NEW INSIGHTS FROM GENOMICS? TESTING NEW APPROACHES TO POPULATION GENETICS IN FLATBACK AND GREEN TURTLE POPULATIONS IN AUSTRALIA.

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Our ability to define marine turtle populations is critical for effective conservation management. Deciphering the genetic structure within and among populations has contributed greatly to our understanding of the extent of interchange among rookeries and provided insights into marine turtle behavior. In Australia we have identified populations and established management units (MUs) as a focus for conservation, largely based on mitochondrial (mt) DNA data, as well as considering nuclear microsatellite data for some species. Extensive new tissue sampling of turtles at rookeries in Western Australia provided an opportunity to apply new genomics tools to investigate genetic structure in green and flatback rookeries around Australia. After the identification of several thousand SNP loci in each species, we analyzed ~1000 loci in flatback turtles and ~2000 loci in green turtles. Where comparisons were possible, genetic diversity at SNP loci was about 50% of that observed at microsatellite loci. Levels of genetic differentiation were very similar between microsatellite and SNP data for flatback turtles, but in green turtles the SNP data often produced lower values. Tests for the significance of genetic differentiation were similar between the two SNP and microsatellite data sets for both species. In contrast, patterns mtDNA genetic differentiation were quite different between species. Estimates of male-mediated gene flow varied among populations and species. Previously defined MUs for both species were supported, and new MUs were defined for flatback turtles in Western Australia. Consistency in the results between the genomic and microsatellite data have provided confidence in both approaches and opened possibilities for future research.

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