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IN THE CIRCUIT COURT OF THE FIRST CIRCUIT

STATE OF HAWAI‘I

STATE OF HAWAI‘I v. ERIC THOMPSON, also known as Eric H. Thompson, Eric Thompson, Defendant.	CASE NO. 1CPC-22-0000500 COUNT 1: MURDER IN THE SECOND DEGREE (§707-701.5 and 706-656 HRS) (REPORT/CITATION NO. 22017454-002) COUNT 2: CARRYING OR USE OF FIREARM IN THE COMMISSION OF A SEPARATE FELONY (§134-21 HRS) (REPORT/CITATION NO. 22017454-003) FINDINGS OF FACT, CONCLUSIONS OF LAW, AND ORDER GRANTING STATE'S MOTION TO DETERMINE ADMISSIBILITY OF "TRUEALLELE" EXPERT TESTIMONY PURSUANT TO HRE 104(A)

FINDINGS OF FACT, CONCLUSIONS OF LAW, AND ORDER GRANTING STATE'S MOTION TO DETERMINE ADMISSIBILITY OF "TRUEALLELE" EXPERT TESTIMONY PURSUANT TO HRE 104(A)

State's Motion To Determine Admissibility Of "TrueAllele" Expert Testimony Pursuant To HRE 104(A), having come on for hearing on December 3, 2024, before the Honorable Paul

jg

B.K. Wong, the State being represented by Deputy Prosecuting Attorney Joel R. Garner and Defendant Thompson being present and being represented by Nelson W.S. Goo, and the Court having received evidence, heard argument of counsel, and being fully advised in the premises, makes the following findings of fact and conclusions of law:

FINDINGS OF FACT

1. The Defendant Eric Thomson is charged with murder in the second degree and use of a firearm in the commission of a separate felony for the alleged killing of Jon Tokuhara.
2. The essential issue for the jury's determination at trial is whether or not the Defendant was or was not the person responsible for the alleged killing; in other words, the essential trial issue is identification.
3. Probabilistic genotyping is a combination of biological modeling, statistical theory, computer algorithms, and probability distributions to produce likelihood ratios for the DNA typing results of forensic samples.[1]
4. Historical methods of mixture interpretation consider all interpreted genotype combinations to be equally probable, whereas probabilistic approaches provide a statistical weighting to the different genotype combinations.[2]
5. Probabilistic genotyping does not utilize a stochastic threshold, but incorporates a probability of alleles dropping out or in.[3]

[1] Scientific Working Group on DNA Analysis Methods (SWGDAM) Guidelines for the Validation of Probabilistic Genotyping Systems, Jun. 15, 2015, State's exhibit 98 at 2.
[2] *Id*.
[3] *Id*.

6. In making use of more genotyping information when performing statistical calculations and evaluating potential DNA contributors, probabilistic genotyping enhances the ability to distinguish true contributors and non-contributors.[4]
7. While the science underlying TrueAllele and probabilistic genotyping is not new, the method of employment is relatively new. The underlying scientific theory is the Bayes Theorem, which was originally developed in the 1700s.[5]
8. The statistical sampling method that TrueAllele uses is based on Monte Carlo Markov Chain algorithms, which is a sampling method for solving complex problems.[6]
9. The Monte Carlo Markov Chain algorithm, originally called the Metropolis algorithm, was developed shortly after World War II at Los Alamos by physicists attempting to model neutron diffusion and multiplication rates in fission devices.[7]
10. The probability calculations involved in the TrueAllele process can be done manually, but because of the sheer amount of calculations, manual work is not feasible.
11. High-powered computing allows the calculation work to be done exponentially faster--and probably more accurately--and makes the employment of the scientific tools possible.
12. TrueAllele produces a Likelihood Ratio (LR) to assess the strength of two separate propositions – that the suspect contributed to the biological evidence versus whether other unknown individuals contributed to the biological evidence.[8]

[4] *Id*.
[5] Testimony of Jennifer Hornyak-Bracamontes, April 26, 2024.
[6] *Id*.
[7] State's exhibit 186 at 383-85.
[8] *See* State's exhibit 181.

13. The use of the LR in reporting is common in Europe, and it has become a standard practice to use the LR to measure the evidential weight of DNA evidence in criminal trials.[9]

14. It is standard practice for probabilistic genotyping systems to report DNA evidence associations using the likelihood ratio.[10]

15. Developmental validation of probabilistic genotyping systems is the acquisition of test data to verify the functionality of the system, the accuracy of the statistical calculations and other results, the appropriateness of analytical and statistical parameters, and the determination of limitations.[11]

16. Developmental validation may be conducted by the manufacturer or developer of the application or the testing laboratory.[12]

17. Internal validation of probabilistic genotyping software systems is the accumulation of test data within the laboratory to demonstrate that the established parameters, software settings, formulae, algorithms, and functions perform as expected.[13]

18. Generally, there are fifty to one hundred (50-100) published validation studies on probabilistic genotyping.[14]

[9] *See* State's exhibit 120 at 556 ("There is now widespread agreement that evidential weight in criminal trials is best measured via likelihood ratios (LRs) comparing prosecution and defense hypotheses.
[10] State's exhibit 114 at 3 (Examining the probabilistic genotyping system likeLTD, and indicating that the evidence will be evaluated using a LR); State's exhibit 115 (Examining EuroForMix, a probabilistic genotyping system using LRs); State's exhibit 117 (proposing a new model for statistical forensic DNA analysis using a LR); State's exhibit 119 (examining "Kongoh", a probabilistic genotyping system that reports results using LRs); State's exhibit 107 (comparing different probabilistic genotyping systems and the use of the LR).
[11] State's exhibit 98 at 5.
[12] *Id*.
[13] *Id*. at 8.
[14] Testimony of Jennifer Hornyak-Bracamontes, April 26, 2024.

19. Cybergenetics's TrueAllele program has been subjected to over forty (40) validation studies, of which eight have been published. The validation studies for TrueAllele have been both developmental and internal.[15]

20. Probabilistic genotyping--of which Cybergenetics's TrueAllele is just one model--is used by fifty percent (50%) of the United States in forensic work. Other countries in the world use probabilistic genotyping, including England, Scotland, Ireland, Finland, Denmark, Canada, Australia, and New Zealand.

21. Probabilistic genotyping is generally accepted in the forensic scientific communities in the western world.

22. The American National Standards Institute and the Academy Standards Board (ANSI/ASB) of the American Academy of Forensic Sciences publishes standards relevant to the use of probabilistic genotyping in casework.[16]

23. The Federal Bureau of Investigation publishes Quality Assurance Standards (FBI QAS) that cover the use of interpretation software such as probabilistic genotyping.[17]

24. The Scientific Working Group on DNA Analysis Methods (SWGDAM) publishes guidelines on the validation of probabilistic genotyping systems.[18]

25. TrueAllele complies with the appropriate ANSI/ASB, SWGDAM, and FBI QAS standards and guidelines, and has provided documentation of their compliance.[19]

[15] *See* State's exhibits 30 through 66, inclusive.
[16] State's exhibits 93 through 95, inclusive.
[17] State's exhibit 96.
[18] State's exhibit 92.
[19] State's exhibit 88 details TrueAllele's compliance with ANSI Standard 018, State's exhibit 89 details TrueAllele's compliance with ANSI Standard 020, State's exhibit 89 details TrueAllele's compliance with ANSI Standard 040, State's exhibit 91 details TrueAllele's compliance with the FBI QAS, and State's exhibit 91 details TrueAllele's compliance with the SWGDAM Guidelines.

26. TrueAllele has written standard operating procedures that guide the proper use of the program.[20]

27. In early 2013, the National Institute of Science and Technology (NIST) and the FBI conducted an interlaboratory study (MIX13) with 108 laboratories, including labs from 46 states, three Federal laboratories, and three Canadian laboratories.[21]

28. Using known DNA profiles, the MIX13 study designers created a series of five mixtures or "cases" that simulate profiles encountered in forensic casework for the participating laboratories to analyze.[22]

29. In "case 5" of the MIX13 study, 74 laboratories incorrectly included a potential suspect "5C" into a four-person mixture and provided a Combined Probability of Inclusion (CPI) match statistic to quantify the inclusion.[23]

30. Only 7 laboratories out of the 108 participants correctly excluded potential suspect "5C', and the sole laboratory in the study using probabilistic genotyping software (TrueAllele) was one of the 7 to correctly exclude "5C". Cybergenetics also submitted results that correctly excluded "5C", but were not considered as part of the 108 participating laboratories as they are not a traditional forensic lab.[24]

31. The MIX13 study highlights how the use of a probabilistic genotyping system can provide more accurate results than the traditional methods of manual DNA mixture interpretation.

[20] State's exhibit 100.
[21] State's exhibit 190 at 84.
[22] State's exhibit 190 at 85.
[23] State's exhibit 190 at 90.
[24] *See* State's exhibit 190 at 90.

32. In 2014, employees from Cybergenetics, the parent company of TrueAllele, and the Virginia Department of Forensic Science published a study comparing manual DNA mixture interpretation and TrueAllele in 72 criminal cases.[25]

33. As part of this 2014 publication, the authors determined the "specificity" of TrueAllele, which "measures the extent to which a mixture interpretation method does not misidentify the wrong person."[26] Essentially, the authors calculated a general error rate of false inclusions – how often TrueAllele gave a positive likelihood ratio for a suspect who did not actually contribute to a mixture.[27]

34. In this study, the authors determined that the error rate of TrueAllele is inversely related to the likelihood ratio – that the higher the likelihood ratio that supports a conclusion that a suspect contributed DNA, the smaller chance of a false inclusion.[28]

35. For likelihood ratios between 1 and 1,000, the false positive rate is 1 in 20,000, and when the likelihood ratio is greater than 1,000, the false positive rate for TrueAllele is 1 in 1,000,000.[29]

36. The likelihood ratios in this case, as applied to Defendant, for item 91-Q7 is 199 million and for item 91-Q8 is 16.4 trillion.[30]

37. While some probabilistic genotyping systems require historical data to form the underlying assumptions needed for the statistical model, TrueAllele uses only the data from the profile under consideration.[31]

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[25] State's exhibit 28.
[26] State's exhibit 28 at 12.
[27] Testimony of Jennifer Hornyak-Bracamontes, October 14, 2024.
[28] *See* Testimony of Jennifer Hornyak-Bracamontes, October 14, 2024.
[29] Testimony of Jennifer Hornyak-Bracamontes, October 14, 2024.
[30] Testimony of Jennifer Hornyak-Bracamontes, October 14, 2024; State's exhibit 281.
[31] Testimony of Jennifer Hornyak-Bracamontes, October 14, 2024; *see* State's Exhibit 187 at 1; *see also U.S. v. Anderson*, 673 F.Supp3d 671, 686 (M.D. Pa. 2023) ("TrueAllele does not rely on that type of external information to generate its results, as it instead 'analyzes the data directly.'")

38. TrueAllele has been validated to calculate the likelihood ratios in mixture samples of up to ten (10) contributors.[32]

39. In this case, Cybergenetics performed TrueAllele analyses on genetic samples to calculate the likelihood ratios for three and four contributors.[33]

40. TrueAllele has been validated and verified to work using the Globalfiler STR kit, and the AB 3500 Genetic Analyzer[34], both of which were used by the Honolulu Police Department in typing the forensic DNA samples in this case.[35]

41. As recommended by the ANSI/ASB Standards, Cybergenetics runs a performance check on the TrueAllele system every time the software is updated to change analytical processes that may impact interpretation or results.[36]

42. When the testing was done, a performance check was done on the TrueAllele system and it was determined that TrueAllele was working properly at the time of the test.[37]

43. Standard operating procedures employed by Cybergenetics in the use of TrueAllele are established and, when followed, the results are generally accepted as reliable.[38]

44. The standard operating procedures were applied by Cybergenetics in the True Allele testing in this case.[39]

45. The Cybergenetics employee who conducted the testing in this case is Jennifer Hornyak-Bracamontes. Ms. Hornyak Bracamontes has a Bachelor of Science degree in biology from Duquesne University and a Master of Science degree in forensic science from

[32] State's exhibit 26.
[33] State's exhibit 281, Testimony of Jennifer Hornyak-Bracamontes, October 14, 2024.
[34] State's exhibit 47, 48.
[35] State's exhibit 303.
[36] State's exhibit 88 at 8.
[37] Testimony of Jennifer Hornyak-Bracamontes, April 26, 2024; *see also* State's exhibits 242 through 264, inclusive (performance checks for TrueAllele from 2017 to 2022).
[38] Testimony of Jennifer Hornyak-Bracamontes, April 26, 2024.
[39] Testimony of Jennifer Hornyak-Bracamontes, April 26, 2024.

Duquesne University. Ms. Hornyak-Bracamontes has completed three in-house trainings with Cybergenetics on the use of TrueAllele. Ms. Hornyak-Bracamontes has been published in three scientific peer-reviewed journals, and has been a co-author in around a dozen other scientific studies regarding TrueAllele. She has worked on around 950 cases for Cybergenetics and has testified in court 54 times. In those 54 times, Ms. Hornyak-Bracamontes was qualified to provide opinion testimony on forensic DNA analysis with a focus on probabilistic genotyping.[40]

46. Based on these Findings of Facts, the Court enters the following Conclusions of Law:

CONCLUSIONS OF LAW

1. "Preliminary questions concerning the . . . admissibility of evidence shall be determined by the court[.]" Hawai'i Rules of Evidence Rule 104(a).
2. Where the preliminary facts necessary for the admissibility of evidence are disputed, the offering party has the burden to prove facts supporting admission by a preponderance of the evidence. *State v. McGriff*, 76 Hawai'i 148, 157, 871 P.2d 782, 791 (1994).
3. For the purposes of this hearing, the admissibility of underlying DNA typing technology is not at issue. *State v. Montalbo*, 73 Haw. 130, 141, 828 P.2d 1274, 1281 (1992) (taking judicial notice that the DNA paradigm is not controversial and is widely accepted in the relevant scientific community).
4. Similarly to *Montalbo*, the issue in this case is the admissibility of evidence and the probability that two DNA profiles are coincidentally matched; i.e., the commonality or rarity of a particular DNA profile. *See id*. at 136, 828 P.2d at 1279.

[40] Testimony of Jennifer Hornayk-Bracamontes, April 26, 2024; State's exhibit 280 (CV of Jennifer Hornyak-Bracamontes).

5. Commonality and or rarity is expressed as a number and is the result of statistical analysis.
6. In *Montalbo*, the Supreme Court of Hawai'i provided a general five-factor test to determine the admissibility of this statistical analysis. *Id*. at 140, 828 P.2d at 1280-81.
7. The Court should weigh general acceptance along with other factors, such as:
    a. Whether or not the evidence will assist the trier of fact to understand the evidence or determine a fact in issue;
    b. The evidence will add to the common understanding of the jury;
    c. The underlying theory is generally accepted as valid;
    d. The procedures used are generally accepted as reliable if performed properly; and
    e. The procedures were applied and conducted properly in the present instance.

    Id.
8. Once that determination is concluded, the Court should then consider whether admitting that evidence is more probative than prejudicial. *Id*.; see also, HRE Rule 403.
9. The commonality and/or rarity of a person's DNA profile and whether or not it coincidentally matches an item of evidence is highly probative of whether or not the Defendant committed the charged offenses. *United States v. Gissantaner*, 990 F.3d 457, 463 (6th Cir. 2021).
10. In applying the *Montalbo* factors, the Court determines that:
    a. The proffered evidence in this case will assist the trier of fact;
    b. Probabilistic genotyping is not common knowledge and expert testimony will assist the jury in understanding the evidence;

c. TrueAllele's use of continuous probabilistic genotyping to generate statistical likelihood ratios is generally accepted in the relevant scientific community; *People v. Wakefield*, 38 N.Y.3d 367, 371, 195 N.E.3d 19, 1 (N.Y. 2022); *United States v. Anderson*, 673 F. Supp. 3d 671, 688 (M.D. Pa. 2023) (stating, "given the forensic science community's broad acceptance of TrueAllele and other probabilistic genotyping software programs, and the widespread use of such programs in the legal context," the court "finds that TrueAllele and the method it employs are generally accepted by the relevant scientific community"); *State v. Simmer*, 304 Neb. 369, 389, 935 N.W.2d 167, 182 (Neb. 2019) ("The wide use of TrueAllele by government crime laboratories and other groups nationwide, Perlin's participation in multiple lectures and conferences, and Helligso's testimony that the scientific community had agreed in recent years that programs like TrueAllele are necessary, all tend to show that TrueAllele has been generally accepted in the relevant scientific community.")

d. The methodology of TrueAllele has been generally accepted by the relevant scientific community based on empirical evidence of its validity as demonstrated by multiple validation studies, including collaborative studies, peer-reviewed publications, and scientific journals;

e. The empirical studies demonstrate that, through deriving reproducible and accurate results from the interpretation of known DNA samples, TrueAllele's reliability is widely accepted and reliable if performed properly; *See Wakefield*, 38 NY.3rd. 367 (2022);

f. The reliability is enhanced from traditional methods, because probabilistic genotyping uses computer programming to mitigate the risk from subjective assessments of multi-person DNA samples and also mitigates the effect of cognitive bias, as the software does not know the other factors of the case; *Gissantaner*, 990 F.3d at 463; and

g. In this case, Cybergenetics employed the procedures properly. Further, Jennifer Hornyak-Bracamontes is duly qualified to operate TrueAllele according to the standard operating procedures.

11. The weighed Montalbo factors all support the admissibility of the proffered evidence of Cybergenetics's use of TrueAllele to calculate the likelihood ratios of the DNA samples in this case. 73 Haw. at 140, 828 P.2d at 1280-81.

12. Although not necessary, the Court also considered the *Daubert v. Merrel-Dow Pharmaceuticals* factors, following *State v. Escobido-Ortiz*, 109 Haw. 359, 467, 126 P.3d 402, 410 (Haw. App. 2005), as corrected (Dec. 30, 2005) (indicating the Daubert factors could be instructive when determining issues of novel scientific admissibility).

13. The Daubert factors are:

a. Whether the technique in question has been tested;

b. Whether the technique has been subjected to peer-review and publication;

c. The error-rate of the technique;

d. The existence and maintenance of standards controlling the technique's operation;

e. Whether the technique has been generally accepted in the scientific community.

Daubert v. Merrell Dow Pharms., Inc., 509 U.S. 579, 113 S. Ct. 2786 (1993).

14. Under the first three of the Daubert factors, TrueAllele has been tested, subjected to peer-review and publication, and has a low error-rate. *Daniels v. State*, 312 So. 3d 926, 934 (Fla. Dist. Ct. App. 2021); *State v. Simmer*, 304 Neb. 369, 386-89, 935 N.W.2d 167, 179-82 (2019).

15. For the fourth *Daubert* factor, there are industry standards applicable to the validation and operation of probabilistic genotyping systems in general. Further, Cybergenetics maintains standard operating procedures that control how the program is used in each case, which if followed yield reliable and accurate results. *Anderson*, 673 F. Supp. 3d at 688.

16. Recently, courts in other jurisdictions have ruled in support of the admissibility of TrueAllele. *E.g., Anderson*, 673 F. Supp. 3d at 688; *Harvin v. State*, 263 Md. App. 326, 340-56, 323 A.3d 481, 490-99 (2024), cert. denied, 489 Md. 338, 330 A.3d 662 (2025) (finding that TrueAllele analysis was based on sufficiently reliable principles and methods so that the results could be profitably applied by a jury); see also, *United States v. Lockett*, No. CR 20-00091-BAJ-RLB, 2023 WL 7181251 at *8 (M.D. La. Nov. 1, 2023).[41]

17. The Court finds probabilistic genotyping to be probative under HRE Rules 401 and 402 and proper under HRE Rule 702.

18. In determining whether the proffered evidence is admissible pursuant to HRE Rule 403, the Court notes that all of the State's probative evidence at trial is necessarily prejudicial to the Defendant.

[41] *See also* State's exhibits 124 through 168 for admissibility rulings regarding TrueAllele.

19. Although evidence of Defendant's guilty may be "necessarily prejudicial" to the Defendant, HRE Rule 403 is concerned with the danger of "unfair prejudice". "Unfair prejudice 'means an undue tendency to suggest decision on an improper basis, commonly, though not necessarily, an emotional one.'" *State v. Gallagher*, 146 Hawaii 462, 481, 463 P.3d 1119, 1138 (Haw. 2020) (citations omitted).
20. The danger of "unfair prejudice" from the proffered evidence is low given the court's findings on the reliability of probabilistic genotyping and the correct application of the TrueAllele program in this case.
21. In this case, the value of identification evidence is extremely high and, consequently, the potential for "unfair prejudice" does not substantially outweigh the probative value of the proffered evidence. Therefore, HRE Rule 403 does not preclude admissibility.
22. In light of all findings of fact and conclusions of law, the Court will allow the presentation of Cybergenetics' TrueAllele testimony at trial.

ACCORDINGLY IT IS HEREBY ORDERED that the State's Motion to Determine Admissibility of "Trueallele" Expert Testimony Pursuant To HRE 104(A) is hereby granted.

Dated at Honolulu, Hawai'i: September 16, 2025.

/S/ Paul B.K. Wong
Judge of the above entitled court

APPROVED AS TO FORM:

Nelson W.S. Goo
Attorney for Defendant Thompson