Hair and fiber analysis plays a key role in the realm of forensic science. A single hair or fragment of clothing could be the key to placing a suspect at the scene of a crime. Most current analyses involve animal hair classification based upon the appearance and physical characteristics of these hairs. However, in the event that two different types of animal hairs are nearly identical in all of their physical characteristics, other analytical methods must be employed. On the physical level, fine cashmere wool hairs are difficult to distinguish based on microscopic techniques from their twins, the lesser-valued yak wool fibers. Studies exploring such qualities as cashmere hair curvature and length, mean fiber diameter and resistance to compression have not been able to conclusively discriminate between the two samples. Another analytical method is needed in order to explore deeper into the molecular and elemental makeup of these fibers to determine if compositional differences may exist, thus aiding in the identification process.

Micro x-ray fluorescence (MXRF) is a nondestructive, analytical method that requires little to no sample preparation. Using MXRF, we were able to successfully determine an elemental difference between a sample of Mongolian cashmere hairs and Mongolian yak wool hairs. Larger amounts of condensed hairs, individual hairs and point spectra of the samples were obtained in order to see if the elemental differences remained constant. It was determined that the cashmere hairs contained a higher sulfur content, while the yak wool hairs were higher in calcium. This pattern was only visible in examining larger amounts of fibers with sample masses of 4 mg at one time. Scans of individual fibers and point spectra were not consistent, thus leading to the conclusion that a ‘bulk effect’ does exist that can be detected by MXRF. This work demonstrates the feasibility of using MXRF to discriminate between cashmere and a yak-wool counterfeit. Further optimization of the minimum amount of hairs and comparisons with a number of other hair samples is needed to extend this method to a routine and reliable identification protocol.