FORENSIC BIOLOGY SECTION

FORENSIC INVESTIGATIVE GENETIC GENEALOGY TEST METHODS

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1. FIGG Methods:

1.1. Scope: This test method is designed to assist investigators in finding leads through Forensic Investigative Genetic Genealogy (FIGG). This method shall only be used for violent crimes (as defined by the database terms of service such as homicide, rape, sexual assault, and robbery) and unidentified human remains (UHR). This test method is designed for the guidance of Biology Section personnel who assist investigations where DNA is available and other investigative leads have been exhausted.

1.2. Precautions/Limitations:

1.2.1. Limitations

1.2.1.1. There shall be an adequate sample of DNA from a suspected perpetrator or unidentified human remains case.

1.2.1.2. An STR profile shall already be uploaded into CODIS.

1.2.1.3. Other reasonable investigative methods have been completed.

1.2.1.4. Single source and mixed DNA samples with appropriate elimination standards may be considered.

1.2.1.4.1. Single source profiles should be evaluated for profile quality.

1.2.1.4.2. Mixtures should be evaluated on a case-by-case basis.

1.2.1.4.3. Mixtures cannot be handled within the Indiana State Police Forensic Services Division and require outsourced SNP profile development.

1.2.2. Case Selection

1.2.2.1. Cases will be chosen based on DNA availability with full permission and agreement with legally responsible law enforcement agencies overseeing the case.

1.2.2.2. Cases may be determined to be unsuitable for FIGG by the FIGG Unit Supervisor.

1.2.2.3. If a developed SNP profile is determined to be unsuitable for upload a memo shall be generated stating FIGG analysis was unable to be performed.

1.3. Related Information:

1.3.1. Appendix 1 Definitions

1.3.2. Appendix 2 DNA Server Instructions

1.3.3. Appendix 3 Investigative Memo Wording

1.3.4. Appendix 4 FIGG Technical Review Worksheet

1.4. Instruments: Not Applicable

1.5. Reagents/Materials: Not Applicable

1.6. Hazards/Safety: Not Applicable

1.7. Reference Materials/Controls/Calibration Checks: Not Applicable

1.8. Procedures/Instructions:

1.8.1. **Public Database Searching**

1.8.1.1. Databases, websites, and tools utilized are not limited to those listed below. However, use of any tools shall follow terms of service and all ISP documentation standards.

1.8.1.2. SNP profiles for database searching may be generated through in-house processing with ForenSeq® Kintelligence, outsourcing, or previous testing performed by other agencies.

1.8.1.3. The DNA Painter Shared cM Project may be utilized to assist in the evaluation of all public database searches. This tool utilizes crowd-sourced data to predict possible relationships based on average shared centimorgans (cM) of categories of relatives.

1.8.1.4. **GEDmatch PRO™**

1.8.1.4.1. GEDmatch PRO™ is the law enforcement portal of the public database GEDmatch that allows users who upload profiles to opt-in for law enforcement searching.

1.8.1.4.2. For the initial search, a project shall be created to invite all members of the FIGG unit to have access to the kit.

1.8.1.4.3. GEDmatchPRO™ new match settings

1.8.1.4.3.1. Under the “manage account” tab, change the “New Match Settings” to 125 cM for Kintelligence kits and 75 cM for Third Party Kits.

1.8.1.4.3.2. If the kit owner is notified of a new match and the case is still active, the kit owner should notify the FIGG researcher assigned to the case. The FIGG researcher should document the new match in the research notebook and download the new .csv file. Exceptions to notifications and documentation requirements may be made when poor Kintelligence sequencing results lead to frequent high level suspected false matches or if a Whole Genome Sequencing has already been requested.

1.8.1.4.4. GEDmatch PRO™ Kit Number is an identifying number needed during research. This number shall be documented in the Research Workbook for easy reference.

1.8.1.4.5. Identification of Matches

1.8.1.4.5.1. Matches may be identified by utilizing information in the email address or alias listed.

1.8.1.4.5.1.1. Internet search engines, social media or other websites may be utilized to identify matches.

1.8.1.4.5.1.2. The effectiveness of search options may be dependent on the popularity of a name or username.

1.8.1.4.5.1.3. Searching for the name on public record websites may also list potential relatives.

1.8.1.4.5.2. Contacting matches should only be done with investigator permission after a reasonably exhaustive alternative search has been conducted first.

1.8.1.4.6. Kintelligence Searches

1.8.1.4.6.1. Match lists generated within GEDmatch PRO™ are divided into the following types:

1.8.1.4.6.2. **High Confidence List**

1.8.1.4.6.2.1. Focus first on the High Confidence matches as these indicate a true genetic connection.

1.8.1.4.6.3. **Expanded Confidence List**

1.8.1.4.6.3.1. This list will include the High Confidence matches as well as those of the Expanded Confidence thresholds. The expanded confidence list includes fifth degree or further removed relatives.

1.8.1.4.6.3.2. These matches should be utilized with caution as they could be false matches.

1.8.1.4.6.4. **All-Matches list**

1.8.1.4.6.4.1. This will include all matches, high and expanded, and many low matches and false positives.

1.8.1.4.6.4.2. These matches should be utilized with extreme caution as they are possible false matches.

1.8.1.4.6.4.3. Particular caution should be utilized when evaluating matches with kits that have low overlap values.

1.8.1.4.7. Tools for evaluating kit results

1.8.1.4.7.1. **Admixture Oracle and Admixture Eurogenes/K13**

1.8.1.4.7.1.1. These reports give basic biogeographical ancestry predictions. The estimates should be utilized with caution due to the limited number of SNP's and limitations in reference populations.

1.8.1.4.7.2. **One-to-Many**

1.8.1.4.7.2.1. This tool generates a match list that displays autosomal and X DNA matches.

1.8.1.4.7.2.2. Input the kit number and hit search to get a match list.

1.8.1.4.7.2.3. One-to-Many can also be accessed by clicking on kit numbers.

1.8.1.4.7.2.4. The .csv file shall be pasted into the workbook and downloaded and retained on the data drive. The case number, item number and date shall be included in the filename.

1.8.1.4.7.2.5. Sort by Overlap to get the best matches (Overlap is a term which refers to the amount of shared SNP locations tested in the target and the match kit. Different companies test different locations so only the overlapping locations can be compared.)

1.8.1.4.7.2.6. Ignore matches with Genera as the source as these are almost always false leads. Their SNP counts do not match those for Kintelligence or other common consumer DNA tests.

1.8.1.4.7.3. **One-to-One Autosomal DNA Comparison**

1.8.1.4.7.3.1. This tools compares the shared autosomal DNA between two kits.

1.8.1.4.7.3.2. Input two kit numbers, click submit and evaluate the shared cM results.

1.8.1.4.7.3.3. To access this directly click on the Longest Segment link on the One-to-Many Match List. The One-to-One list will be displayed including the shared cM values.

1.8.1.4.7.4. **One-to-One X**

1.8.1.4.7.4.1. This tool allows detailed comparisons between X-DNA kits. Two kits are required for this comparison.

1.8.1.4.7.5. **Generation Chart**

1.8.1.4.7.5.1. This tool is similar to the Shared cM Project but is designed specifically for Kintelligence kits. Reference both for

potential cM relationships but more weight should be placed on the Generation Chart on GEDmatch PRO™ when using a Kintelligence kit.

1.8.1.4.7.6. **A-Matrix**

1.8.1.4.7.6.1. This tool is used to compare all DNA matches to one another to see if they share DNA.

1.8.1.4.7.6.2. Select kits to compare and click visualization options; then select Matrices and A-Matrix. A chart will be generated to view shared cM between DNA matches.

1.8.1.4.7.7. **Are My Parents Related?**

1.8.1.4.7.7.1. This tool displays similarities in segments of DNA from maternal and paternal sides and makes a determination if the parents are likely related within recent generations.

1.8.1.4.7.7.2. In cases of incest or close familial relationships, this is an important tool as the amount of DNA shared between the unknown individual and the DNA matches may be elevated affecting relationship predictions.

1.8.1.4.7.7.3. Provides an estimated number of generations between parents before a Most Recent Common Ancestor could be found.

1.8.1.4.7.7.4. If parents are likely related, caution should be utilized when working with the clustering tools.

1.8.1.4.7.7.5. If the parents are determined to be likely related, this information should be included in the investigative memo.

1.8.1.4.7.8. **AutoTree Clustering**

1.8.1.4.7.8.1. This tool organizes matches into shared match clusters with each color representing kits that share DNA with each other and the target kit.

1.8.1.4.7.8.2. Gray cells represent a shared match that may be related to multiple clusters of individuals.

1.8.1.4.7.8.3. If no clusters or too many clusters are generated the default cM thresholds can be adjusted.

1.8.1.4.7.9. **Triangulation**

1.8.1.4.7.9.1. This tool groups matches that share a common ancestor by visualizing shared DNA segments on each chromosome.

1.8.1.4.7.9.2. The Upper Segment Threshold limit may need to be lowered to get fewer very close relatives in the groupings.

1.8.1.4.7.10. **Match One or Both**

1.8.1.4.7.10.1. This tool shows matches in common between two kits.

1.8.1.4.7.10.2. Enter two kits in the tool and click submit. Three match lists are generated, one for each kit and one shared list.

1.8.1.4.7.11. **Multiple Kit Analysis**

1.8.1.4.7.11.1. Autosomal Matrix Comparison: a tool to help with visualizing a genetic network by comparing a set group of individuals against each other into a table which then can

be used to determine commonalities and shared DNA groups. Green colors are close relatives, yellow is a second or third cousin match and Red\pink are more distant relatives.

1.8.1.4.7.11.2. Generations Matrix Comparison: This tool is similar to the Autosomal Matix but estimates how many generations to the most recent common ancestor instead of comparing cM.

1.8.1.4.7.12. **Segment Search**

1.8.1.4.7.12.1. This tool identifies kits with matching chromosome segments to evaluate the potential for common ancestors.

1.8.1.4.7.12.2. The segment information can be additionally visualized utilizing chromosome mapping on DNApainter.com**.**

1.8.1.4.7.13. **AutoKinship**

1.8.1.4.7.13.1. This tool predicts trees based on shared DNA between clusters identified from the Autocluster tool. It also identifies segment clusters based on triangulating segments using AutoSegment. AutoKinship reports integrate AutoTree and AutoSegment results.

1.8.1.4.7.14. **Your Tag Groups**

1.8.1.4.7.14.1. Tag Groups can be created based on relationships, clusters, and close relationships.

1.8.1.4.7.14.2. It is most effective when used in combination with the Multiple Kit Analysis Tool.

1.8.1.4.7.15. **Find GEDcoms by Kit**

1.8.1.4.7.15.1. Search for an uploaded GEDcom by searching for a Kit Number.

1.8.1.4.7.15.2. GEDcoms and Wiki Trees are available on the Match lists through a link.

1.8.1.4.7.16. **Search GEDcoms**

1.8.1.4.7.16.1. Search all uploaded GEDcoms uploaded to GEDmatch.

1.8.1.5. **FamilyTreeDNA (FTDNA)**

1.8.1.5.1. FTDNA is a public database that allows users that upload to opt-in for law enforcement searching.

1.8.1.5.2. Requests for searching by Law Enforcement for a qualifying case should be added to the sFTP portal and appropriate paperwork sent by email to solves@othram.com. Alternatively, other methods for upload as directed by Othram may be utilized. Copies of paperwork shall be retained in the casefile.

1.8.1.5.2.1. Additional information about a user might require a court order, search warrant or subpoena. These requests will only be handled through court proceedings from valid law enforcement agencies.

1.8.1.5.2.1.1. These requests shall be sent through post office letter and not email.

1.8.1.5.2.1.2. Requests shall be sent to mailing address in User Agreement.

1.8.1.5.3. The .csv file of the match list shall be pasted into the workbook and downloaded and retained on the data drive. The case number, item number and date shall be included in the filename.

1.8.1.5.4. Information found on DNA Match List:

1.8.1.5.4.1. Includes the name or username of the DNA match

1.8.1.5.4.2. Shared DNA and longest block of each shared segment

1.8.1.5.5. “In Common With” and “Not in Common With” tool

1.8.1.5.5.1. A matched individual can be evaluated to view shared matches or individuals who do not share matches to aid in clustering.

1.8.1.5.6. Uploaded family trees of matches may be utilized with caution.

1.8.1.5.7. MyOrigins

1.8.1.5.7.1. This is an Ethnicity Report for FTDNA.

1.8.1.5.8. Family Finder Matrix: Add up to ten people to see if they share each other in a cluster.

1.8.1.6. **DNA Justice**

1.8.1.6.1. DNA Justice is a database that allows users to upload their profiles specifically for law enforcement searching.

1.8.1.6.2. Unlike other databases, DNA Justice will notify DNA uploaders if they match to an uploaded profile.

1.8.1.6.3. Requires registration and uploading of a SNP profile before access to the site is given. A match list is then generated.

1.8.2. **FIGG Research Workbook**

1.8.2.1. Every new case shall receive a new FIGG Research Workbook that is saved in the FIGG folder in the data drive.

1.8.2.1.1. The workbook shall be named with the Case Number_item#_G# (ex. 24I-01234_001A_G1).

1.8.2.1.1.1. A new version shall be saved with each additional research or testing.

1.8.2.1.1.2. Previous documentation shall be retained in each new workbook version.

1.8.2.1.2. Case number, investigator’s name, contact information, type of case (criminal vs. UHR) and any other identifying information shall be included.

1.8.2.1.3. Basic background information for the case with helpful details such as biological sex, gender, race or ethnicity, approximate age, when and where located, or other pertinent case information should be recorded.

1.8.2.1.4. Progress notes each day research is being conducted should include latest hypotheses, summary of the work completed, possible links between trees, and the next tasks.

1.8.2.1.4.1. As trees are built, daily progress notes should include possible connections between families.

1.8.2.1.4.2. If there are surnames, localities or unique places of origin found linking DNA matches, these should be documented in the research workbook.

1.8.2.1.5. A downloaded copy of the matches shall be placed within the Workbook on the appropriate tab. This copy will list all DNA matches and their cM information for easy reference.

1.8.2.1.6. Each DNA match investigated should have an individual tab within the workbook.

1.8.3. **Ancestry Trees and Research**

1.8.3.1. Each tree shall be named with the Case Number_item# (ex. 24I-01234_001A).

1.8.3.2. Resources are not limited to those mentioned below.

1.8.3.3. Privacy

1.8.3.3.1. Trees set to “private” cannot be viewed by individuals not invited to collaborate on the tree. Changing the searchability setting shall also be done to prevent limited information from deceased individuals from appearing in Ancestry tree searches.

1.8.3.3.2. When the tree is created the Privacy Settings shall immediately be adjusted prior to entering any information.

1.8.3.3.2.1. Go to the family tree, in the toolbar on the left, click More (three dots) and select Tree Settings. On the Tree Settings Page, select the “Private Settings” tab; select Private tree and click the box saying “Also prevent your tree from being found in searches” in the Private Tree section.

1.8.3.3.2.2. Privacy settings should be documented in the research workbook by a screenshot added to the general information tab.

1.8.3.3.3. When sharing a tree, the level of someone’s control over that tree can be determined as well as their ability to view living individuals.

1.8.3.4. The unknown individual (UHR or suspect) should be the first person entered into the tree.

1.8.3.4.1. The individual shall be listed as “Unknown Individual” in the name field.

1.8.3.4.2. The biological sex of the individual should be entered, if known, at the time of tree creation.

1.8.3.4.3. After the potential identification of the unknown individual is hypothesized, the name field and information may be updated.

1.8.3.5. After grouping DNA matches, the highest and most helpful matches that are identified will be entered into the tree. The name shall be entered into the tree, if known. An alias can be substituted and edited as more information is gathered. In the suffix box, “DNA Match” and their cM number should be written. The original username may be entered into the suffix box at the analyst’s discretion.

1.8.3.6. All trees shall be shared with all members of the FIGG team.

1.8.3.6.1. Invitations to the tree should be sent via Ancestry through the *Invite* button and then on the *Email* tab using the ISP email addresses.

1.8.3.6.1.1. Each member of the FIGG team shall be given access to the “Editor” level of privacy.

1.8.3.7. A family tree showing 4-5 generations should be built for the best matches whenever possible.

1.8.3.7.1. If a most recent common ancestor is likely farther back from 5 generations, research should be conducted focused upon most likely connections.

1.8.3.8. “Quick and Dirty” Trees

1.8.3.8.1. The focus is placed on building accurate family trees quickly without fully documenting every family member to identify a most recent common ancestor.

1.8.3.8.2. The tree should not include every fact about every family member.

1.8.3.8.3. “Quick and dirty” trees should assist in finding the Most Recent Common Ancestors quickly.

1.8.3.9. Most Recent Common Ancestor (MRCA)

1.8.3.9.1. When building trees, there should be times when the same individuals appear as families intersect.

1.8.3.9.2. Merging individuals in the tree shall be done once they are identified as being the same.

1.8.3.9.3. Based on the shared cM numbers, the likely generations for a most recent common ancestor can be estimated.

1.8.3.10. Saving Ancestry.com Images and Records:

1.8.3.10.1. Ancestry.com images and records utilized during research shall be linked to the applicable individuals in the family tree.

1.8.3.11. Saving Photos:

1.8.3.11.1. Saving photographs directly to one’s tree from another tree compromises the privacy of the tree and makes the private tree partially searchable and able to be located. Saving photos directly in this manner shall not be done.

1.8.3.11.2. If a photo needs to be retained, a copy shall be retained in the FIGG Research Workbook.

1.8.3.11.3. Only photographs which are applicable to the case (such as a potential close relative of the unknown individual) should be retained.

1.8.3.11.3.1. Artificial Intelligence (AI) created photographs or photographs that do not aid in the research such as ships, tombstones, or family homes should not be downloaded and stored.

1.8.3.12. Using Newspapers.com or other resources available within the Ancestry subscription.

1.8.3.12.1. Copies of obituaries or records shall be linked directly to the Ancestry tree.

1.8.3.13. Newspapers or other web sources

1.8.3.13.1.1. Sources may be added in Ancestry through “Add web link” or “Add fact or event” and copying the web link. Additionally, a web link may be added under an existing life event.

1.8.3.14. Naming of individuals

1.8.3.14.1. Maiden or birth surnames should be used, if known. If it is unknown the surname shall be left blank.

1.8.3.14.2. First and middle names should be added when known.

1.8.3.14.3. Aliases should be listed with quotations after the birth name.

1.8.3.14.4. Occupations shall not be included in any name, including suffix or prefix.

1.8.3.14.4.1. The suffix can be utilized for other identifying information.

1.8.3.14.5. Surnames should not be in all capital letters.

1.8.3.14.6. When foreign names are known, standardized foreign spellings should be used including any foreign letter characters.

1.8.3.15. Creating Unlinked Individuals within a tree

1.8.3.15.1. For every DNA match which is being pursued, an unlinked tree shall be created within the Ancestry Tree for that case.

1.8.3.15.2. To create an unlinked tree for a DNA match, open to the pedigree view in Ancestry Trees. Click on “Add Father” or “Add Mother” and add that individual’s known information. This will create a false relationship. Click on the person to go to their profile. Click “edit icon”, then “edit relationships”, and delete the false relationship. This will create an unlinked person in the tree.

1.8.4. **Match Evaluation**

1.8.4.1. The research analyst has the discretion to determine if matches are insufficient to move forward with family tree building.

1.8.4.1.1. An investigative memo shall be issued to inform the investigator that the profile will continue to be searched in the databases.

1.8.4.1.2. Additional technologies such as Whole Genome Sequencing or other specialized targeted sequencing techniques may be recommended to provide potential for additional matches.

1.8.4.2. Cases with no resolution shall be searched at least every six months for at least five years to check for new matches.

1.8.4.2.1. The .csv of the match list shall be retained for periodic checks. The case number, item number and date shall be included in the filename.

1.8.4.2.2. If informative new matches are found tree building research should resume.

1.8.5. **Target Testing**

1.8.5.1. Target testing involves choosing specific people to help narrow the search for potential candidates for the unknown individual.

1.8.5.1.1. All requests for target testing should be issued in a memo.

1.8.5.1.2. Requests should include the name, address and contact information of the target tester for the investigator to collect the DNA standard.

1.8.5.1.3. The Forensic Services Division shall not use target testing standards collected with surreptitious methods.

1.8.5.1.4. A copy of the signed informed consent shall be required for DNA target testing performed by ISP.

1.8.5.1.5. For unknown suspects, recommended target test subjects should be no closer than second cousins of the individual.

1.8.5.1.5.1. Multiple target test subjects may be needed to identify the subject.

1.8.5.1.6. In-house target testing is subject to the same standards and practices of other DNA testing including all standard laboratory procedures and protocols for FIGG.

1.8.5.1.7. Target testers should be notated within the research workbook.

1.8.5.1.8. These testers shall be notated as a DNA match in the Ancestry Tree with the phrase “DNA Match” and their cM number in the suffix name area. “Target Test” should be listed in the prefix for ease of access in searching the Tree for individuals’ names.

1.8.5.2. Self-uploading target testers

1.8.5.2.1. Law enforcement may initiate target testing utilizing a FTDNA Family Finder™ kit.

1.8.5.2.2. If a target tester is located who has already tested with DNA, they should be given the option to upload their information to GEDmatch and/or FTDNA.

1.8.5.2.2.1. If possible, the investigator should assist in uploading of their profile. Instructions shall be provided to the target tester to assist with upload.

1.8.5.2.2.2. Law enforcement should encourage the individual to provide their email used for upload or GEDmatch kit number for future identification in any match list.

1.8.5.2.2.3. Any individuals who voluntarily upload their own DNA to GEDmatch or FTDNA and opt-in to law enforcement are in control of their test results. These are not required to be deleted at the time of case closure.

1.8.6. **Reference Testing**

1.8.6.1. Reference tests will be recommended through an investigative memo in order to verify the POI identified through genealogy.

1.8.6.2. If a single individual is named for reference testing the individual may be made the "home" person in the Ancestry tree.

1.8.6.3. Reference testing utilizes STRs to perform a direct comparison or relationship comparison with a close family reference standard (such as parent, child, or sibling).

1.8.6.4. Reference testing is subject to the same standards and practices of other DNA testing including all standard laboratory procedures and protocols in the Biology Casework Test Methods.

1.8.7. **Communication with Biological Relatives or Individuals Outside of Law Enforcement**

1.8.7.1. Permission shall be obtained from the investigating officer before contact is made with any individuals outside of law enforcement. Documentation of permission shall be retained within the casefile.

1.8.7.2. Individuals shall be informed of the genealogist's position and role in a law enforcement investigation upon initial contact.

1.8.7.2.1. Genealogist contact information shall also be provided to allow multiple lines of communication.

1.8.7.3. Limited information about the case should be shared for criminal cases. For unidentified remains cases all necessary information should be shared.

1.8.7.4. Information and documentation from contacted biological relatives should be utilized with caution.

1.8.7.5. Contacted individuals should be discouraged from participating in the investigation outside of providing records and information.

1.8.7.6. Match lists or other confidential investigative information shall not be provided.

1.8.7.7. First contact for DNA matches or kit managers should be made via email.

1.8.7.8. Contact with DNA matches shall not be made through social media or through Ancestry or other website messaging systems.

1.8.7.9. First contact for Target Testers shall be made by law enforcement.

1.9. Records

1.9.1. Case Closure

1.9.1.1. Closure of FIGG research can be due to any of the following reasons:

1.9.1.1.1. STR confirmation testing is complete.

1.9.1.1.2. Confirmation of the identification by the coroner.

1.9.1.1.3. At the request of the agency.

1.9.1.2. Documentation of case closure and completed steps shall be documented within the casefile.

1.9.1.3. If a case is closed during the initial research process, a memo documenting withdrawal of the case shall be written.

1.9.2. Deletion of DNA Samples

1.9.2.1. After the closure of a case, all third-party samples processed in-house for target testing and the original SNP profile shall be removed from GEDmatch PRO™, FTDNA and any other databases that were utilized.

1.9.2.2. All original research located in Ancestry Trees shall be deleted from Ancestry accounts.

1.9.2.2.1. GEDcoms of original research shall be downloaded and stored in the FIGG data drive.

1.9.2.2.1.1. GEDcoms shall be named “Case Number_item#.

1.9.2.2.1.2. Instructions for downloading a tree as a GEDcom can be found here: https://support.ancestry.com/s/article/Uploading-and-Downloading-Trees.

1.9.3. File Organization

1.9.3.1. All files shall be saved into the case folder on the FIGG data drive.

1.9.3.2. Folder name shall include Case Number.

1.9.3.3. Within each folder, there shall be a copy of the FIGG Research Workbook.

1.9.3.4. All .csv files generated from match lists shall be retained in this folder. The case number, item number and date shall be included in the filename.

1.10. Investigative Memos

1.10.1. All investigative leads for an unknown individual shall be included in an investigative memo.

1.10.1.1. Investigative memos should be brief, concise and contain enough to explain the findings without going into extreme detail.

1.10.1.2. Dates should use the month, day, year format in all memos.

1.10.1.3. Images of any tool results (ex. biogeographical ancestry) shall have reference to the tool used and date information was generated.

1.10.1.4. Investigative memos shall be sent by email to the investigating officer. Delivery and/or read receipts should be documented in the case record.

1.10.1.5. Investigative memos and FIGG technical review sheets shall be stored in Laboratory Information Management System (LIMS) imaging module.

1.10.1.5.1. Memos shall be named in LIMS utilizing the following nomenclature: “FIGG_Case#_memo_G#_PE#_V#” (ex. FIGG_26I1234_Memo_G1_7457_V1).

1.10.1.5.2. Technical review worksheets shall be named in LIMS utilizing the following nomenclature: “FIGG_Case#_TR_G#_PE#_V#” (ex. FIGG_26I1234_TR_G1_7457_V1).

1.10.1.6. All Target Testers and DNA matches are Confidential Genetic Informants; therefore, a redacted investigative memo shall be generated upon request for Discovery that removes names of all living relatives.

1.10.1.6.1. Names, birth and death dates, and other identifying or personal information of Target Testers and DNA matches shall be fully redacted.

1.10.1.6.2. The redacted report shall be saved in a subfolder of the case folder.

1.10.2. Draw-IO webtool

1.10.2.1. Draw-IO is an open-source program which can be located on diagrams.net.

1.10.2.2. This webtool can create charts showing the relationship between the individual and their DNA matches.

1.10.2.3. Draw-IO may be utilized during family tree research.

1.10.2.4. Draw-IO charts may be generated or utilized for investigative memos.

1.10.2.5. Multiple Draw-IO charts might need to be created for each group of DNA matches showing most recent common ancestors or shared ancestors.

1.10.2.6. Individuals shall be listed by first, middle (if known), and last name with their birth and death years (ex. John Doe 1905-1999), if known, matching their listing in the Ancestry tree. Birth and death years for DNA matches are optional.

1.10.2.6.1. Suffixes (ex., Jr.) may be added if needed to distinguish between individuals with the same first and last name.

1.10.2.7. Shared cM numbers shall be reported between the Unknown Individual and each Confidential Genetic Informant in any report and Draw-IO chart.

1.10.2.8. Charts shall be saved in the FIGG data drive.

1.10.2.9. Target Testers should be referred to by name in Draw-IO charts. “Target Testing” shall be indicated below the box for clarity. When preparing Reference Test Memos, their shared cM amount shall be included.

1.11. Technical Review and Administrative Review

1.11.1. Each FIGG investigative memo issued shall undergo technical and administrative review.

1.11.2. Technical Review shall verify:

1.11.2.1. All required protocols in the FIGG process were followed.

1.11.2.2. FIGG Research Workbook contains required documentation.

1.11.2.3. Formatting of the Ancestry and memo trees meets requirements including name formats and privacy settings and contains appropriate information.

1.11.2.4. Investigative recommendations are logically sound and supported by documentation.

1.11.2.5. Investigative memos contain appropriate and correct information.

1.11.3. An Administrative Review shall be completed for all FIGG investigative memos. “Reviewed By: PE#” shall be added to the memo for documentation.

1.12. References

1.12.1. Bettinger, B.T. *Guide to DNA Testing and Genetic Genealogy 2nd Edition*. Family Tree Books, 2019. Print.

1.12.2. United States Department of Justice Interim Policy: Forensic Genetic Genealogical DNA Analysis and Searching; September 24, 2019. Web. https://www.justice.gov/opa/pr/department-justice-announces-interim-policy-emerging-method-generate-leads-unsolved-violent

1.12.3. National Technology Validation and Implementation Collaborative (NTVIC): Guidelines for establishing Forensic Investigative Genetic Genealogy (FIGG) programs, *Forensic Sci. Int. Synergy* 7 (2023). Print.

1.12.4. Wickenheiser, R.A., Naugle, J., Hoey, B., Nowlin, R., Kumar, S.A., Minton, A., Allen, L., Glynn, C. National technology validation and implementation collaborative (NTVIC) policies and procedures for forensic investigative genetic genealogy (FIGG), *Forensic Sci. Int. Synergy* 6 (2023), 100316. Print.

1.12.5. GEDmatch.com Terms of Service and Privacy Policy: Web. https://www.gedmatch.com/terms-of-service-privacy-policy/

1.12.6. FamilyTreeDNA Law Enforcement Guide: Web. https://www.familytreedna.com/legal/law-enforcement-guide

1.12.7. DNA Justice Foundation Terms of Service: Web. https://www.dnajustice.org/tos

APPENDIX 1
DEFINITIONS

1. Centimorgan: A unit of genetic measurement to represent the distance between two points on a chromosome. A unit used to measure the amount of shared DNA between two people.
2. Combined DNA Index System (CODIS): Refers to the DNA database and its software. It is composed of National (NDIS), State (SDIS), and Local (LDIS) components. It contains DNA profiles from offenders, crime scenes and includes a missing person database.
3. DNA Cluster: A group of interconnected DNA matches to the person of interest.
4. Confidential Genetic Informant: A DNA match to the person of interest in a FIGG case. This term is utilized to protect the privacy of individuals who are not directly involved in the criminal matter if records must be provided to individuals outside of the investigation.
5. DNA Justice Foundation: A non-profit organization that manages a genetic database specifically for Law Enforcement applications of genetic genealogy.
6. FamilyTreeDNA (FTDNA): A genealogical company that maintains a publicly accessible genetic database that allows searching by law enforcement.
7. Forensic Investigative Genetic Genealogy (FIGG): A technique created by genealogists and law enforcement to find leads using DNA found at scenes of violent crimes or for identification of human remains.
8. GEDmatch/GEDmatch PRO: An online service established in 2010 used to compare DNA data files from different testing companies; they are known for being cooperative with Law Enforcement. GEDmatch PRO is the portal utilized for law enforcement upload and searching of kits that are opted in for law enforcement searching.
9. Match: A general FIGG term referring to individuals who share segments of DNA with the person of interest.
10. Most recent common ancestor (MRCA): The closest shared ancestor between two or more individuals
11. National Technology Validation and Implementation Committee (NTVIC): An organization of federal, state and local crime laboratory leaders, university researchers, and private companies that establish guidelines and recommendations for FIGG programs.
12. Reference testing: The comparison of a person of interest's direct reference standard back to the STR profile. When a direct reference standard isn't available, kinship analysis of a close family member can be utilized.
13. Short Tandem Repeat (STR): Small sections of DNA that contain short segments (2, 3, 4 or more base pairs) which repeat several times. The number of repeat units may vary between individuals. STRs are utilized in traditional DNA analysis and CODIS searching.
14. Single Nucleotide Polymorphism (SNP): A genetic variation of a single base pair of DNA. SNP profiles are utilized for FIGG searching.
15. Targeted sequencing: The process of generating data on a pre-determined set of SNPs that have been selected for FIGG.
16. Target testing: Requesting a more distantly related individual voluntarily test to help include or exclude certain branches of the family tree as descendants of the person of interest.
17. Quick and dirty trees: Quickly researched trees created to find connections between two genetically related individuals.

18. Whole Genome Sequencing (WGS): The process of determining nearly the entirety of the DNA sequence of an individual’s profile at a single time. Large panels of targeted sequencing methods that include hundreds of thousands of SNPs may also be referred to as WGS.

APPENDIX 2
DNA SERVER INSTRUCTIONS

The DNA data drive ("DNA Data") will be used for storage and archiving of case documentation, data and photos. The FIGG folder within the IRL data folder will contain all documentation for FIGG cases. Within the FIGG folder, there shall be one folder for each year or range of years of FIGG casework. A case folder shall be created for each case number, which will contain all associated electronic data for that case. The case folder shall be contained within the year or range folder that matches the case number, not the year the case was completed.

The following nomenclature shall be used:

- FIGG Research Workbook: case number_item#_G# (ex. 24I-01234_001A_G1)
- Ancestry Trees: case number_item# (ex. 24I-01234_001A)
- GEDcoms: case number_item# (ex. 24I-01234_001A)
- Match lists: the case number, item number and date shall be included in the filename.

APPENDIX 3
INVESTIGATIVE MEMO TEMPLATES

INSUFFICIENT MATCHES

FIGG INVESTIGATIVE MEMO

Investigator Name
Agency
Address
City, IN Zip

Date
Agency Case Number:
ISP Forensic Services Division Case Number:
Item Number:

Case Information

The following case details have been compiled from law enforcement files and were utilized in the evaluation of genealogical research. [Add relevant case information here.]

Introduction

Forensic Investigative Genetic Genealogy (FIGG) is a technique which generates leads in violent unsolved crimes and unidentified human remains cases. DNA from an evidence sample or human remains is analyzed and the SNP profile is uploaded to law enforcement accessible public genealogy databases to locate genetic relatives of the Person of Interest (POI). Genealogical research is conducted on those relatives to build family trees, locating common ancestors and evaluating their descendants to determine which individual(s) may be the POI. Confirmation should be verified through direct comparison to a reference standard from the POI or through kinship analysis of standards of close living relatives.

Biogeographical Ancestry

[Optional - Add chart here?]
Data from [Kintelligence Ancestry Estimation Report/other source – date]

DNA analysis indicated that the POI is consistent with an individual of [X] Ancestry. [if no chart add source here]

Research Summary

[In order to generate more DNA matches and investigative leads, it is recommended to outsource this case for Whole Genome Sequencing (WGS). Please contact the analyst for more information.

AND/OR

At this time there are not enough available DNA Matches to complete Forensic Investigative Genetic Genealogy. The case will continue to be monitored, and new information will be provided in a separate memo.]

All information provided is for investigative purposes only. This information is based only on the data and information developed at the time of reporting and does not supersede any additional DNA matches or information that may be identified. The Indiana State Police Forensic Services Division recommends that all investigatory conclusions be confirmed through final STR comparisons.

Analyst
Biology Section
Indiana State Police
Forensic Services Division
Analyst work phone number
Analyst work email

Year/Lab/Memo#

INVESTIGATIVE LEAD MEMO

FIGG INVESTIGATIVE MEMO

Investigator Name
Agency
Address
City, IN Zip

Date
Agency Case Number:
ISP Forensic Services Division Case Number:
Item Number:

Case Information

The following case details have been compiled from law enforcement files and were utilized in the evaluation of genealogical research. [Add relevant case information here.]

Introduction

Forensic Investigative Genetic Genealogy (FIGG) is a technique which generates leads in violent unsolved crimes and unidentified human remains cases. DNA from an evidence sample or human remains is analyzed and the SNP profile is uploaded to law enforcement accessible public genealogy databases to locate genetic relatives of the Person of Interest (POI). Genealogical research is conducted on those relatives to build family trees, locating common ancestors and evaluating their descendants to determine which individual(s) may be the POI. Confirmation should be verified through direct comparison to a reference standard from the POI or through kinship analysis of standards of close living relatives.

Biogeographical Ancestry

[OPTIONAL: Add chart here]
Data from [Kintelligence Ancestry Estimation Report/other source – date]

DNA analysis indicated that the POI is consistent with an individual of African ancestry. [if no chart add source here]

Research Summary

X [groups of] DNA matches were found to be biologically connected to the POI. The following summary will include charts displaying the connections between the POI and these DNA matches. These DNA matches will be listed by their name or username.

DNA Cluster #

This cluster contains X matches. These matches include:

1) NAME sharing X cM.
2) NAME sharing X cM.
3) etc…

Figure # shows the relationships within the cluster to the most recent common ancestor. The most recent common ancestor[s] [was/were] determined to be [NAME OR NAMES]. The POI descends from [these/this] ancestor[s].

Figure #

[insert draw.i.o. chart]

DNA Match #

NAME sharing X cM.

Figure # shows the relationship to the possible POI.

Figure #
[insert draw.i.o. chart]

Investigative Recommendations

Research indicates the possible POI may be NAME[S]. [IF POI LIVING]
Please submit an appropriate DNA standard (such as an oral/buccal swab standard) for confirmation of this investigative lead.]

Name:
Parents:
Birthdate:
Birthplace:
Last Known Address:
[other appropriate investigative information]

[IF POI DECEASED]
Please consult the reporting analyst for further recommendations on approaching reference testers and explaining why testing is needed. The recommendations provided are based on genealogical research and family relationships can be complex, sensitive topics. Care should be utilized when approaching family members for these discussions. The contact information listed below should be confirmed prior to contact with the individual.

To confirm this investigative lead, please submit an appropriate DNA standard (such as an oral/buccal swab standard) from at least one of the following individuals:

1) Name:
   Birthdate:
   Last Known Address:
   Relationship to POI:

2) Name:
   Birthdate:
   Last Known Address:
   Relationship to POI:

All information provided is for investigative purposes only. This information is based only on the data and information developed at the time of reporting and does not supersede any additional DNA matches or information that may be identified. The Indiana State Police Laboratory recommends that all investigatory conclusions be confirmed through final STR comparisons.

Analyst
Biology Section
Indiana State Police
Forensic Services Division
Analyst work phone number
Analyst work email

Note: DNA matches and other genetic relatives of the POI are considered confidential genetic informants. To protect the privacy of individuals not directly involved in the case, the laboratory recommends redaction of names and identifying information of DNA matches and living ancestors before distribution of this memo to individuals not involved in the investigation of the criminal matter. Please contact the laboratory for a redacted version prior to utilization of this memo in any court filings or discovery fulfilment unless otherwise directed through court order.

Year/Lab/Memo#

TARGET TESTING MEMO

FIGG INVESTIGATIVE MEMO

Investigator Name
Agency
Address
City, IN Zip

Date
Agency Case Number:
ISP Forensic Services Division Case Number:
Item Number:

Case Information

The following case details have been compiled from law enforcement files and were utilized in the evaluation of genealogical research. [Add relevant case information here.]

Introduction

Forensic Investigative Genetic Genealogy (FIGG) is a technique which generates leads in violent unsolved crimes and unidentified human remains cases. DNA from an evidence sample or human remains is analyzed and the SNP profile is uploaded to law enforcement accessible public genealogy databases to locate genetic relatives of the Person of Interest (POI). Genealogical research is conducted on those relatives to build family trees, locating common ancestors and evaluating their descendants to determine which individual(s) may be the POI. Confirmation should be verified through direct comparison to a reference standard from the POI or through kinship analysis of standards of close living relatives.

Biogeographical Ancestry

[OPTIONAL: Add chart here]
Data from [Kintelligence Ancestry Estimation Report/other source – date]

DNA analysis indicated that the POI is consistent with an individual of African ancestry. [if no chart add source here]

Research Summary

X [groups of] DNA matches were found to be biologically connected to the POI. The following summary will include charts displaying the connections between these DNA matches. The DNA matches will be listed by their name or username.

DNA Cluster #

This cluster contains X matches. These matches include:

1) NAME sharing X cM.
2) NAME sharing X cM.
3) etc…

Figure # shows the relationships within the cluster to the most recent common ancestor. The most recent common ancestor[S] [was/were] determined to be [NAME OR NAMES]. The POI descends from [these/this] ancestor[s]. Collection of voluntary DNA standards from the specified individuals within the family cluster is recommended to assist in continued genealogical research.

Figure #

[insert draw.i.o. chart]

DNA Match #

NAME shares X cM with the POI. The possible relationships to the POI include:

Collection of voluntary DNA standards from the specified individuals within Figure # is recommended to assist in continued genealogical research.

Figure #

[insert draw.i.o. chart]

Investigative Recommendations

Collection of DNA standards from specified individuals within the family clusters is necessary to assist in continued genealogical research. Please consult the reporting analyst for further recommendations on approaching voluntary target testers and explaining why testing is needed. The recommendations provided are based on genealogical research and family relationships can be complex, sensitive topics. Care should be utilized when approaching family members for these discussions. The information listed below should be confirmed prior to contact with the individual.

DNA standards for voluntary target testers require signed informed consent paperwork so the tester understands how their DNA will be utilized and how their genetic information will be retained.

DNA standards should be collected from the following individual[s]:

1) Name:
   Birthdate:
   Last Known Address:
   Relationship to POI:

2) Name:
   Birthdate:
   Last Known Address:
   Relationship to POI:

All information provided is for investigative purposes only. This information is based only on the data and information developed at the time of reporting and does not supersede any additional DNA matches or information that may be identified. The Indiana State Police Laboratory recommends that all investigatory conclusions be confirmed through final STR comparisons.

Analyst
Biology Section
Indiana State Police
Forensic Services Division
Analyst work phone number
Analyst work email

Note: DNA matches and other genetic relatives of the POI are considered confidential genetic informants. To protect the privacy of individuals not directly involved in the case, the laboratory recommends redaction of names and identifying information of DNA matches, living ancestors and potential target testers before distribution of this memo to individuals not involved in the investigation of the criminal matter. Please contact the laboratory for a redacted version prior to utilization of this memo in any court filings or discovery fulfilment unless otherwise directed through court order.

Year/Lab/Memo#

APPENDIX 4

FIGG TECHNICAL REVIEW WORKSHEET

Case _____ Memo_____ Technical Reviewer _____

Analyst _____

	Yes	NA	Comments
General			
1. All electronic data were stored properly (GEDcoms, .csv files, workbook).	☐	☐	_____
2. Relevant SNP data has been uploaded to law enforcement database(s).	☐	☐	_____
3. Case information added to appropriate tracking list(s).	☐	☐	_____
FIGG Research Workbook			
4. Proper daily notes were present.	☐	☐	_____
5. All match information contained in .csv files were copied to correct tabs.	☐	☐	_____
6. Documentation was added from all genealogists aiding in the tree building process.	☐	☐	_____
7. Tools used to analyze DNA matches were documented.	☐	☐	_____
Genealogical Trees			
8. Trees were properly formatted.	☐	☐	_____
9. Privacy of tree verified.	☐	☐	_____
10. Each step in the tree is supported by appropriate documentation.	☐	☐	_____
Investigative Memo			
11. Correct agency case number was used.	☐	☐	_____
12. All names were spelled correctly throughout.	☐	☐	_____
13. Family chart details match Ancestry trees.	☐	☐	_____
14. Memo wording guidelines were followed.	☐	☐	_____
15. Investigative recommendations are logically sound and supported by documentation.	☐	☐	_____