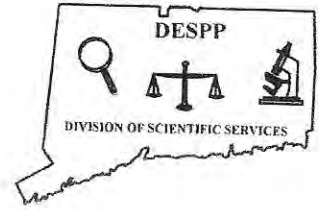




STATE OF CONNECTICUT

DEPARTMENT OF EMERGENCY SERVICES and PUBLIC PROTECTION DIVISION OF SCIENTIFIC SERVICES



Guy M. Vallaro, Ph.D. Director

DNA REPORT

Laboratory Case DSS-19-004168

Submitting Agency CSP - EDMCS 1320 Tolland Stage Road Tolland, CT 06084

Date of Request 7/28/2019

Agency Case CFS1900358671 Xref: 19-13419GV

Xref: Office of the Chief Medical Examiner

Date of Report 8/9/2019

EVIDENCE DESCRIPTION

- #002 (#2) Box with "Smith & Wesson SW9VE handgun, snRBF6116 w/magazine and 16 rounds"
#002-001 S&W pistol model SW9VE 9mm caliber, SN: RBF6116
#002-001-01 Swabbing - Grip area of firearm
#002-001-01-01 Extract of 002-001-01
#002-001-02 Swabbing - Trigger of firearm
#002-001-02-01 Extract of 002-001-02
#002-001-03 Swabbing - Slide area of firearm
#002-001-03-01 Extract of 002-001-03
#002-001-04 Swabbing - LP designated area "L1"
#002-002 S&W 9mm pistol magazine
#002-002-01 Swabbing - Magazine
#002-002-01-01 Extract of 002-002-01
#002-003 Sixteen 9mm Luger cartridges
#002-003-01 Swabbing - Cartridges
#002-003-01-01 Extract of 002-003-01
#006 (#10) Bag with "Fifteen (15) Winchester S&W .40 cal bullets & empty mag from item #12"
#006-001 One (1) magazine
#006-001-01 Swabbing - magazine base
#006-001-01-01 Extract of 006-001-01
#006-001-02 Swabbing - Remainder of magazine
#006-002 Fifteen (15) cartridges
#006-002-01 Swabbing - cartridges
#007 (#12) Box with "Glock 22, .40 cal pistol, s/n: BKKZ517"
#007-001 Reddish-brown stain on right side of slide of firearm
#007-001-01 Extract of 007-001
#007-002 Swabbing - Grip area of firearm

278 Colony Street, Meriden, Connecticut 06451 Phone (203) 639-6400 Fax (203) 639-6485

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- #007-002-01 Extract of 007-002
- #007-003 Swabbing - Top of slide of firearm
- #007-003-01 Extract of 007-003
- #007-004 Other reddish-brown stains on slide of firearm
- #007-005 Swabbing - Trigger of firearm
- #007-005-01 Extract of 007-005
- #008 (#13) Bag with "Blackhawk, Glock 19 holster, color black"
- #008-001 Swabbing - Exterior of holster
- #008-001-01 Extract of 008-001
- #012 Bag with "Autopsy sample - Alphonso Zaporta"
- #012-001 Envelope labeled "scalp hair"
- #012-002 Envelope labeled "left fingernails"
- #012-003 Envelope labeled "right fingernails"
- #013 Known blood sample, Alphonso Zaporta
- #017 (#42) Envelope with "Fired bullet w/BLS in Rx bottle"
- #017-001 Reddish-brown staining on projectile
- #017-001-01 Extract of 017-001

TESTING SUMMARY

Item #	Screening	Profile Obtained ¹	CODIS Entry
		F6C	
002-001-01		Yes	No - Complex Mixture
002-001-02		Yes	No - Complex Mixture
002-001-03		Yes	No - Complex Mixture
002-002-01		Yes	No - Complex Mixture
002-003-01		Yes	No - Insufficient
006-001-01		Yes	No - Eligible Portion Insufficient
007-001	Blood(+)	Yes	No - Not Appropriate
007-002		Yes	No - Complex Mixture
007-003		Yes	No - Eligible Portion Insufficient
007-005		Yes	No - Eligible Portion Insufficient
008-001		No	
013		Yes	
017-001	Blood(+)	Yes	No - Not Appropriate

¹F6C = Fusion 6C STR DNA amplification kit

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CONCLUSIONS SUMMARY

Item #	Description	Type	Alphonso Zaporta (#013)
002-001-01	Swabbing - Grip area of firearm	Mixture	No Comparison
002-001-02	Swabbing - Trigger of firearm	Mixture	No Comparison
002-001-03	Swabbing - Slide area of firearm	Mixture	No Comparison
002-002-01	Swabbing - Magazine	Mixture	Eliminated
002-003-01	Swabbing - Cartridges	Mixture	Cannot be Eliminated
006-001-01	Swabbing - magazine base	Mixture	Included
007-001	Reddish-brown stain on right side of slide of firearm	Male	Consistent with Source
007-002	Swabbing - Grip area of firearm	Mixture	Included
007-003	Swabbing - Top of slide of firearm	Mixture	Included
007-005	Swabbing - Trigger of firearm	Mixture	Included
017-001	Reddish-brown staining on projectile	Male	Consistent with Source

CONCLUSIONS

1. #002-001-01 (Swabbing - Grip area of firearm)

The results are consistent with the DNA profile from item #002-001-01 being a mixture of five contributors with at least one of them being male. This profile is too complex for STRmix interpretation. Due to the complexity of the DNA profile from item #002-001-01, no comparisons will be made.

2. #002-001-02 (Swabbing - Trigger of firearm)

The results are consistent with the DNA profile from item #002-001-02 being a mixture of five contributors with at least two of them being male. This profile is too complex for STRmix interpretation. Due to the complexity of the DNA profile from item #002-001-02, no comparisons will be made.

3. #002-001-03 (Swabbing - Slide area of firearm)

The results are consistent with the DNA profile from item #002-001-03 being a mixture of five contributors with at least three of them being male. This profile is too complex for STRmix interpretation. Due to the complexity of the DNA profile from item #002-001-03, no comparisons will be made.

4. #002-002-01 (Swabbing - Magazine)

The results are consistent with the DNA profile from item #002-002-01 being a mixture of three contributors. The results do not support the hypothesis that Alphonso Zaporta is a contributor to this profile. Assuming three contributors, Alphonso Zaporta is eliminated as a contributor to the DNA profile from item #002-002-01.¹

¹Profile analyzed and comparison made using STRmix™ analysis software.

DNA REPORT

5. #002-003-01 (Swabbing - Cartridges)

The results are consistent with the DNA profile from item #002-003-01 being a mixture of two contributors with at least one of them being male. Assuming two contributors, the DNA profile from item #002-003-01 is at least 41,000 times more likely to occur if it originated from Alphonso Zaporta and one unknown individual than if it originated from two unknown individuals.¹

6. #006-001-01 (Swabbing - magazine base)

The results are consistent with the DNA profile from item #006-001-01 being a mixture of two contributors with at least one of them being male. Assuming two contributors, the DNA profile from item #006-001-01 is at least 100 billion times more likely to occur if it originated from Alphonso Zaporta and one unknown individual than if it originated from two unknown individuals.¹

7. #007-001 (Reddish-brown stain on right side of slide of firearm)

The results are consistent with the DNA profile from item #007-001 originating from a single male individual. Assuming one individual, the DNA profile from item #007-001 is at least 100 billion times more likely to occur if it originated from Alphonso Zaporta than if it originated from an unknown individual.¹

8. #007-002 (Swabbing - Grip area of firearm)

The results are consistent with the DNA profile from item #007-002 being a mixture of four contributors with at least two of them being male. Assuming four contributors, the DNA profile from item #007-002 is at least 100 billion times more likely to occur if it originated from Alphonso Zaporta and three unknown individuals than if it originated from four unknown individuals.¹

9. #007-003 (Swabbing - Top of slide of firearm)

The results are consistent with the DNA profile from item #007-003 being a mixture of three contributors with at least two of them being male. Assuming three contributors, the DNA profile from item #007-003 is at least 100 billion times more likely to occur if it originated from Alphonso Zaporta and two unknown individuals than if it originated from three unknown individuals.¹

10. #007-005 (Swabbing - Trigger of firearm)

The results are consistent with the DNA profile from item #007-005 being a mixture of two contributors with at least one of them being male. Assuming two contributors, the DNA profile from item #007-005 is at least 100 billion times more likely to occur if it originated from Alphonso Zaporta and one unknown individual than if it originated from two unknown individuals.¹

11. #017-001 (Reddish-brown staining on projectile)

The results are consistent with the DNA profile from item #017-001 originating from a single male individual. The results from item #017-001 are identical to the results from item #007-001. Therefore, assuming one individual, the DNA profile from item #017-001 is at least 100 billion times more likely to occur if it originated from Alphonso Zaporta than if it originated from an unknown individual.

¹Profile analyzed and comparison made using STRmix™ analysis software.

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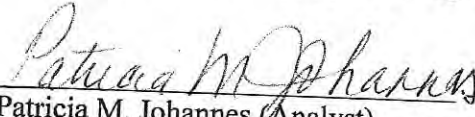
REMARKS


Hair-like fibers were collected from items #002 and #017 and returned to the submission packaging.

Items #002-001-04, #006-001-02, #006-002-01, #007-004, #012-001, #012-002 and #012-003 were not tested at this time.

Items #002-001-01, #002-001-02, #002-001-03, #002-002-01, #002-003-01, #006-001-01, #007-002, #007-003, #007-005 and #008-001 were consumed in testing. Items #002-001-04, #006-001-02, #006-002-01, #007-001, #007-004, #012, #013 and #017-001 were retained at the laboratory. Items #002, #006, #008 and #017 were forwarded to the Firearms unit of the laboratory. Item #007 was forwarded to the Latent Print unit of the laboratory. All DNA extracts listed were retained at the laboratory.

Results apply to the evidence as received by the Division of Scientific Services and relate only to the items tested. This report reflects the test results, conclusions, interpretations, and/or the findings of the analyst as indicated by their signature below.


Patricia M. Johannes (Analyst)
Forensic Science Examiner 2


Daniel T. Renstrom (Technical Reviewer)
Forensic Science Examiner 2

DNA REPORT

APPENDIX

Fusion 6C STR Alleles Detected

Item #	AMEL	D3S1358	D1S1656	D2S441	D10S1248	D13S317	Penta E	D16S539	D18S51
002-001-01	X, Y	14, 15, 16, 17, 18	12, 14, 15, 16, 17, 17.3, 18.3	10, 11, 11.3, 12, 14	12, 13, 14, 15	8, 9, 11, 12, 13	5, 7, 10, 12, 13, 15	9, 11, 13	12, 14, 15, 16, 18, 19, 22
002-001-02	X, Y	14, 16, 17, 18	13, 14, 15, 17, 17.3, 18.3	10, 11, 11.3, 14	12, 13, 14, 16, 17, 19	8, 11, 12	5, 7, 10, 11, 12, 13, 21	9, 11, 13	12, 14, 15, 16, 18, 19
002-001-03	X, Y	14, 15, 16, 17, 18	13, 14, 15, 17, 17.3, 18.3	10, 11, 11.3, 14	12, 13, 14, 16, 17, 19	8, 11, 12	5, 7, 12, 21	8, 9, 11, 12, 13	12, 14, 15, 16, 18, 19
002-002-01	X	14, 16, 17, 18	15, 17, 17.3	10, 11.3, 14	13, 14	8, 11, 12	12	9, 11, 13	12, 14, 15, 16, 18, 19
002-003-01	X, Y	NR	14, 18.3	10, 11.3, 14	12, 14	8, 11, 12	NR	13	19
006-001-01	X, Y	14, 16	12, 14, 18.3	14	12, 17	12	7, 12	9, 11, 13	12, 15, 19
007-001	X, Y	14, 16	14, 18.3	14	12, 17	12	7, 12	9, 13	15, 19
007-002	X, Y	14, 15, 16, 17, 18	12, 13, 14, 15, 17.3, 18.3	10, 11, 11.3, 14	12, 13, 14, 15, 16, 17	10, 11, 12, 13	5, 7, 11, 12, 15	9, 11, 13	12, 13, 15, 16, 19
007-003	X, Y	14, 16, 17	14, 18.3	11, 14	12, 16, 17	12	7, 12	9, 13	15, 19
007-005	X, Y	14, 16	14, 18.3	14	12, 17	12	7, 12	9, 13	12, 15, 19
013	X, Y	14, 16	14, 18.3	14	12, 17	12	7, 12	9, 13	15, 19
017-001	X, Y	14, 16	14, 18.3	14	12, 17	12	7, 12	9, 13	15, 19

NR = No Results.

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APPENDIX (Cont'd.)

Fusion 6C STR Alleles Detected

Item #	D2S1338	CSF1PO	Penta D	TH01	vWA	D21S11	D7S820	D5S818	TPOX
002-001-01	17, 18, 19, 23, 24	10, 11, 12, 13	2.2, 7, 8, 10, 11, 12, 14	6, 7, 8, 9, 9.3	14, 15, 16, 17, 18, 19	24.2, 28, 30, 31.2	9, 10, 11, 12, 13	10, 11, 12, 13	8, 10, 11
002-001-02	16, 17, 18, 19, 24	10, 11, 12	7, 10, 11, 12, 13, 14	6, 7, 8, 9, 9.3	14, 15, 16, 17, 18, 19	24.2, 28, 30, 31.2	8, 10, 11, 12, 13	10, 11, 12, 13	8, 9
002-001-03	16, 17, 18, 19, 23, 24	10, 11, 12, 13	2.2, 7, 8, 10, 11, 12, 13, 14	6, 7, 8, 9, 9.3	14, 15, 16, 17, 19	24.2, 28, 29, 30, 31.2, 32	8, 10, 11, 12, 13	10, 11, 12, 13	8, 9, 10
002-002-01	17	10, 12	11	9	15, 16, 17, 19	24.2, 28, 31.2	11, 12, 13	13	8
002-003-01	NR	10	NR	NR	15	28, 32	11	NR	NR
006-001-01	17, 23	10, 13	2.2, 10	6, 7	14, 16	28, 32	10, 11	10, 13	9, 10
007-001	17, 23	10, 13	2.2, 10	6, 7	14, 16	28, 32	10, 11	10, 13	9, 10
007-002	17, 19, 23, 24	10, 11, 12, 13	2.2, 10, 11, 13, 14	6, 7, 8, 9, 9.3, 10	14, 16, 17, 18, 20	28, 29, 31.2, 32, 32.2	9, 10, 11, 12	10, 11, 12, 13	8, 9, 10
007-003	17, 23	10, 13	2.2, 10	6, 7	14, 16, 17	28, 32	10, 11	10, 13	9, 10
007-005	17, 23	10, 13	2.2, 10	6, 7	14, 16	28, 31, 32	10, 11	10, 13	9, 10
013	17, 23	10, 13	2.2, 10	6, 7	14, 16	28, 32	10, 11	10, 13	9, 10
017-001	17, 23	10, 13	2.2, 10	6, 7	14, 16	28, 32	10, 11	10, 13	9, 10

NR = No Results.

DNA REPORT

APPENDIX (Cont'd.)

Fusion 6C STR Alleles Detected

Item #	D8S1179	D12S391	D19S433	SE33	D22S1045	DYS391	FGA	DYS576	DYS570
002-001-01	10, 11, 12, 13, 14, 16	17, 18, 19, 21	10, 12, 14, 14.2, 15.2	14, 16, 17, 18, 26.2, 27.2, 28.2	11, 13, 15, 16	NR	22, 23, 24, 25, 26	18	NR
002-001-02	10, 12, 13, 14, 16	17, 18, 19, 20, 21	12, 14, 15.2	14, 16, 17, 18, 21, 27.2	13, 15, 16	10	19, 20, 22, 23, 24, 25, 26	15	18, 19
002-001-03	10, 12, 13, 14, 16	17, 18, 19, 21	12, 14, 14.2, 15.2	14, 16, 17, 26.2, 27.2	15, 16	10	20, 21, 22, 23, 24, 25, 26	15, 17, 18	18, 19
002-002-01	12	18, 19	12, 14, 15.2	17	15	NR	23, 24, 25, 26	NR	NR
002-003-01	NR	NR	NR	16	NR	NR	25	NR	NR
006-001-01	12, 13	18, 19	12, 14	16, 26.2	15, 16	10	24, 25	18	18
007-001	12, 13	18, 19	12, 14	16, 26.2	15, 16	10	24, 25	18	18
007-002	10, 12, 13, 14, 15, 16	18, 19, 22, 23	12, 13, 14, 15, 15.2	16, 17, 18, 26.2, 27.2	14, 15, 16, 17	10, 11	19, 22, 23, 24, 25	17, 18	18, 19
007-003	12, 13	17, 18, 19	12, 14	16, 26.2	15, 16	10	24, 25	17, 18	18
007-005	12, 13	18, 19	12, 14	16, 26.2	15, 16	10	24, 25	18	18
013	12, 13	18, 19	12, 14	16, 26.2	15, 16	10	24, 25	18	18
017-001	12, 13	18, 19	12, 14	16, 26.2	15, 16	10	24, 25	18	18

NR = No Results.

DNA Report Glossary of Terms and Important Concepts

The following supplemental information is to provide our clients with a more comprehensive description of the methods used by our laboratory for the examination/analysis of items submitted for forensic testing.

Definitions

DNA Analyses and Results Interpretation

Allele. A form of a gene, or region of DNA that is located at a specific physical location or site (a locus, plural is loci) on a particular chromosome. Humans generally have either one or two alleles at each locus. When individuals inherit two copies of the same allele, they are **homozygous** at that locus. When they inherit two different alleles, they are **heterozygous** at that site.

Analytical Threshold. The peak height value below which a peak cannot be reliably distinguished from background machine noise.

Autosome. A chromosome that is not one of the sex chromosomes—chromosomes 1–22 in humans.

CODIS. Combined DNA Index System. A compilation of state and national DNA databases (all 50 states, FBI, USACIL, DC, Puerto Rico) containing STR profiles from convicted offenders, evidentiary samples, missing persons, and other categories. CODIS is maintained by the FBI.

DNA REPORT

Deconvolution. The virtual separation of DNA mixtures into the genotypes of the individual contributors based on quantitative peak height information and assumptions pertaining to the profile, such as the number of contributors and any known/assumed contributors.

Deoxyribonucleic acid (DNA) testing involves multiple steps, including DNA extraction, quantitation, amplification, electrophoresis and analysis of the resulting data.

DNA extraction. The recovery of purified DNA from biological samples.

DNA quantitation. A means of measuring the amount of DNA (total human DNA, male DNA, and degradation index) recover from biological samples by a specialized PCR method called quantitative polymerase chain reaction (qPCR) or real-time PCR.

DNA Profile. The DNA test results (single source or mixture) generated at 1 or more loci.

Differential DNA extraction. A method of separating semen-containing mixed body fluid samples into two fractions, a sperm-rich fraction (SF) and an epithelial-rich fraction (EF), based on differences between sperm cells and other cell types.

Electropherogram. A representation of the DNA profile (PCR products separated on the basis of their size by capillary electrophoresis) in the form of peaks on a graph. The height of the peaks is measured in relative fluorescent units (RFUs).

Fusion 6C PCR Amplification Kit (F6C). F6C is a 6 dye system manufactured by Promega that amplifies 27 loci (23 autosomal STRs, 3 Y-STRs, and the Amelogenin gender marker) in a single reaction. F6C contains all 20 loci now required for CODIS.

Known/Assumed contributor. The assumption that a person is the source of (or contributor to) a DNA profile. The assumption must be consistent with the DNA profile results and there must be objective support for the assumption i.e., there must be a reasonable scientific expectation that an individual's DNA is in the evidentiary profile. In general, this would apply to non-probative comparisons for intimate samples and other items that have been regularly handled or worn by the assumed contributor.

Loci. Specific locations in the DNA molecule (singular is locus).

Polymerase Chain Reaction (PCR). Also known as DNA amplification. PCR can be thought of as "molecular photocopying", where small segments of DNA (typically, short tandem repeats or "STRs" in forensics) are copied many times in a thermal cyclers.

Probabilistic Genotyping (PG). A DNA profile analysis tool. Probabilistic genotyping is the use of biological modeling to infer genotypes for the DNA typing results and to calculate likelihood ratios. PG analysis provides a statistical weighting to the different genotype combinations that could explain the evidentiary profile.

STRmix. A probabilistic genotyping DNA analysis software system that models (analyzes) DNA profile results. STRmix is a software tool used to assist the DNA analyst in interpreting DNA profiles and in performing statistical calculations. STRmix can accurately deconvolute DNA mixtures—a virtual separation of mixture profiles into their individual components (genotypes) based on quantitative peak height information.

Stochastic threshold. The peak height value above which it is reasonable to assume that allelic dropout has not occurred at any given locus. Allelic dropout is when one or more alleles present in the sample are not detected above the analytical threshold.

Yfiler PCR Amplification kit. The Yfiler kit, manufactured by Applied Biosystems, amplifies 17 Y-STRs in a single reaction. Yfiler is a 5 dye system containing the SWGDAM recommended Y-STRs and other highly variable markers.

DNA methods for the analysis of biological material employ three basic types of DNA testing:

- **Autosomal STR testing** (loci not on the X or Y chromosomes) offers the greatest potential for individualization. Such tests detect both male and female DNA equally, but an excess of female DNA (e.g. >50:1) may render a male profile undetectable.
- **Y-STR testing** detects only male DNA. As a result, a male DNA profile can be detected even in the presence of a significant excess of female DNA (>100:1). Since all paternally-related males (and an unknown number of unrelated males in the general population) have identical Y-STR profiles, a Y-STR profile cannot be individualized to a single male.
- **Mitochondrial DNA sequencing.** The specific order of the 4 DNA bases (A, C, G, T) is determined for HV1 and HV2.

DNA REPORT

General Categories of Testing Conclusions

- Mixture.** A DNA profile that contains results from more than 1 individual.
- Major contributor.** A DNA profile that is present in a higher quantity within a DNA mixture.
- Minor contributor.** A DNA profile(s) that is present in a lower quantity within a DNA mixture.
- Inconclusive.** Per DSS SOPs, no conclusion can be drawn from the comparison between the known sample and the evidentiary sample.
- Insufficient profile results/Insufficient for comparison.** When insufficient data is obtained for the questioned DNA Profile for comparison purposes, the following statement is reported: "Due to limited data detected from the item, the comparison to the known profile is inconclusive." This statement is made for low-level, partial DNA profiles when there is insufficient data from the evidentiary profile for comparison to a particular known.
- Consistent with Source.** The results are consistent with the tested individual being the source of a single-source DNA profile.
- Inclusion.** The results demonstrate that the tested individual is a potential contributor to a DNA mixture.
- Cannot be eliminated.** Analogous to a "partial match". An individual cannot be eliminated (CBE) as the source of (or contributor to) a DNA profile if there is a strong positive association (LR is at or above the DSS inconclusive threshold of 10,000) between the known profile and the evidentiary profile but some of the alleles present in the known sample are not detected in the evidentiary profile.
- Eliminated.** The DNA profile for a questioned sample is not consistent with originating from the known sample tested.

General Categories of Statistical Conclusions

- The Likelihood Ratio (LR)** assesses the probability of the evidentiary profile occurring given two alternate (mutually exclusive) hypotheses; (H_1 and H_2). H_1 is typically where the data is explained by an inclusion of the person of interest (POI). H_2 is typically where the data is explained by a person selected at random from the general population and not the POI (match is coincidental). An LR is typically calculated using STRmix™ Analysis software for forensic unknown DNA profiles when the known individual(s) is not eliminated as the source of or a contributor to the evidence profile by a manual comparison. The LR is the probability of the profile occurring if hypothesis 1 (H_1) is true compared to the probability of the profile occurring under the alternate hypothesis (H_2).
- The Y-STR statistic (counting method)** reflects the number of times that a given Y-STR profile is observed in a search of the National Y-STR Database. The counting method provides an estimate of the random match probability for a Y-STR profile.
- Random Match Probability (RMP).** RMP estimates the rarity of a DNA profile in the general population (unrelated individuals). It is the probability that a person selected at random from the general population (unrelated) would match the evidentiary profile.
- Criminal Parentage Testing.** The random man not excluded (RMNE) statistic is calculated when the tested individual is not eliminated. The statistic calculated is the expected frequency (parentage inclusion probability) of individuals who could contribute the paternally (or maternally) transmitted alleles.
- Combined Kinship Index (CKI).** CKI compares the relative support for two competing hypotheses (non-criminal cases): the two individuals are related, versus the hypothesis that they are unrelated individuals selected at random from the population.