The case of quantitative genetics and underlying heterogeneity

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- 1. In-principle question
- 2. Specific case
- 3. Some things I have done re: #2

1. In-principle question

What to do if we think that researchers have overlooked a significant issue for 100 years?

1. In-principle question

What to do if we think that researchers have overlooked a significant issue for 10 or 5 years?

U.S. philosophy of biology-last 30 years

Emphasis on conceptual systemization of biologists' work

Conceptual structure of Chapters 1-4 of Darwin's *On the Origin of Species*

```
IF
    [#1 & 2] Variation among organisms in characters
    & Inheritance (reproducibility) of characters
    [# 3] Hyperfecundity
THEN
    not all can survive
=> struggle for existence
=> differential representation of variant characters in lineages
    of organisms over time
= evolution (or "modification by descent")
```

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=> struggle for existence
=> differential representation of variant characters in lineages
Q: Which survive?
A: most fit to their environment
IF [#4] Survival (& reproduction) of the fitter (=N.S.)
THEN evolution will result in (local) improvement of
       adaptation to conditions of existence
```

Audiences

for Conceptual Systemization?

Students:

Economical account (for didactic effect)

Other philosophers:

"My systematization is better than yours (b/c ...)"

Audiences for Conceptual Systemization?

Researchers:

- "We make systematic and clear what you had not." [Or more systematic and clearer.]
- "We endorse researcher A over researcher B."
- "We can extend researcher A's thinking."
- Systemization in philosophy of biology => philosophers want to show researchers some things they have overlooked

Aside:

Science = rational interpretation + empirical discrimination

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Q: What is needed to demonstrate that change and the resulting characters were produced by a process of natural selection?

```
"We" =
scientists
as well as
  philosophers, sociologists & historians
  of science
```

Audience participation:

Your response?

Example: Submit your ideas to science journals

Think -> pair -> share

Some answers:

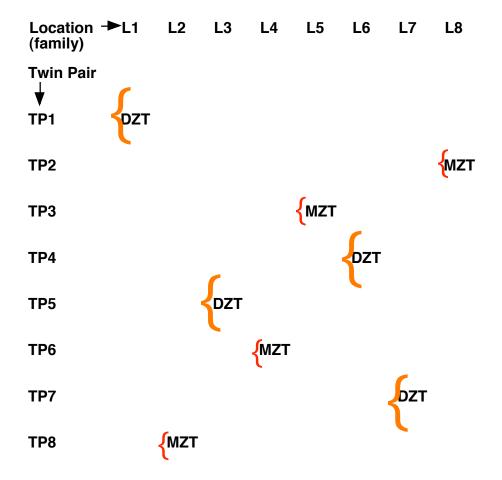
- 1. Stay quiet
- 2. Submit ideas to science journals
- 3. Submit ideas to philosophy of science journals
- 4. Tease out hist., social., pol., cultural implications
- 5. Tease out the political implications

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Q: Case studies or systematic treatment of range of ways (direct -> backdoor) to influence scientific debates?

2. Specific Case: Quantitative Genetics and Underlying Heterogeneity



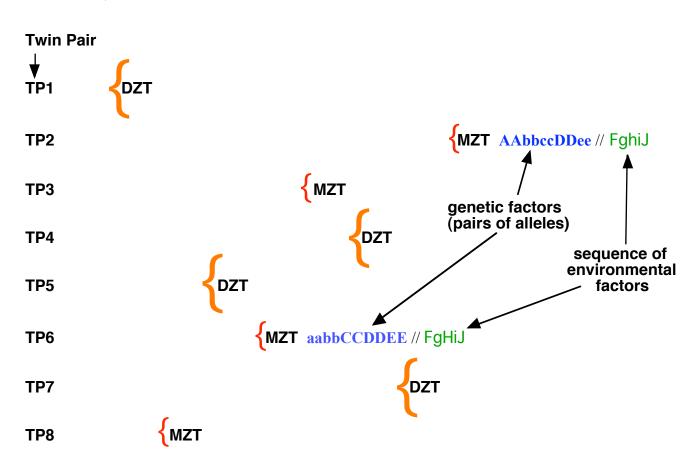
TRAIT is height

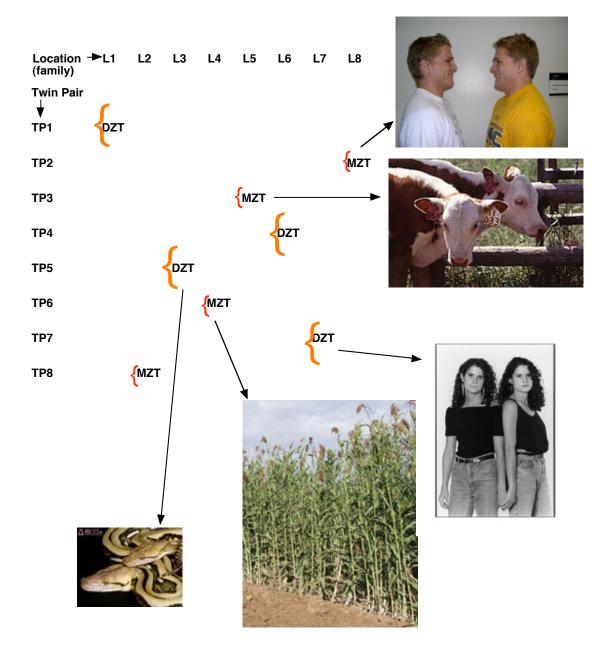
DZT less similar on average than MZT

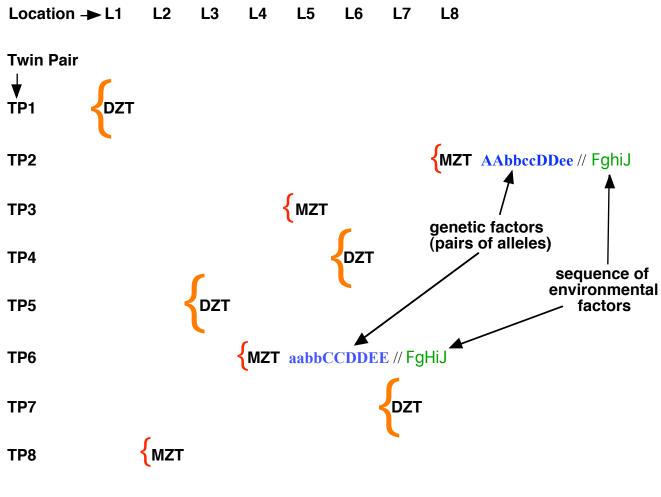
& MZT share all genes, while DZT do not

=> genetic similarity is associated with similarity in trait (substantial heritability of height)

Location → L1 L2 L3 L4 L5 L6 L7 L8







-> Qs: Implications?
Why overlooked?

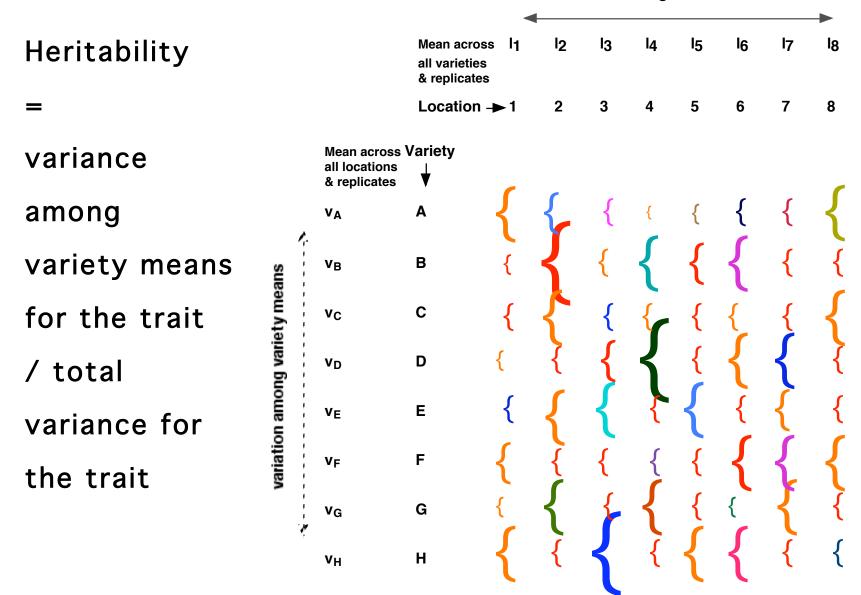
Why overlooked?

Terminology

genetic ₁	quantitative	trait	variance of trait,
	genetics		partitioned (AnOVa)
genetic ₂	relatedness	variable	fraction of variable
		part of	part of genome
		genome	shared
genetic ₃	genetics	site(s) on	heterozygosity at
		genome	site(s)

variation among location means lз Mean across 11 12 14 15 16 17 18 all varieties & replicates Location → 1 2 3 5 6 8 4 7 **Mean across Variety** all locations & replicates Α \mathbf{v}_{A} В v_B variation among variety means C ٧c D v_D Ε ٧E F ۷F G v_{G} Н \mathbf{v}_{H}

variation among location means



Why overlooked?

Terminology

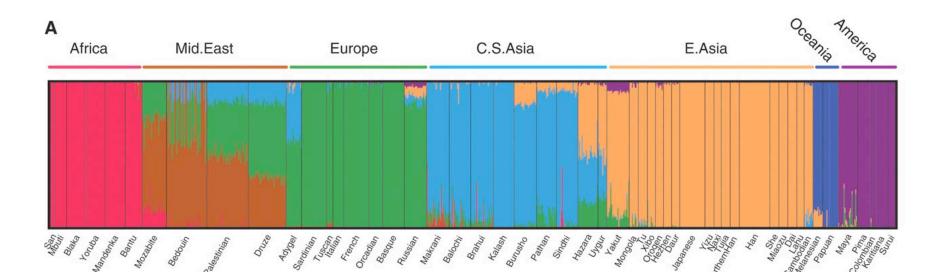
"contribution of genetic differences to observed differences among individuals"

(Plomin et al. 1997, 83)

"fraction of the variance of a phenotypic trait in a given population caused by (or attributable to) genetic differences"

(Layzer 1974, 1259).

Genetic gradient: Not shown by QG, but plausible



Li, J. et al. (2008) Science 319: 1100-1104

Implications?

Undertake research w/o reference to trait's heritability
 (heterogeneity, not polygenic, as explanation of GWA results)

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- Use high heritability => trait is potentially worthwhile
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- Restrict range of varieties or locations

Why overlooked? —Historical Origins

Mendelian model at base of classical quantitative genetics

- single locus + dominance, duplicated over many loci
- + noise + variance across locations of the average value of the trait in each location
- = "polygenic"

Gene-free model

Must be possible

Instead of assumption

All other things being equal, similarity in traits for relatives is proportional to the fraction shared by the relatives of all the genes that vary in the population

Resemblance among relatives -> empirically determined parameter

Gene-free model

1. Simulations => Assumption is not reliable

- 2. VxL interaction variance subsumed in augmented "Variety" variance
- => Human heritability estimates unreliable—usually overestimates
- => Acknowledge alternative assumptions & implications

3. Some things I have done re: specific case

1. Stay quiet	Almost quiet	
3. Submit ideas to philosophy of	Most effort here.	
science journals	No errors identified yet.	
	NSF SGER.	
2. Submit ideas to science journals	Progressively stripped back.	
	NSF-funded visits with researchers.	
	Unpublished mss.	
	Write book & move on.	
4. Tease out the historical,	Session at joint meetings of STS societies, Vancouver	
sociological, political, cultural	2006.	
implications	Visiting fellowship at KLI near Vienna 2008 & 2010.	
	Planned blog of manuscripts and reviews.	
	New book in the works.	
5. Tease out the political	Genetic Studies Working Group.	
implications	Long interview with reporter for Science.	

1. In-principle question

Q: Case studies or systematic treatment of influencing research re-direction

2. Specific case

Terminology. Implications. Origins & alternative. Implications.

3. Some things I have done re: #2

Range from direct -> backdoor/indirect ways to influence scientific debate

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Latest installment: Come to IU -> discussion??