

**DIET ANALYSIS OF THE MEDITERRANEAN SHAG
(*PHALACROCORAX ARISTOTELIS DESMARETSII*) USING
CONVENTIONAL TECHNIQUES AND NEXT GENERATION
SEQUENCING**

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The recent development of next generation sequencing technologies allows the molecular identification of a species' diet from prey remains by the direct characterization of dozens of samples with several thousand sequences per sample, and has the potential to reveal many consumed species simultaneously (DNA metabarcoding). The Mediterranean shag is a subspecies of high conservation concern, with global population of less than 10,000 pairs, 10% of which lives in the Greek islands of the Aegean and the Ionian Sea. Within the frame of the EU LIFE project "ConShagAudMIBAGR", a diet analysis is carried out using both conventional prey identification and next generation sequencing. Regurgitates (undigested prey remains) and feces have been collected from a large colony of the species in the N. Aegean Sea. A conventional prey analysis has been carried out in the regurgitates, by identifying indigestible part remains, mainly fish otoliths. The regurgitates as well as fecal samples are being subjected to amplicon sequencing using the 454 GS-FLX platform. By analyzing the same samples (i.e. regurgitates) both by conventional and molecular techniques, we will be able to check whether molecular approaches perform better for prey identification at the species level and if they can give reliable quantitative estimations. Moreover, the analysis of fecal samples will show whether there are prey items that were not detected in the regurgitates. Finally, it will be estimated which approach is more cost effective for determining the diet of the Mediterranean shag.