactions are common.**

**Illustrative example:** case study of Asian stalk-eyed fly, *Cyrtodiopsis dalmanni*. David et al. 'Condition-dependent signalling of genetic variation in stalk-eyed flies'. Nature 406 186-188 (2000).

A G\*E approach was useful in assessing whether male eyespan signals genetic benefits to females. The underlying logic is that male ornamental traits can be viewed as costly handicaps. Can only high quality males afford to bear large ornaments? Are large ornaments costlier for low quality males?

One way to resolve these issues is to examine the condition dependence of male sexual traits in comparison with other non-sexual traits. In benign environments, it is predicted that the cost differential of traits will be low with low variance between individuals. In stressful environments, trait cost differentials will be elevated with a high variance between individuals. Are these patterns exaggerated for sexual traits?

What was already known? Data on phenotypes indicated that male eyespan was strongly informative about condition. Compared to non-sexual traits, male ES was especially sensitive to deteriorating environmental conditions. This was true of both absolute male ES and relative (to body size) male ES. Relative male ES signals male phenotypic quality to females over and above any information conveyed by body size.

What is the **genetic** basis of this condition=dependence?

Reared full- and half-sibling families in 3 environments of decreasing value (corn, spinach, cotton wool). Measured progeny traits (male ES, female ES, male and female wing length, male and female body size).

#### *Absolute trait values*

Significant differences between effects of environments for all traits in both sexes (Corn > Spinach >>> Cotton wool).

Also, genetic variation in all traits in all environments.

Significant G\*E for absolute male ES. Variance between genotypes increased as environmental quality decreased but genotypic ranks of families maintained across environments. That is, a genotype which performed well in one environment tended to do well in other environments.

#### *Relative trait values*

Relative male ES shows similar pattern to absolute pattern. But removing the effect of body size from the non-sexual traits greatly reduced their environmental condition-dependence.

G\*E interaction for relative male ES similar to absolute story: genotype ranks maintained across environments, genetic variance increased under stress. For non-sexual traits, G\*E interactions seen for their absolute values were eliminated or greatly reduced.

#### *Conclude*

Genetic basis of pattern of heightened sensitivity of sexual ornaments to environmental conditions strongly implicates “good genes” as target and potential benefit of female mate choice.