

Project Title	The role of copy number variation in environmental adaptation in corals
University (where student will register)	University of Warwick
Which institution will the student be based at?	As above
Theme (Max. 2 selections)	Climate & Environmental Sustainability <input type="checkbox"/> Organisms & Ecosystems <input checked="" type="checkbox"/> Dynamic Earth <input type="checkbox"/>
Key words	Coral reefs, climate change, copy number variation, adaptation
Please explain how the project fits within the NERC remit	This project is focused on the adaptive capacity of corals. This aligns strongly with NERC’s Strategic Delivery Plan 2022-2025 by addressing environmental challenges associated with climate change.
Supervisory team (including institution & email address)	PI: Dr Ed Smith (University of Warwick, ed.g.smith@warwick.ac.uk) Co-I: Prof Robin Allaby (University of Warwick, R.G.Allaby@warwick.ac.uk)

Project Highlights:

- Investigate coral adaptation to the world’s warmest reefs. In this project, you will be analysing gene copy number variation, an often overlooked but important source of genomic variation.
- You will develop cutting-edge bioinformatic skills analysing short- and long-read sequencing datasets.
- You will be working at the forefront of ecological genomics research whilst contributing to a growing body of research working to conserve coral reefs for future generations.

Overview (including 1 high quality image or figure:

Coral reefs have suffered dramatic declines over the past three decades due to a myriad of natural and anthropogenic stressors. As the threats to coral reefs are expected to increase under climate change, it is imperative that we understand the ecological and evolutionary mechanisms underpinning coral stress tolerance. An improved understanding of corals’ adaptive capacity will help improve forecasts of reef futures in response to climate change, identify vulnerable populations for conservation, and enhance reef restoration efforts.

To date, research on the genomic basis for coral adaptation has focussed on using single nucleotide polymorphisms (SNPs) to identify regions of the genome under selection (e.g., Smith et al., 2022). The focus on SNPs has largely resulted from the ease at which they can be obtained through short-read sequencing technologies, however, SNPs are only one of many types of genomic polymorphisms (e.g., inversions, translocations, copy number variation). Copy number variation (CNV) is a form of genomic variation that arises from the duplication of genomic segments, which can alter gene expression through dosage effects, as well as provide substrate for adaptive

evolution. CNV has been recognised as an important source of variation between coral species (Noel et al., 2023), yet remains understudied at the species level (i.e., intraspecific variation). This project will take advantage of recent technological and methodological advances to investigate whether copy number variation (CNV) is an important driver of coral adaptation to distinct thermal environments.

In this project, you will quantify the extent of CNV among individuals of the same coral species collected from the extreme environmental gradient located between the Persian/Arabian Gulf and the Gulf of Oman. You will identify gene family expansions associated thermal and salinity gradients, and assess how CNV at the genomic level impacts the transcriptome/proteome.

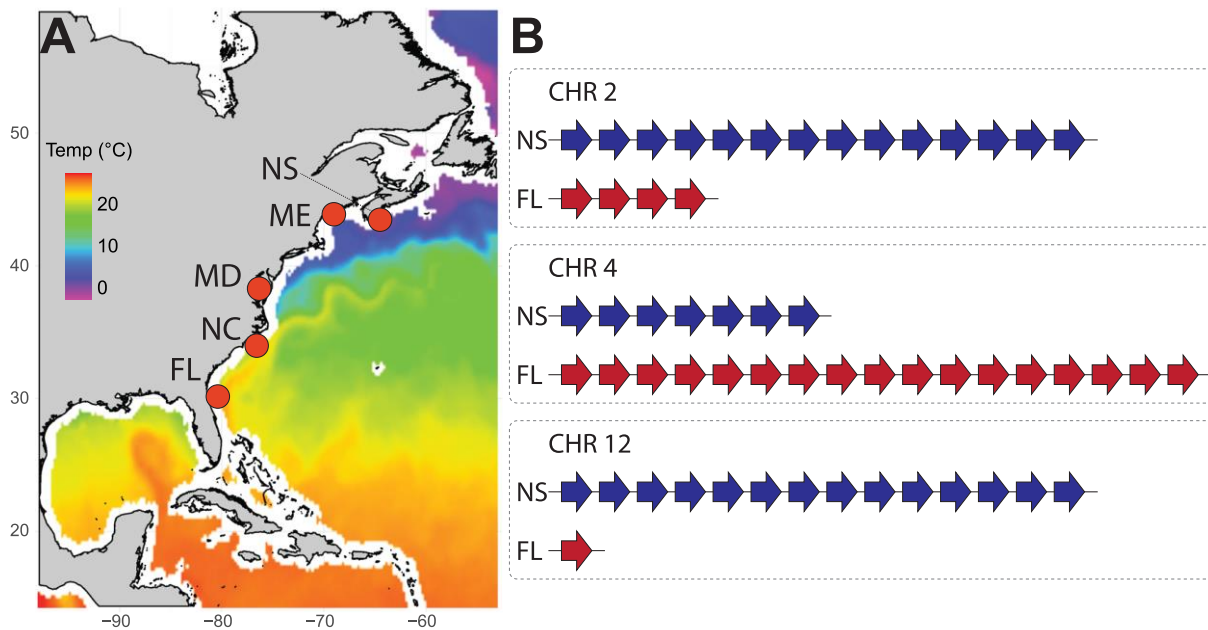


Figure 1: Our recent research on the starlet sea anemone (*Nematostella vectensis*) along the Atlantic Coast of the U.S. has revealed extensive copy number variation (CNV) between populations (e.g., Smith et al. 2023). In this project, you will be using similar techniques to investigate CNV differences in corals.

Alt Text: This image shows distinct gene copy number differences between anemones sampled at the extremes of a thermal gradient.

Methodology:

Copy number variation among individuals of the same coral species will be compared using whole genome sequencing. There is freedom for the student to target particular genes of interest and quantify copy number differences and sequence divergence using multiple approaches including qPCR, amplicon sequencing, and comparative genomics (see Smith et al. 2023). In order to gain functional insights, we plan to supplement these analyses with additional approaches that could include common-garden experiments, transcriptomics, proteomics, and/or microscopy.

Training and skills:

Students will be awarded CENTA2 Training Credits (CTCs) for participation in CENTA2-provided and 'free choice' external training. One CTC equates to 1/2 day session and students must accrue 100 CTCs across the three years of their PhD.

Training will be provided in a range of different techniques, as required, including molecular biology (e.g., high molecular weight DNA extractions, qPCR, sequencing library preparation), bioinformatics (e.g., genome assembly, comparative genomics), and experimental design.

Partners and collaboration (including CASE):

Further information on partners and collaboration (including CASE):

This project will involve collaboration with Dr. John Burt and members of Burt Lab at New York University Abu Dhabi.

Possible timeline:

Year 1: Genome-wide characterisation of intraspecific CNV using population genomics WGS data or genome assemblies.

Year 2: In-depth analyses of target genes across different environments.

Year 3: Integrating experimental approaches to gain mechanistic insights into the functional effects of genomic copy number variation.

Further reading:

Dorant, Y., Cayuela, H., Wellband, K., Laporte, M., Rougemont, Q., Mérot, C., Normandeau, E., Rochette, R. and Bernatchez, L. (2020) Copy number variants outperform SNPs to reveal genotype–temperature association in a marine species. *Molecular Ecology*, 29(24), pp.4765-4782.

Noel, B., Denoeud, F., Rouan, A., Buitrago-López, C., Capasso, L., Poulain, J., Boissin, E., Pousse, M., Da Silva, C., Couloux, A. and Armstrong, E. (2023) Pervasive tandem duplications and convergent evolution shape coral genomes. *Genome Biology*, 24(1), pp.1-38.

Smith, E.G., Hazzouri, K.M., Choi, J.Y., Delaney, P., Al-Kharafi, M., Howells, E.J., Aranda, M. and Burt, J.A. (2022) Signatures of selection underpinning rapid coral adaptation to the world's warmest reefs. *Science advances*, 8(2), p.eabl7287.

Smith, E.G., Surm, J.M., Macrander, J., Simhi, A., Amir, G., Sachkova, M.Y., Lewandowska, M., Reitzel, A.M. and Moran, Y. (2023) Micro and macroevolution of sea anemone venom phenotype. *Nature Communications*, 14(1), p.249.

Further details:

Please see the lab page [here](#).

To learn more about the project, contact Ed Smith (ed.g.smith@warwick.ac.uk). Please include a CV, details of past research, and outline your interest in the project.