

Use of DNA Testing in Police Investigative Work for Increasing Suspect Identification, Arrest, Conviction, and Case Clearance

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Synopsis

Abstract

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Background

The use of DNA (deoxyribonucleic acid) testing as part of police investigative work has increased substantially since its emergence in the 1980s (e.g., Roman et al., 2008; Home Office, 2005; Lovrich et al., 2003). Initially used primarily in serious cases, such as homicides and rapes, recent use has expanded to include additional crimes, such as property offenses (e.g., Asplen, 2004, Home Office, 2005). The fundamental question motivating this review is: Does the use of DNA testing improve the effectiveness of the police in identifying and convicting perpetrators of crime, particularly if expanded beyond its traditional use in serious and violent offenses?

Assessment of the importance of the use of DNA in police investigations comes in part from the low clearance rates (i.e. rates of solved crimes) that are often achieved using conventional investigative techniques. This problem was noted in the National Research Council (NRC) report on *Fairness and Effectiveness in Policing* (Committee, 2004) which concluded “that most property crimes and many violent crimes are unsolved” (p. 227). The problem is particularly acute for property crimes where clearance rates are often much below 20% (Cordner, 1989; Weisburd et al., in press). Low clearance rates in property crime are the result of a combination of factors, but are often attributed to a lack of evidence in property crime investigations (where eye witness accounts are rare) and the large number of cases relative to investigators available (Eck, 1983; Greenwood, Chaiken, & Petersilia 1977). The NRC report (2004) also notes that studies have shown “that if clues pointing to specific suspects were not provided by citizens to the first responding officers, then follow-up investigators had great difficulty solving the case” (p. 228).

Despite the strong advances in police innovations and their evaluation in the 1980s and 1990s (Weisburd and Braga, 2006), there is more generally little evidence regarding whether technology (e.g. advanced computing, automatic finger print systems, and DNA analysis) has impacted on the success of investigations (Committee, 2004). In this regard Horvath et al. (2001:5) argue that "in many fundamental respects, the police criminal investigation process has remained relatively unaffected by the significant changes that have occurred in policing, the crime problem and technology in the past thirty years."

DNA is essentially a long string of information that is represented by combinations of four possible acid pairings of adenine, cytosine, guanine, and thymine (AT, GC, TA, CG). Long sequences of these pairs contain each individual's genetic information, much the same way strings of 1s and 0s in binary code can contain the information used by computers (i.e. 00110101101100).

While over 99.9% of the sequence of acid pairs is exactly the same in everyone's DNA, the relatively small portions of DNA that are unique for each individual (United States, About Forensic DNA). Within this unique portion, there are several known points, or loci, where short sequences of these acid pairs are repeated over and over. By counting the number of times these short sequences repeat at each of these loci, it is possible to determine, with a very high degree of certainty, whether a sample of DNA came from a particular individual. In a recent report from the National Research Council, the Committee on Identifying the Needs of the Forensic Sciences Community investigated many aspects of the forensic sciences currently being used in the United States. While the report was critical of many of the other methods, the committee concluded that DNA was the only "forensic method [that] has been rigorously shown to have the capacity to consistently, and with a high degree of certainty, demonstrate a connection between evidence and a specific individual source" (Committee on Identifying the Needs of the Forensic Sciences Community, 2009, p. 7)

Measuring the number of times a short string of acid pairs repeats at a particular locus is known as STR (short tandem repeats) analysis. STR analysis has largely replaced the previously used RFLP (restriction fragment length polymorphism) method of analysis, which measured much longer strings of repeating acid pairs over much larger portions of the DNA string than the several loci used in STR analysis. The FBI has identified 13 specific loci that are used in forensic analyses, and when the number of repeats for each of these loci is the same in two samples, the odds of the similarity being a coincidence are about one in a billion (U.S. Department of Energy, 2008). This method of DNA analysis can result in three possible outcomes: inclusion, exclusion, or inconclusive result (United States, Possible Results from DNA Tests). It is important to recognize that an inclusion is not actually the same as a "match." Rather, it only means that the odds of a sample coming from another source are extremely unlikely.

Just as the STR method improved DNA analysis from the earlier RFLP method, other developments in the scientific aspects of forensic DNA are continuing to advance the capabilities of the discipline. The new techniques of mtDNA (mitochondrial DNA) and Y-STR (Y chromosome STR) analysis can be used to identify people through their familial lines (United States, Mitochondrial Analysis; United States, Y-Chromosome Analysis). Automation and robotics are being incorporated into crime laboratories "to improve the speed and to reduce the cost of DNA analysis" (United States, Miniaturization and Automation). New portable analysis systems, which are the size of a briefcase, can be used at the crime scene to produce a profile in about 30 minutes (NEC, 2007). More sensitive methods of collecting samples are allowing analysis of even the minuscule amounts of DNA left from simply touching a surface (Gill, 2001).

As fast as these new technologies related to forensic DNA have been developing, new policies and applications of that science have developed just as quickly. As mentioned earlier, the use of DNA testing as part of police investigative work has increased substantially since its emergence in the 1980s and DNA databases, such as CODIS (Combined Offender DNA Index System) in the United States and NDNAD (National DNA Database) in the United Kingdom, have also been developed to provide an entirely new method of investigating crime. Instead of using DNA analysis simply to corroborate the guilt (or innocence) of a previously identified suspect, DNA databases can themselves identify suspects before there is any other evidence implicating the individual. The offenses for which DNA is collected and entered into these databases have broadened so that within the United States, as of April 2009, 47 states collect DNA samples from all convicted felons, and 35 states collect samples from those convicted of certain misdemeanors (DNA Resource, 2009). Many states are either considering, or have already implemented, policies of collecting DNA samples from arrestees.

In addition to identifying suspects, forensic DNA has also contributed to the exoneration of those wrongfully convicted of crimes they did not commit. Thus far, forensic DNA has contributed to the exoneration of 238 individuals convicted of serious crimes in the United States, 17 of whom have served time on death row (The Innocence Project, 2009).

Along with the benefits of any new advance, there are also challenges. The utility and popularity of forensic DNA has also proved to be one of its shortcomings. Misconceptions about the capabilities of DNA analysis and other forensic sciences, commonly known as the CSI effect, are common (Schweitzer & Saks, 2007). With the promise of forensic answers in difficult criminal investigations, increased submissions to crime laboratories have made backlogs of unprocessed evidence a frequent occurrence (Lovrich, et al., 2004). Stories of thousands of rape cases remaining unanalyzed and sitting on lab shelves are unfortunately frequent (CA NOW, 2009; Nadler, 2002; Weiner).

The goal of this systematic review is to summarize the relevant and accessible evidence on the effectiveness of DNA testing in routine police work. Specifically, the fundamental question motivating this review is: Does the use of DNA testing improve the effectiveness of the police in identifying and convicting perpetrators of crime, particularly if expanded beyond its traditional use in serious and violent crime investigations?

Objectives

The objective of this review is to synthesize credible evidence on the effectiveness of DNA testing as part of routine police investigative practices compared to other more traditional forms of investigation or other methods of forensic DNA analysis. Of interest are the effects on the apprehension of individuals responsible for crimes and reductions in the likelihood of the involvement of innocent individuals in the criminal justice system. We are also interested in the effect of DNA on the cost, speed, clearance rates, arrest rates, and conviction rates of investigations.

It is anticipated that this review will help inform policy makers and the police department decisions regarding the routine use of DNA testing in investigative police work. Many police agencies are expanding the use of DNA testing, and a critical examination of the existing evidence is warranted.

Methods

Criteria for considering studies for this review

Types of interventions

The scope of the review will be limited to the use of DNA testing by police as part of their investigations of crime. We will not consider the use of DNA testing by criminal defendants or by prosecutors. Of particular interest is the routine or expanded application of DNA testing in cases that often do not make use of available DNA evidence. The primary basis for eligible studies requires some variation in the use of DNA in the investigation.

Types of studies

Given the limited amount of research in this area, we will include a broad range of study designs. All designs, however, must estimate the effect of DNA testing relative to an alternative or more limited type or application of analysis (i.e., varying degrees of DNA testing, but not necessarily effects sizes).

The ideal design type would randomly assign cases to either a DNA testing condition or a traditional investigative practices condition, and then assess the outcomes of both conditions from the same time-frame. We will consider any such designs that vary the degree of DNA testing used and examine one or more of the outcomes discussed above. The comparison condition does not need to

represent the absence of DNA analysis, but simply a variation of DNA from the treatment condition.

We will also consider quasi-experimental designs in which there is a control group that is either matched to the DNA testing group, or identified as comparable. To include these less methodologically rigorous designs will require statistical justification of the suitability of the control groups identified.

Interrupted time-series designs will also be included in this review, or other regression-based analyses that estimate the impact of DNA testing on a relevant outcome, but these designs will be handled separately as they especially vulnerable to historical threats to validity. An essential feature of time-series designs is the multiple baseline estimates of the rate of interest (e.g., identification of a suspect). This allows for an assessment of both the natural change over time and change that may be associated with the start of an intervention, such as the use of DNA testing or some other change related to the use of DNA in police investigative work.

Basic pre-post designs with a single pre-DNA and a single post-DNA estimate will be included, but these designs will also be handled separately as they provide a weak basis for drawing causal inferences. Other quasi-experimental designs will be included, such as a design that contrasts the clearance rates for different police agencies (without statistically justifying the validity of the comparison), but these will be reported separately.

Types of outcome measures

This review will extend to all crime types. We recognize, however, that the utility of DNA testing is likely to vary substantially across crime type. The current trend toward increased use of DNA testing in burglary cases reflects that burglary is often a high volume crime, with offenders engaged in serial burglaries (Roman et al., 2008). The serial nature of this crime increases the likelihood that a suspect may be identified in an existing database and helps police connect crimes committed by the same individual. The added value of DNA testing may be less for other crimes. As such, we will examine the evidence separately by type of offense.

DNA testing may improve outcomes at several stages of the investigative process. It may facilitate the identification of suspects through the use of DNA databases, such as *CODIS* in the United States or the *UK National Criminal Intelligence Database* in the United Kingdom. DNA testing also may help eliminate suspects or identify one suspect among multiple suspects found through traditional police

investigative methods. These processes may increase the likelihood of an arrest and a conviction, raising the number of cleared cases. Studies under review may examine the effectiveness of DNA testing as measured by one or more of these outcomes. As such, we will examine as part of our review the following aspects of effectiveness as outcomes: the rate at which suspects are identified, the arrest rate of a suspect, the conviction rate, length and speed of an investigation, the cost of the investigation, and the case clearance rate (i.e., how often cases are successfully solved).

The source of the data will generally be from official records or reports of some form. However, we will not restrict eligibility based on the source of the outcome data. All sources will be considered.

Search methods for identification of studies

We will consult with an information retrieval specialist on the selection of keywords to use and databases to search. Preliminary searches will be conducted with the terms “DNA” and “Police” or “Policing” or “Investigation”. The terms will be refined and expanded as we gain greater familiarity with the existing literature and how it is cataloged. In addition to searching the databases listed below (see electronic sources), we will also search the UK Home Office website for relevant publications. Google Scholar will be searched to help identify publications not already captured through the formal databases. Key individuals working in this field will be solicited for assistance in identifying relevant studies (e.g., Peter Neyroud at the National Policing Improvement Agency). We will also be searching for studies in languages other than English. If we identify any such studies, we will solicit assistance in translating these documents.

Search Strategy for the Identification of Relevant Studies

A search strategy for electronic databases was developed in order to reach an optimal balance between potentially relevant search results and the large number of results using similar terms, yet addressing issues other than those of interest in this project. This search strategy is broad, but avoids the combination of terms that would include the large body of technical research done on DNA, as well as studies exclusively addressing non-DNA forensic sciences.

Search Terms

Two categories of keywords were developed for this search. The first category addresses the technology of interest (DNA). The second category addresses the

application of DNA testing in police investigative work, and includes terms such as policing, detective, arrest, etc. The intention of separating the terms in this manner was to include all the potentially relevant results, while simultaneously excluding the large bodies of literature on DNA from non-forensic disciplines. These two sets of keywords were combined with a Boolean AND. Unfortunately, the body of literature on the application of DNA to criminal investigations is much smaller than the literature on aspects of DNA addressed by other disciplines (i.e., the basic science of DNA testing). This has resulted in search results in the low hundreds for some databases.

1. Particular Technology of Interest

DNA or "DEOXYRIBONUCLEIC ACID"

2. Application context

FORENSIC! or LAW or LEGAL or COURT* or TRIAL! or CSI or C.S.I. or "CRIME SCENE" or "CRIME LAB*" or ANALYSIS or INVESTIGATION! or POLIC* or DETECT* or PROSECUT* or DEFEN* or CRIM* or CODIS or C.O.D.I.S. or "COMBINED DNA INDEX SYSTEM" or NON-VIOLENT or "RAPE KIT!" or IDENTI* or ARREST! or COST! or CLEARANCE! or CLOSURE! or SPEED or "COLD CASE!" or EXCULPAT* or "WRONGFUL CONVICTION!" or "ACTUAL INNOCENCE" or BACKLOG

Electronic Sources

The search strategy described above was applied to the following databases, which cover both the more accessible sources as well as the grey literature.

Association of Chief Police Officers ACPO
Association of Chief Police Officers of Scotland ACPOS
Association of Police Authorities APA

Australian Research Council Centre of Excellence in Policing and Security (CEPS)
ASSIA – Applied Social Science Index and Abstracts
Canadian Police Research Centre
CINCH – Australian Institute of Criminology
Criminal Justice Abstracts
Dissertation Abstracts
Ebsco

EconLit
ENFSI – European Network of Forensic Science Institutes
Forensic Science Communications
Forensic Science Society
HeinOnline
Her Majesty's Inspectorate of Constabulary HMIC
Ingenta
Jill Dando Institute of Crime Science (JDI)
JSTOR
Medline/Embase
NCJRS (National Criminal Justice Reference Service)
NCSTL (National Clearinghouse for Science, Technology, and the Law)
Policy Archive
PolicyFile
PROQUEST
Public Affairs Information Service
RAND Documents
ResearchNow
Science Direct
Scottish Institute for Policing Research SIPR
Social Sciences Citation Index
Social Services Abstracts
Sociological Abstracts
SSRN – Social Science Research Network
Worldwide Political Science Abstracts

Data collection and analysis

Assessment of risk of bias in included studies

The methodological quality of the studies will be assessed by coding the features contained in the attached coding forms. The types of information that will be considered include: (1) nature of assignment to conditions; (2) use of matching of cases or the use of statistical controls, such as regression analysis to adjust for potential selection bias in the case of non-random assignment to conditions; (3) representativeness of the sample of cases (e.g., census, random sample, convenience sample); (4) attrition of cases from the study; and, (5) replication of findings in multiple jurisdictions.

The methodological quality information will be reported in tabular form and presented along with the effect size information. If a meta-analysis is performed, effect sizes will be compared on the above dimensions to assess for potential bias.

Measures of treatment effect

The odds-ratio will be the effect size of choice for all outcomes of a dichotomous or binary nature. For example, an odds-ratio will be computed to represent the effect of DNA testing relative to an alternative on the proportion of cases cleared. In contrast, the standardized mean difference effect size will be used for outcomes measured on a continuous measure or outcomes that represent counts or rates. Standard methods of computing effect sizes will be used (see Lipsey and Wilson, 2001). In the case of quasi-experimental designs, preference will be given for effect sizes adjusted for baseline differences. For example, a coefficient for a treatment dummy variable from a logistic regression model can be converted into a treatment effect odds-ratio that is adjusted for the other variables in the model. Similarly, covariate adjusted means can be used in the computation of a standardized mean difference of effect sizes (Lipsey and Wilson, 2001). Preference will also be given to quasi-experimental designs that use a control/comparison condition that is assessed at the same time as the treatment condition.

Unit of analysis issues

The primary unit-of-analysis within the studies of interest will usually be a criminal case, such as a sexual offense or a burglary. Within studies, these cases will typically be aggregated across a police station or some other jurisdiction. Effects from studies that report results separately for distinct and independent policing units, such as units in different cities, will be coded separately and treated as statistically independent.

Multiple reports or manuscripts based on the same study or data will be treated as a single entity for purposes of this review. We will either select the most complete references if all of the relevant information in secondary reports (e.g., journal manuscript) is contained within the primary report (e.g., technical report). However, if the multiple reports each provide unique information (e.g., different outcomes or different jurisdictions), then all reports will be coded as part of this review.

Assessment of reporting biases

Reporting bias will be addressed in several ways. First, the search for and inclusion of unpublished works, such as technical reports, will help guard against reporting and publication bias. If possible, we will compare the results from published and unpublished studies as one estimate of potential bias. Second, we will list any outcomes (dependent measures) included in a study for which an effect size could not be computed. These outcomes are more likely to have negative or null results. A large number of such outcomes, particularly for primary outcome measures, raise concerns regarding reporting bias. We will only perform more formal statistical assessments of publication bias if sufficient data permit, such as the Duval and Tweedie trim-and-fill method and funnel plots (Duval & Tweedie, 2000).

Data synthesis

Once we have completed our search, we will make the determination of whether meta-analysis is the most appropriate method of analyzing the data. Our decision rule for performing meta-analysis will be as follows: two or more studies, each with a computable effect size of a common outcomes construct (potentially measured in different ways), and similar comparison condition. Instances that satisfy this decision rule will be meta-analyzed using standard methods (i.e., inverse-variance weighted, random effects model; see Lipsey and Wilson, 2001). We will also use meta-analysis to synthesize results across multiple sites within a single study if results are reported separately. If data permit, we will explore potential moderators of the effectiveness of DNA, such as crime type, nature of the comparison or counterfactual condition (e.g., finger-print or other non-DNA methods).

In the absence of meta-analysis, synthesis of the findings across studies and inferences about the effectiveness of DNA use in policing will be based on the size and direction of the effects and the confidence intervals. Greater emphasis will be placed on the direction of effects and consistency of effects across similar studies. A single high quality evaluation with an effect size of a meaningful magnitude that is also statistically significant will be interpreted as evidence that DNA use *can* be

effective, assuming there is not an equally strong study with a negative result (multiple studies of the same relationship would, however, be meta-analyzed). Statements about the generalizability of the findings will be limited to the range of conditions examined. Studies with weak internal validity (i.e., plausible bias in the estimate of the causal relationship) will be viewed cautiously. Positive findings of a meaningful magnitude will be interpreted as promising, but will also be viewed as providing limited evidence of the potential effectiveness of forensic DNA use in police investigations.

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Declarations of interest

We have no conflicts of interest related to the use of DNA testing in policing or the studies included in this review.

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Coding Forms

Study Level Code Sheet

Use one study level code sheet for each study. If multiple documents report on the results from the same study, identify one of the documents as primary and use its document ID as the StudyID below. Record the document ID for the related documents in the CrossRef# fields.

Identifying Information:

1. Study (document) identifier StudyID _____
2. Cross reference document identifier CrossRef1 _____
3. Cross reference document identifier CrossRef2 _____
4. Cross reference document identifier CrossRef3 _____
5. Coder's initials SCoder _____
6. Date coded Date ____ - ____ - ____

General Study Information:

7. Author Author _____
8. Funder (e.g., NIJ) Funder _____
9. Geographical Location of Study SLocale _____
10. Geography (1=single site; 2=multiple sites; 9=cannot tell) Sites _____
11. Country Country _____
10. Date range for research (when conducted, not published):
StartDate ____ - ____ - ____
DoneDate: ____ - ____ - ____
11. Publication Type PubType ____
 1. Book
 2. Book Chapter
 3. Journal (peer reviewed)
 4. Federal Gov't Report

- 5. State/Local Gov't Report
- 6. Dissertation/Thesis
- 7. Unpublished (tech report, conference paper)

12. Number of DNA groups (not sample size, but distinct groups, such as police departments, cities, etc.; these are units on which results are reported separately and will be coded separately below)

TxGrps

13. Number of comparison/control groups (not sample size, but distinct groups, such as police departments, cities, etc.; these are units on which results are reported separately and will be coded separately below)

CgGrps ____

14. Number of jurisdictions included in the study

NumJuris _____

DNA-Comparison Level Code Sheet

Use one DNA-comparison level code sheet for distinct geographic or policing unit on which results are reported. For example, if a study is conducted in five cities and results are reported separately for each city, then you will code the information below five times, once for each city. Assign each geographic or policing unit a unique substudy ID, starting at 1 for each treatment-comparison within a study. For example, if a study has three treatment conditions and each is compared to a single control condition, code the information below separately for each treatment compared to the single control condition resulting in three treatment-comparison code sheets. Give each treatment-comparison a unique treatment-comparison identifier (TxID), such as 1, 2, 3, etc.

Identifying Information:

1. Study (document) identifier StudyID _____
2. DNA-comparison identifier GrpID _____
Label for this group/unit _____
3. Coder's initials GrpCoder _____

Sample size information:

4. Sample size (e.g., number of cases) for DNA (treatment) condition DNAN _____
5. Sample size (e.g., number of cases) for comparison/control condition
CompN _____
6. Attrition in the DNA (treatment) condition (number of case; -999 missing)
DNAattrit _____
7. Attrition in the comparison/control condition
DNAattrit _____

Type of cases:

8. Type of cases TypeCases _____

1. Burglary
2. Sexual assault/rape
3. Murder
4. Sexual assault/rape & murder
5. All case types
8. Other _____

Nature of the Control Condition:

9. Nature of the comparison group CgType ____
1. Fingerprinting
 2. No DNA; routine police investigative practices
 3. Routine investigative practices that may include some cases with DNA use
 8. Other _____
 9. Cannot tell

Methodological Rigor:

10. How were cases assigned to conditions? TxRandom ____
1. Random (simple)
 2. Random (matching pairs)
 3. Quasi-random (alternative cases, alternative blocks of cases)
 4. Historical (comparison cases prior to DNA cases in time)
 5. Different jurisdictions
 8. Other _____
11. Missassignment rate (percentage of cases that violated the random assignment protocol) (999 if missing; 888 if non-randomized study) TxMsRate ____
12. How did the researchers handle violations of random assignment? TxAnalyz ____
1. Analyzed as assigned
 2. Analyzed as treated
 3. Both 1 and 2 above (only code effect sizes for 1)
 4. Removed cases
 5. Other _____
 8. NA (non-randomized study)
 9. Not indicated
13. Did the researchers test for baseline (pretest) differences? TxDiff1 ____
(1=yes; 0=no)

14. If yes to above, what was the nature of any pretest differences?TxDiff2 ____

1. No significant differences or substantive differences if n<100 per group
2. Minor differences or differences on variables unlikely to be related to offending
3. Major or important differences
8. Not applicable

15. Baseline (pretest) differences judged to bias the results in which direction? TxBias ____

1. Positive bias (treatment effect likely to be larger than it really is)
2. Negative bias (treatment effect likely to be smaller than it really is)
3. No bias (no differences or differences on variables that should have no effect)
4. Cannot make a judgment (differences have an uncertain effect)
8. Not applicable (answered no to question 13)
9. Cannot tell

16. Credibility of matching (1=low; 2; 3; 4; 5=high; 8=not applicable)CrMatch ____

17. Census or sample of all cases (1=census; 2=sample; 9=cannot tell)Census ____

18. Type of sampling (1=random; 2=convenience; 8=not applicable; 9=cannot tell)

Sampling ____

Outcome (Dependent Variable) Level Code Sheet

Code the information below separately for each dependent variable (outcome) for which an effect size will be coded.

Identifying Information:

1. Study (document) identifier StudyID _____
2. Dependent measure identifier DVID _____
3. Coder's initials DVCoder _____
4. Date coded DVDate ____ - ____ - ____

Dependent Variable Information:

5. Label _____
6. Source of information DVSource ____
 1. Official reports (police reports, etc.)
 2. Survey
 3. Other _____
7. What is the variable measuring? DVcnstr ____
 1. case clearance rate
 2. arrest rate
 3. conviction rate
 4. time to case clearance
 5. time to arrest
 6. time to conviction
 7. other _____
8. Was there any reported difference between the DNA and comparison condition in how this measure was collected? (1=yes, 0=no, 9=cannot tell) DVDiff ____
9. Level of measurement DVLOM ____
 1. Dichotomous indicator
 2. Frequency count
 3. Rate (frequency divided by population base)
 4. Other _____

Effect Size Level Coding Sheet

Code this sheet separately for each eligible effect size.

Identifying Information:

1. Study (document) identifier StudyID _____
2. DNA-Comparison identifier GrpID _____
3. Outcome (dependent variable) identifier DVID _____
4. Effect size identifier ESID _____
5. Coder's initials ESCoder _____
6. Date coded ESDate ____ - ____ - ____

Direction of Effect:

7. Direction of effect. (Note: Specify the direction of the effect. Do not leave as missing or this effect size cannot be used.)
 1. Effect favors treatment (DNA) condition
 2. Effect favors comparison/control condition
 3. Effect favors neither condition (no difference; effect size equals 0)
 9. Cannot tell
8. Effect reported as statistically significant (1=yes, 0=no, 8=not tested, 9=cannot tell)

ESDirect

ES_Sig ____

Effect Size Data:

9. DNA group sample size ES_TxN _____
10. Control group sample size ES_CgN _____

Effect Size Data---Record for Continuous Type Measures Only:

11. DNA (treatment) group mean ES_TxM _____
12. Comparison/Control group mean ES_CgM _____

13. Are the above means adjusted (e.g., ANCOVA adjusted)? (1=yes, 0=no)

ES_MAdj _____

14. DNA (treatment) group standard deviation ES_TxSD _____

15. Comparison/Control group standard deviation ES_CgSD _____

16. DNA (treatment) group standard error ES_TxSE _____

17. Comparison/Control group standard error ES_CgSE _____

18. *t*-value from an independent *t*-test or square root of *F*-value from a one-way analysis of variance with one *df* in the numerator (only two groups)

ES_t _____

Effect Size Data---Dichotomous Measures:

19. DNA (treatment) group; number of successes ES_TxNf _____

20. Comparison/Control group; number successes ES_CgNf _____

21. DNA (treatment) group; proportion successes ES_TxPf _____

22. Comparison/Control group; proportion successes ES_CgPf _____

23. Are the above proportions adjusted for pretest variables?
(1=yes; 0=no)

ES_PAAdj _____

24. Logged odds-ratio ES_LgOdd _____

25. Standard error of logged odds-ratio ES_SELgO _____

26. Logged odds-ratio adjusted? (e.g., from a logistic regression analysis with other independent variables) (1=yes; 0=no)

ES_OAdj _____

27. Chi-square value with *df* = 1 (2 by 2 contingency table) ES_ChiSq _____

28. Correlation coefficient (phi) ES_RPhi _____

Effect Size Data---Hand Calculated:

29. Hand calculated *d*-type effect size ES_Hand1 _____

30. Hand calculated standard error of the d -type effect size ES_Hand2 _____

31. Hand calculated odds-ratio effect size ES_Hand3 _____

32. Hand calculated odds-ratio standard error ES_Hand4 _____