Evolution in invasive populations:
Using genomics to explore selection in the Australian European starling (*Sturnus vulgaris*) introduction

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BACKGROUND

The future will favor invasive species:
- Increased intercontinental travel = new or reinforced invasion pathways
- Habitat clearing and global warming expected to favor invasive species over native ones

In order to successfully model range shifts in invasive species, we must have a thorough understanding of the changes the species has undergone, and may continue to undergo, as it occupies the new, invaded ecosystem.

Invasive species as models:
- Investigate evolutionary mechanisms behind invasive species' rapid evolutionary change
- Explore a species' ability to change and survive
- Investigate the relationship between genotype, local adaptation & invasion success

Sturnus vulgaris – the globally invasive European starling
- Native to the Palearctic and invasive on other continents, introduced into Australia in 1860's
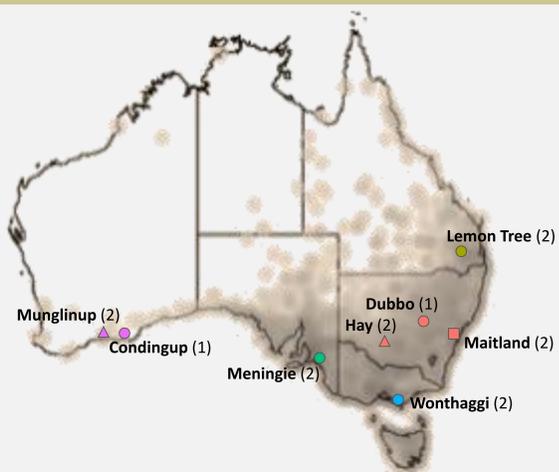- Already show signs of local adaptation within the Australian range

What are some candidate drivers of the starlings' rapid differentiation across their invasive novel environment?
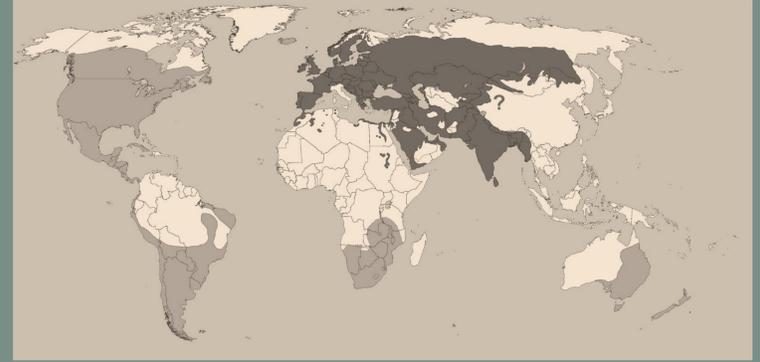
Global Range
Native Populations
Invasive Populations

METHODS

Fig. 1 (Left): Map of the invasive European starling's Australian distribution. Points indicate a sampling site. Corresponding label indicates location in bold, and number of individuals sampled at that site in brackets. Total N = 14, total pops = 8. Whole genome sequencing (WGS) data was used to characterise genetic differentiation across the range by analysing single nucleotide polymorphisms (SNPs).

Fig. 2 (Right): Sequencing workflow diagram for all 14 WGS starling samples. Key bioinformatic approaches used to generate below results figures are listed in the corresponding figure legend.
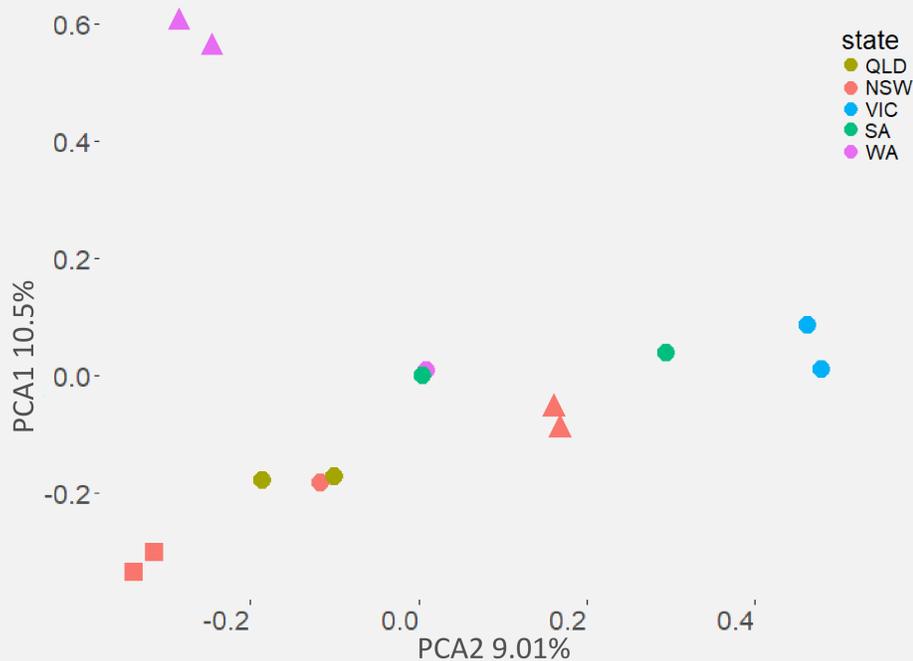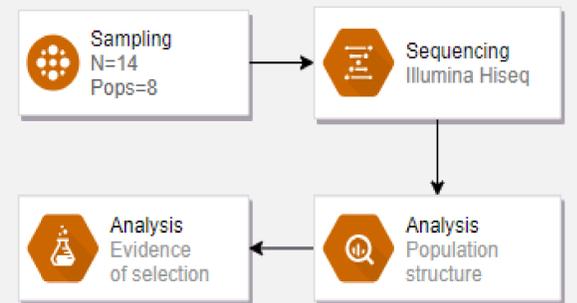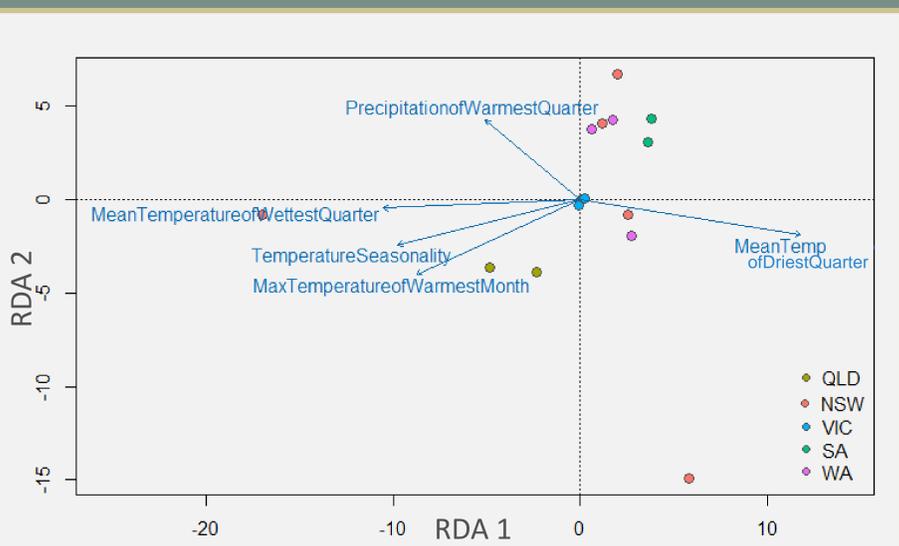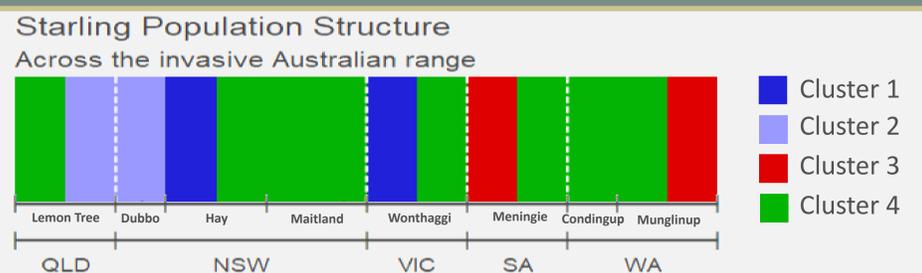
Lemon Tree (2)
Dubbo (1)
Hay (2)
Maitland (2)
Munglinup (2)
Condingup (1)
Meningie (2)
Wonthaggi (2)

Sampling N=14 Pops=8 → Sequencing Illumina Hiseq
Analysis Evidence of selection ← Analysis Population structure

Fig. 3 (Left): Principal component analysis of whole genome SNPs across all 14 starlings (Fig. 1). SNPs were processed and filtered using GATK and VCFtools, and prepared for visualisation in R using SNPRelate.

Fig. 4 (Below): Structure plots of whole genome SNPs. Population structure was calculated using fastSTRUCTURE, and visualised in R using pophelper.

Fig. 5 (Bottom Left): Redundancy analysis (RDA) examining genotype-environment association (GEA) in candidate 'outlier SNPs'. Fst was examined along genomes in windows of 10kb. SNPS were located within windows reporting Fst > 0.5, and were designated as 'outlier SNPs'. This genetic data was analysed against the corresponding locations' environmental data using multivariate linear regression. PCA was used on the resulting matrix to produce linear combinations of the predictors.

PCA1 10.5%
PCA2 9.01%

state
- QLD
- NSW
- VIC
- SA
- WA

Starling Population Structure
Across the invasive Australian range
- Cluster 1
- Cluster 2
- Cluster 3
- Cluster 4

Lemon Tree | Dubbo | Hay | Maitland | Wonthaggi | Meningie | Condingup | Munglinup
QLD | NSW | VIC | SA | WA

PrecipitationofWarmestQuarter
MeanTemperatureofWettestQuarter
TemperatureSeasonality
MaxTemperatureofWarmestMonth
MeanTemp ofDriestQuarter

RDA 2
RDA 1

- QLD
- NSW
- VIC
- SA
- WA

CONCLUSION

Starling population differentiation and structure
- Differentiation appears to be occurring at the northern (Dubbo and Lemon Tree) and western (WA) range edges, as well as midrange (VIC and Hay).
- Population differentiation appears to be tied heavily to temperature, as well as precipitation throughout the starlings' range.

Despite a relatively young age 160 years, the invasive starling population in Australia appears to show local adaptation to environmental factors.

Future directions of research
- RDA GEA approach can be used to begin examining candidate SNPs and hence genes likely playing a role in local adaptation and hence invasion success.

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