

the early 19th century

their native environment, with the northern type crab exhibiting superior cold tolerance and the southern type exhibiting superior heat tolerance (Somero and Somero 2014).

Interestingly, cold tolerance was later found to be correlated with mitochondrial haplotype, indicating that variation in the mitochondrial genome is driving the disparity between the northern and southern crabs (Coyle et al. 2011). True, this suggests that mitochondria can influence phenotype—an idea that has had increasing evidence in recent years. The exact mechanism of this phenomenon in green crabs remains a mystery. 50-60 crabs were

site from Harpswell, Downeast Maine. For each variant, crabs were dissected, and DNA was extracted and amplified for the CO1 gene. For each variant, a primer pair was selected for sequencing the entire mitochondrial genome. RNA was extracted from the heart, gill, and muscle tissue then sent to Novogene for a process known as RNA-Seq for sequencing genes. Finally, the data was analyzed for differences among variants.

### RESULTS

A total of 9 samples were successfully sequenced, representing two of each variant (except for B2, which only had one). During the initial CO1 screening, a new warm type variant was discovered (henceforth referred to as A3), but this was not sequenced. The RNA-Seq process yielded approximately 9000 nucleotides of the mitochondrial genome for each sample. Although this was not the complete genome, two-thirds of the genes were recovered for analysis. A total of 77 nucleotide substitutions were identified among variants—73 were synonymous (i.e. the resulting amino acid was unchanged), and 4 were nonsynonymous (i.e. the resulting amino acid was different). The two most notable nonsynonymous mutations were found in the ATP6 gene and Cox3 gene of both B1 replicates.

These are of significance as ATP6 and Cox3 can influence the amount of ATP available at different temperatures. In fact, variation in ATP6 has been shown to affect the thermal tolerance of mammals (Ballard and Whitlock 2004). However, this only accounts for B1, not B2 nor C. In the future, additional work should be done to recover the remaining mitochondrial genome to assess for nonsynonymous mutations in B2 and C. Nevertheless (12):