

# Population genetic signatures of a recent marine range extension

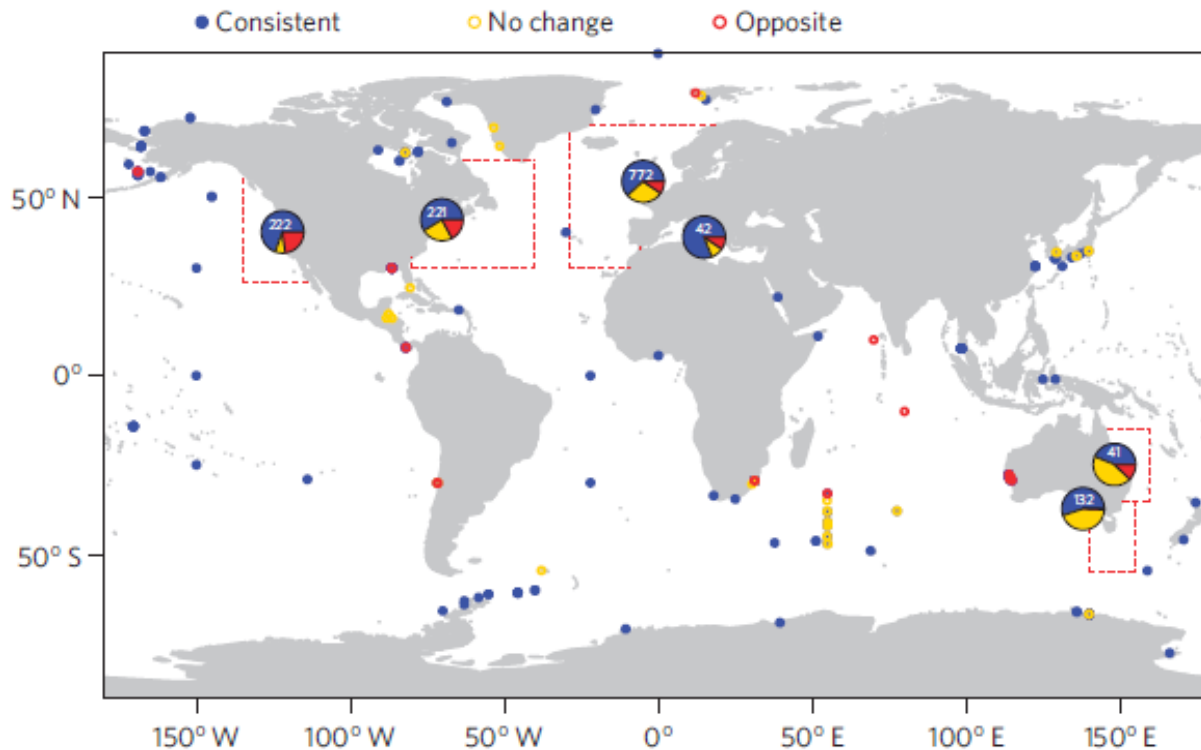
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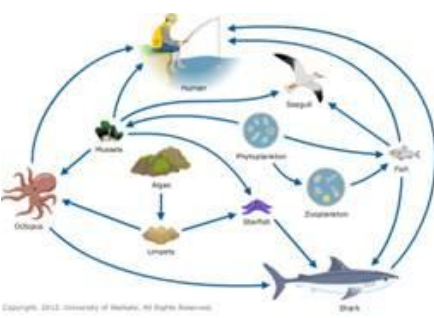
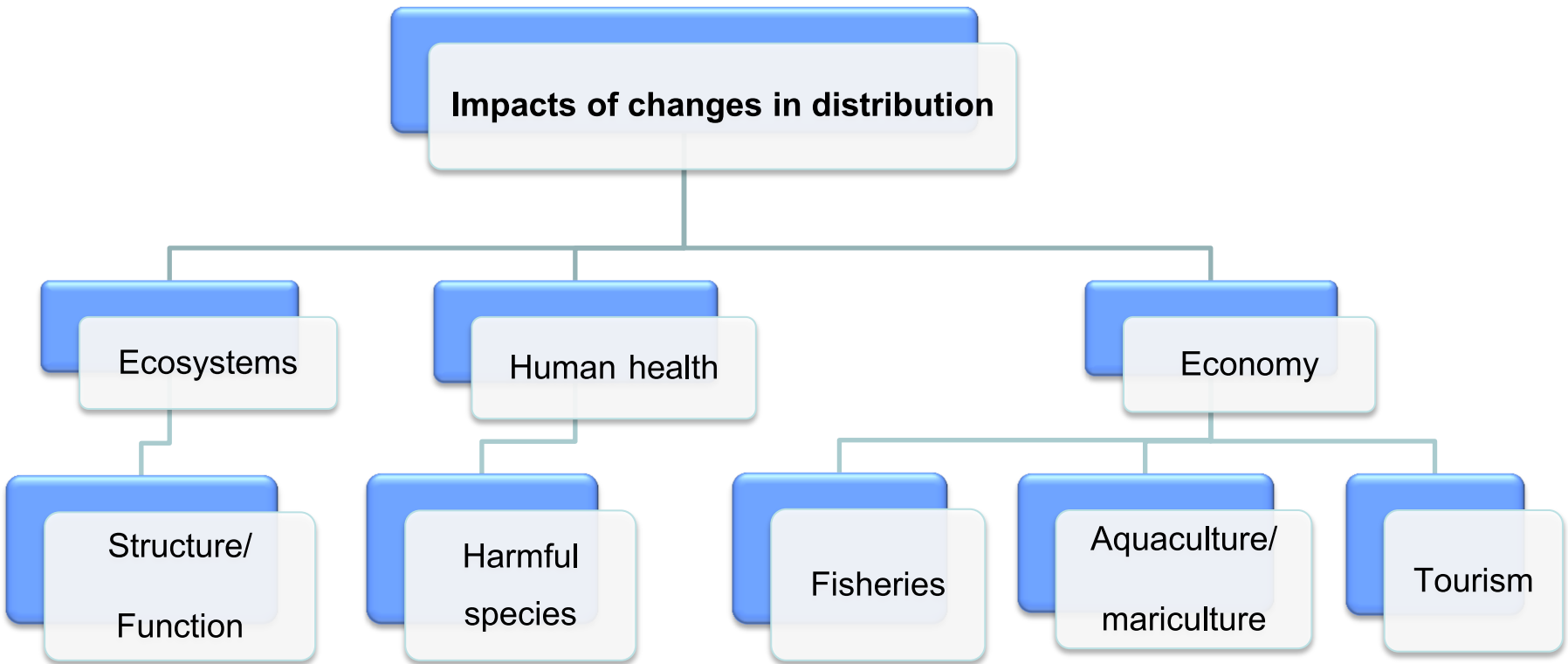
translatingnatureintoknowledge

## Changes in distribution driven by oceanic warming

- Several marine species are **changing** their **patterns of geographic distribution, abundance, and phenology** in response to oceanic warming
- The magnitude in **responses** is **highly variable** (e.g. 25-85% in the expected direction)



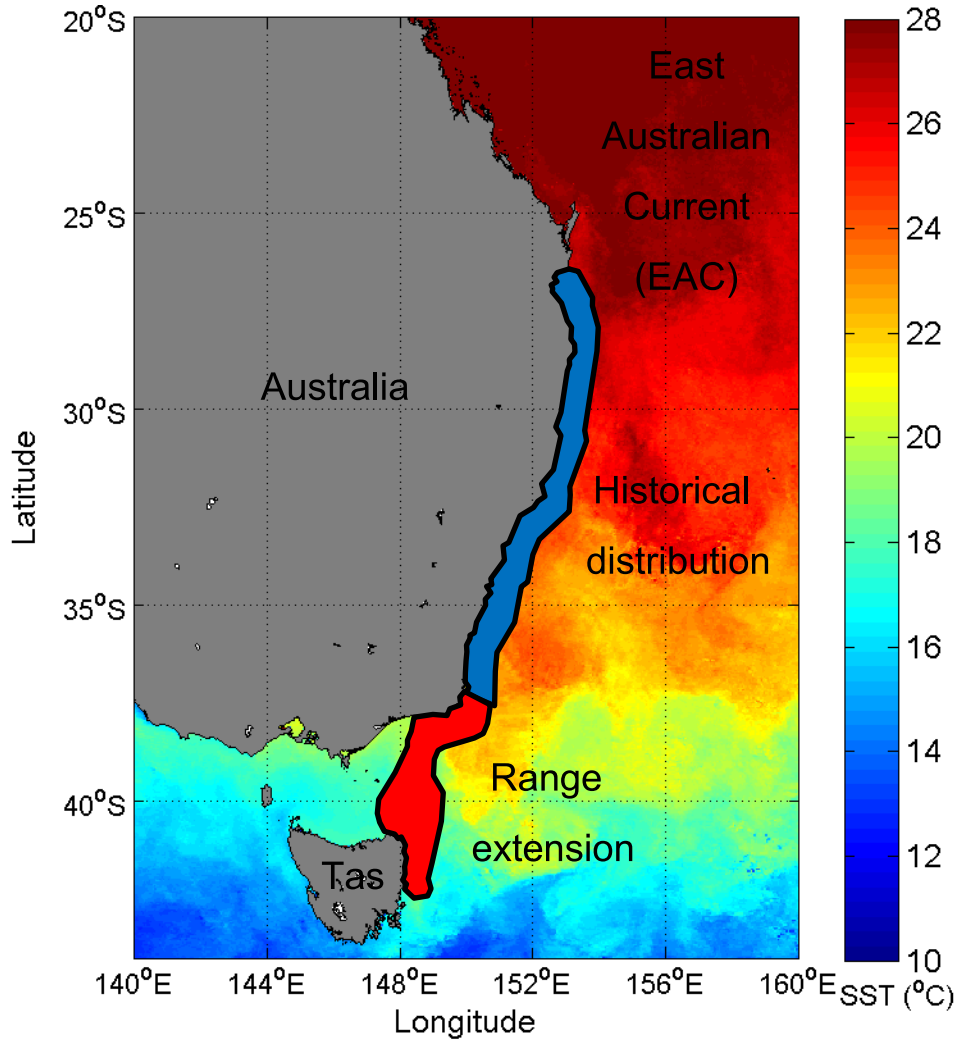
# The issue



**What species are likely to undertake changes in distribution  
driven by oceanic warming**



# Case study: range extension of *Octopus tetricus*



*Octopus tetricus* (Gould 1852)

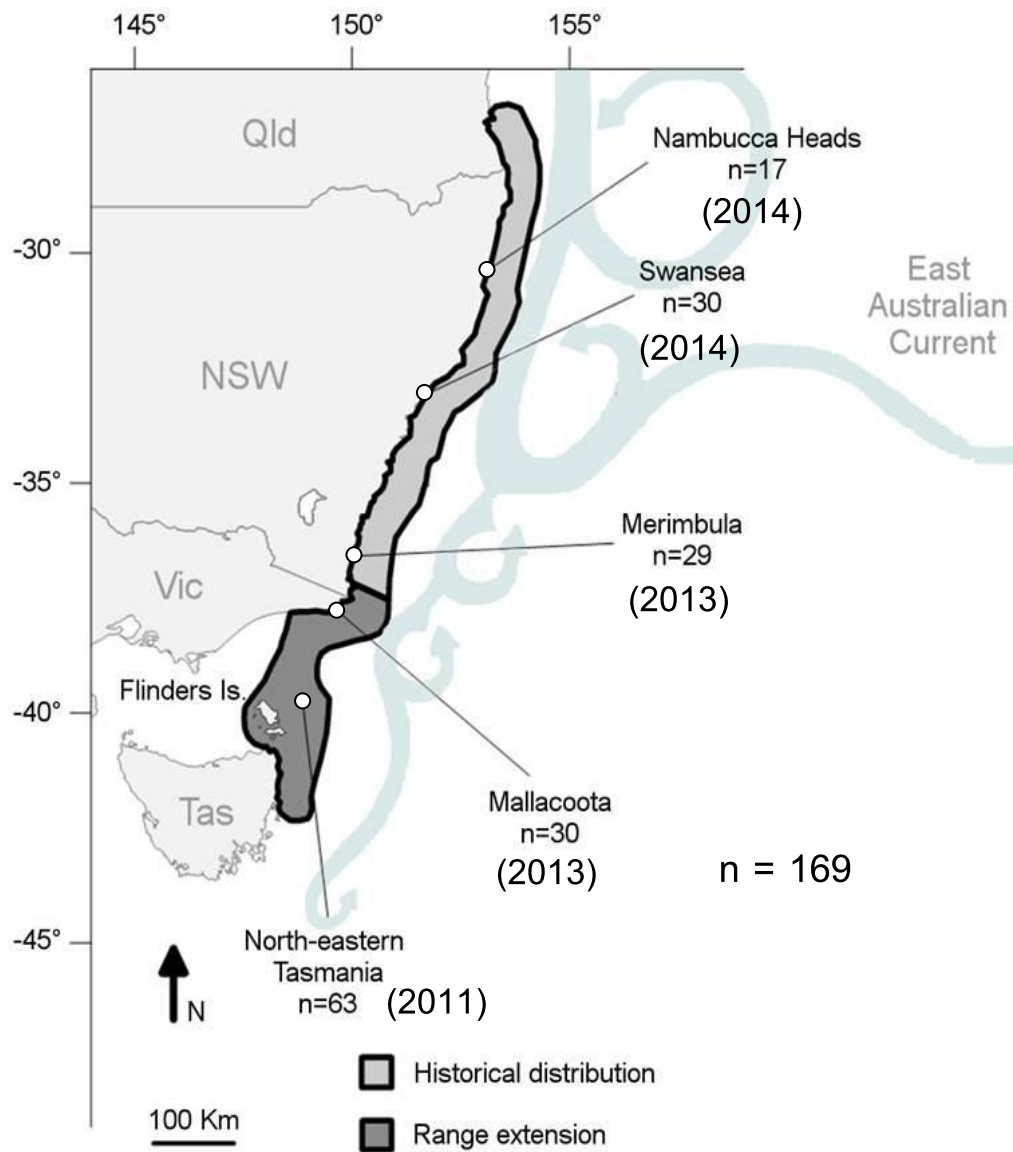


1. What is the **population genetic structure** of *O. tetricus* along its entire distribution?
2. Does *O. tetricus* have **phenotypic plasticity**?
3. What is the **gene flow** between historical and extension areas?
4. Where are the **source populations** located that contribute to the range extension areas?
5. What is the **genetic diversity** of the range extension vs other population components?
6. Are there any **bottleneck or demographic effects**?

**How these genetic signatures influence persistence in new areas?**



# Samples collection

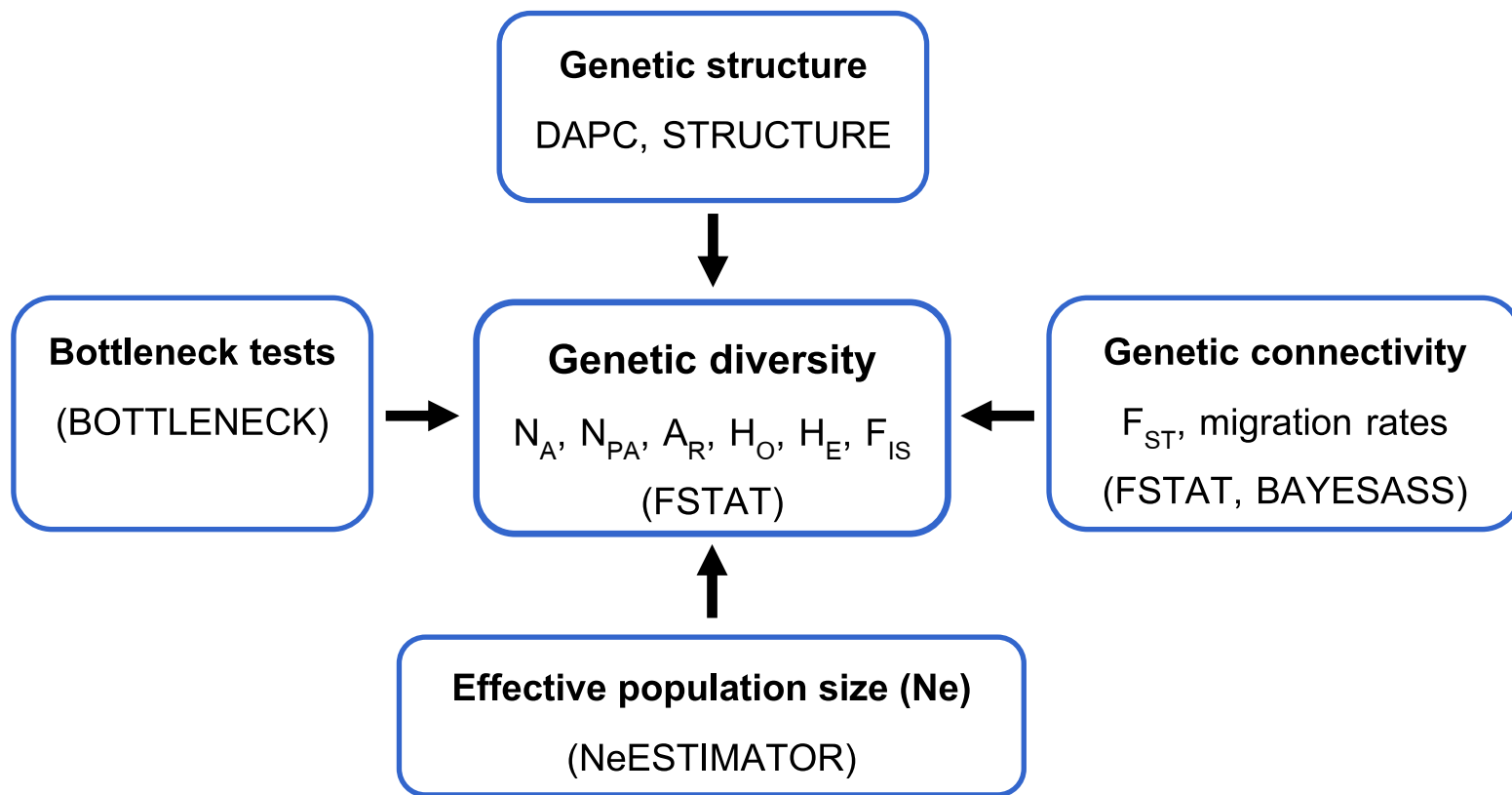
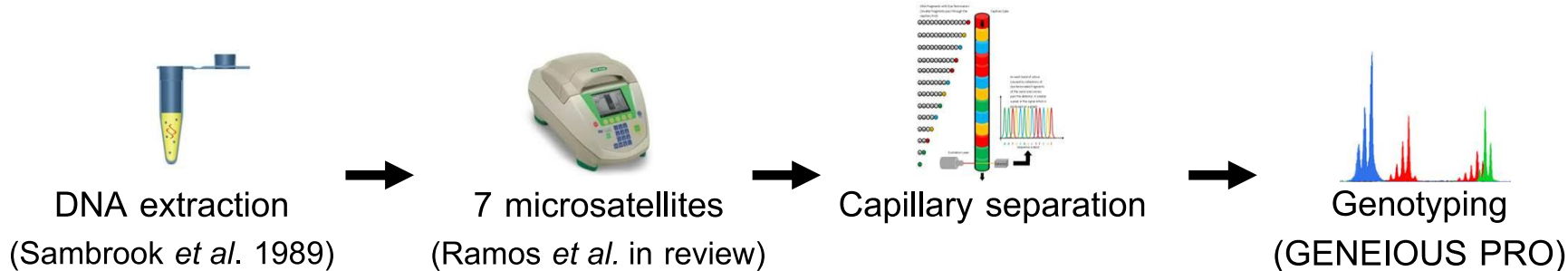


Anaesthesia in 2% MgCl solution



Tissue in 95% ethanol

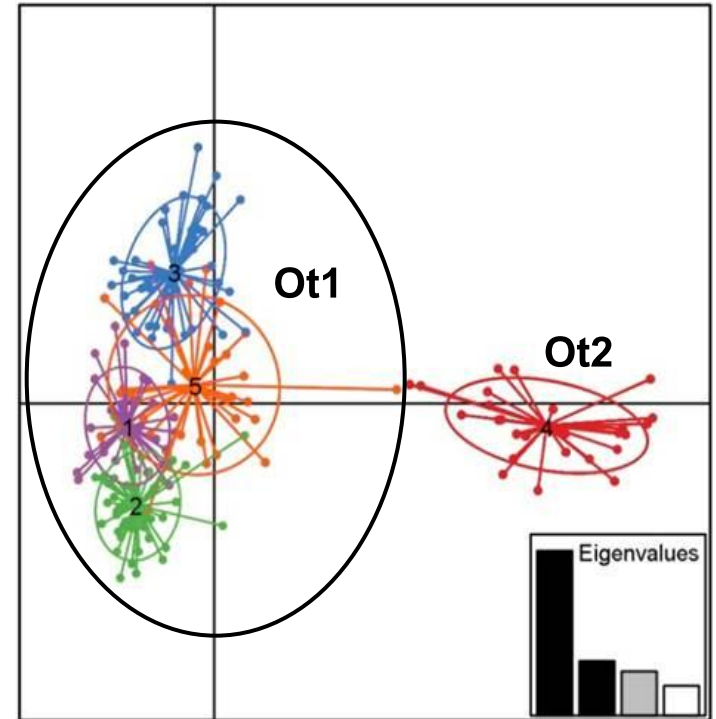
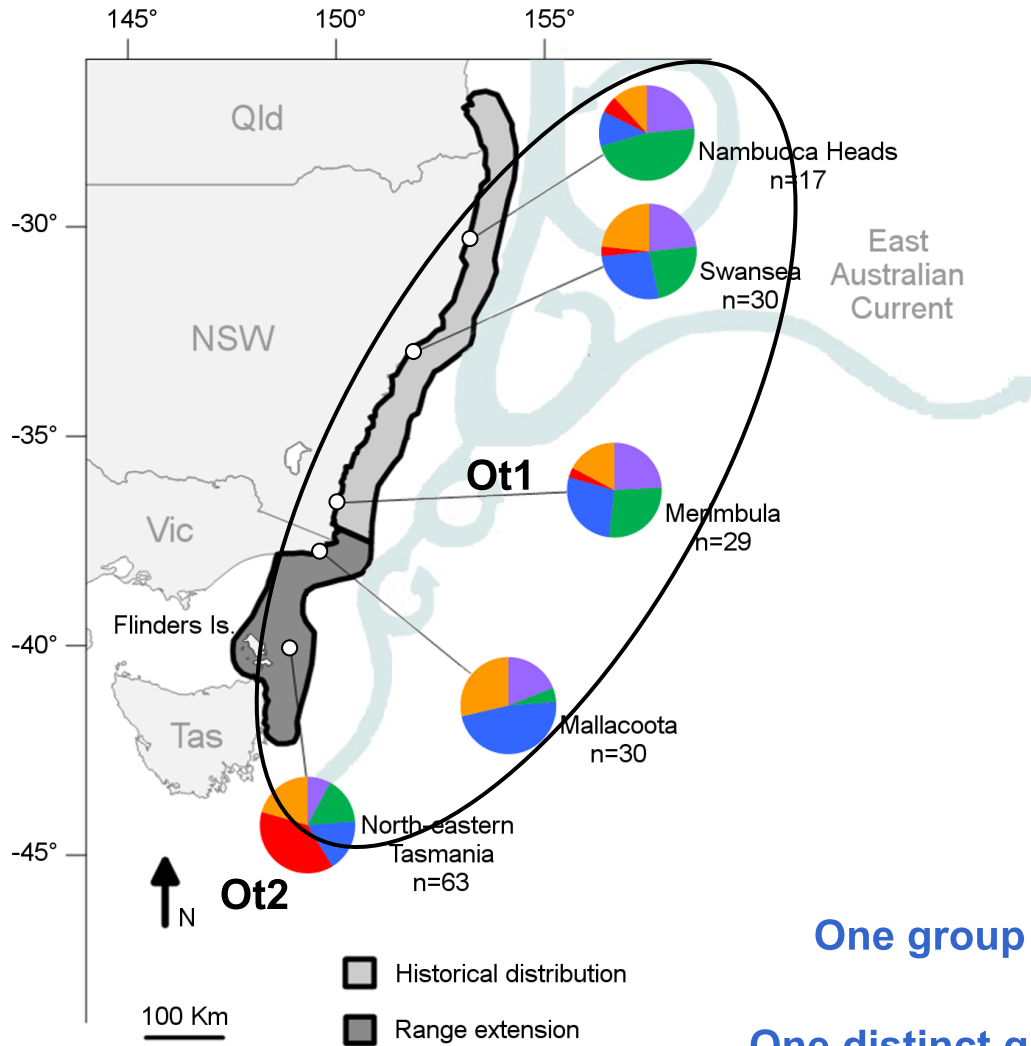
## Lab work and data analyses



Linkage disequilibrium & Hardy-Weinberg equilibrium (GENEPOP)



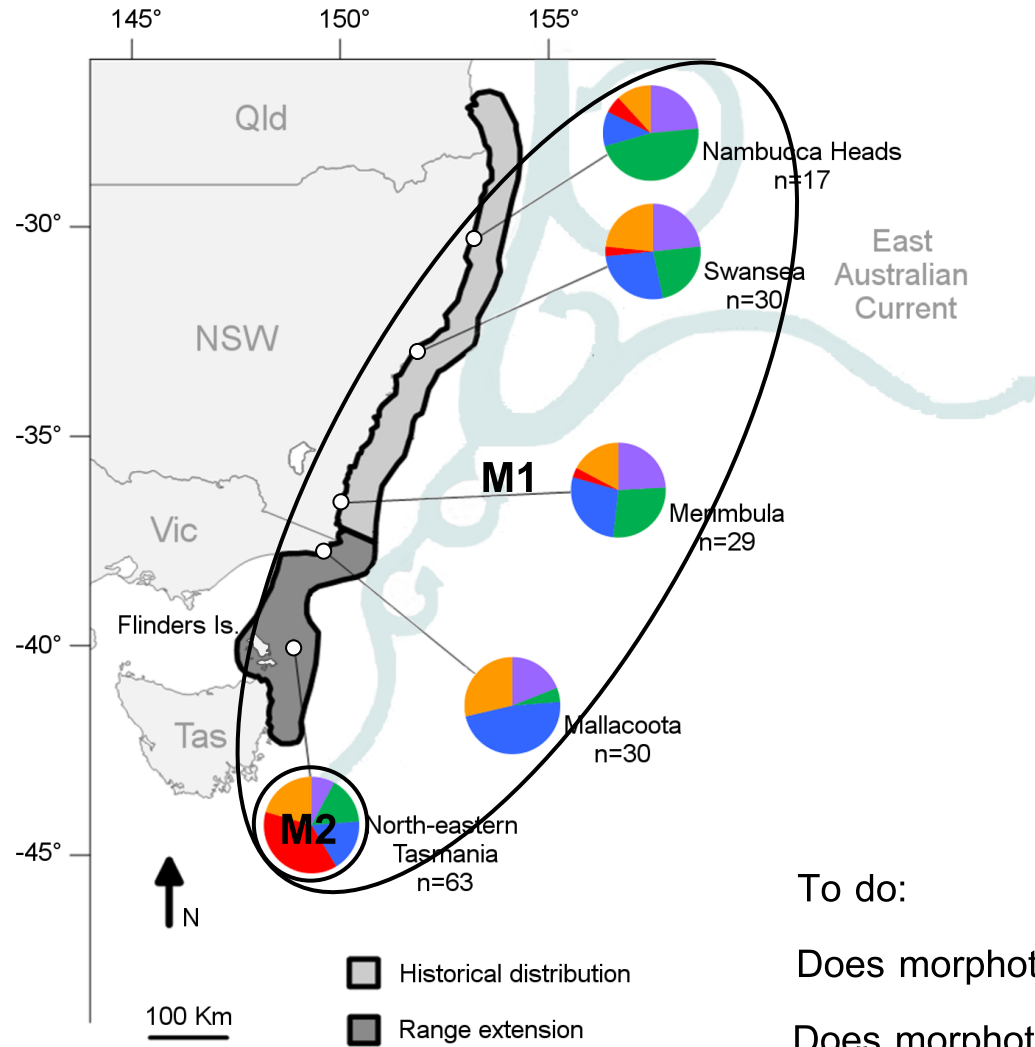
# Population genetic structure



One group along the entire distribution (Ot1)

One distinct group at north-eastern Tasmania (Ot2)

# Phenotypic plasticity?



Morphotype 1 (M1) Morphotype 2 (M2)

All along

Tasmania



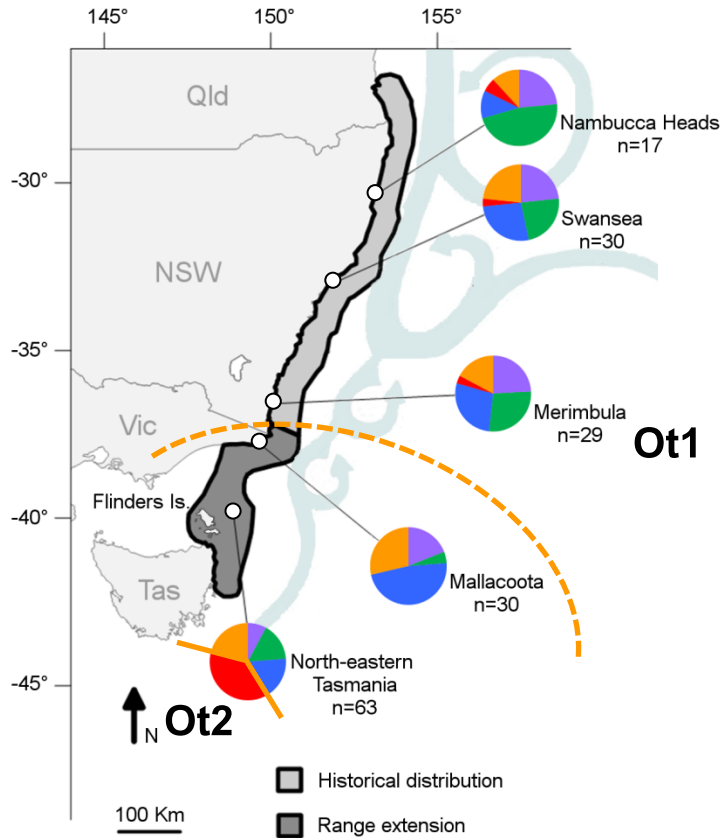
To do:

Does morphotype 1 correspond to common group Ot1?

Does morphotype 2 correspond to distinct group Ot2?

Morphology-genetics for more samples

# Genetic connectivity ( $F_{ST}$ )



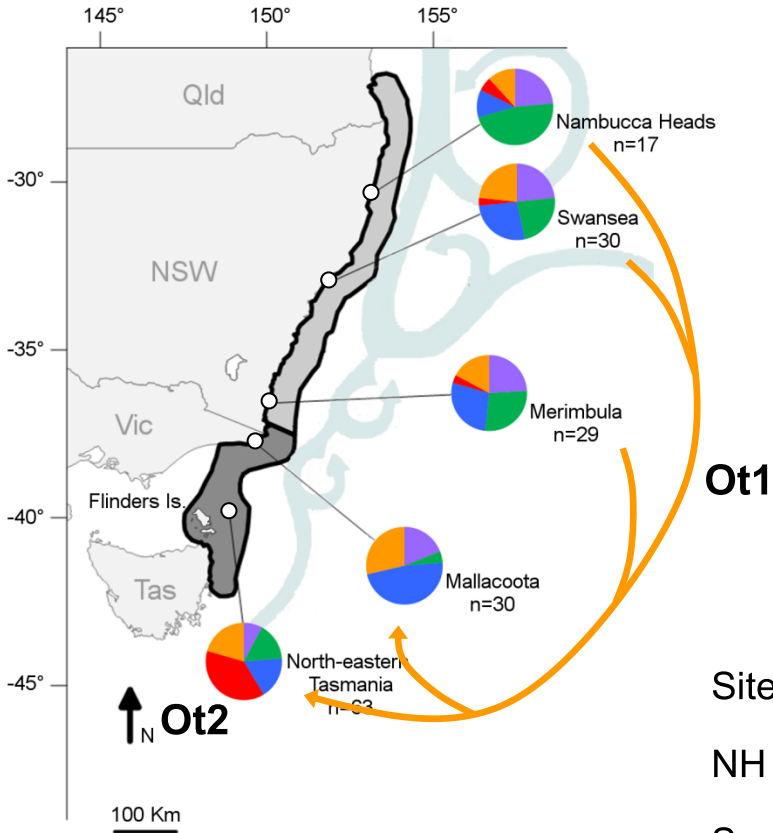
Site	NH	Swa	Mer	Mal	Tas (Ot1)
Swa	0.0005				
Mer	0.0026	0.0001			
Mal	0.0182	<b>0.0117</b>	0.0126		
Tas (Ot1)	<b>0.0173</b>	<b>0.0083</b>	<b>0.0051</b>	0.0051	
Tas (Ot2)	<b>0.1609</b>	<b>0.1380</b>	<b>0.1336</b>	<b>0.1648</b>	<b>0.1314</b>

Bold indicates significant values after Bonferroni correction of  $P < 0.005$

Ot2 different from the rest of the population

Range extension partially different from the historical distribution

# Genetic connectivity (migration)



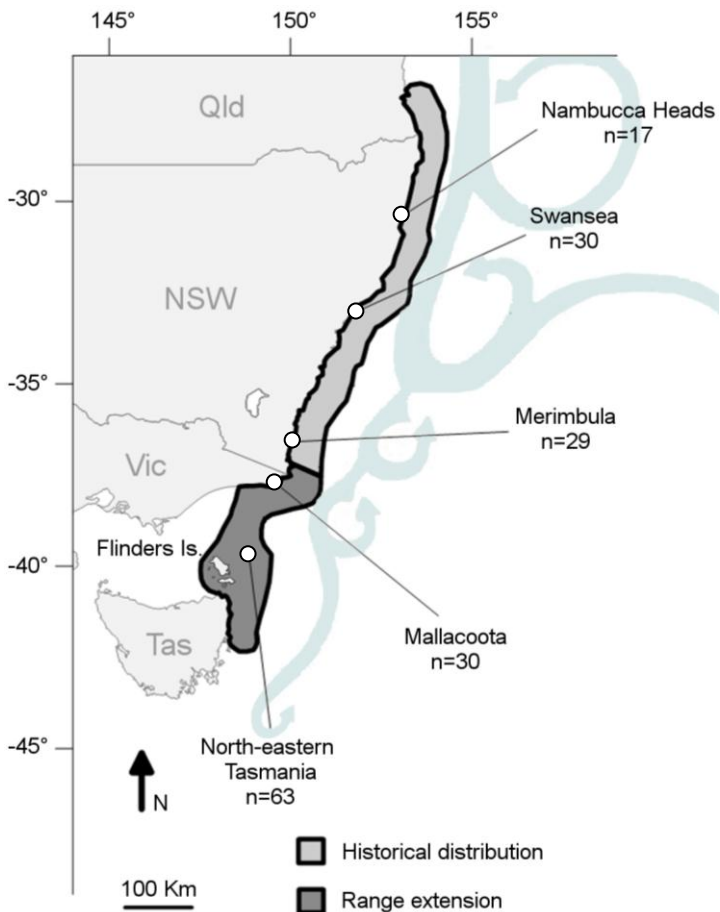
Migration from all sites

Mallacoota is the main source of migrants

Ot1  
Sink

Site	Source					
	NH	Swa	Mer	Mal	Tas (Ot1)	Tas (Ot2)
NH	0.680	0.013	0.014	0.210	0.021	0.025
Swa	0.009	0.676	0.009	0.237	0.019	0.025
Mer	0.009	0.009	0.676	0.236	0.016	0.028
Mal	0.009	0.009	0.009	0.796	0.143	0.010
Tas (Ot1)	0.007	0.008	0.007	0.256	0.690	0.009
Tas (Ot2)	0.010	0.010	0.010	0.013	0.020	0.910

## Genetic diversity



Zone/Site	n	$N_A$	$N_{PA}$	$A_R$	$H_O$	$H_E$	$F_{IS}$
<b>Historical distr.</b>	88	14.00	2.71	13.73	0.57	0.63	0.09
NH	17	7.43	0.57	7.29	0.51	0.57	0.11
Swa	30	10.14	0.86	8.04	0.58	0.64	0.11
Mer	29	10.00	0.57	8.05	0.62	0.65	0.05
<b>Range ext.</b>	91	15.14	4.43	14.60	0.63	0.69	0.08
Mal	30	9.86	0.86	7.87	0.58	0.62	0.07
Tas (Ot1)	35	10.57	1.14	7.76	0.67	0.65	-0.05
Tas (Ot2)	24	9.00	1.00	7.81	0.64	0.66	0.05

n, sample size;  $N_A$ , number of alleles;  $N_{PA}$ , number of private alleles;  $A_R$ , allelic richness (standardized to 17 samples);  $H_O$ , observed heterozygosity;  $H_E$ , expected heterozygosity;  $F_{IS}$ , Fixation index.

**Genetic diversity is similar in the extension area compared with the historical distribution**

Rapid demographic expansion (Excoffier *et al.* 2009)

## Bottleneck tests

	Infinite Allele Model				Overall
	i	ii	iii	iv	
<b>Historical distr.</b>	0.318	0.165	0.469	No	No
NH	0.349	0.220	0.766	No	No
Swa	0.593	0.339	0.406	No	No
Mer	0.598	0.441	0.406	No	No
<b>Range ext.</b>	0.576	0.245	0.766	No	No
Mal	0.586	0.094	0.656	No	No
Tas (Ot1)	0.589	0.385	0.766	No	No
Tas (Ot2)	0.606	0.303	0.594	No	No

**No evidence of a bottleneck effect**

i) “sign test” for heterozygosity excess; ii) “standardized differences test” for differences in allele frequencies; iii) “Wilcoxon test” for reduced mean heterozygosity; iv) “mode-shift qualitative test” for distortion of allele frequency distributions.

Significance at  $P < 0.05$

Kimura & Crow 1964; Ohta & Kimura 1973; Cornuet & Luikart 1996; Luikart *et al.* 1997; Luikart *et al.* 1998; Luikart & Cornuet 1998



**Effective population size (Ne)**

Zone	Ne	CI (Inferior)	CI (Superior)
Historical distribution	1665	244	$\infty$
Range extension	96	67	154

Ne, Effective population size; CI, Confidence interval; P = 0.02

**Ne at the extension area is small compared with the historical distribution**

Ne  $\geq$  100: limits loss in total fitness to  $\leq$  10%, avoids inbreeding depression;

Ne  $\geq$  1000: Retains evolutionary potential (Frankham *et al.* 2014)

1. What is the **population genetic structure** of *O. tetricus* along its entire distribution?

**Two groups:** 1) entire distribution; 2) Tasmania (Ot2).

2. Does *O. tetricus* have **phenotypic plasticity**?

**Phenotypic plasticity seems to occur** at the range extension area.

3. What is the **gene flow** between historical and range extension areas?

There is moderate **gene flow** between sites.

4. Where are the **source populations** located that are contributing to the range extension of *O. tetricus*?

**All along the distribution.** The main source of migrants is located off Mallacoota.

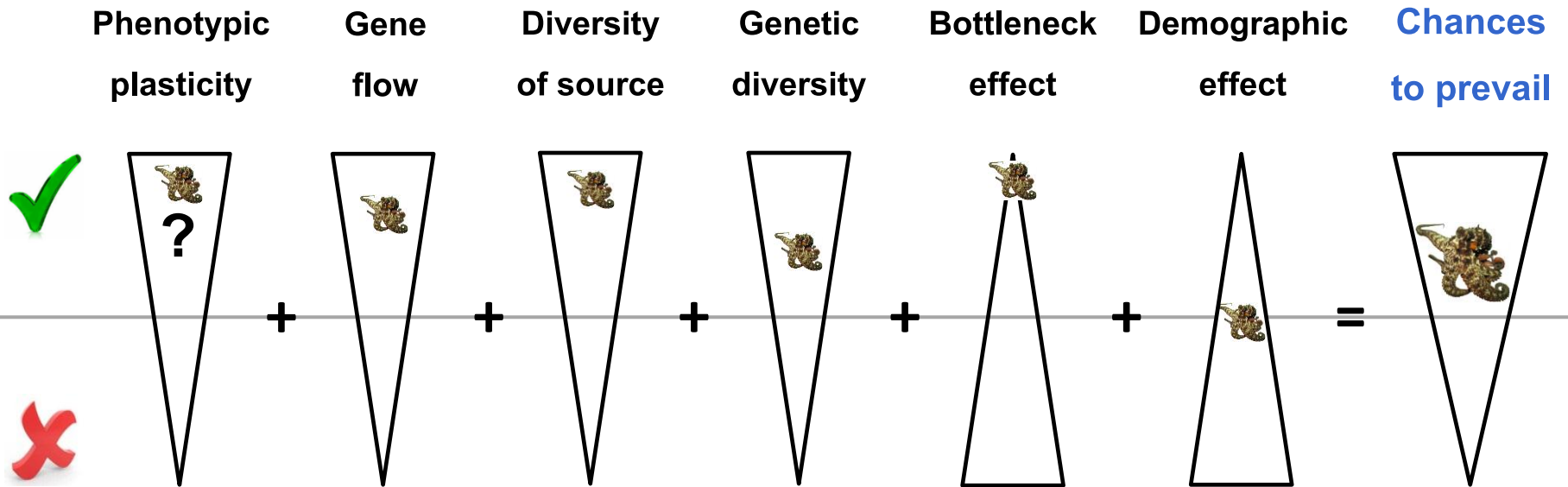
5. What is the **genetic diversity** of the range extension vs other population components?

**Genetic diversity is similar at the extension area** compared to the historical area.

6. Are there any **bottleneck** or **demographic effects** at extension areas?

**No evidence of a bottleneck effect.** **Effective population size in the range extension area is small** compared with the historical distribution.

How these genetic signatures influence persistence in new areas?





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