

Genetic variance in
temperature tolerance
and potential to adapt
to ocean warming in
Heliocidaris
erythrogramma armigera



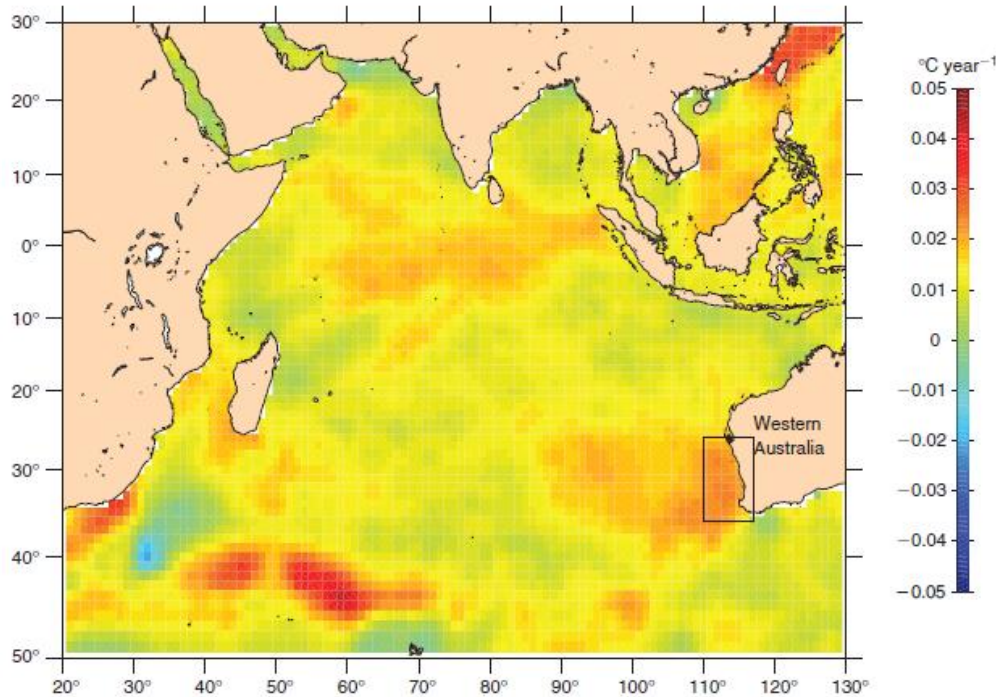
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Project Outline

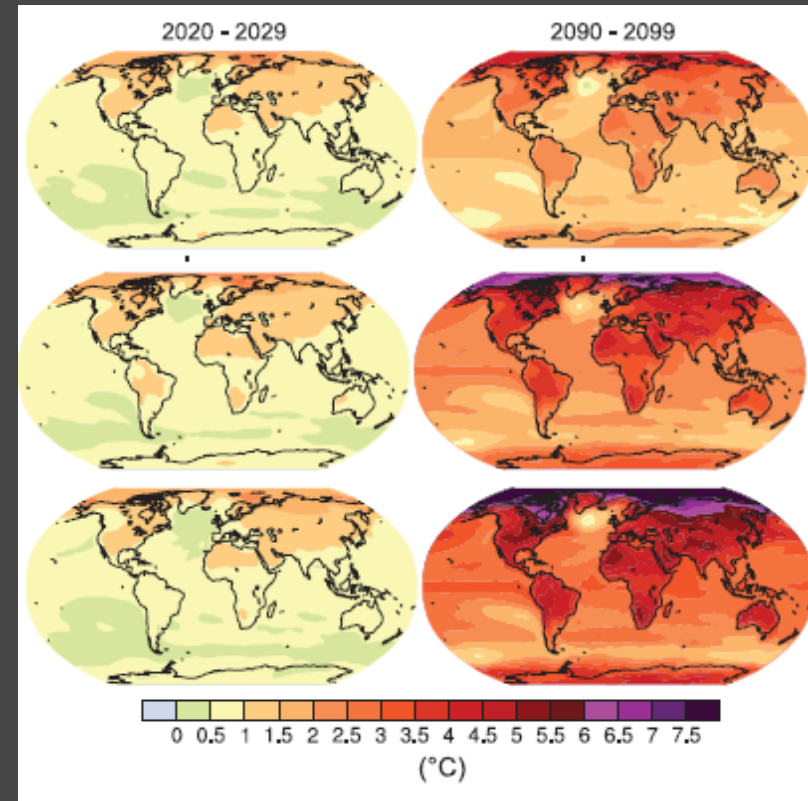
- Climate change: how will biodiversity respond, and how do we manage it?
- Genetic adaptation is required for long-term responses
- Is there potential for *Heliocidaris erythrogramma armigera* to adapt genetically to ocean warming?

Ocean Warming

Rate of warming from 1951 to 2004.



Projected temperature changes in the early and late 21st century for three emissions scenarios.



Responses to Climate Change

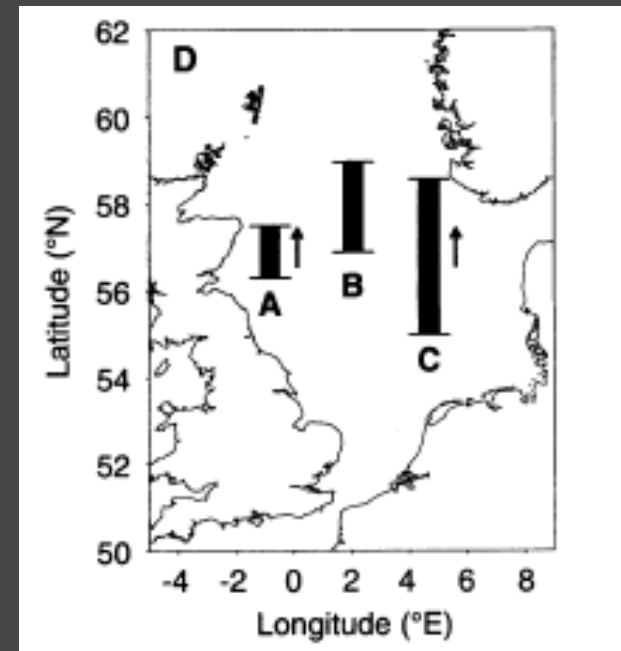


- Range shifts
- Plasticity
- Genetic adaptation

Responses to Climate Change

- Range shifts
 - ▣ Problems: Barriers; reduction in range size; mismatch with other environmental variables
- Plasticity
- Genetic adaptation

Latitudinal shifts in distribution of three fish species in the English Channel with climatic warming.



Responses to Climate Change

- Range shifts

- Plasticity

- ▣ Problems: limited, short-term responses; reaction norms may not remain adaptive

- Genetic adaptation

Phenotypic plasticity: genotypes produce different phenotypes in different environments.



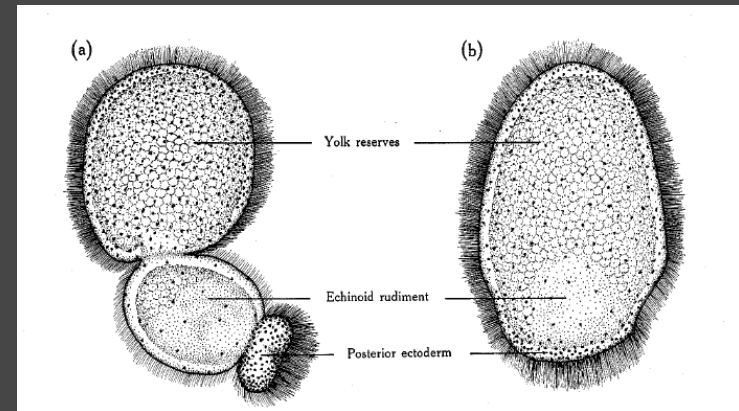
Responses to Climate Change

- Range shifts
- Plasticity
- Genetic adaptation
 - ▣ Evolution needed for long term responses
 - ▣ Genetic variation needed for evolution
 - ▣ Is there standing genetic variation for adaptive traits in populations?

Study Species

- Two subspecies: *H. e. armigera* and *H. e. erythrogramma*
- Broadcast spawners with planktonic larval stage
- *H. e. armigera* are autumn breeders, spawning March-May

Larvae of *H. erythrogramma* after hatching; (a) constricted; (b) unconstricted.



Williams and Anderson (1975) *Australian Journal of Zoology*, 23: 371-403.

Evans *et al.* (2007) *Evolution*, 61: 2832-2838.

Byrne *et al.* (2009) *Proceedings of the Royal Society B*, 267: 1883-1888.

Project Aims

- Determine if there are significant heritable components to temperature tolerance in *Heliocidaris erythrogramma armigera*
- Project will use quantitative sibling analyses to partition environmental and genetic sources of variance in larval survival to hatching and temperature tolerance



Phenotypic Variance

$$V_P = V_G + V_E$$

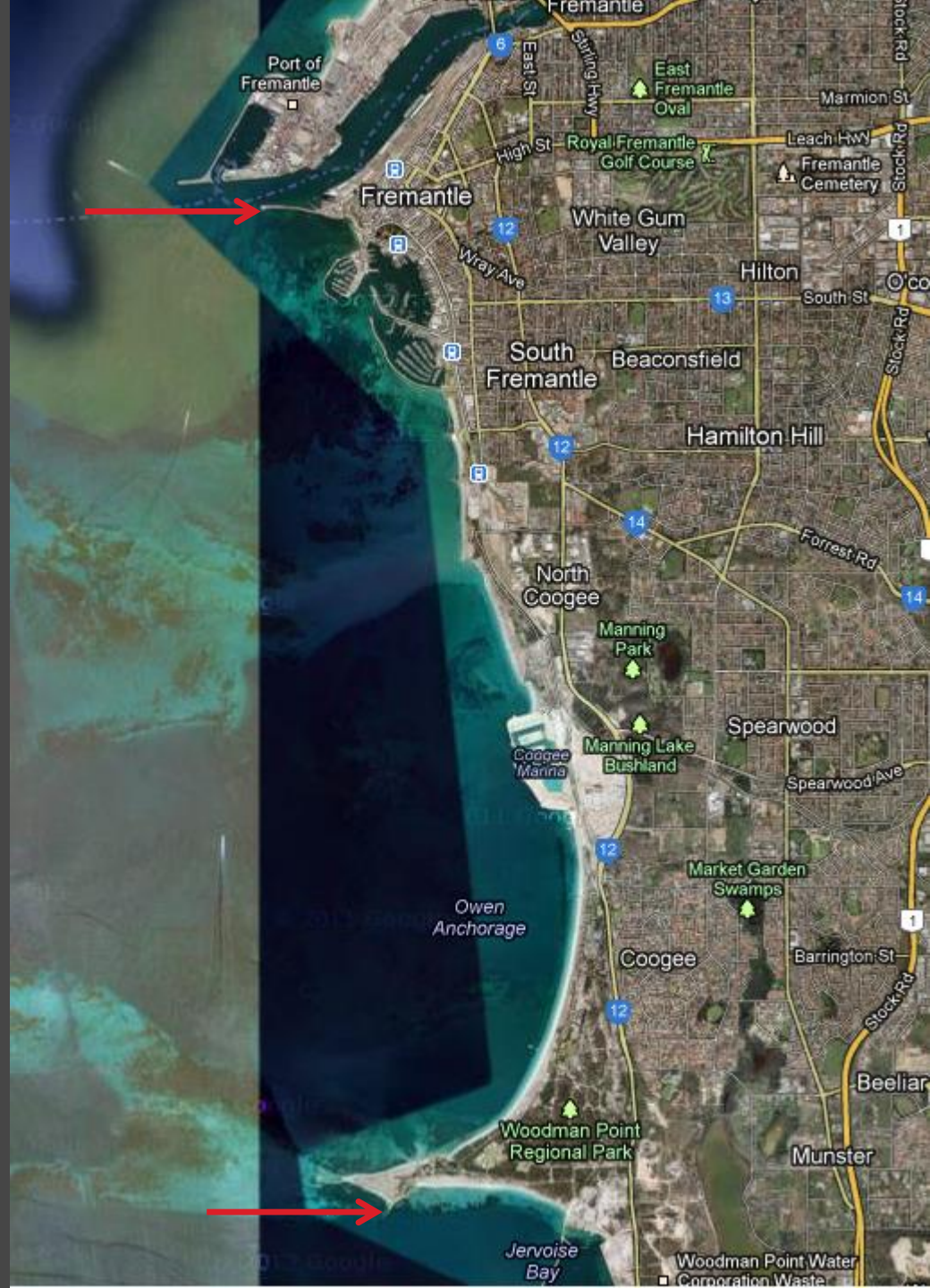
$$V_P = V_A + V_D + V_I + V_E$$

- Covariance among half-sibs: estimates V_A
- Covariance among full-sibs: includes $V_D + V_I$

Study Populations

South Mole,
Fremantle

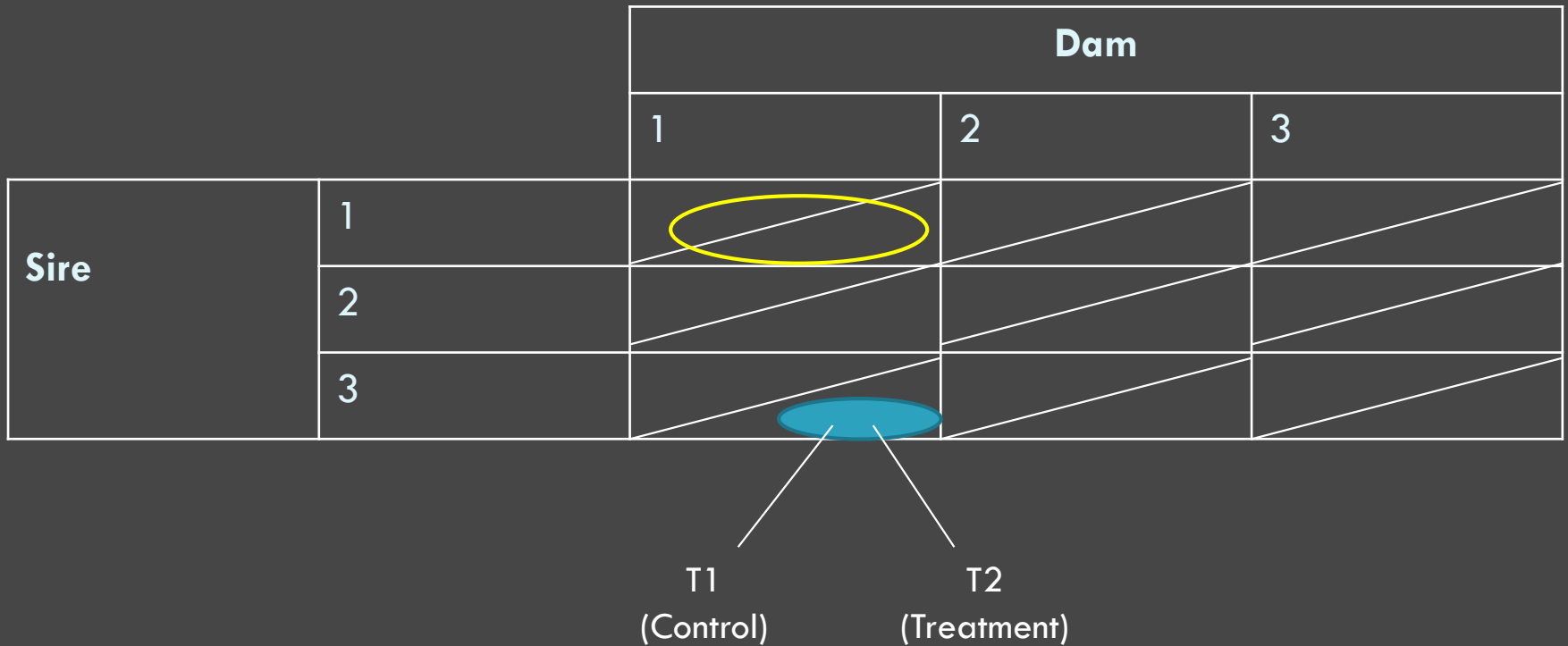
Woodman Point,
Cockburn



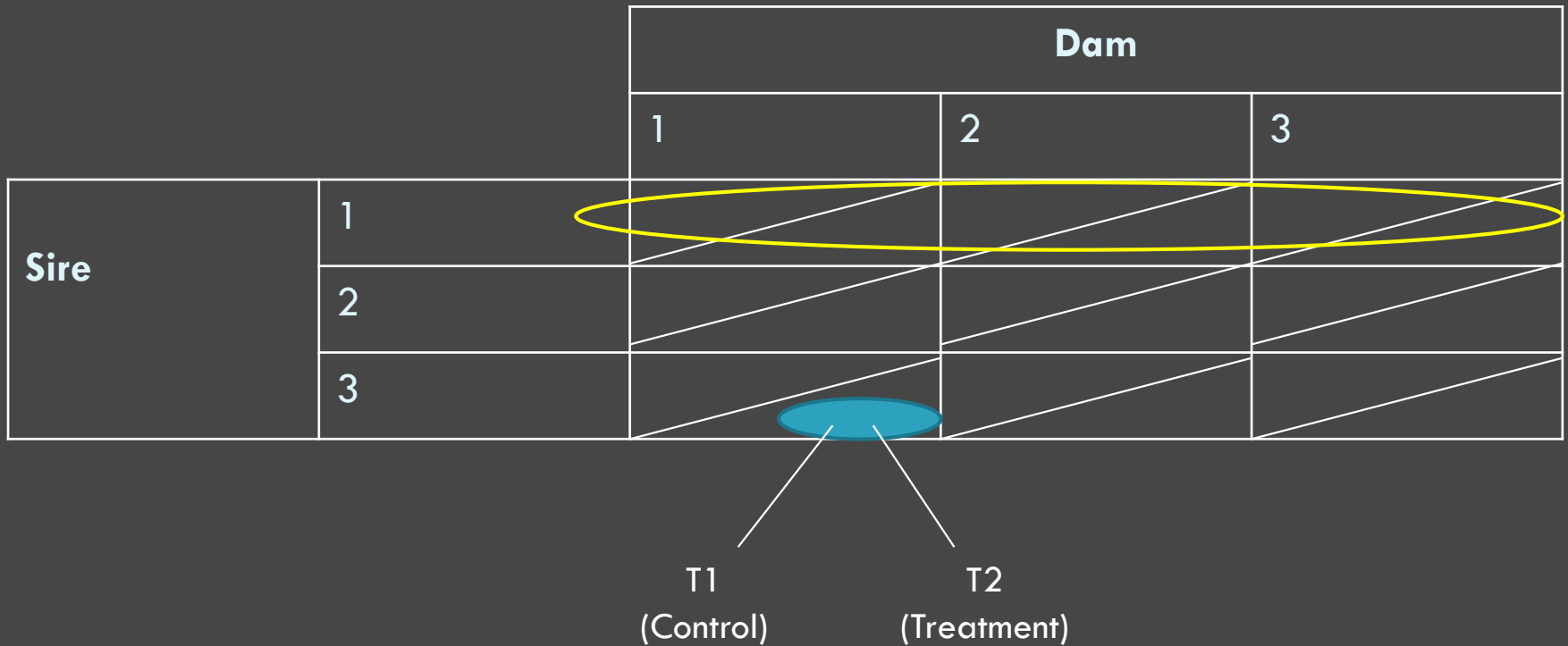
Methods

- Males (sires) and females (dams) crossed in 3×3 blocks
- Offspring reared at control (22°C) and treatment (25°C) temperatures
- Survival to hatching assayed, and variance partitioned into causal components

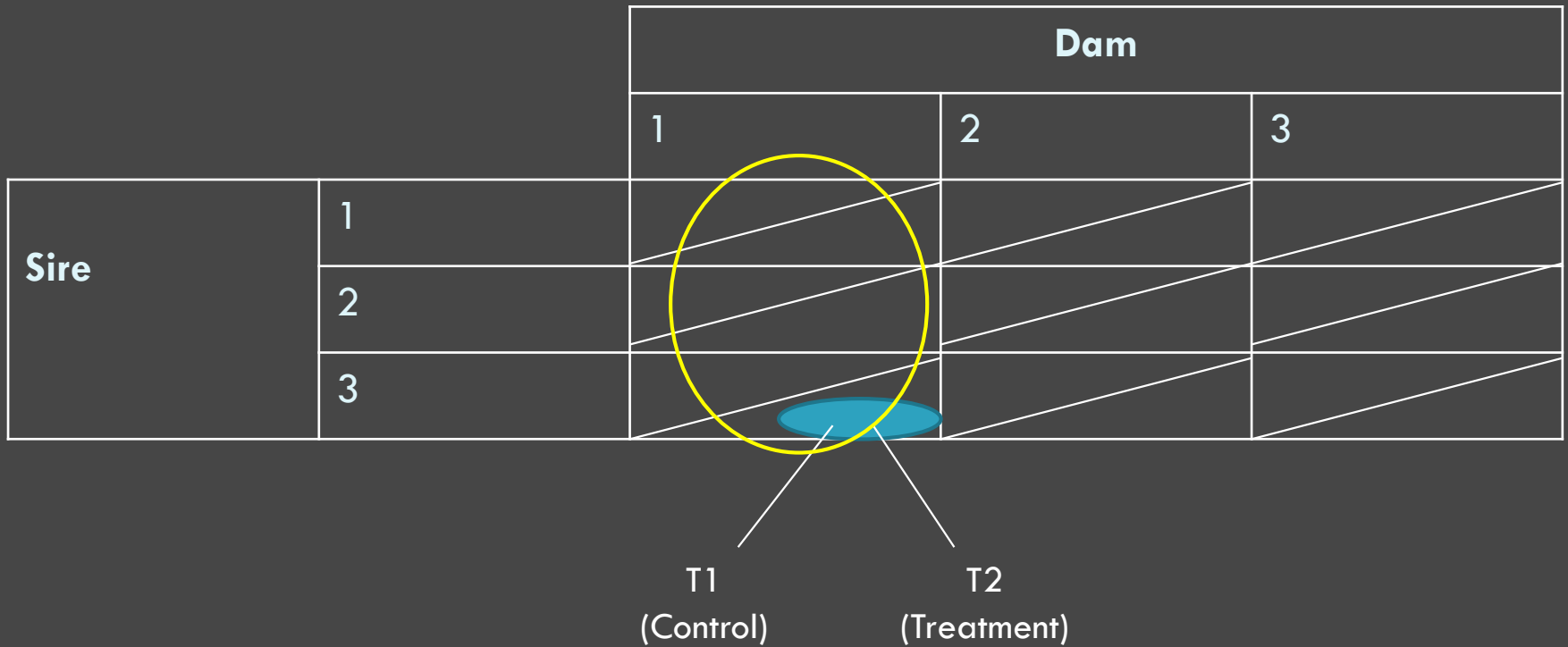
Experimental Design



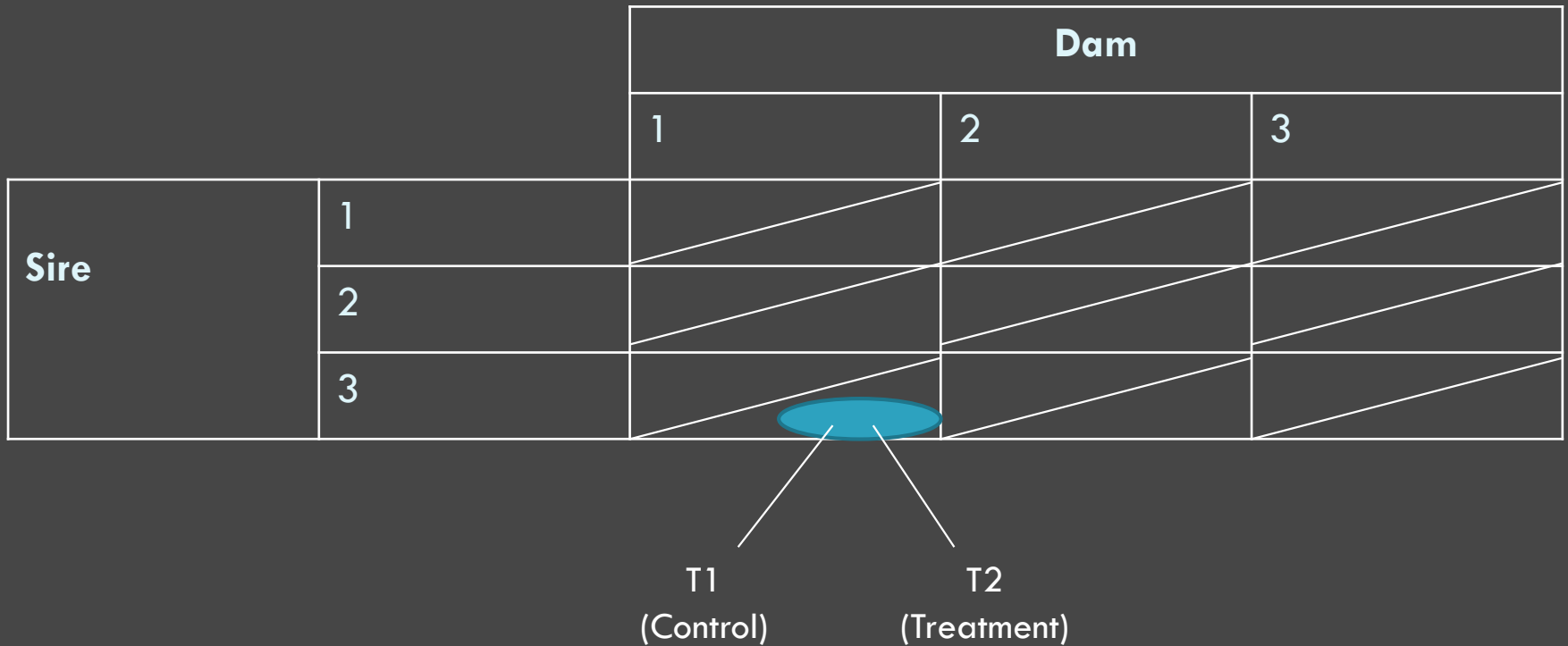
Experimental Design



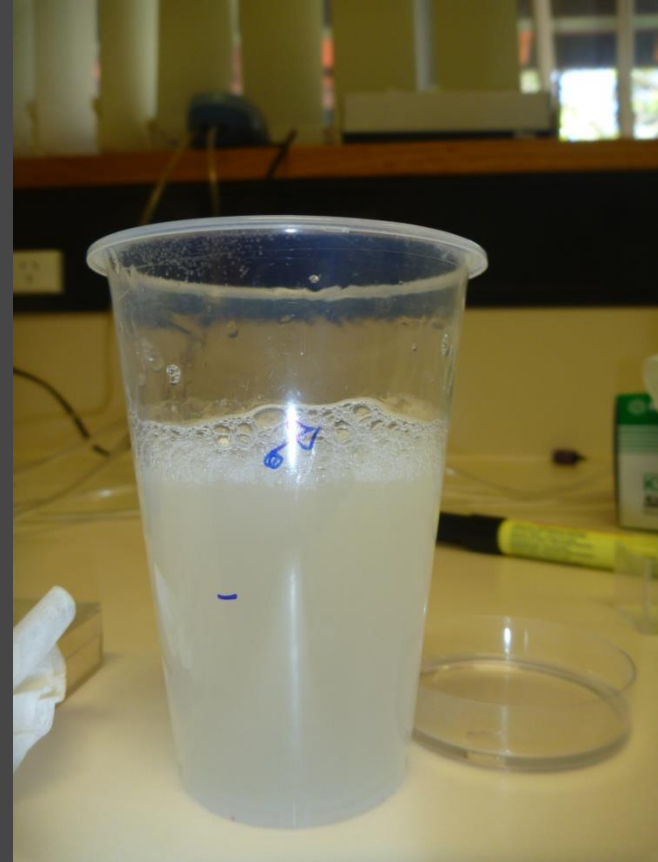
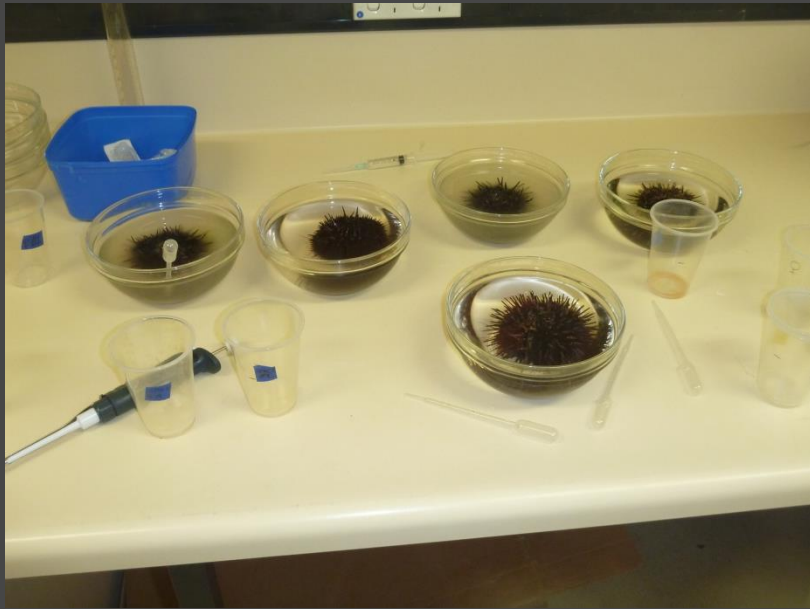
Experimental Design



Experimental Design



Fertilisations



Temperature Treatments



Analysis

□ Mixed effects model:

- Sire (Random)
- Dam (Random)
- Temperature (Fixed)
- S×D (Random)
- S×Temperature (Random)
- D×Temperature (Random)
- S×D×Temperature (Random)
- Block (Random)



Survival to hatching

Summary

- Genetic adaptation is important for long-term responses of populations to climate change
- This project will assess standing genetic variation for temperature tolerance in *H. erythrogramma armigera*
- A quantitative sibling analysis will be used to partition genetic and environmental sources of variance

Acknowledgements

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Thank you for listening!