Genome-wide SNPs unravel population structure and variability in the Fijian Black-lip Pearl Oyster

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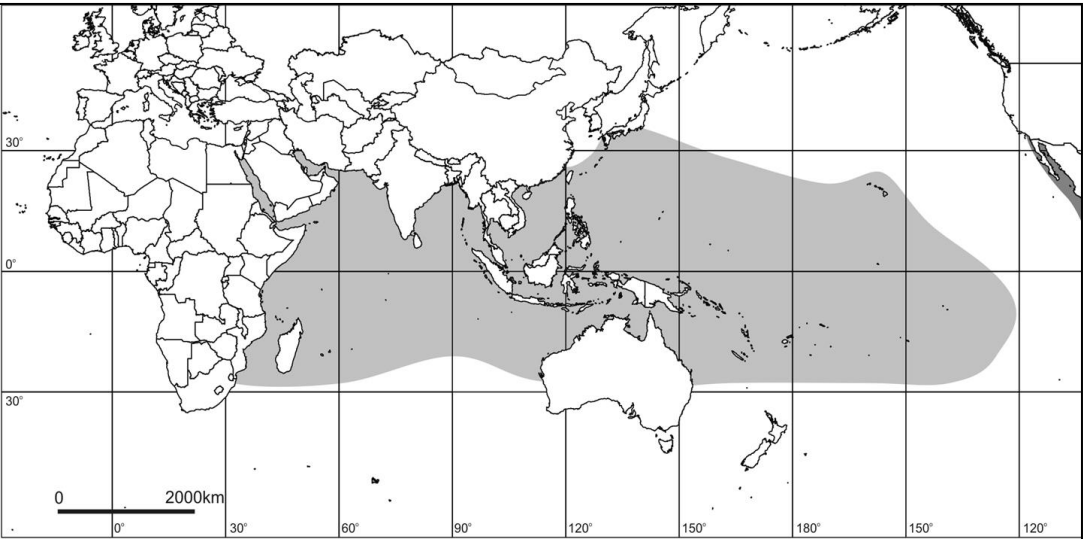
Secretariat of the Pacific Community

Overview

- Black-lip Pearl Oyster and Fijian cultured pearl industry.
- Research problem/knowledge gaps.
- Study overview and methods.
- Results and future directions.

Pinctada margaritifera (L.)



- Broad Indo-Pacific natural distribution, 0-20m, reef.
- ~120 mm DVH, ~ 100 mm DVM. 26-29 °C, 28 – 32 ‰.
- Primary species for aquaculture in the Pacific Islands.
- Broadcast spawner, 40-50 million eggs.

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Pinctada margaritifera (L.)

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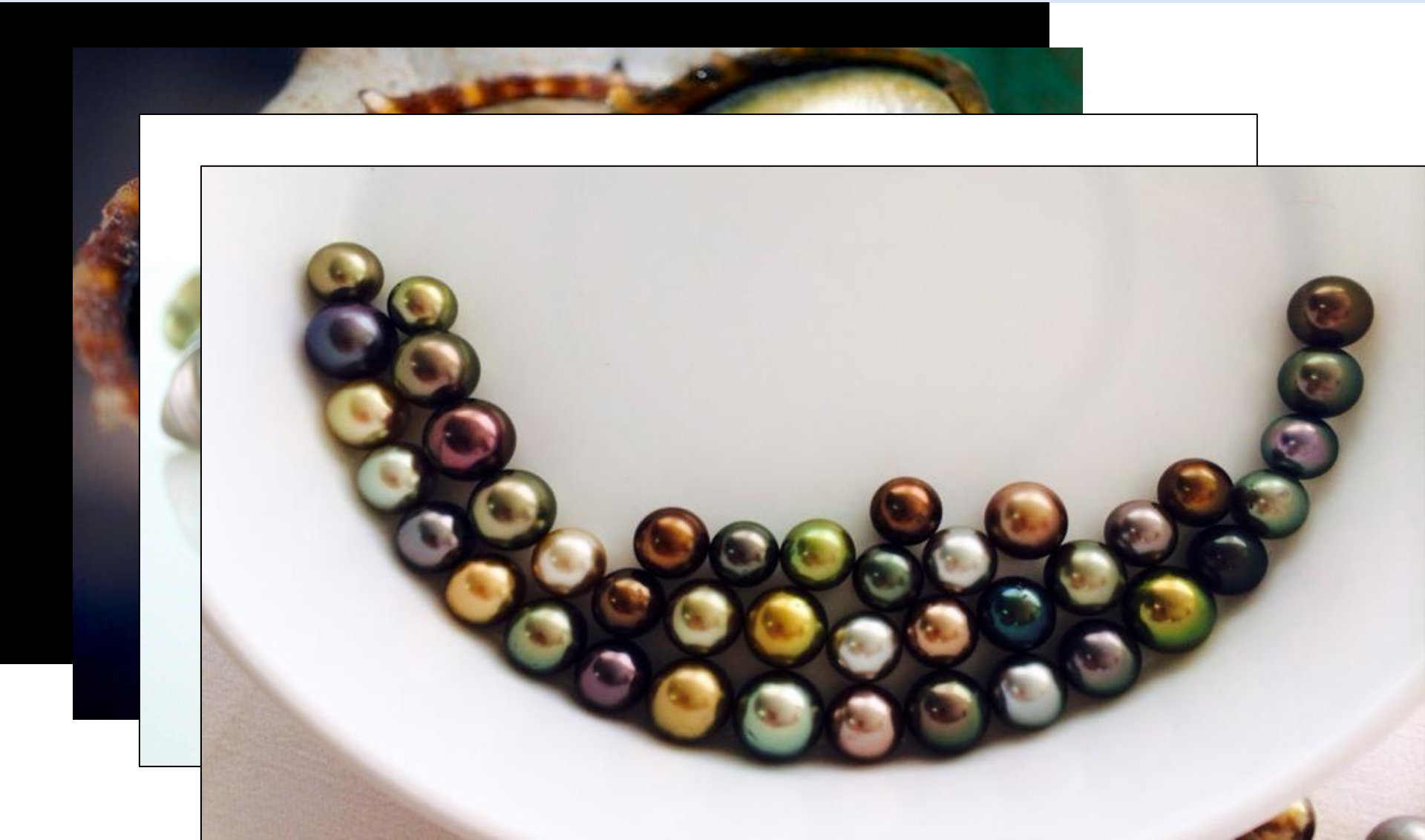
Traditional black and coloured “Fiji’’ pearls



Pearl oyster aquaculture in Fiji

- *Pinctada margaritifera* is the main species.
- Most valuable aquaculture commodity: ≈ 13 million USD annually.
- ~7 farms, reliant on mainly wild-caught + hatchery produced spat.
- Farm expansion and establishment set to grow the industry.

Research problems/knowledge gaps

- Wild oyster stocks reduced.
- No fishery management policy.
- Population genetic status unknown.
- Biological data needed for conservation and aquaculture efforts.
- Population genomic tools will provide the answer!

Source: Richards *et al*. (1994)

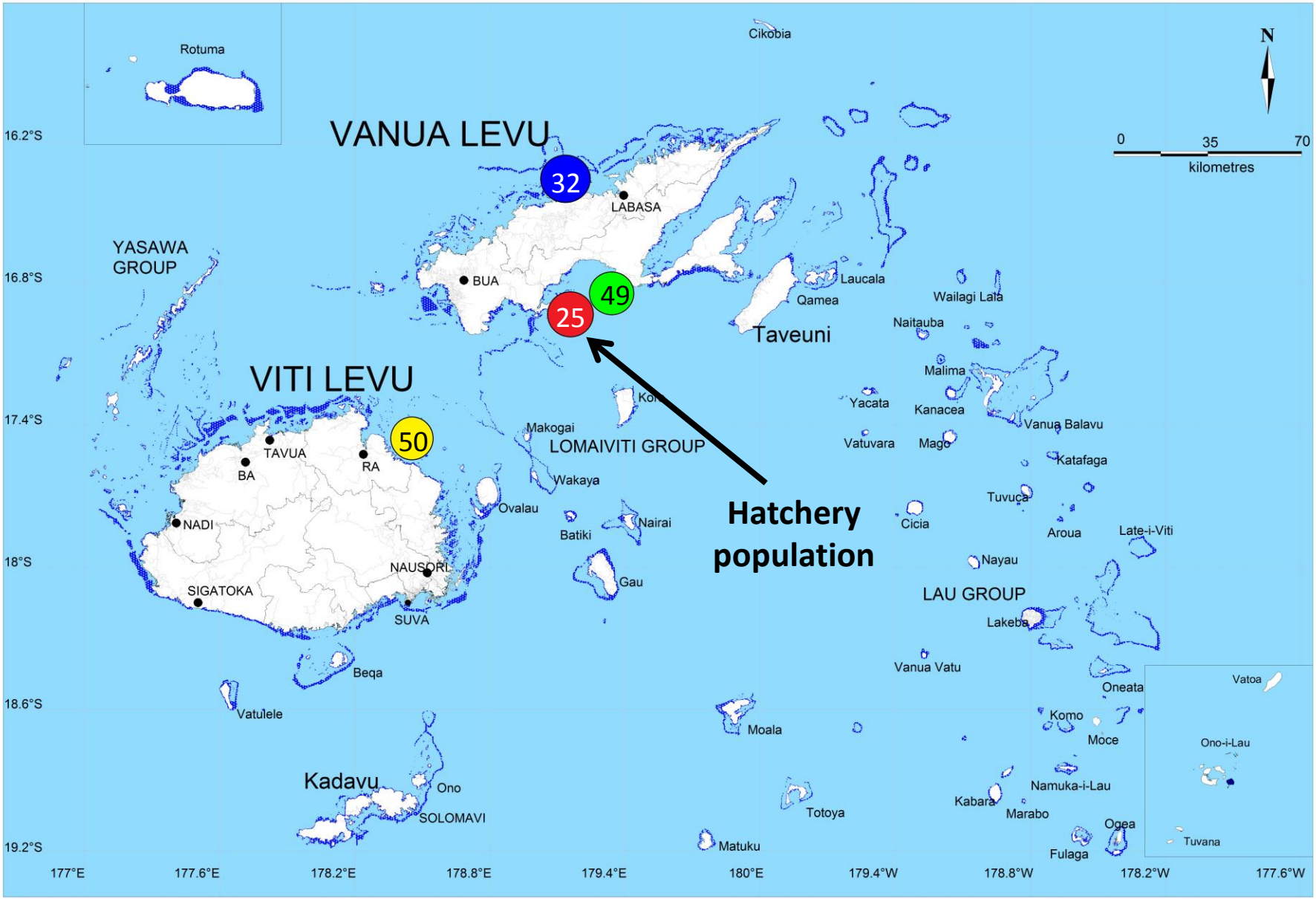
Study overview

Specific aims:

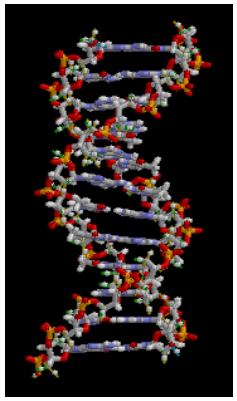
- For Fijian *P. margaritifera* develop genome-wide SNPs to determine:

- Genetic diversity levels.
- Population structure.
- Relatedness and gene flow.
- Investigate colour morphotypes.
- Formulate recommendations for management of fishery and sustainable aquaculture.

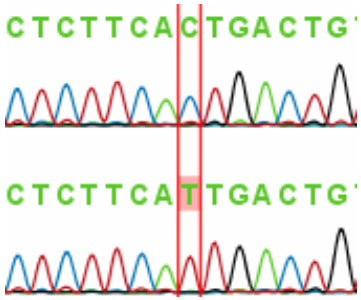
Methods: tissue sampling.



Methods: population genomics



ddRADseq:
Genome-wide
SNP markers

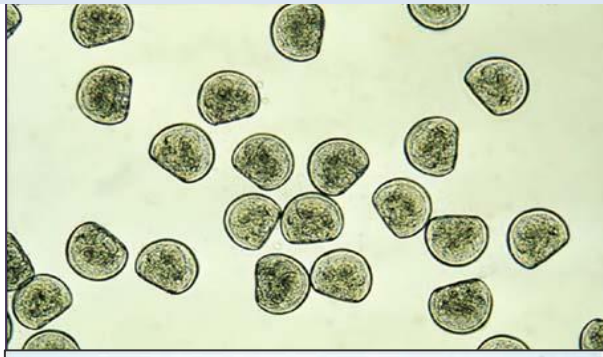


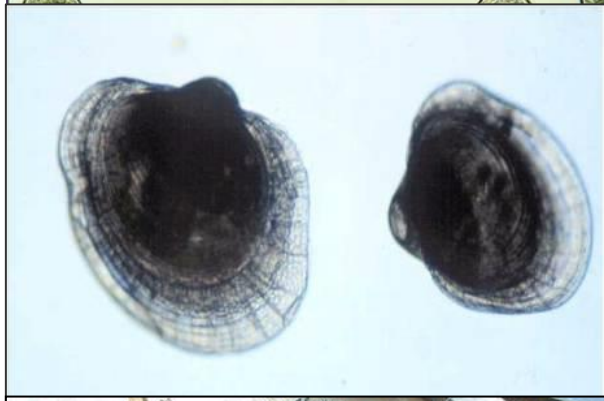
- ARLEQUIN
- GenePop
- GENETIX
- *adegenet*
- *DiveRsity*
- NeESTIMATOR
- NETVIEW
- BayeScan
- LOSITAN

- Differentiation
- Gene flow
- Structure
- Diversity

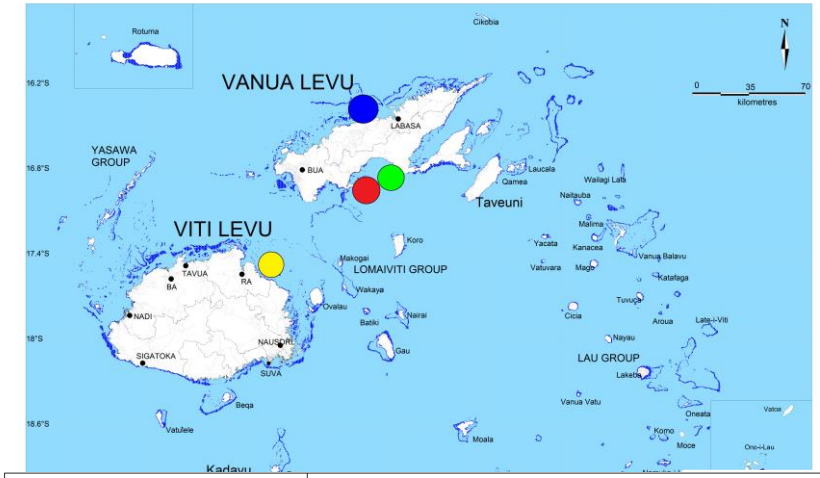
Results: population genomics

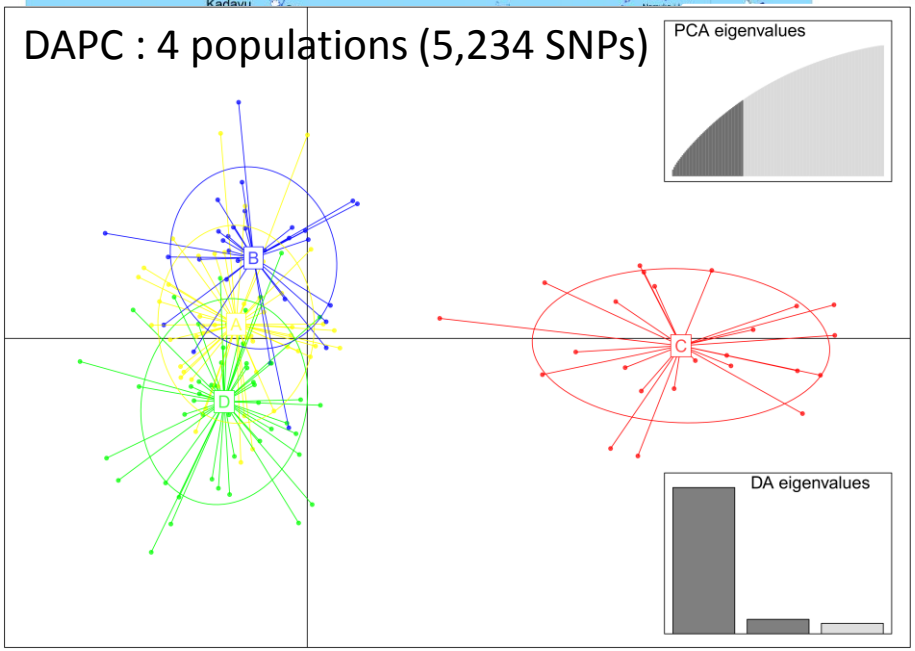
- 5,234 genome-wide SNPs discovered.
- Low levels of genetic differentiation (average F_{st} = 0.042).
- N_e > 192 for all wild populations. Hatchery N_e = 6.1.
- Outlier analyses detected ~100 SNPs between colour morphs.

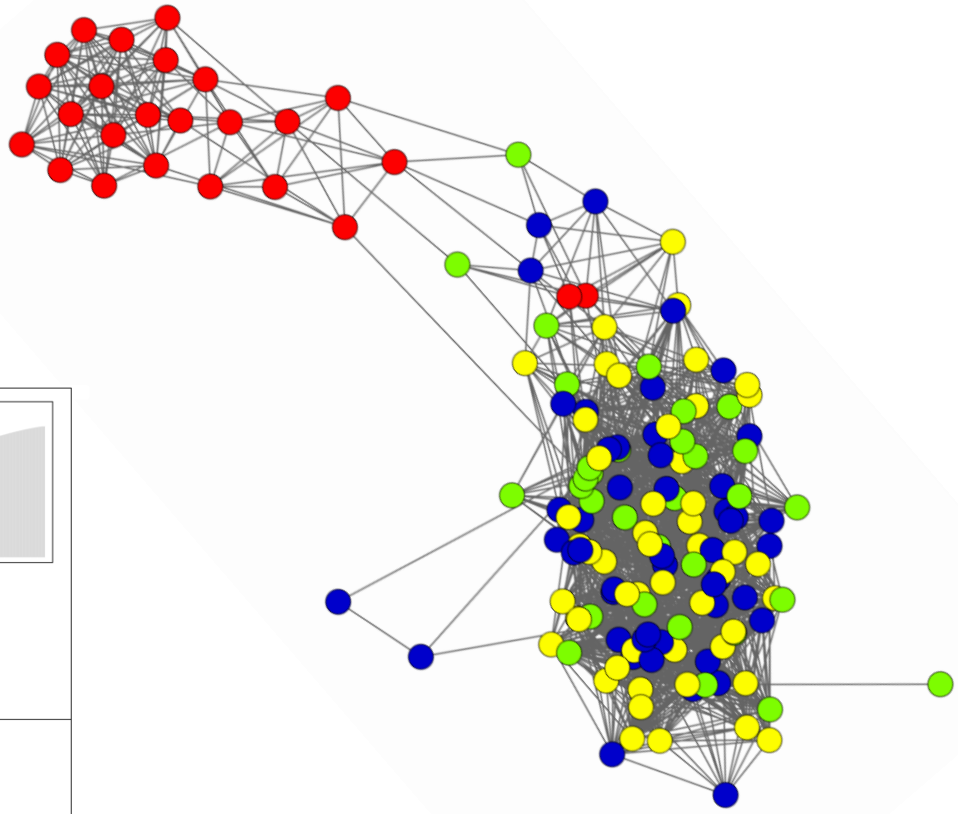




Results: population genomics

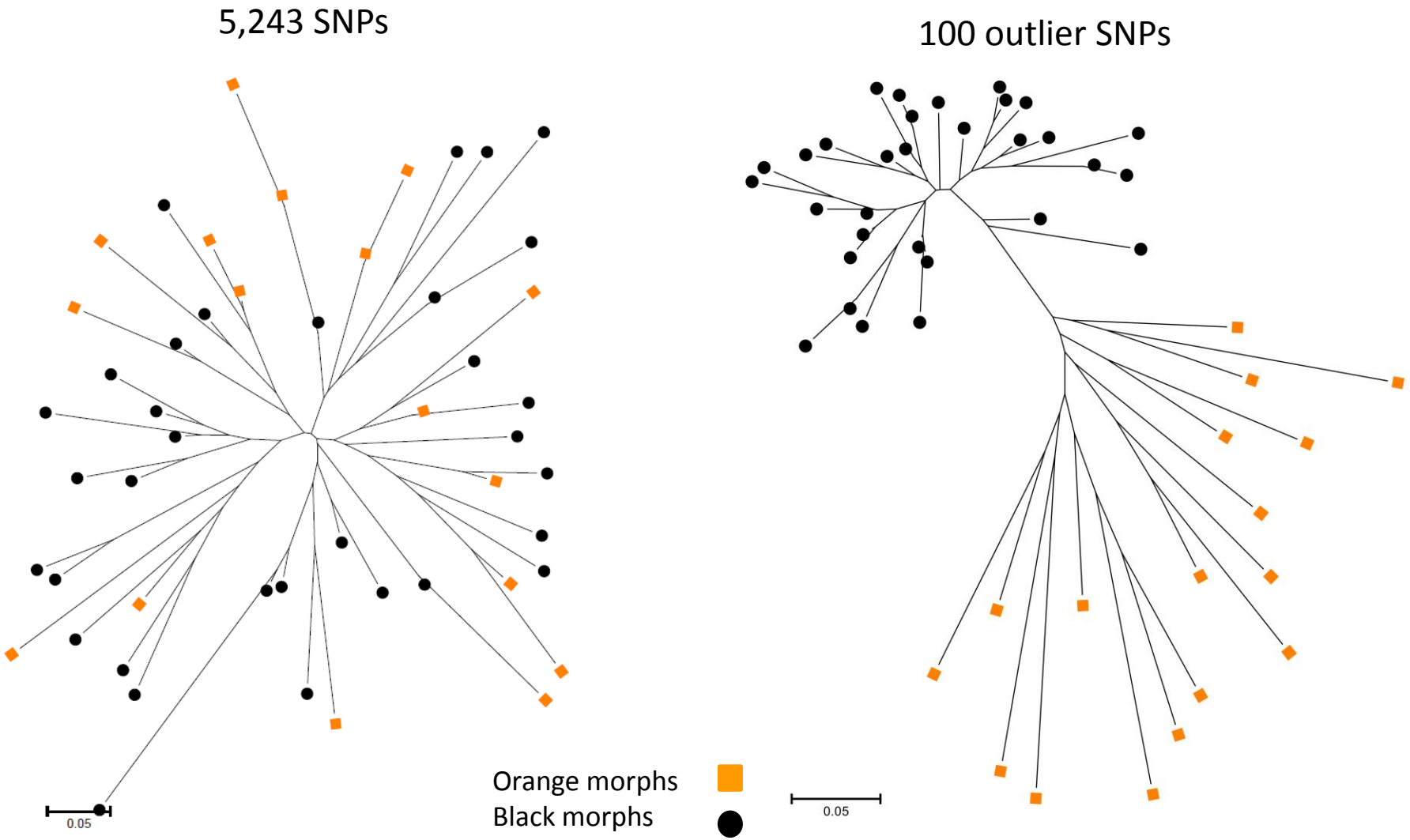






NETVIEW : 4 populations, 156 individuals (k-NN = 40, 5,234 SNPs)

Results: colour morphs



Conclusions and future directions

- Genome-wide SNPs revealed panmixia for *P. margaritifera* within Fiji.
- High utility of SNPs to detect population structure and differentiation
- Outlier testing able to differentiate between tissue colour morphotypes.
- Sound fishery management possible given informativeness of dataset.

Acknowledgements

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Questions?