A NEW WAY TO TAG

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If you have ever worked on a sea turtle nesting beach project, then you have probably had the experience of snapping a metal tag to the trailing edge of a sea turtle's flipper. You have probably also thought about how the process of tagging itself might have affected the behavior of that turtle, or you may have wondered if you would ever see her or the tag again. Tagging studies have taught us a lot over the years, but the fact is that for some populations, most tagged females are indeed never seen again, likely because of low nest site fidelity relative to the scale of the tagging effort. And saturation tagging is difficult; patrolling a study area every hour during the nesting season to intercept nesting females can require an enormous number of participants and can pose significant and costly logistical challenges. Yet until recently, flipper tagging has been the only option for obtaining reliable demographic data about how many females are nesting, how many clutches of eggs they are laying, and how often they are remigrating (i.e., how frequently they are returning to nest).

In recent years, however, a new technique has emerged as an alternative means of collecting individual fecundity data. The method uses genetic tagging of females through nest sampling. Each female leaves behind a DNA record in her eggshells, and researchers can now exploit nuclear genomic variation between turtles to identify unique genetic fingerprints for each individual. Those intrinsic genetic tags permit researchers to assign clutches sampled during morning surveys to individual females without the need to physically intercept the adult turtles. The data collected are analogous to those collected through conventional tagging, and they allow researchers to estimate nesting female population size and annual survival, as well as clutch frequency and remigration intervals.

Nest sampling confers a few critical advantages over conventional tagging. First, the ability to fingerprint eggs opens up possibilities for tagging on geographical scales that would be logistically impossible with standard tagging patrols. Second, nest sampling is noninvasive to nesting females and alleviates concerns about how tagging might affect their behavior. Perhaps most significantly, the same genetic markers used for individual identification can clarify relationships among nesting females. Long-term projects linking daughters to their mothers could ultimately assess natal site fidelity, reproductive longevity, reproductive fitness, and recruitment patterns.

Genetic tagging of eggs is not without its drawbacks, however. Eggs ideally would be sampled within the first few days of incubation to reduce the likelihood of contamination from embryonic nuclear DNA. This approach requires the collection of a single viable egg from each clutch, unless eggshells are available through depredation or natural breakage. Also, genetic analysis must currently be conducted in a specialized laboratory. However, with rapidly evolving genetic technologies, we may one day be able to undertake such work at field sites.

Undeveloped eggs sampled following hatchling emergence can yield maternal DNA. Unfortunately, the warm, moist conditions ideal for embryo development promote rapid degradation of the maternal nuclear DNA present in the eggshell. Even in fresh eggs, the amount of DNA present is markedly lower than in a tissue or blood sample, so additional analyses are often necessary in approximately 10 to 15 percent of samples to resolve genetic fingerprinting errors. Nevertheless, the wealth of information gained through egg-derived tagging outweighs the disadvantage of destructive sampling and the technical challenges of analyzing small amounts of DNA. Moreover,

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researchers can use stable isotope signatures of yolks from sampled eggs to assign females to major foraging areas. By having researchers combine those powerful techniques, it is possible to determine the reproductive consequences of foraging in different regions.

We are currently conducting a genetic tagging project with the goal of sampling every recorded loggerhead nest north of Florida in collaboration with state agency sea turtle programs and with state and federal biologists, researchers, and volunteer groups in Georgia, Maryland, North Carolina, South Carolina, and Virginia. This range encompasses the majority of nesting habitats of the Northern Recovery Unit of loggerheads that nest in the southeastern United States. Genetic tagging is ideal for this subpopulation because nesting densities are low to moderate. Moreover, validating the egg chamber is standard morning survey protocol for all nests in this region.

Genetic tagging of unincubated eggs is a robust technique for individual identification in situations where direct interception of nesting females is not feasible or is too expensive and labor intensive. Some projects have ceased flipper tagging altogether. For instance, the Little Cumberland Island Sea Turtle Project, one of the longest-running saturation tagging efforts in the world (1964–present),

switched entirely to genetic tagging in 2010. Former intern Jocelyn Coulter inspired the idea of egg tagging in 2005 when she froze depredated eggs from a freshly laid clutch where the turtle had evaded patrollers. We were later able to match the eggs' genetic fingerprint to a skin sample from a female they had tagged earlier in the season.

Although this modern approach is not appropriate for all nesting populations, it provides an alternative to flipper tagging for turtle rookeries where nest sampling is logistically manageable. Fully exploiting the benefits of egg sampling requires partnerships with agencies and volunteer networks that conduct nest surveys across the potential range of the nesting population. For rookeries where all those elements come together, this technique will continue to yield novel insights into sea turtle behavior for the foreseeable future. ■

CLOCKWISE, FROM TOP: An olive ridley deposits eggs into her nest chamber. © SERGIO PUCCI / WWW.PUCCI.CR ; A researcher collects an eggshell for genetic analysis to identify the individual turtle that laid the eggs. © MATTHEW GODFREY / NCWRC; Eggshell samples await analysis. © MATTHEW GODFREY / NCWRC