Michael Coble, PhD
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Area of Expertise

Complex DNA mixtures of two or more contributors can be challenging for the forensic scientist to interpret. My research focuses on issues associated with DNA mixture interpretation and probabilistic methods of interpretation using software analyses. Other areas of research include haploid marker systems for forensic testing (mitochondrial DNA and Y-chromosome testing), and non-traditional marker systems (e.g. X-chromosomal STRs, insertion-deletion markers, etc.) to gather genetic information from challenged samples.

Qualifications

BS in Biology, Appalachian State University

MFS in Forensic Molecular Biology, The George Washington University

PhD in Genetics, The George Washington University

Recent Publications

A new implementation of a semi-continuous method for DNA mixture interpretation
Alfieri, J., Coble, M. D., Conroy, C., Dahl, A., Hares, D. R., Weir, B. S., Wolock, C., Zhao, E., Kingston, H. & Zolandz, T. W., Dec 2022, In: Forensic Science International: Reports. 6, 100281.

Study of CTS DNA Proficiency Tests with Regard to DNA Mixture Interpretation: A NIST Scientific Foundation Review
Bille, T., Coble, M. D., Kalafut, T. & Buckleton, J., 21 Nov 2022, In: Genes. 13, 11

Assessment of human nuclear and mitochondrial DNA qPCR assays for quantification accuracy utilizing NIST SRM 2372a
Cropper, E., Coble, M. D. & Kavlick, M. F., Jul 2022, In: Forensic Science International: Genetics. 59, 102711.

Re: Riman et al. Examining performance and likelihood ratios for two likelihood ratio systems using the PROVEDIt dataset
Buckleton, J., Bright, J. A., Taylor, D., Wivell, R., Bleka, Ø., Gill, P., Benschop, C., Budowle, B. & Coble, M., Jul 2022, In: Forensic Science International: Genetics. 59, 102709.

Exploring likelihood ratios assigned for siblings of the true mixture contributor as an alternate contributor
Kelly, H., Coble, M., Kruijver, M., Wivell, R. & Bright, J. A., May 2022, In: Journal of Forensic Sciences. 67, 3, p. 1167-1175 9 p.

Exploring the advantages of amplifying the entire extract versus splitting the extract and interpreting replicates using a continuous model of interpretation
Bille, T., Coble, M. D. & Bright, J. A., 2022, In: Australian Journal of Forensic Sciences. 54, 5, p. 584-595 12 p.

Analysis of forensic mixtures
Coble, M., Budowle, B. & Erlich, H., 1 Jan 2020, *Silent Witness: Forensic DNA Evidence in Criminal Investigations and Humanitarian Disasters.* Oxford University Press, p. 49-66 18 p.

Mitochondrial DNA control region variation in Lebanon, Jordan, and Bahrain
Zimmermann, B., Sturk-Andreaggi, K., Huber, N., Xavier, C., Saunier, J., Tahir, M., Chouery, E., Jalkh, N., Megarbane, A. , Bodner, M., Coble, M., Irwin, J., Parsons, T. & Parson, W., Sep 2019, In: Forensic Science International: Genetics. 42, p. 99-102 4 p.

STRmix™ collaborative exercise on DNA mixture interpretation
Bright, J. A., Cheng, K., Kerr, Z., McGovern, C., Kelly, H., Moretti, T. R., Smith, M. A., Bieber, F. R., Budowle, B., Coble, M. D., Alghafri, R., Allen, P. S., Barber, A., Beamer, V., Buettner, C., Russell, M., Gehrig, C., Hicks, T., Charak, J., Cheong-Wing, K., & 34 othersCiecko, A., Davis, C. T., Donley, M., Pedersen, N., Gartside, B., Granger, D., Greer-Ritzheimer, M. M., Reisinger, E., Kennedy, J., Grammer, E., Kaplan, M., Hansen, D., Larsen, H. J., Laureano, A., Li, C., Lien, E., Lindberg, E., Kelly, C., Mallinder, B., Malsom, S., Yacovone-Margetts, A., McWhorter, A., Prajapati, S. M., Powell, T., Shutler, G., Stevenson, K., Stonehouse, A. R., Smith, L., Murakami, J., Halsing, E., Wright, D., Clark, L., Taylor, D. A. & Buckleton, J., May 2019, In: Forensic Science International: Genetics. 40, p. 1-8 8 p.

Expanding beyond the current core STR loci: An exploration of 73 STR markers with increased diversity for enhanced DNA mixture deconvolution
Novroski, N. M. M., Wendt, F. R., Woerner, A. E., Bus, M. M., Coble, M. & Budowle, B., Jan 2019, In: Forensic Science International: Genetics. 38, p. 121-129 9 p.