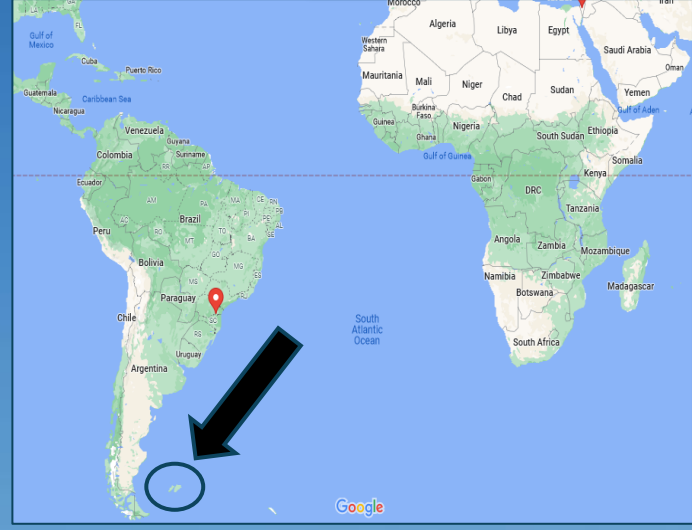
The role of the Last Glacial Maximum in shaping patterns of phylogeographic structure in brooding sea star, *Anasterias antarctica,* in the Falkland Islands and southern Chile



Amy Guest

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Why, what, when?

Understand how phylogeographic structure is driven by glaciation

Last Glacial Maximum (18,000 - 25,000 ya)

Anasterias antarctica, ‘Common Sea Star’

Brooding reproductive strategy

Aims

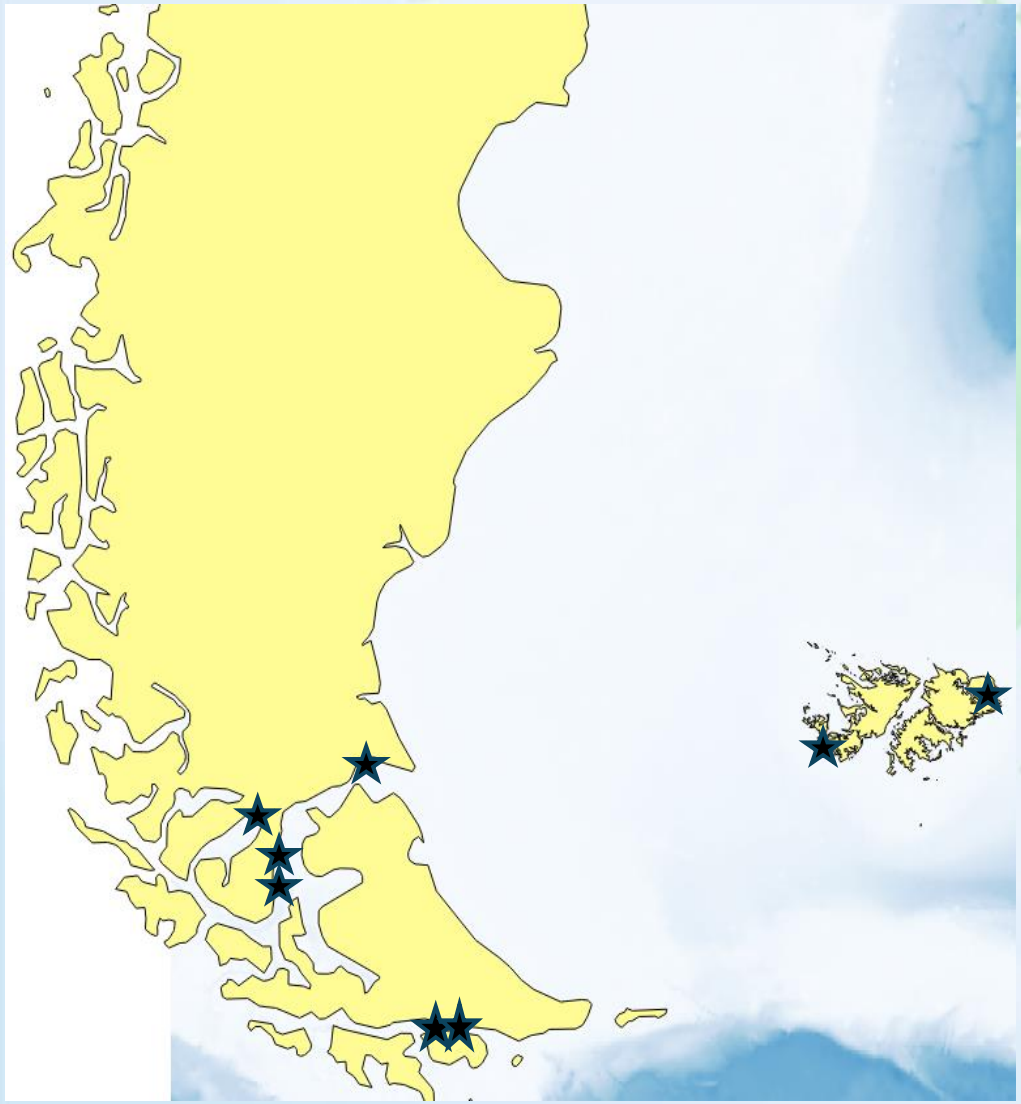
Falkland Islands as a refugium?

Reconstruct phylogeographic relationships

Infer mechanisms of movement

Predictions

What would allow us to accept the refugia hypothesis?



Unique Falklands haplotypes

Fewer unique Chilean haplotypes

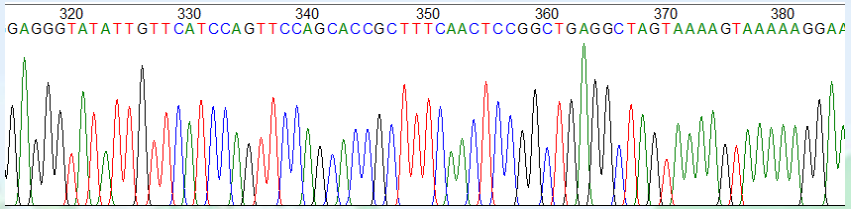
Higher nucleotide and haplotype diversity in Falklands populations

More mutational steps between Falklands haplotypes

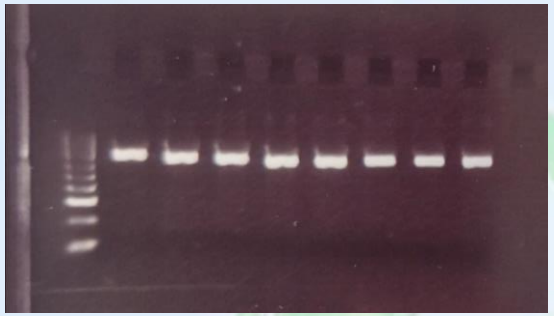
Few shared haplotypes between Chile-Falklands

Methods

Sequencing



DNA Extraction and Amplification mtDNA COI + 16S

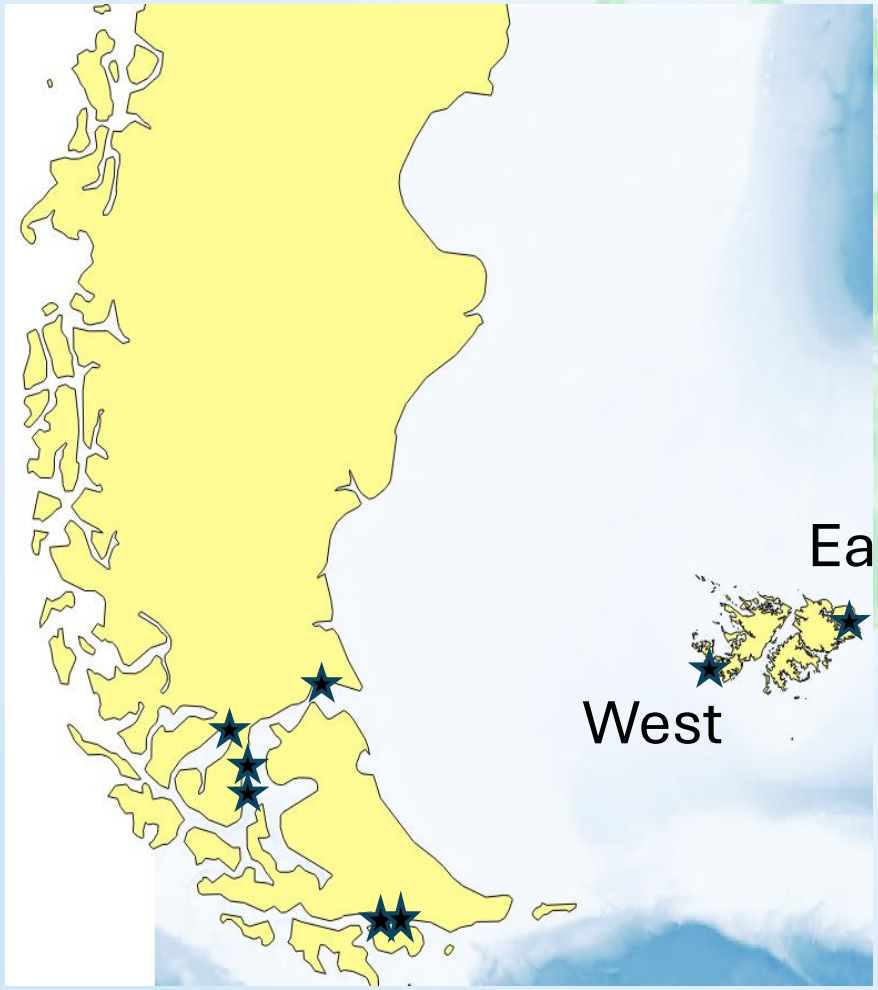


Maximum-likelihood trees

Haplotype network

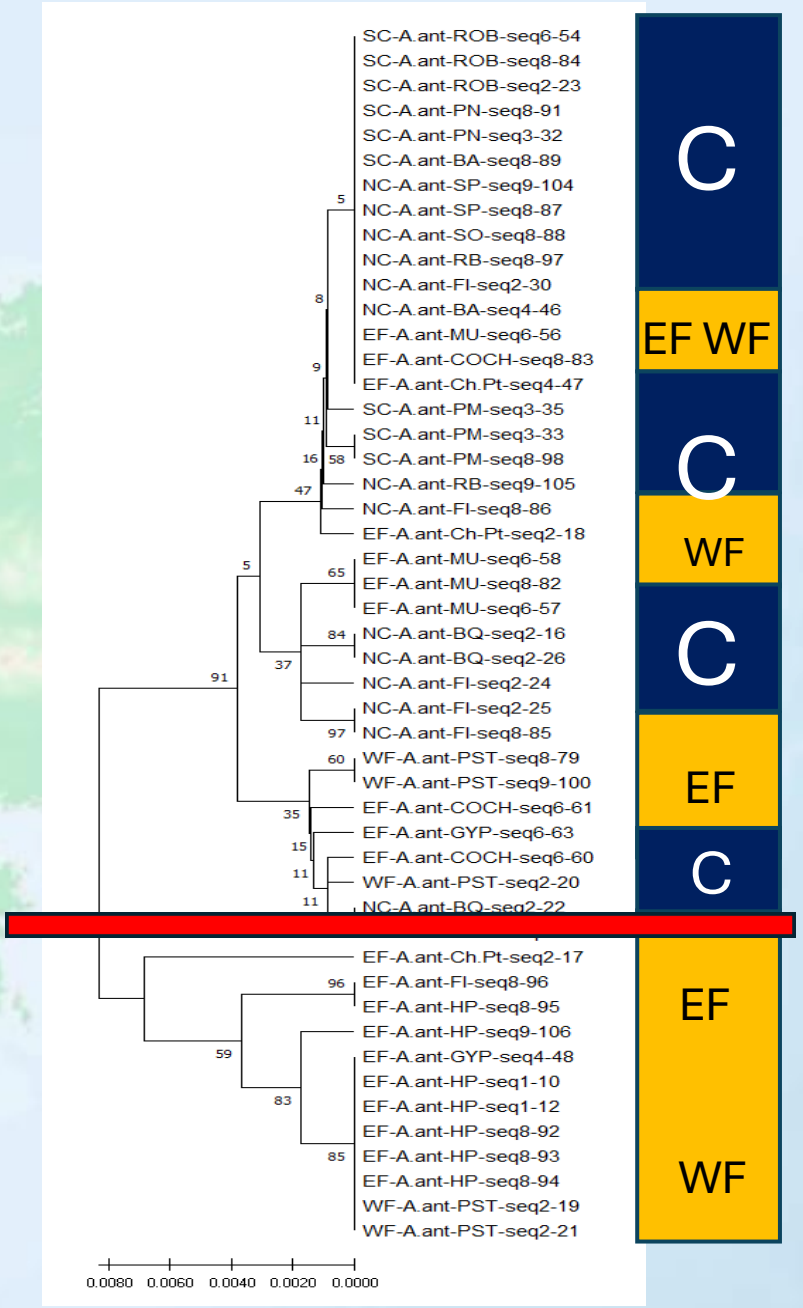
Haplotype & Nucleotide diversity

Results



2 main clades = refugium

Mixed sub-groups = dispersal



Results

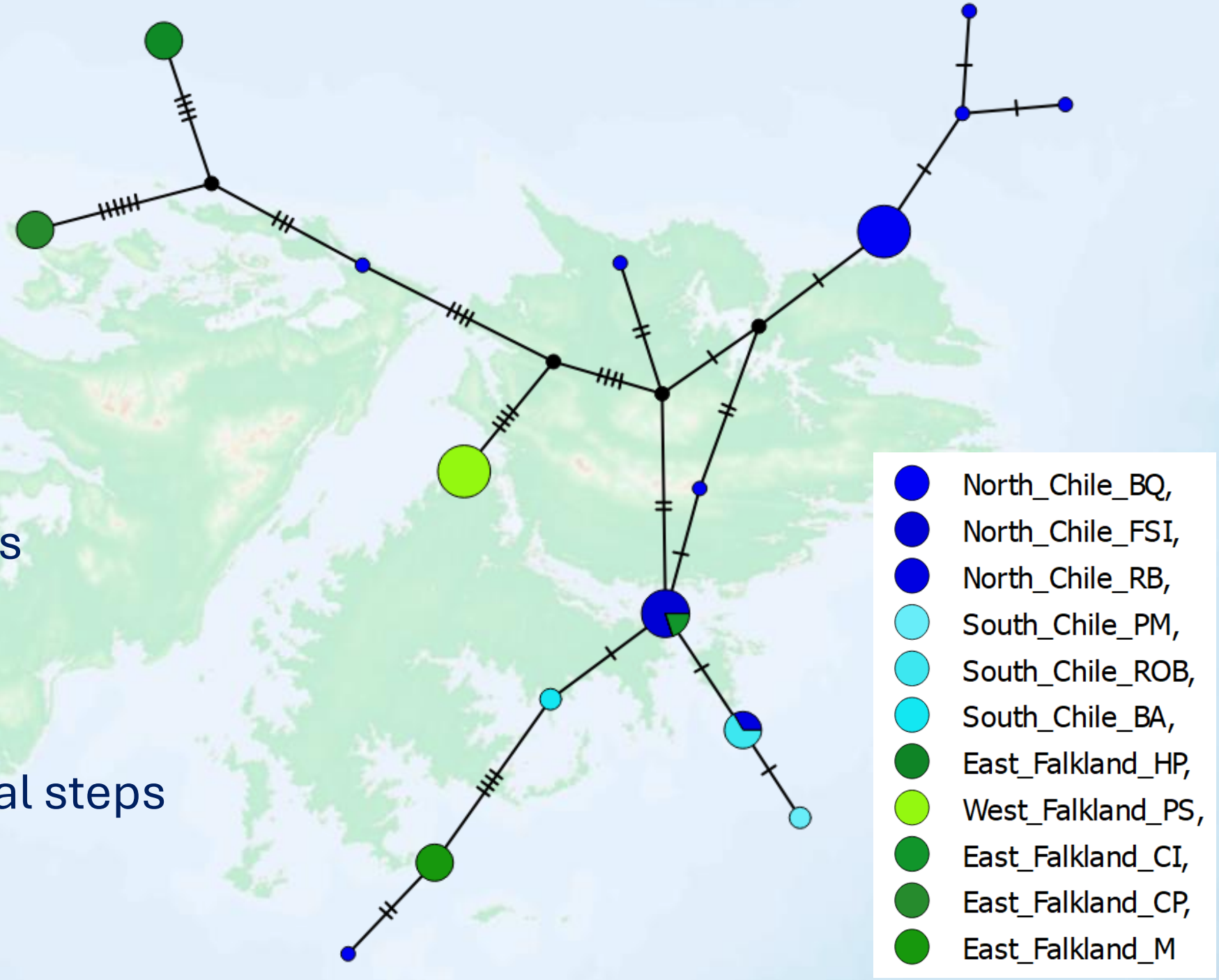
16 haplotypes

4 median vectors

14 unique haplotypes

2 shared haplotypes

Quantified mutational steps



Results

	Falkland Islands	Chile
Haplotype diversity (h)	0.917	0.848
Nucleotide diversity (π)	0.009	0.004

Falklands > Chile, as predicted

Discussion

Partial support for refugium hypothesis

Phylogeographical relationships shown, the first Chile- Falklands study of a brooding sea star

Shared ancestral haplotypes pre-glaciation *with* occasional dispersal via kelp rafting the most parsimonious explanation

Thanks for listening

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