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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

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., 2021, (Accepted/In press) In: Australian Journal of Forensic Sciences.

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 others, Ciecko, 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.

Probabilistic genotyping software: An overview

Coble, M. D. & Bright, J. A., Jan 2019, In: Forensic Science International: Genetics. 38, p. 219-224 6 p.

NIST interlaboratory studies involving DNA mixtures (MIX05 and MIX13): Variation observed and lessons learned

Butler, J. M., Kline, M. C. & Coble, M. D., Nov 2018, In: Forensic Science International: Genetics. 37, p. 81-94 14 p.

NIST interlaboratory studies involving DNA mixtures (MIX13): A modern analysis

Buckleton, J. S., Bright, J. A., Cheng, K., Budowle, B. & Coble, M. D., Nov 2018, In: Forensic Science International: Genetics. 37, p. 172-179 8 p.

Non-autosomal forensic markers

Coble, M., Andersen, M. M., Buckleton, J. S., Taylor, D. & Bright, J. A., 3 Sep 2018, *Forensic DNA Evidence Interpretation*. Taylor and Francis, p. 315-352 38 p.

A response to “Likelihood ratio as weight of evidence: A closer look” by Lund and Iyer

Gittelsohn, S., Berger, C. E. H., Jackson, G., Evett, I. W., Champod, C., Robertson, B., Curran, J. M., Taylor, D., Weir, B. S., Coble, M. D. & Buckleton, J. S., Jul 2018, In: *Forensic Science International*. 288, p. e15-e19

The peopling of South America and the trans-Andean gene flow of the first settlers

Gómez-Carballa, A., Pardo-Seco, J., Brandini, S., Achilli, A., Perego, U. A., Coble, M. D., Diegoli, T. M., Alvarez-Iglesias, V., Martínón-Torres, F., Olivieri, A., Torroni, A. & Salas, A., Jun 2018, In: *Genome Research*. 28, 6, p. 767-779 13 p.