B40 Coupling DNA and Gas Chromatography/Mass Spectrometry (GC/MS) Analysis of Skeletal Remains: A Case Study of the USS *Oklahoma*

Suni M. Edson, MS, Armed Forces DNA ID Laboratory, Dover Air Force Base, DE 19902*

Learning Overview: The purpose of this presentation is to provide information on a novel application of Gas Chromatography/Mass Spectrometry (GC/MS) analysis that could improve the speed at which persons are identified in mass fatality incidents.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by showing a novel application of GC/MS and how this data may be coupled with DNA testing results from skeletonized human remains.

The Armed Forces Medical Examiner System-Armed Forces DNA Identification Laboratory (AFMES-AFDIL) partners with the Defense POW/MIA Accounting Agency (DPAA) to provide DNA testing of skeletonized human remains of missing service members from past military conflicts. Most commonly, the remains found are not those of a single individual, but comprise commingled individuals from aircraft crashes, ground losses, ships, or other incidents. One of the largest single assemblages of remains ever analyzed is that of the remains of the individuals killed-in-action on the USS *Oklahoma*.

On 7 December 1941, torpedoes sank the USS *Oklahoma* during an attack on Pearl Harbor, HI. In the process of sinking, the ship rolled over and then remained inverted in the harbor until 1943. The ship was righted at that time and the remains of approximately 429 individuals were recovered and placed in group burials. Efforts to identify the remains made in the late 1940s resulted in 35 persons being buried as individuals. The remainder were buried in 46 plots at the National Memorial Cemetery of the Pacific (NMCP) in Hawaii.

Beginning in 2003, the DPAA initiated an effort to identify the 394 individuals from the graves at the NMCP. The testing of the first casket to be disinterred generated over 100 different mitochondrial DNA (mtDNA) profiles. The remaining 45 caskets were disinterred in 2015, and to date nearly 5,000 osseous fragments have been submitted to AFMES-AFDIL for mtDNA testing, and approximately 3,000 have been completed.

As part of the DNA extraction protocol at AFMES-AFDIL, the exterior of the bone is removed using a sanding tool. For the USS *Oklahoma* samples, the detritus was often sticky with the residue of fuel oil and adipocere. Rather than being discarded, this material was collected from a selection of samples by the analysts and retained as part of a study on the carry-over of inhibitory materials from skeletal materials to the associated extracted DNA.

The skeletal detritus from 208 individual elements was treated sequentially with acetonitrile and dichloromethane. The eluate was removed and allowed to evaporate in an effort to concentrate materials found in the osseous elements. The concentrated materials were then re-suspended in methanol for injection on an Agilent 7890A-5975C GC/MS. Contained within the skeletal materials were products of decomposition, such as fats and esters, fat-soluble medications, and chemicals inherent to the ship itself, such as anthracene and other fuel oil components.

It was expected that the remains would show largely the same chemical profile, especially with regards to the fuel oil present. However, this was not found to be so. The GC/MS traces showed fuel profiles consistent with what should have been on the ship, the USS *Oklahoma* being one of the first ships to be powered by fuel oil. However, they were not all the same. In between the peaks of fuel and decomposition by-products were traces of medications and other chemicals. When the GC/MS data from the different solvents were compiled and paired with the DNA extracted from the remains, it was found that the generated chemical profiles were unique to the individual.

While GC/MS analysis of skeletonized human remains still needs to be perfected, it has far-reaching implications for human identification. Coupling DNA testing with GC/MS profiling could greatly improve the speed with which large assemblages of commingled remains can be sorted. Once a GC/MS profile is paired with the DNA profile, one only needs to test skeletal elements in GC/MS, which is a markedly faster and cheaper method than DNA testing and requires very little training.

Skeletonized Remains, DNA, GC/MS