THE EFFECTS OF CYANOACRYLATE FUMING ON THE QUANTITY AND QUALITY OF DNA RECOVERED FROM DEFLAGRATED PIPE BOMBS

By

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ABSTRACT

THE EFFECTS OF CYANOACRYLATE FUMING ON THE QUANTITY AND QUALITY OF DNA RECOVERED FROM DEFLAGRATED PIPE BOMBS

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Low copy number DNA deposited on an improvised explosive device (IED) is typically subjected to and degraded by the high temperatures during deflagration, creating a situation where it is difficult to identify the assembler. Often, when IED fragments are sent for analysis, they are analyzed both for explosive residue and fingerprints, leading to the potential loss of remaining DNA. This research examined cyanoacrylate (CA) fuming of pipe bomb fragments immediately after deflagration and its effects on the quantity and quality of DNA collected from the IED. This allows for determination of a proper order of processing for IED fragments. Twenty-four volunteers were asked to mock-assemble pairs of pipe bombs, one of which was CA fumed after deflagration and one that was not. DNA was quantified, amplified using an AmpFlSTR® Minifiler™ PCR Amplification Kit, and consensus profiles were developed. Comparisons indicated that CA fuming did not hinder DNA recovery, but due to high variation it could not be determined if it resulted in greater DNA recovery. Additionally, fuming did not alter the quality of the amplification product or consensus profiles. The decision as to the order of processing of the pipe bomb fragments, including whether or not to fume them, should be made as soon as possible when they arrive at the laboratory.

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Introduction

Improvised Explosive Devices

An improvised explosive device (IED) has been defined as "an explosive device that is placed or fabricated in an improvised manner, incorporates destructive, lethal, noxious, pyrotechnic, or incendiary chemicals and is designed to destroy, incapacitate, harass or distract" (National Research Council, 2008). They may be used in what is termed "asymmetric warfare," where a weaker side or terrorist group, which has decisive disadvantages in manpower or resources, attacks a stronger enemy. Chosen because of easy concealment and adaptability, IED use is relatively common both domestically and internationally in a wide variety of situations, such as the bombing of the World Trade Centers in 1993, the Olympic Park Bombing in 1996, the 2004 train bombings in Madrid, the 2005 London bus bombings, and the almost daily use in Iraq and Afghanistan (Burke, 2007; National Research Council, 2008). In 2008, approximately 656 IEDs were utilized across the United States, up from approximately 564 in 2007 (US Bomb Data Center, unpublished).

All IEDs are composed of an initiation system and a main charge (Thurman, 2006). Initiation systems vary widely, ranging from a simple fuse to more elaborate electronic triggering mechanisms. Explosive charges are classified as either high or low. Regardless of whether or not it is confined, a high explosive will detonate, that is, instantaneously convert from a solid phase to the gaseous phase at a rate faster than the speed of sound, 3300 ft/s, creating a supersonic shock wave (Thurman, 2006). Low explosives, if not confined, will simply burn. For a deflagration (explosion where the

velocity is subsonic) to occur a low explosive needs to be confined. Additionally, ignition can occur with heat, a sudden shock, or friction (Thurman, 2006; Burke, 2007).

A common low explosive is smokeless powder, which produces little smoke and enjoys a wide variety of usages, and is found in three forms: single, double, and triple base. A single base powder is the weakest of the smokeless powders and includes, among other ingredients, nitrocellulose dissolved in ether alcohol. A double base smokeless powder contains nitrocellulose and, usually, nitroglycerin, creating a more powerful explosive than the single base. Composed of nitrocellulose, nitroglycerin, and nitroguanidine, a triple base smokeless powder does not necessarily create a more powerful explosion than a double base; the addition of nitroguanidine serves to suppress the flash produced by the burning powder (Thurman, 2006).

There are three major classes of IEDs: incendiary, explosive-incendiary, and explosive. Incendiary devices may not always explode, but serve to ignite an accelerant (a substance used to cause the spread of fire) with a fuse. Explosive-incendiary devices use an explosive charge to ignite an accelerant. Explosive IEDs use charges to cause both casualties and damage, and can be further sub-categorized into platter, shaped, claymore, blast-fragmentation and blast. A platter IED propels a disc at a target, and is usually used against armored vehicles. A shaped charge is used to achieve a specific result, such as creating a hole in a wall to gain entry into a building, and may result in a specific pattern. Claymores and blast-fragmentations are both combined with shrapnel; however, claymores are usually coupled with high explosives and direct the shrapnel in a specific direction, whereas blast-fragmentation devices may contain either high or low explosives, usually in a metal container, and shrapnel is added to increase casualties.

Blast IEDs are similar to blast-fragmentation, but do not have the added shrapnel, although they still cause casualties and destruction (Thurman, 2006). The different types of IEDs are often constructed using pipes or tubes to contain the explosive, with steel pipes and end caps being the most common owing to their ability to withstand the high pressure created by the released gases, which generates a more destructive explosion (Thurman, 2006). Since components are easily obtained from local hardware stores and instructions found on the Internet, the complexity of IEDs is only limited by the abilities of the assembler and available materials (Thurman, 2006; Burke, 2007).

Low Copy Number DNA

It has been shown that genetic profiles can be obtained from a fingerprint and other brief contact between a person and an object (van Oorschot and Jones, 1997; Schulz and Reichert, 2002; Balogh *et al*., 2003; Esslinger *et al*., 2004). In fact, Findley *et al*. (1997) reported the ability to obtain short tandem repeat (STR) profiles from single cells, while noting allelic dropout (the loss of one or both alleles at a locus) was observed in approximately 40% of their samples. Balogh *et al*. (2003) used a simple strategy of raising the number of polymerase chain reaction (PCR) cycles to increase its sensitivity with low copy number (LCN) DNA recovered from fingerprints on paper. However, the increase in cycle number must be balanced against the increase in extraneous alleles, often from laboratory sources, that can be observed in the subsequent electropherogram (Gill *et al*., 2000). Furthermore, Gill (2001) proposed reducing PCR volume to obtain profiles from LCN DNA samples.

Multiple complications have been identified when working with both LCN and highly degraded DNA. In a review by Alaeddini *et al*. (2010), it was noted that human

somatic cells contain roughly 6 pg of genomic DNA and that LCN DNA is generally defined as a sample that contains less than 100 pg of DNA, or approximately 17 cells worth. Conventional STR kits produce amplicons that range from approximately 100 – 450 bp, and are generally optimized for use with 1 ng of DNA (Coble and Butler, 2005; Alaeddini *et al*., 2010). LCN DNA samples analyzed with conventional STR kits show greater heterozygotic peak imbalances and increased stutter products (Whitaker *et al*., 2001; Alaeddini *et al*., 2010). Stutter products are caused by slipped strand mispairing, a situation where a single repeat can loop out, usually resulting in a product that is one repeat shorter than the actual allele (Walsh *et al*., 1996). A suggested solution for dealing with both amplification failure and stochastic effects (where one allele is preferentially sampled or amplified over another) is to repeat the analysis to confirm results (Wiegand and Kleiber, 2001; Alaeddini *et al*., 2010).

Researchers also sought to reduce the overall size of STRs by identifying flanking regions suitable for primers that were closer to the desired core repeat region, resulting in amplicon sizes ranging from approximately 70 – 270 bp (Wiegand and Kleiber, 2001; Coble and Butler, 2005). Studies showed an increase in sensitivity when these primers were used on LCN or highly degraded samples (Weigand and Kleiber, 2001; Coble and Butler, 2005; Lopes *et al*., 2009, Müller *et al*., 2010). Eventually, a commercial kit (Minifiler™) was developed based on this miniSTR concept, requiring 0.5 – 0.75 ng DNA (Applied Biosystems, 2007). Mulero *et al*. (2008) conducted a validation study of the kit, and showed that there was a slight increase in stutter when compared to a standard STR kit. Additionally, partial profiles were obtained from samples diluted to 125 pg, as well as samples artificially degraded with DNase I. Lopes *et al*. (2009) also

tested the sensitivity of the miniSTR kit with samples ranging from 0.010 – 0.756 ng of DNA, and obtained complete profiles from 68% of them, while an additional 11% yielded callable alleles for seven of the eight genetic markers. Furthermore, there were no inconsistencies between the profiles obtained from a conventional STR kit and the miniSTR kit. Luce *et al*. (2009), in a validation study for the use of the Minifiler™ kit for forensic casework, noted an increased occurrence of forward stutter and other artifacts not attributable to other sources. Stutter percentages reached approximately 15% of the allele peak height. Heterozygotic peak height imbalances ranged from 35 – 100%, greater than that of conventional STR kits, making the identification and separation of mixtures more difficult. However, the miniSTR kit is more sensitive for the analysis of degraded DNA samples (Luce *et al*., 2009; Müller *et al*., 2010).

Multiple Analyses of a Single Sample to Determine a Profile

Navidi *et al*. (1992) developed a mathematical model that indicated analysis of multiple aliquots of a single sample might be an effective way to manage allelic dropin or dropout when dealing with LCN DNA. The model assumes that each locus has the same probability of encountering PCR reagents and replicating, and showed that a minimum of ten analyses would be needed to determine homozygosity with a statistical level of certainty. Taberlet *et al*. (1996) tested the proposed method, only calling an allele if it was seen twice, and found it to be sufficient to obtain reliable results. Using dilutions from 1 ng to 0.8 pg of DNA, Gill *et al*. (2000) studied the utility of applying conventional STR interpretation rules to LCN DNA. They noted that negative controls could not be used to detect low-level contamination as spurious alleles (dropin) can occur, but not

consistently across all samples extracted concurrently with the negative control. Furthermore, attempts to concentrate samples above stochastic levels before amplification were generally not successful. Therefore, the authors recommended that a single sample should be analyzed multiple times to identify allelic dropin. Alleles consistently seen in the electropherograms were called, while alleles that were not encountered repeatedly were considered dropins.

In a blind study, Hoffmann (2008) used consensus profiling to obtain profiles from IED containers. Consensus profiling seeks to develop a profile by using multiple assays of a single sample to determine which alleles are consistently observed; those that are inconsistently observed may be due to allelic dropin or dropout. After volunteers used backpacks for 11 days, they served as containers for pipe bombs that were deflagrated within them 11 regions of each backpack were swabbed and DNA was amplified. Consensus profiles were developed for each backpack and 7/8 matched the reference samples, while the eighth had a single ambiguous allele.

Past Studies on DNA Recovery from Pipe Bombs

An early attempt to identify the handler of deflagrated pipe bombs DNA was made by Esslinger *et al*., (2004). Analyzed with a conventional 9 locus STR kit (Profiler^{TM}), one pipe bomb out of 20 yielded a full profile, with an additional four yielding partial profiles.

Seeking to counteract the low amounts of nuclear DNA obtained from bomb fragments, Foran *et al*. (2009) investigated the utility of mitochondrial DNA (mtDNA) for identifying the assembler of a pipe bomb using a single swab per bomb. Robin and

Wong (1988) estimated mammalian cells contain between 200 and 1700 copies of mtDNA depending on cell type, which increases the likelihood of recovering DNA post-deflagration. Foran (2006) found that the location of mtDNA (within the double-membrane bound mitochondria) might also provide protection against degradation. Foran *et al*. (2009) were able to assign approximately 50% of yielded profiles to a single donor, with an additional 18% assigned to a correct subset of individuals. Similarly, Kremer (2008) used mtDNA in concert with miniSTRs [miniSGM (http://www.cstl.nist.gov/strbase/miniSTR.htm) and miniNC01 (Coble and Butler, 2005)] to increase successful handler identification. When both miniSTR and mtDNA were used, 70% of the pipe bombs were correctly assigned to the assemblers, while only 50% were correctly assigned using miniSTRs. However, the drawbacks of using mtDNA for assembler identification are threefold. First, many crime laboratories do not perform mtDNA analysis, and to do so would require validation of new reagents and protocols. Second, analysis of mtDNA is more labor-intensive than analysis of STRs. The statistical calculation used to determine the frequency of haplotypes for mtDNA, the counting method, is much less discriminatory than random match probabilities or likelihood ratios used for STRs, which is based off the product rule (Butler, 2005) Furthermore, Kremer (2008) noted that with the greater sensitivity of miniSTRs, extraneous alleles were frequently observed, leading to an increased possibility that an incorrect handler assignment might be made. In an attempt to optimize the recovery of DNA from deflagrated pipe bombs, Gomez (2009) used miniSTRs to compare DNA recovery rates from samples that were swabbed and samples that were soaked in 20 mL of digestion buffer. She found that the double swab technique was more effective.

Additionally, the results were similar to those of Kremer (2008) in that extraneous peaks caused difficulty in determining a handler's profile.

Cyanoacrylate Fuming

Cyanoacrylate (CA) or 'Superglue' fuming is a process by which fingerprints, a potential source of LCN DNA, are developed when exposed to CA and water vapors in an enclosed chamber. An optimal humidity level for CA fuming is approximately 80% (Lewis *et al*., 2001). The technique is commonly used to visualize latent fingerprints on non-porous surfaces (Lewis *et al*., 2001; von Wurmb *et al*., 2001). Fingerprints are composed of eccrine sweat secreted by the hairless surfaces of the body, and principally contain NaCl, lactic acid, urea, and amino acids (Lewis *et al*., 2001; Wargacki, *et al*., 2007). Low amounts of fatty acids may be present in the print, although these are usually transferred from hairy portions of the body where sebaceous glands secret lipids (Lewis *et al*., 2001). Latent prints are visualized when monomeric CA (Figure 1) polymerizes, coating the print. Lewis *et al*. (2001) further noted that oily fingerprints can be visualized up to 6 months after being laid down, most likely because the oil can delay the evaporation of water needed to begin polymerization.

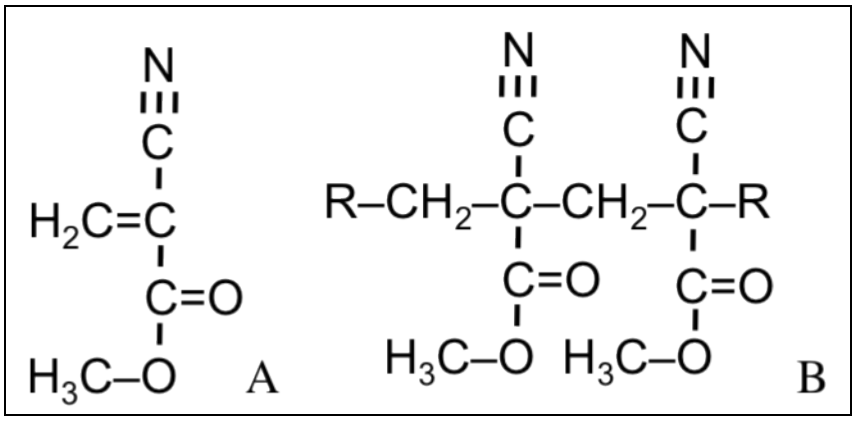

Figure 1: Molecular structure of a CA monomer and CA polymer
The molecular structure of methylcyanoacrylate monomer (A) and its polymer (B)

Attempting to determine if CA fuming inhibited PCR, Von Wurmb *et al*. (2001) extracted DNA from blood and saliva samples (5 μL, 10 μL and 50 μL stains) using two methods — Chelex and Invisorb (a kit that binds DNA to silica oxide). CA decreased peak height on small bloodstains, but did not affect the profile. Large blood and saliva stains were not affected. Grubwieser *et al*. (2003) placed bloody fingerprints and fingerprints with saliva on porous and non-porous surfaces, including envelopes, stamps, glass slides and cans. Prints were visualized using a variety of methods including CA fuming in either a fuming chamber or vacuum, and DNAs were extracted organically. Complete profiles were obtained and there were no differences in amplification results between CA fumed test samples and controls. Bille *et al*. (2009) spotted cells containing approximately 30 ng of DNA at multiple locations on six different pipe bombs, which were then wrapped in wire fencing, placed in trenches, and deflagrated. The pipe bomb fragments were transported back to the laboratory where three were fumed with CA the following day. DNA extractions were completed with a QIAamp® DNA Micro Kit. Overall, 1 – 35% of the original amount of DNA was recovered post-deflagration,

depending on the area of the pipe bomb that was swabbed. Additionally, CA fuming was found to have no effect on the amount of DNA recovered.

Study Aims: Determination of the Effects of Cyanoacrylate Fuming on DNA Recovery from IEDs

Typically when an IED is submitted for processing in a laboratory, an explosives examiner visually inspects the evidence for intact explosive particles (communication from the ATF). If none are seen, the interior surfaces of the IED are washed to capture any residue for subsequent analysis. The evidence is then transferred to the latent prints section of the lab for CA fuming. If usable prints are not found, the evidence is sent to a trace evidence examiner for collection of any hairs, fibers, etc. that are attached. The IED is then transferred to a DNA analyst for swabbing. However, the order of analysis can be altered depending on specific circumstances pertaining to a particular case, and the most productive method for processing such evidence is unknown.

It is possible that CA fuming is advantageous in recovering DNA from post-blast IEDs. Fuming could cause cells to adhere to the surface of the pipe bomb, thus retaining DNA as it is being transported. Alternatively, fuming might hinder the collection of DNA by hindering removal of cells from the surface when swabbed. Additionally, CA could have an inhibiting effect on PCR or even degrade DNA through chemical interactions. To date, none of the potential ramifications of CA fuming of IEDs have been quantified using real-world examples of post-blast LCN DNA analysis. Given this, the goal of this current research was to determine the impact of CA fuming on the quantity and quality of DNA recovered from deflagrated pipe bombs. A preliminary study was conducted using compact discs (CDs) with fingerprints placed in known areas

to determine the effects of CA on DNA recovery from an inert surface. A second study involving 1-in zinc galvanized steel end caps was conducted to assess the effects of zinc, handling, and CA, on the quantity of DNA recovered. A final blind study was conducted examining CA fuming of handled and deflagrated pipe bomb fragments and DNA recovery, using pairwise comparison of non-fumed and fumed pipe bombs. Multiple extractions from a single pipe bomb were used to develop a consensus profile, and compared to reference samples for accuracy.

Materials and Methods

Fuming Chamber Assembly

A fuming chamber was constructed from a 24 x 16 x 13 in, 15-gallon storage container (Incredible Plastics, Warren, Ohio) and contained a candle warmer (Rimports USA LLC, Provo, UT). A hole was cut in the bottom corner of the storage container to allow insertion of the candle warmer's power cord. Potential areas for leakage around the hinges and electrical cord were sealed using duct tape.

Cyanoacrylate Fuming Procedures

A plastic beaker was filled with 250 mL of pre-heated, distilled water and placed on the candle warmer. The bottom of a 1-in diameter foil boat was covered with cyanoacrylate (E-Z Bond Instant Glue, Cyanoacrylate, K & R International, Laguna Niguel, CA) and positioned on the candle warmer. Objects to be fumed were situated as close as possible to the cyanoacrylate (Figure 2). Preliminary trials were conducted by placing a print on a plastic container in the fuming chamber for varying amounts of time until the print was easily visualized.

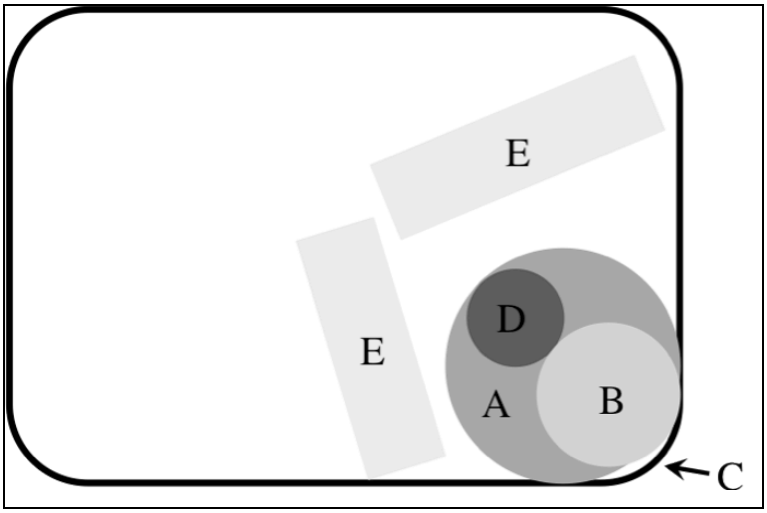

Figure 2: Relative positioning of the fuming chamber components. (A) Candle warmer. (B) Pre-heated distilled water in a 250 mL plastic beaker. (C) Location of the hole cut for the candle warmer's electrical cord. (D) Foil boat containing cyanoacrylate (E) Positions of samples being fumed.

Collection of DNA from Compact Discs

Compact discs (CDs) were soaked in 10% solution of 101 Bleach (James Austin Company, Mars, PA) for 1 h. After being rinsed and dried with paper towels, they were UV irradiated in a Spectrolinker XL-1500 (Spectronic Corporation, Westbury, NY) for 5 min on each side, wiped down with ELIMINase on a lab wipe (Decon Laboratories Inc, Bryn Mawr, PA) followed by distilled water, and placed in a laminar flow hood to dry.

Two volunteers did not wash their hands, handle cleaning agents, or use lotions for 1 h prior to and during the experiment. Subjects rubbed their fingers together in an attempt to equalize the amount of cells on corresponding fingers of each hand. Prints from four fingers on the dominant hand were laid down in predetermined areas on one disc, while four prints from the non-dominant hand were laid down on a second disc. Approximately 1 h later, a second set of prints was collected. Prints from the dominant hand were placed in unused areas on the disc on which prints from the non-dominant

hand had previously been placed, and vice versa. For each person, one disc was immediately fumed, while the second disc remained un-fumed. DNA from each print was isolated, purified and quantified for both the fumed and non-fumed discs, as detailed below. The use of human subjects was in accordance with guidelines established by the University Committee on Research Involving Human Subjects (IRB # 07-557).

Collection of DNA from End Caps

Threaded, galvanized, 1-in steel end caps were purchased from local hardware stores. Each end cap was washed with soap and water, followed by decontamination with a 10% bleach solution using a lab wipe. End caps were placed in the Spectrolinker for 5 min on each side, and were dried in a laminar flow hood. Each individual cap was sealed in a new paper bag.

Ten volunteers were asked to refrain from washing their hands or using cleaning agents or lotions for a minimum of 1 h prior to handling the end caps, both before and during the study. Participants tightened an end cap and then removed it from a 12-in galvanized steel pipe using their dominant and non-dominant hands on separate end caps. Approximately 2 h later, volunteers tightened and then removed an additional end cap for each hand. Immediately, one end cap handled with the dominant hand and one end cap handled with the non-dominant hand were fumed with cyanoacrylate. The remaining two end caps remained unfumed. After fuming, DNA from each end cap was isolated, purified, and quantified as detailed below.

Collection of DNA from Pipe Bombs

Forty-nine galvanized, nippled, steel pipes (12-in long by 1-in diameter) and 98 (1-in diameter) end caps were purchased from local hardware stores. Adhesive Remover (Manco, Inc., Avon, OH) was used to remove adhesive residue. A 1/4-in diameter hole was drilled through half of the end caps to allow insertion of a fuse. All pipes and end caps were washed with soap and water, and wiped down with 10% bleach solution. End caps were UV-irradiated in the Spectrolinker for 5 min on each side, while the pipes were rotated 180^{o} after 5 min. The components were dried in a laminar flow hood and sealed in paper bags.

Twenty-four volunteers were asked to refrain from washing their hands and using cleaning agents or lotions for a minimum of 2 h prior to handling the components, both before and during the study. Participants mock-assembled one pipe bomb by screwing the end caps on each pipe and removing the end cap containing the hole. The components were returned to their original paper bags and resealed. The volunteers resumed their daily activities for approximately 2 h, and then repeated the assembly procedure. One pipe bomb was not handled and served as a reagent blank. It was swabbed prior to deflagration, and after being cleaned again, was deflagrated. No data from it were included in comparisons between the non-fumed and fumed data sets. Each pipe bomb was blindly designated with the combination of a number (1 – 24), representing the individual, and letter [“C” for control (non-fumed) and “F” for fumed]. Volunteers also provided buccal swabs as reference samples, which were given a random letter designation.

Deflagration of Pipe Bombs and Collection of Fragments

Six pipe bombs were transported to the Lansing Fire Fighting Training Facility (Lansing, MI), while the rest were transported to the Operating Engineers Local Education Center 324 (Howell, MI), where members of the Michigan State Police Bomb Squad loaded the pipe bombs with 1.5 oz of Green Dot Smokeless Shotshell Powder (Alliant Powder Co., Radford, VA). A 40 s fuse was then inserted. Pipe bombs 10C, 11C, 11F, 13C, 13F, 14C and 14F were deflagrated in a steel crate (Figure 3) at the training facility's smoke room. The steel crate was placed within a concrete cylinder with the ends blocked by concrete slabs (Figure 4) at the Education Center. After deflagration, fragments were collected and returned to their original bags. Pipe bombs designated for fuming were immediately taken to a safe location at each site and fumed as described above.

Figure 3: Steel crate in which the pipe bombs were deflagrated.

The crate was designed to retain pipe bomb fragments, while at the same time abating blast pressure. The sides and top were made of steel, while the bottom was made of wood, which was covered by a steel plate.

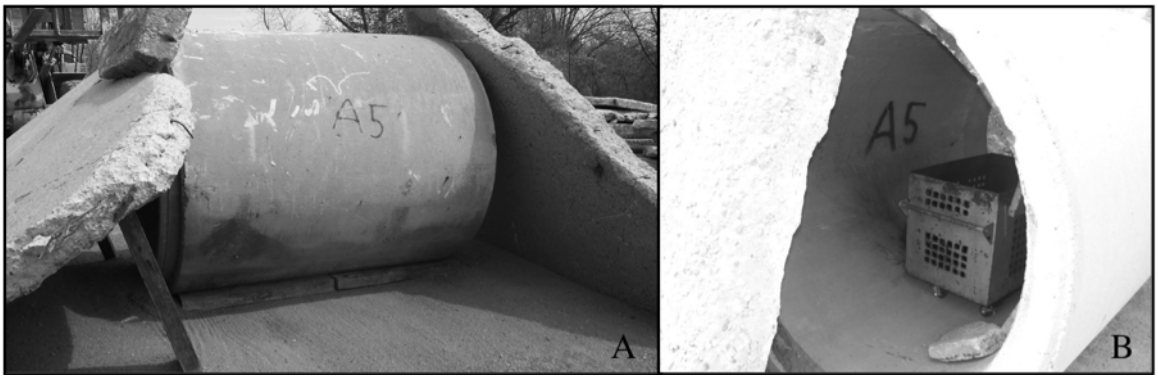

Figure 4: Construct for deflagrations at Operating Engineers Local Education Center 324.

A large concrete cylinder was laid on its side, with concrete slabs propped on either opening to deflect down any fragments that may have escaped the steel crate (A), which was placed within the cylinder (B).

DNA Isolation and Purification

Sterile cotton swabs were UV irradiated for 5 min with the Spectrolinker. Using the double swab technique (Sweet *et al*., 1997), a swab was moistened with approximately 200 μL of digestion buffer (20 mM Tris, 50 mM EDTA, 0.1% SDS, pH 7.5) and rubbed over the targeted area, immediately followed by a dry swab. The swabs from the pipe bombs were visually inspected to note if they had relatively large amounts (enough to cover the swab) or small amounts of powder residue. They were placed in a 2 mL dolphin tube containing 400 μL of digestion buffer and 4 μL of proteinase K (20 mg/mL), vortexed, and incubated overnight at 55^{o}C.

Swabs were centrifuged in spin baskets inserted in the same dolphin tube at 14,000 rpm for 3 min. The contents of the tube were transferred to a 1.5 mL microfuge tube. Four hundred microliters of phenol (Fisher BioTech, Fair Lawn, NJ) were added to each extract, briefly vortexed, and centrifuged at 14,000 rpm for 5 min. The aqueous layer was transferred to a new 1.5 mL microfuge tube containing 400 μL of chloroform (Mallinckrodt Baker, Inc., Phillipsburg, NJ), vortexed, and centrifuged for 5 min at

14,000 rpm. For the CDs and end caps the aqueous layer was transferred to Millipore YM-30 columns (Millipore, Bedford, MA), and centrifuged at 14,000 x g for 12 min, followed by two washes with 300 μL of TE (10 mM Tris, 1 mM EDTA, pH 7.5) and 12 min centrifugation at 14,000 x g. The extractions were eluted with 20 μL of TE buffer and stored at -20 ^{o}C.

Six extractions were performed for each pipe bomb: two for each end cap and pipe, each time approximating half the surface area. Isolation of DNA was achieved as detailed above. The DNAs were purified using Millipore YM-100s and centrifuged at 500 x g for 24 min, followed by two washes with 300 μL of low TE (10 mM Tris, 0.1 mM EDTA, pH 8.0) and another centrifugation of 24 min at 500 x g. Extracts were eluted with 20 μL of low TE and stored at -20 ^{o}C.

DNA Quantification

DNAs were quantified using a Quantifiler® Human DNA Quantification Kit (Applied Biosystems, Foster City, CA). Each reaction contained 6.3 μL of Primer Mix, 7.5 μL of Reaction Mix and 1.2 μL of DNA. A double-row of standards was composed of DNA concentrations ranging from 50 ng to 0.023 ng was used. PCR was performed on an iQ^{TM} 5 Multicolor Real-Time PCR Detection System (Bio-Rad Laboratories, Hercules, CA). The reactions were heated to 95^{o}C for 10 min, followed by 40 cycles of 95^{o}C for 15 s and 60^{o}C for 60 s.

The iQ^{TM} 5 – Standard Edition v 2.0.148.60623 software calculated a standard curve. If the R^2 value was below 0.98, standards that appeared to be outliers were

removed and the standard curve was recalculated. The software calculated the concentration of DNA per sample.

DNA Amplification with Minifiler™

Extracted DNA was amplified in 10.0 μL reactions using Minifiler™ (Applied Biosystems). Each reaction contained 1.0 μL Primer Mix, 4.0 μL of Master Mix and 5.0 μL of a combination of DNA and low TE. Five microliters of DNA were added if the results indicated a minimum of 5 μL would be needed to reach the target of 0.5 ng per reaction. Thermocycling consisted of an initial step of 95°C for 11 min was followed by 30 cycles of 94°C for 1 min, 59°C for 2 min, 72°C for 1 min and a final extension at 60°C for 45 min.

Capillary Electrophoresis

Two microliters of each reaction were added to a 0.5 mL microfuge tube containing 24.5 μL of formamide and 0.5 μL of GeneScan™ - 500 LIZ™ Size Standard (Applied Biosystems). An allelic ladder was prepared using AmpFlSTR® MiniFiler™ Kit Allelic Ladder (Applied Biosystems), containing 1.5 μL of the ladder, 24.5 μL of formamide, and 0.5 μL of size standard. Tubes were incubated at 95°C for 3 min, followed by incubation on ice for 5 min. The lids of the microfuge tubes were removed, a drop of mineral oil was added, and the tubes were loaded onto a 48-well plate. DNAs were electrophoresed on an ABI 310 Genetic Analyzer (Applied Biosystems), beginning

with a 5 s, 15 kV injection, followed by a 15 kV run for 26 min at 60°C. The allelic ladder was electrophoresed for 30 min at 60°C.

Processing of Reference Samples

Reference buccal swabs were transferred to a 2 mL dolphin tube containing 400 μL of digestion buffer, and incubated at 55°C for two hours. Extraction, purification and elution, and quantification were performed as previously described, followed by dilution to 1 ng/μL. Amplification reactions were carried out as detailed above, with 1.0 μL of the diluted DNA added to the Minfiler™ reaction along with 4.0 μL of TE. Products were electrophoresed as detailed above, with the exceptions that 1 μL of the reaction was added to the formamide and size standard, and the injection time was 3 s.

STR Analysis of Electropherograms and Development of Consensus Profiles

STR data were analyzed using GeneMapper® ID Software v3.2.1 (Applied Biosystems). Electropherograms were manually reviewed and callable peaks recorded for each extraction using a minimum threshold value of 50 relative fluorescence units (RFUs). Alleles that were most consistent among the six profiles obtained from a single pipe bomb, though not necessarily occurring in all six electropherograms, were identified as the genotype at that locus. Any additional peaks were considered dropin. Using this information, a consensus profile (Hoffmann, 2008) was developed blindly for each sample.

A second individual independently analyzed the reference buccal samples (to ensure elimination of bias) using GeneMapper® ID software, and profiles were determined manually with a minimum peak height of 50 RFUs. Consensus profiles were then compared to the reference handler profiles and placed into one of the following categories depending on their quality:

A. A full, correct consensus profile.
B. The handler's alleles were present, but so were others.
C. The developed profile was inconsistent with the handler's profile by one allele.
D. The developed profile was inconsistent with the handler's profile by two alleles.
E. The developed profile was inconsistent with the handler's profile by three alleles.
F. The developed profile was inconsistent with the handler's profile by four or more alleles.

When the consensus genotype contained three alleles at a locus but all other loci were consistent with the handler, the consensus profile was placed in category B. If any alleles were inconsistent with the handler's profile the consensus was placed in categories C, D, E, or F as appropriate.

Each consensus genotype was given a rank corresponding the confidence that the author was that it was the correct genotype. The ranks were:

1. Confident.
2. Somewhat confident.
3. Low confidence/Could not distinguish among three alleles.
4. Uncallable.

Loci were individually examined for quality and callable peaks were placed into one of six categories:

I. Only the handler's alleles.
II. Multiple alleles were called, but the handler's alleles constituted the major contributor.

III. The handler's alleles were not the major contributor.
IV. Only one of the handler's allele.
V. No alleles belonged to the handler.
VI. No alleles.

"Major contributor" genotypes were alleles that had peak height ratios of approximately 60 – 70%. The percentages of alleles that fell into each category were calculated for the fumed and non-fumed samples, and compared.

Statistical Analysis

Pairwise t-tests compared DNA recovery between non-fumed and fumed CDs, end caps, and pipe bombs. Extractions that quantified with 0 ng of DNA were removed, as wells as outliers identified using the extreme studentized deviate test. An F-test and subsequent t-test were used to compare DNA recovery once outliers were removed. Further, the same tests were used to compare DNA recovery between swabs with relatively large and small amounts of powder residue. An ANOVA was performed to determine if there was an association between the accuracy of consensus profiles and the quantity of DNA recovered per pipe bomb. All statistical tests were calculated using a 95% confidence interval ($\alpha = 0.05$).

Results

Establishment of Fuming Time

Control prints were most easily visualized when the fuming time was approximately 15 min.

DNA Quantities Obtained from CDs

The average DNA quantity recovered from the non-fumed CDs was $6.49 \times 10^{-3} \pm 1.75 \times 10^{-2}$ ng, while $1.57 \times 10^{-3} \pm 1.96 \times 10^{-3}$ ng was recovered from fumed CDs (Table 1). There was no significant difference between the amount of DNA recovered from non-fumed and fumed CDs ($p = 0.293$). After removing extracts that quantified with 0 ng of DNA the averages were $8.65 \times 10^{-3} \pm 1.99 \times 10^{-2}$ ng and $2.78 \times 10^{-3} \pm 1.83 \times 10^{-3}$ ng for non-fumed and fumed, respectfully. There was a significant difference in the variances ($p = 2.60 \times 10^{-7}$), however the subsequent t-test again showed no difference between the averages ($p = 0.332$).

Non-Fumed	ng of DNA	Fumed	ng of DNA
1CA	0.00E+00	**1FA**	4.21E-03
1CB	3.41E-03	**1FB**	3.49E-03
1CC	2.90E-04	**1FC**	6.21E-03
1CD	3.42E-03	**1FD**	3.62E-03
1CE	5.42E-03	**1FE**	4.27E-04
1CF	7.13E-02	**1FF**	0.00E+00
1CG	1.27E-03	**1FG**	0.00E+00
1CH	0.00E+00	**1FH**	0.00E+00
2CA	2.22E-03	**2FA**	0.00E+00
2CB	1.25E-03	**2FB**	2.24E-03
2CC	0.00E+00	**2FC**	4.95E-04
2CD	1.02E-02	**2FD**	0.00E+00
2CE	0.00E+00	**2FE**	2.40E-03
2CF	3.69E-03	**2FF**	1.97E-03
2CG	9.89E-04	**2FG**	0.00E+00
2CH	3.07E-04	**2FH**	0.00E+00
Average	6.49E-03	**Average**	1.57E-03
Standard Deviation	1.75E-02	**Standard Deviation**	1.96E-03
p-value	0.293		

Table 1: Quantities and pairwise t-test of DNA obtained from fingerprints on CDs. "C" indicates control (non-fumed) samples, while "F" indicates fumed samples. A – D indicate fingers on the right hand excluding the thumb, while E – H indicate fingers on the left hand, excluding the thumb. A and E: index finger, B and F: middle finger, C and G: ring finger, D and H: little finger.

DNA Quantities Obtained from End Caps

The average amount of DNA obtained from the non-fumed end caps was 4.88 x $10^{-1} \pm 4.82 \times 10^{-1}$ ng, while the average from the fumed end caps was 4.73 x $10^{-1} \pm 6.00$ x 10^{-1} ng (Table 2). There was no significant difference in DNA recovery (p= 0.939). With removal of 0 ng quantities, the averages were 4.88 x $10^{-1} \pm 4.82 \times 10^{-1}$ ng and 5.25 x $10^{-1} \pm 6.47 \times 10^{-1}$ ng for non fumed and fumed end caps respectively, and no

significant difference was found between the variances (p = 0.216) or averages (p = 0.837).

Non-fumed	ng of DNA	Fumed	ng of DNA
1CD	4.65E-02	**1FD**	0.00E+00
1CN	3.02E-02	**1FN**	6.02E-03
2CD	5.23E-01	**2FD**	3.37E-02
2CN	8.20E-02	**2FN**	9.96E-02
3CD	1.53E+00	**3FD**	3.31E-01
3CN	2.80E-01	**3FN**	1.89E+00
4CD	5.65E-01	**4FD**	4.98E-01
4CN	1.65E+00	**4FN**	4.25E-01
5CD	8.41E-01	**5FD**	2.00E-01
5CN	3.51E-03	**5FN**	2.75E-01
6CD	6.31E-01	**6FD**	7.36E-01
6CN	3.47E-01	**6FN**	1.10E-01
7CD	5.91E-01	**7FD**	8.76E-02
7CN	4.54E-01	**7FN**	1.53E-01
8CD	7.49E-02	**8FD**	2.43E+00
8CN	1.15E+00	**8FN**	5.89E-01
9CD	1.27E-01	**9FD**	3.27E-01
9CN	7.30E-02	**9FN**	8.48E-01
10CD	4.22E-01	**10FD**	0.00E+00
10CN	3.29E-01	**10FN**	4.20E-01
Average	4.88E-01	**Average**	4.73E-01
Standard Deviation	4.82E-01	**Standard Deviation**	6.33E-01
p-value	0.939		

Table 2: Quantities and pairwise t-test of DNA recovered from end caps.
"C" indicats control (non-fumed) samples, while "F" indicates fumed samples. "D" indicates the dominant hand was used, while "N" indicates the use of the non-dominant hand.

Fragmentation of Pipe Bombs

Fragmentation of the pipes and end caps was highly variable despite the consistent use of 1.5 oz of powder. The amount of fragmentation ranged from little damage with pipe and end caps remaining relatively intact to more complete destruction

where both the pipe and end caps were highly fragmented (Figure 5). End caps generally fragmented into three or more pieces, usually with at least one large piece. The top, flat portions of the end caps were rarely recovered in pieces large enough to swab. Aside from intact end caps, fragments that were large enough to be swabbed were only recovered from two pipe bombs, 6F and 24C (Figure 6).

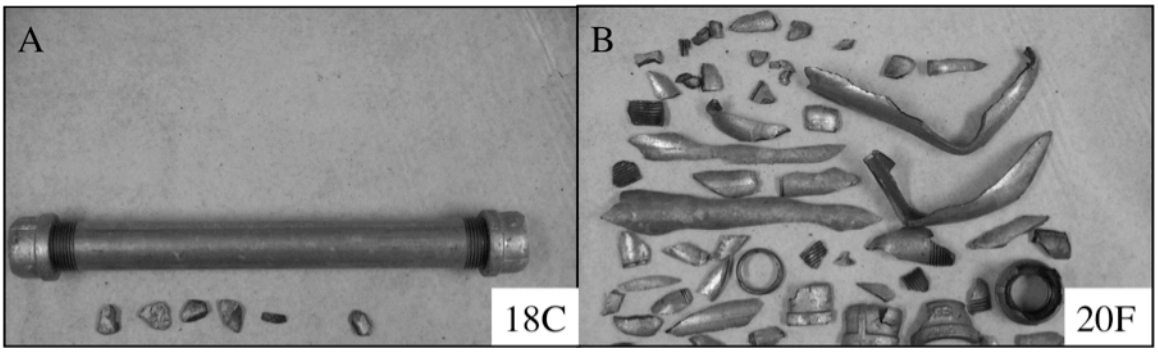

Figure 5: Range of fragmentation among the pipe bombs.
Fragmentation varied widely, ranging from little more than fragmentation of the tops of the end caps (A) to more complete disintegration (B).

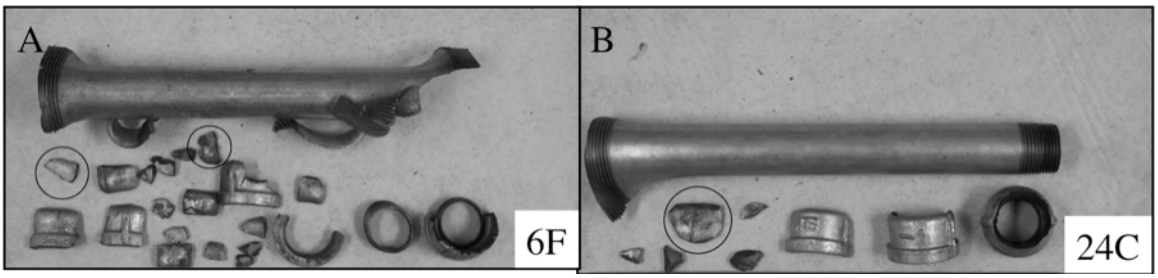

Figure 6: Pieces from the tops of end caps that were large enough to swab.
The tops of the end caps were rarely recovered in large enough pieces to allow swabbing. Three exceptions are shown here (circled) in pipe bombs 6F and 24C.

Relatively large amounts of powder residue (enough to cover the swab) were recovered on 120/288 (42%) of the swabs during isolation. The residual powder often settled to the bottom of the dolphin tube during incubation, and was avoided when the supernatants were transferred to the 1.5 mL microfuge tubes. A deep pink or red color developed with the addition of phenol and remained until the samples were washed in the column purification step.

DNA Quantities Obtained from Pipe Bombs

The average amount of DNA recovered from the non-fumed pipe bombs was 1.91 x 10^{-2} ± 2.73 x 10^{-2} ng, while the average of the fumed pipe bombs was 2.92 x 10^{-2} ± 6.21 x 10^{-2} ng (Table 3). Some, though not a highly significant difference was found between the amounts of DNA recovered from non-fumed and fumed pipe bombs (p = 0.052). Removal of 0 ng quantities and outliers resulted in an average of 1.91 x 10^{-2} ± 1.87 x 10^{-2} ng and 2.02 x 10^{-2} ± 2.29 x 10^{-2} ng for non-fumed and fumed respectively. A highly significant difference in the variances existed (p = 3.74 x 10^{-18}), but there was no significant difference in the averages (p = 0.69). Two of the six swabs from the undeflagrated, unhandled pipe bomb quantified with DNA approximately one-tenth the average of the handled pipe bombs. Similarly, after deflagration of the unhandled pipe bomb four of the six swabs displayed levels of DNA approximately one-tenth of the amount recovered from the handled pipe bombs.

	Non-fumed	**Fumed**
Average DNA (ng)	1.91E-02	2.92E-02
Standard Deviation	2.73E-02	6.21E-02
p-value	0.052	

Table 3: Results of the two-tailed pairwise t-test for DNA recovered from deflagrated pipe bombs.
The pairwise t-test indicated more DNA was recovered from fumed pipe bombs than non-fumed pipe bombs, although it was not significant. After removal of 0 ng quantities and outliers there was no significant difference (p=0.69).

There was a significant difference between the variances (p = 1.43 x 10^{-9}) among swabs with relatively large amounts of powder residue and relatively small amounts of

powder residue, but no significant difference in the amount of DNA recovered from swabs with the relatively different amounts of powder residue ($p = 0.303$).

	Large Amounts of Observed Powder Residue	Little Amounts of Observed Powder Residue
Average DNA (ng)	2.11E-02	2.66E-02
Standard Deviation	3.34E-02	5.74E-02
F-Test p-value	1.43E-09	
t-Test p-value	0.303	

Table 4: F-test and t-test comparing the variances and average amounts of DNA recovered from swabs with different amounts of powder residue.
A significantly greater variation in DNA recovery from swabs with relatively large amounts of powder residue as opposed to those with relatively small amounts of powder residue, but no significant difference in the averages.

No DNA was recovered from 24 of 144 (17%) swabs from non-fumed pipe bombs, while 19 of 144 (13%) swabs from fumed pipe bombs gave the same result. Only Pipe bomb 17C had no DNA recovery from any of the six swabs.

Comparison of Consensus Profiles and Handlers' Profiles

Consensus profiles from non-fumed and fumed pipe bombs are displayed in Appendix B and are characterized in Figure 7. Four of twenty-four complete profiles from the non-fumed pipe bombs were consistent with the handler at all alleles (17%, category A, Figure 7A), while an additional seven profiles (no alleles inconsistent with the handler's profiles, but others were called) were also developed (29%, category B). Full, handler profiles were developed from seven of twenty-four fumed pipe bombs (29%, category A, Figure 7B), while no partial profiles were developed. Seven profiles

developed from non-fumed bombs (29%) and eight from fumed bombs (33%) had one allele inconsistent with the handler (category C). Profiles that were inconsistent at two alleles accounted for four (17%) and three (13%) non-fumed and fumed bombs, respectively (category D). No non-fumed bombs were inconsistent at three alleles, while two fumed pipe bombs (8%) fell into category E. Profiles of two non-fumed (8%) and four fumed (17%) pipe bombs were inconsistent at four or more alleles (category F). Negative controls showed several peaks, but were attributed to artifacts because the peaks were either too sharp or too broad and were not consistent with the shape of allelic peaks.

A consensus genotype of one or two alleles could neither be developed for 18 loci from 11 different non-fumed bombs, nor 14 loci from 9 fumed bombs (Table 5). In these cases the consensus genotype was narrowed to three alleles, all of which included the handler's alleles. The third allele was in a stutter position (one repeat before or after the handler's allele) in 8 loci of non-fumed samples (44%) and 10 loci of fumed samples (71%). The handler of pipe bomb 16F was a homozygous 11 at CSF1PO; both stutter position peaks (10 and 12) were also present. Half of the inconsistent genotypes occurred when a locus was typed as heterozygous while the handler was homozygous. There were certain cases when the author had low confidence in the consensus genotype, but was the handler's (e.g., 5C, D18S51); however, there were other cases when the author had high confidence, but the consensus genotype was inconsistent with the handler's genotype (e.g., 8F, D18S51).

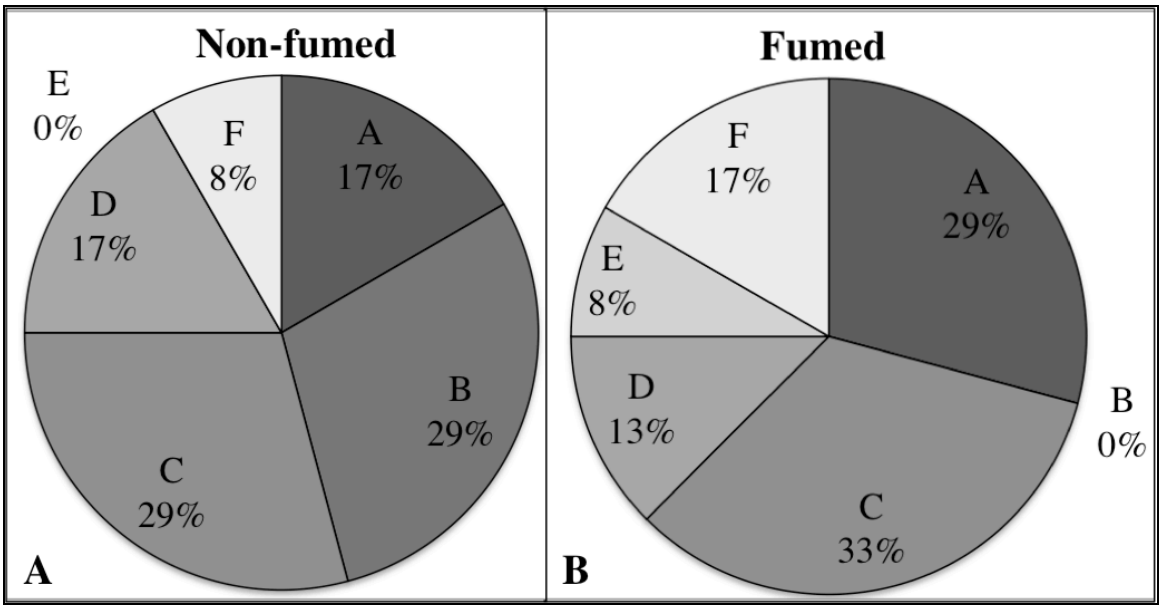

Figure 7: Characterization of consensus profiles for non-fumed and fumed pipe bombs. Consensus profiles from 24 non-fumed and fumed pipe bombs were divided into 6 categories according to their concordance with the handler's actual profile. A: A full consensus profile was developed and matched the handler's profile. B: The handler's alleles were present, but so were others. Categories C, D, E, and F encompass consensus profiles that were inconsistent with the handler's profile by one, two, three and four, or more, respectively. When three alleles were noted at a locus in the consensus profile, the locus was categorized where the handler's alleles were present, but so were others (category B) if remaining loci were consistent with the handler.

Non-Fumed	Locus	Called Alleles	Handler's Alleles	Fumed	Locus	Called Alleles	Handler's Alleles
1C	D13S317	11, 12, 13	12, 13	**1F**	D13S317	11, 12, 13	12, 13
	D16S539	9, 11, 13	11, 13		D2S1338	17, 19, 20	17
	D18S51	15, 17, 18	17, 18	**3F**	FGA	20, 21, 24	20, 21
2C	FGA	22, 23, 24	22, 24	**6F**	FGA	20, 21, 22	20, 21
3C	D13S317	11, 13, 14	13, 14	**10F**	D13S317	8, 11, 12	8, 12
	D2S1338	16, 19, 21	16, 21		D21S11	28, 29, 31	28, 29
	CSF1PO	10, 11, 12	11, 12		D16S539	11, 12, 13	11, 12
	FGA	20, 21, 23	20, 21		CSF1PO	10, 11, 12	11, 12
7C	FGA	20, 24, 25	24, 25	**11F**	D13S317	9, 11, 12	9, 12
9C	D2S1338	17, 24, 25	24, 25	**12F**	D16S539	9, 11, 12	9, 11
	D18S51	12, 13, 15	12, 13	**16F**	CSF1PO	10, 11, 12	11
10C	D13S317	8, 11, 12	8, 12	**17F**	D7S820	8, 9, 11	8, 11
14C	CSF1PO	10, 11, 12	10, 11		D21S11	28, 30, 32.2	28, 32.2
	FGA	21, 23, 24	23, 24	**24F**	CSF1PO	10, 11, 12	10, 12
16C	D13S317	8, 11, 12	8, 12				
19C	D7S820	10, 11, 12	10, 12				
20C	D2S1338	17, 20, 25	17, 25				
23C	D13S317	10, 11, 12	10, 12				

Table 5: Loci at which three allele calls were made in non-fumed and fumed pipe bombs. "C" indicates control (non-fumed) samples, while "F" indicates fumed samples. Consensus profiles for 1C, 2C, 3C, 7C, 9C, 10C, 14C, and 19C were placed in category B because the consensus genotypes for the remaining loci (not shown) were correct. The remaining consensus profile for the non-fumed and all consensus profiles for the fumed pipe bombs listed above were placed in categories C, D, E or F as appropriate because at least one allele at the remaining loci was inconsistent with the handler.

Accuracy of Consensus Profiles Compared to DNA Yields

The average amount of DNA recovered per pipe bomb for each consensus profile is shown in Table 6. Category A profiles from both non-fumed and fumed pipe bombs had the highest DNA recovery. Category F and C profiles had the second highest and lowest average DNA recovery from non-fumed pipe bombs, respectively. Category C and F profiles had the second highest and lowest recovery from fumed pipe bombs, respectively. There was no difference between or within the groups ($p = 0.153$) showing no correlation between the average amounts of DNA recovered per pipe bomb and the accuracy of the consensus profiles.

	Consensus Profile Category					
	A	**B**	**C**	**D**	**E**	**F**
Non-Fumed (ng)	3.37E-02	1.88E-02	1.03E-02	1.60E-02	--	2.75E-02
Fumed (ng)	5.08E-02	--	1.77E-02	4.69E-02	1.10E-02	7.11E-03

Table 6: Comparison of consensus profile quality and average DNA recovery per pipe bomb.
A: A full consensus profile was developed and matched the handler's profile. B: The handler's alleles were present, but so were others. Categories C, D, E, and F encompass consensus profiles that were inconsistent with the handler's profile by one, two, three, and four or more, respectively. When three alleles were noted at a locus in the consensus profile, the locus was categorized as a partial profile (category B) if the alleles at the remaining loci were consistent with the handler.

Characterization of Allele Calls Inconsistent with the Handler

Seventeen alleles were inconsistent with the handler's profile (consensus profiles were placed in categories C, D, E, and F) at loci where only one or two alleles were called in non-fumed pipe bombs (Figure 8A). Five were called at D18S51, three at CSF1PO, two at D2S1338 and FGA, and one at D13S317, D7S820, amelogenin,

D21S11, and D16S539. Eighteen alleles were inconsistent with the handler's profile at loci where one or two alleles were called in fumed pipe bombs (Figure 8B), with six at D18S51, three at CSF1PO, two at D16S539 and FGA, and one at D13S317, D7S820, and amelogenin; no alleles were inconsistent with the handler's profile at D21S11.

Alleles were in stutter positions in 8/17 (47%) of those that were inconsistent with the handler's profile from non-fumed pipe bombs. The remaining nine alleles (53%) were not in a stutter position, and could not be attributed to the researchers. The handler's genotype was not in any of the six respective electropherograms for pipe bombs 12C, 17C, and 18C even some though alleles were. One consensus genotype (at D18S51 for pipe bomb 20C) was inconsistent with the handler because the handler's alleles were minor peaks in the electropherograms. Alleles were in stutter positions in 10/18 (56%) of those that were inconsistent with the handler from fumed pipe bombs.

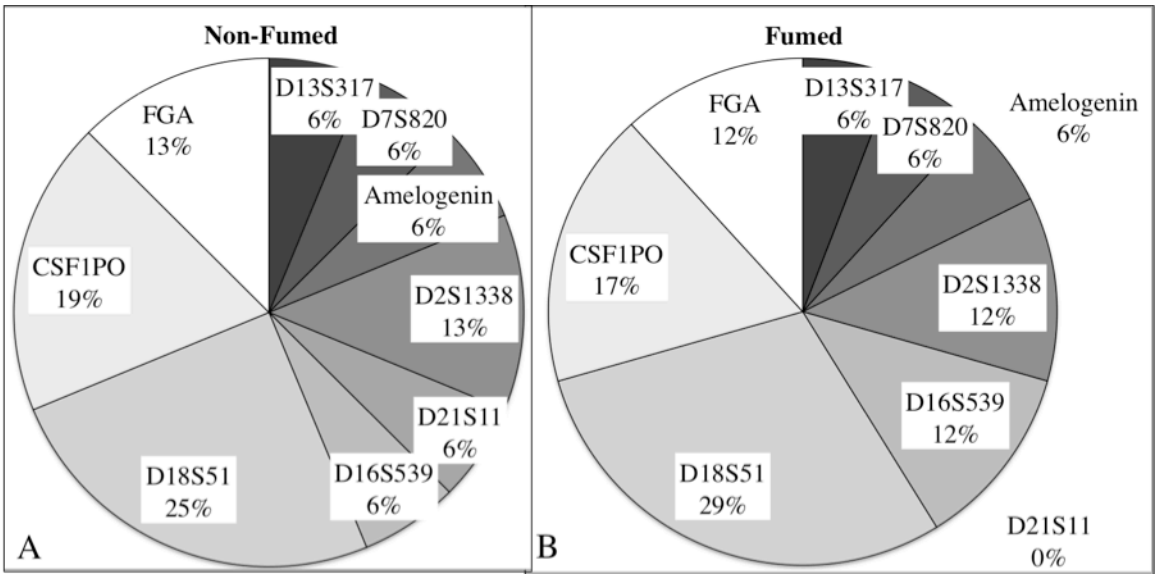

Figure 8: Characterization of consensus calls inconsistent with the handler.
For both non-fumed (A) and fumed (B) samples inconsistent allele calls occurred most frequently at D18S51. No inconsistent consensus alleles were called at D21S11 in non-fumed pipe bombs.

Analysis the Alleles at Each Locus

Forty percent (519/1296) of loci from non-fumed pipe bombs (Figure 9A) fell into categories I (only the handler's alleles) and II (the handler's alleles constituted the major profile) while 43% (555/1296) of loci from fumed pipe bombs (Figure 9B) fell into the same categories. Forty-four percent (576/1296) and forty-one percent (539/1296) of non-fumed and fumed pipe bombs, respectively, fell into categories III (the handler's alleles did not constitute the major profile) and IV (only one handler allele). Sixteen percent (201/1296) of the loci from non-fumed bombs, and sixteen percent (202/1296) of the loci from fumed pipe bombs fell into the categories V (no alleles belonged to the handler) and VI (no alleles). There was no statistical difference between the non-fumed and fumed bombs in the number of alleles per locus ($p=0.840$). Furthermore, the ratio of alleles to the expected number of alleles at a locus in non-fumed and fumed samples showed no significant difference ($p=0.821$).

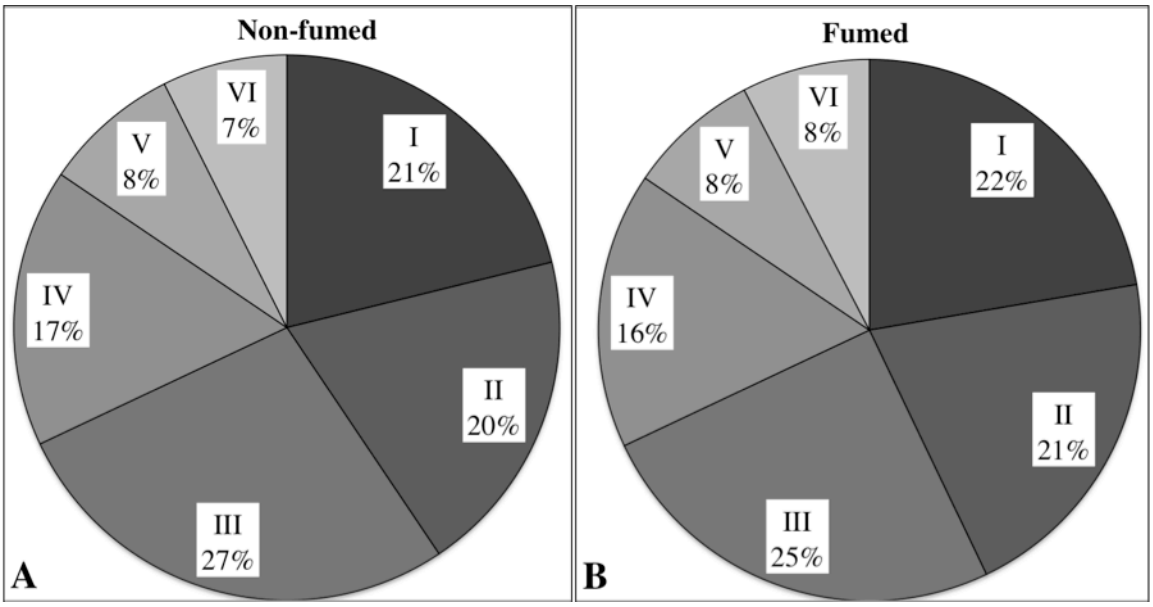

Figure 9: Breakdown of loci for non-fumed and fumed pipe bombs.
Loci for each electropherogram were assigned to one of six categories. I: Only the handler's alleles. II: Multiple alleles were called, but the handler's alleles constituted the major contributor. III: The handler's alleles were not the major contributor. IV: Only one handler allele. V: No alleles belonged to the handler. VI: No alleles.

Discussion

The purpose of the study was to assess the effects of CA fuming on the quantity and quality of DNA recovered from deflagrated pipe bomb fragments. This stems from previous attempts to increase the amount of biological information obtained from IEDs and to determine if there should be a defined order of processing post-deflagrated IED fragments. Typically, a laboratory, such as the ATF, receives IED components, collects explosive residue, and CA fumes the fragments for fingerprints prior to DNA analysis (communication from the ATF). This study was designed to determine if CA fuming immediately after pipe bomb deflagration would affect the order of laboratory analysis. It was possible that greater quantities of DNA could be recovered from the fragments or that DNA collection and subsequent analysis might be inhibited.

Retention of pipe bomb fragments differed between the two deflagration locations. The latch used to keep the lid of the crate closed failed as a result of the deflagrations, allowing fragments to be strewn across the room in the training facility; however, when the crate was placed inside the large concrete cylinder with additional large concrete slabs partially blocking the open ends at the Howell, MI location (with a large block of wood used to lodge the crate shut), few fragments escaped the cylinder. The reduction in area that needed to be searched for pipe bomb fragments streamlined the process of deflagration and fragment collection. The one drawback of the Howell, MI location was that it was outdoors, making the process heavily dependent on the weather.

The end caps in the preliminary study produced approximately 100 times more DNA than CDs, which may have been due to differences in composition of the materials

or the amount of surface area that was touched. The end caps were rougher than the CDs and could capture more cells from the handler. Additionally, volunteers solely laid down fingerprints on the CDs, while they tightened the end caps with the palm of their hand, providing a greater surface area from which cells could be shed. Conversely, the quantities of DNA recovered from the pipe bombs were approximately ten times less than those recovered from the end caps in the preliminary study. This was most likely a result of the extreme environmental conditions of the deflagration process, where the forces of the explosion dislodged cells from the relatively smooth surface of the pipe bombs, while the heat from the blast destroyed DNA. Further, the end caps were processed within a few days of the volunteers handled them, whereas several months passed before all pipe bombs were deflagrated, which may have allowed some DNA to degrade or cells fall off.

Von Wurmb *et al.* (2001) suggested that CA fuming might inhibit amplification of DNA. The authors placed blood and saliva on glass slides and fumed them for 60 min at 55ºC. Additionally, the Chelex procedure (an extraction where polystyrene divinylbenzene iminodiacetate ions bind metal ions that can facilitate the breakdown of DNA) was used, which co-purified the CA polymers with DNA, and may have resulted in inhibition. To confirm this, the authors added CA polymers directly to a PCR, which resulted in inhibition. The shorter fuming time used in the present study, in combination with the use of organic extraction, may have removed the CA polymers, thus reducing the presence of inhibition. In fact, there was no difference in DNA recovery between non-fumed and fumed samples in the preliminary CDs and end caps studies.

Numerous studies have been performed investigating the mechanism of CA deposition on handled materials, including initiating reactions with tertiary amines, fatty

acids, proteins, and water (Czekanski *et al*., 2006; Eromosele *et al*., 1989; Pepper and Ryan, 1983). Czekanski *et al*. (2006) stated that the OH group on one CA monomer or water reacts with a carbon atom on another monomer and continues the chain propagation results in long many-branched chains. Wargacki *et al*. (2007) also studied the polymerization of CA, but with solutions of sodium lactate and alanine at similar concentrations as found in eccrine sweat, and concluded that the carboxyl group can initiate polymerization. Further, the condition under which CA polymerizes affects the length of the polymer. If the pH of the system is acidic many short chains develop, as opposed to longer chains when the environment is more basic. Burns *et al*. (1998) found that the addition of ammonia might help with CA polymerization, due to its basic pH. If the polymer chains on the pipe bomb fragments were short, remaining cells might have been more easily lost during transport. It is unknown whether the fuming environment in the current study was acidic or basic; however the addition of ammonia to the fuming chamber could have allowed the CA monomers to begin polymerization on the carboxyl groups of proteins on cells more efficiently and led to longer, branched chains, potentially increasing the overall adhesion of the remaining cells to the pipe bomb. Further studies would need to be conducted to examine if the addition of ammonia to the fuming process adversely affects downstream DNA analysis.

Lewis *et al*. (2001) studied the processes involved in the development of fingerprints with CA fuming. Clean and oily fingerprints were laid down on stainless steel discs and glass slides, and were developed using 1 g of CA heated to 150^{o}C. Clean, fresh fingerprints resulted in visible polymer on the print ridges, while older prints showed reduced contrast. High relative humidity resulted in better visualization with old

oily prints. Lewis *et al*. (2001) noted that clean prints resulted in "noodle structures," while oily prints emulsify water in the oily phases and form capsules, but both prints provide enough contrast for visualization. Further, it was noted that oil can delay evaporation of water needed to initialize polymerization and that optimization of humidity was needed to reduce deposition of CA in the background. Bille *et al*. (2009), in their study of time on DNA recovery from deflagrated pipe bombs, returned the fragments to the laboratory, and followed a controlled, defined humidifying (75% relative humidity) and glue heating (10 min at 120 ºC) steps. The fuming chamber constructed for the present study had minimal temperature controls, with placement of heated water on a candle warmer. Humidity levels and temperature were not monitored; thus, they certainly fluctuated due to environmental factors such as outdoor temperature and wind. This can lead to variability in the consistency of CA residue deposited on the fragments and potentially influence the adherence of cells on the pipe bomb during transport. More controlled fuming could optimize the CA residue formation on pipe bomb fragments, but would likely require transport of the fragments back to a laboratory before the process can be completed, which itself could lead to a loss of cells.

When fuming in the field, a test print might be placed on a similar substrate (in this case galvanized steel) in the fuming chamber behind the pipe bomb fragments. When the test print is easily visualized, it is likely that the fuming process is complete for the fragments. This would ensure a more consistent deposition of CA residue, allowing the fumer to better deal with environmental conditions.

Bille *et al*. (2009) found no statistical difference or trend in the amount of DNA recovered from non-fumed and fumed pipe bomb fragments, similar to the present study

when 0 ng quantities and outliers were removed (p=0.69). However, Bille *et al*. (2009) only tested three pairs of pipe bombs, whereas 24 pairs were analyzed in this study. With such a small sample size, it is unlikely that Bille *et al*. (2009) could detect a difference in DNA yield. Furthermore, CA fuming was not performed immediately after deflagration, but was carried out after the fragments were transported back to the laboratory, nullifying any possible effect that CA fuming had on adhering cells to the pipe bombs during transport.

Another factor that could have influenced DNA yields was the presence of powder residue. Variances in the amounts of DNA between swabs with relatively large and low amounts of residue were statistically different ($p=1.43 \times 10^{-9}$), with pipe bombs having lower amounts of powder residue showing greater variability. Such variation is probably a result of the extremely low amounts of DNA recovered from all pipe bombs. The powder likely did not interfere with DNA recovery, as there was no significant difference between swabs with high or low amounts of powder residue.

A specific amount of input DNA is recommended with Minifiler™ . Luce *et al*. (2009), in their validation of Minifiler™ for casework, found that peak height ratios could be as low as 36% when the optimal quantity of DNA was added to the PCR. The average quantity of DNA added to the reactions in the current study was well below this optimum, and only 9/288 extractions recovered enough DNA to add 0.5 ng. The remaining 97% of extractions yielded less than 100 pg/5 μL, and thus were amplified under conditions where the resulting peak height imbalances could be greater than those observed by Luce *et al*. (2009) when optimal DNA input was used. Such peak

imbalances can lead to the misinterpretation of major and minor contributors, resulting in the development of an incorrect consensus profile.

One or more of the handler's alleles dropped out at 32% of the loci. Further, two of the nine extractions that were not LCN (19FP1 and 24CP2) experienced dropout even with optimal DNA input into the Minifiler™ reaction. This, in combination with only the handler's alleles being present or were the major peaks at 42% of the loci, reduced the ability to accurately develop a consensus profile. Interestingly, 41 extractions (from 21 pipe bombs) showed that 0.00 ng of DNA were recovered when quantified with Quantifiler™ (Appendix A); however, the subsequent amplification resulted in at least partial profiles, although these generally had few alleles. Most of the peaks did not add weight to the subsequent development of consensus profiles, as 55% of the loci had zero or one of the handler's alleles. Amplification of 13CE3 produced a profile that contained all but one of the handler's alleles, while 15CE2 produced a profile that contained all of the handler's alleles. However, even in these instances the handler's alleles were not always the major peaks. Thus this shows that, while rare, profiles obtained from extractions that quantify as having no DNA can help in the development of consensus profiles.

The ability to develop a partial profile when Quantifiler™ indicates that there are 0 ng of DNA indicates that it may not be the best measure of DNA quality for subsequent DNA analysis. The Quantifiler™ assay probes a DNA segment 62 bp in length, shorter than alleles amplified with Minifiler™ . Andréasson *et al*. (2002) developed a real time quantification assay for nuclear and mitochondrial DNA, and noted that longer products

would better estimate larger amplicons, while failing to detect smaller targets in degraded samples. A better estimate of amplifiable DNA may be obtained by using a combination of large and small amplicons similar to the quantification system developed by Swango *et al*. (2007), whose multiplex qPCR probed both TH01 and CSF1PO with amplicon sizes of ~170 – 190 and 67 bp, respectively. The assay was sensitive to approximately 44 pg, and allowed a quantitative determination of the level of degradation in a DNA sample by calculating the ratio of the CSF1PO quantity to the TH01 quantity. If this method had been used to quantify DNAs in the present study, the level of degradation could have been assessed. Knowledge of degradation levels prior to amplification would have allowed determination of which extractions would result in the best data, potentially increasing the likelihood and confidence that the handler's alleles could be determined in the consensus profile.

DNA was also recovered from the pipe bomb that was cleaned and unhandled both before and after deflagration; however, the average DNA quantity was one tenth that of the average of pipe bombs handled by volunteers. The two extractions (RBE3 and RBP2) that recovered DNA before the pipe bomb was deflagrated did not result in any alleles upon amplification with Minifiler™ . Because DRBE1, DRBE2 and DRCP1 exhibited alleles at all loci, an attempt was made to develop a consensus profile to determine the source, however a full consensus could not be established, as none of the alleles were consistent among the three extractions. Specifically, three or more alleles occurred at 11 loci from three of the six extractions from the unhandled pipe bomb (Appendix B), demonstrating a mixture. At least one male was a contributor at DRBE1 and DRCP1, while it was possible that there was a male/female mixture from DRBE2 as

the Y peak was approximately 40% of the X peak at amelogenin. Further, some alleles were not consistent with any of the researchers associated with the current study. This shows that dropin most likely resulted from the non-sterile environment in which the pipe bombs were deflagrated.

Budowle (2007) noted that contamination could originate from laboratory personnel, sample-to-sample carry over, reagents, or consumables. Additionally, artifact alleles can be caused by stutter or dropin. The increased sensitivity and detection of contamination in LCN DNA analysis may explain the peaks from the unhandled pipe bomb. Negative controls throughout the study showed several peaks, but were attributed to artifacts because the peak morphologies were not consistent with alleles (either too sharp or too broad). Although a remote possibility, extraneous DNA may have also come in contact with the pipe bombs when they were placed (and returned after deflagration) inside an unused paper bag because the bag were not pretreated and the inner surface was not UV irradiated. Additionally, the pipe bombs were assembled and deflagrated in an open environment where extraneous DNA may have come in contact with it. The impact of peaks in the stutter position is illustrated by the 19 loci for the non-fumed and 14 loci for fumed pipe bombs where three alleles were noted in the consensus. Approximately 60% of the time the non-handler allele was in a stutter position (either one repeat before or after the handler's allele). Further, other common problems encountered when analyzing LCN DNA, namely allelic dropin, dropout, and heterozygous peak imbalances (Gill *et al*., 2001; Whitaker *et al*., 2001), resulted in genotypes inconsistent with the handler for 16 loci in non-fumed and 17 loci for fumed pipe bombs.

Approximately 70% (23/33) of alleles called in the consensus profiles that were inconsistent with the handler in the present study were made at FGA, CSF1PO, D18S51 and D2S1338. Because of their larger amplicon sizes, FGA, D18S52, and D2S1338 are more susceptible to slippage products (Applied Biosystems, 2007). The resulting allele calls that were inconsistent with the handler were most likely a result of the elevated stutter at these loci, which was compounded by the fact that the DNA was LCN. CSF1PO, on the other hand, has an amplicon size up to approximately 130 bp (comparable to D13S317 and D16S539), but displayed results similar to the larger loci. This shows that some loci may have decreased reliability when DNA is analyzed after deflagration. Additionally, Both FGA and CSF1PO are labeled with PET, which typically shows higher background, which might have lead to more erroneous calls, particularly since the 50 RFUs was set as the threshold for detection. The remaining 10 non-handler allele calls (five between non-fumed and fumed pipe bombs) were made at D13S317, D7S820, amelogenin, D21S11 and D16S539. Amplicon sizes for these loci ranged from approximately 70 – 140 bp, making them less sensitive to degradation. Consequently, it may be advantageous to explore the feasibility of using alternative miniSTRs in the development of consensus profiles for highly degraded DNA. The alternative loci should have a longer core sequence (e.g. 5 bp instead of 4 bp), which would decrease stutter percentages.

Conclusion

Overall, full consensus profiles were developed for 21% (5/24) of non-fumed pipe bombs and 33% (8/24) of fumed pipe bombs. The remaining consensus profiles had either one allele inconsistent with the handler's profile or contained the handler's alleles in addition to others at a locus. Results of this study show that CA fuming pipe bomb fragments immediately after deflagration does not hinder subsequent recovery of DNA. However, the standard deviation of DNA recovery was high relative to the average DNA recovery, and made it difficult to ascertain whether CA fuming led to an increase in DNA recovery. Further, there were no differences in the consensus profiles developed between non-fumed and fumed pipe bombs, indicating that CA fuming does not affect the accuracy of the consensus profile.

While ideally it may be preferable to fume IED fragments on site, this is not practical as laboratory personnel are often not at the scene. Instead it might be feasible to determine whether or not to fume pipe bomb fragments immediately upon their submission to the laboratory. This would provide the advantage of having a controlled fuming environment, optimizing CA deposition, while at the same time causing the remaining cells to adhere to fragments so they are not lost as the evidence is stored, awaiting analysis.

APPENDICIES

Appendix A. Quantity of DNA Recovered from Pipe Bombs

Extractions were labeled as follows: the first position denoted the pipe bomb pair; "C" denoted control (non-fumed) pipe bombs; "F" denoted a fumed pipe bombs; "E" denoted an extraction from an end cap, "P" denoted an extraction from the pipe; the last position denoted extraction number for the particular pipe bomb component. For example, 13-E4 represented the 13^{th} pair of pipe bombs, extraction from an end cap, swab 4. Non-fumed (C) and fumed (F) bomb pairs are adjacent in the table to allow comparison.

RB identified the pipe bomb that was swabbed prior to deflagration. DRB denoted the pipe bomb that was decontaminated but not handled by volunteers. Neither were CA fumed. Values obtained from it were not included in any calculations.

Shaded cells were swabs that had relatively large amounts of powder residue, nearly covering the swabs used. Bolded numbers highlight extractions that showed no DNA when quantified.

Set and Swab Number	Non-Fumed (C)	Fumed (F)	Set and Swab Number	Non-Fumed (C)	Fumed (F)	Set and Swab Number	Non-Fumed (C)	Fumed (F)
1-E1	1.27E-2	1.06E-2	**7-E1**	1.18E-2	**0.00E+0**	**13-E1**	3.32E-2	6.63E-3
1-E2	1.04E-2	2.38E-2	**7-E2**	1.22E-2	1.45E-3	**13-E2**	**0.00E+0**	6.52E-2
1-E3	1.95E-1	4.83E-3	**7-E3**	9.87E-3	4.30E-3	**13-E3**	2.91E-2	2.24E-1
1-E4	3.04E-2	4.02E-3	**7-E4**	1.96E-2	6.49E-4	**13-E4**	3.61E-2	1.93E-1
1-P1	6.44E-2	9.29E-2	**7-P1**	1.67E-2	**0.00E+0**	**13-P1**	5.10E-2	1.72E-1
1-P2	5.54E-2	2.49E-2	**7-P2**	6.57E-3	1.46E-3	**13-P2**	7.13E-2	3.68E-1
2-E1	2.93E-3	1.11E-2	**8-E1**	**0.00E+0**	8.44E-3	**14-E1**	1.93E-2	3.70E-2
2-E2	2.13E-2	2.20E-2	**8-E2**	**0.00E+0**	9.83E-3	**14-E2**	1.52E-2	5.08E-2
2-E3	9.26E-3	1.10E-2	**8-E3**	2.94E-2	**0.00E+0**	**14-E3**	**0.00E+0**	5.62E-2
2-E4	6.87E-3	1.10E-2	**8-E4**	9.60E-3	**0.00E+0**	**14-E4**	1.78E-2	5.65E-3
2-P1	5.50E-3	9.57E-2	**8-P1**	2.68E-2	1.28E-2	**14-P1**	8.37E-3	7.10E-2
2-P2	8.42E-3	1.52E-1	**8-P2**	1.90E-2	1.15E-2	**14-P2**	2.33E-2	4.83E-2
3-E1	**0.00E+0**	**0.00E+0**	**9-E1**	6.27E-3	5.77E-3	**15-E1**	5.92E-3	3.11E-2
3-E2	7.09E-4	0.00E+0	**9-E2**	1.58E-2	**0.00E+0**	**15-E2**	**0.00E+0**	4.15E-2
3-E3	1.55E-2	1.27E-3	**9-E3**	6.60E-3	1.15E-2	**15-E3**	5.22E-2	5.11E-1
3-E4	1.10E-2	2.79E-3	**9-E4**	1.60E-2	2.85E-2	**15-E4**	2.64E-2	5.95E-2
3-P1	8.43E-3	4.87E-3	**9-P1**	2.75E-3	1.04E-2	**15-P1**	1.21E-2	9.86E-2
3-P2	7.58E-3	1.28E-2	**9-P2**	1.16E-2	1.12E-2	**15-P2**	3.41E-2	5.27E-2
4-E1	2.69E-2	**0.00E+0**	**10-E1**	2.31E-3	**0.00E+0**	**16-E1**	**0.00E+0**	1.33E-2
4-E2	2.75E-2	1.44E-3	**10-E2**	3.98E-3	1.45E-3	**16-E2**	7.17E-3	1.06E-2
4-E3	7.72E-3	1.04E-2	**10-E3**	1.23E-2	4.30E-3	**16-E3**	6.88E-3	1.55E-2
4-E4	4.00E-2	1.17E-2	**10-E4**	**0.00E+0**	6.49E-4	**16-E4**	3.35E-2	2.33E-2
4-P1	2.17E-2	7.11E-2	**10-P1**	4.33E-3	**0.00E+0**	**16-P1**	3.74E-2	1.28E-2
4-P2	3.91E-3	8.76E-3	**10-P2**	**0.00E+0**	1.46E-3	**16-P2**	1.82E-2	1.08E-2
5-E1	2.12E-3	2.14E-3	**11-E1**	1.54E-3	2.66E-3	**17-E1**	**0.00E+0**	4.87E-3
5-E2	7.51E-2	1.27E-2	**11-E2**	2.45E-3	1.56E-2	**17-E2**	**0.00E+0**	2.34E-3
5-E3	7.25E-2	2.35E-2	**11-E3**	**0.00E+0**	4.40E-4	**17-E3**	**0.00E+0**	8.45E-3
5-E4	6.26E-2	1.06E-2	**11-E4**	**0.00E+0**	4.91E-2	**17-E4**	**0.00E+0**	4.71E-3
5-P1	6.73E-3	3.28E-2	**11-P1**	1.28E-2	3.96E-3	**17-P1**	**0.00E+0**	1.28E-2
5-P2	1.11E-1	1.75E-2	**11-P2**	1.18E-2	1.63E-3	**17-P2**	**0.00E+0**	**0.00E+0**
6-E1	3.69E-3	7.69E-3	**12-E1**	**0.00E+0**	3.55E-3	**18-E1**	8.82E-2	3.25E-3
6-E2	6.54E-3	4.54E-3	**12-E2**	3.69E-3	**0.00E+0**	**18-E2**	7.88E-2	2.36E-2
6-E3	4.07E-3	2.31E-3	**12-E3**	6.38E-3	9.59E-3	**18-E3**	1.79E-2	4.90E-2
6-E4	7.11E-3	4.34E-3	**12-E4**	**0.00E+0**	**0.00E+0**	**18-E4**	4.47E-2	4.02E-2
6-P1	1.67E-3	4.66E-3	**12-P1**	6.35E-3	**0.00E+0**	**18-P1**	2.35E-2	2.26E-2
6-P2	**0.00E+0**	1.90E-3	**12-P2**	**0.00E+0**	7.70E-3	**18-P2**	6.38E-3	1.43E-2

Table 7: Quantity of DNA recovered from pipe bomb pairs 1 - 18

Set and Swab Number	Non-Fumed (C)	Fumed (F)	Set and Swab Number	Non-Fumed (C)	Fumed (F)	
19-E1	2.60E-3	1.05E-2	**23-E1**	1.17E-2	9.65E-3	
19-E2	1.59E-2	8.18E-2	**23-E2**	1.95E-3	2.73E-3	
19-E3	2.08E-2	3.08E-2	**23-E3**	3.46E-3	3.02E-2	
19-E4	6.51E-2	1.04E-1	**23-E4**	3.54E-2	1.51E-2	
19-P1	2.72E-2	1.38E-1	**23-P1**	2.43E-2	8.86E-2	
19-P2	8.34E-3	1.52E-2	**23-P2**	3.14E-2	7.19E-2	
20-E1	5.81E-3	**0.00E+0**	**24-E1**	7.97E-2	8.77E-3	
20-E2	1.96E-2	**0.00E+0**	**24-E2**	3.29E-2	1.14E-2	
20-E3	**0.00E+0**	2.19E-3	**24-E3**	3.32E-3	**0.00E+0**	
20-E4	7.86E-3	7.72E-3	**24-E4**	1.03E-2	**0.00E+0**	
20-P1	3.56E-3	**0.00E+0**	**24-P1**	4.11E-2	2.22E-2	
20-P2	**0.00E+0**	1.03E-2	**24-P2**	1.37E-1	**0.00E+0**	
21-E1	2.50E-2	2.56E-2	**RBE1**	0.00E+0	**DRBE1**	4.55E-3
21-E2	7.87E-3	1.57E-2	**RBE2**	0.00E+0	**DRBE2**	3.41E-3
21-E3	2.27E-2	1.27E-2	**RBE3**	1.22E-3	**DRBE3**	0.00E+0
21-E4	1.80E-2	1.21E-2	**RBE4**	0.00E+0	**DRBE4**	1.21E-3
21-P1	9.71E-3	1.77E-2	**RBP1**	0.00E+0	**DRBP1**	2.56E-3
21-P2	1.57E-2	5.49E-2	**RBP2**	1.29E-3	**DRBP2**	0.00E+0

Table 8: Quantities of DNA recovered from pipe bomb pairs 19 – 24, including reagent blanks

Appendix B. Alleles in Each Electropherogram

Column headings were labeled with the swab nomenclature. "Alleles" are the alleles in the electropherogram. Numbers in parentheses denoted minor peaks.

"Locus Category" (Loc Cat) is one of the six categories describing the results for each

I. Only the correct alleles were seen.
II. The correct alleles were seen, and constituted the major profile.
III. The correct alleles were seen, but did not constitute the major profile.
IV. Only one correct allele was seen.
V. Alleles were seen, but none were correct.
VI. No alleles were seen.

"Consensus" (Con) is the consensus profile. "Score" is how confident the researcher was in making the consensus call:

1. Confident
2. Somewhat confident
3. Low confidence/Could not distinguish between three alleles
4. Uncallable

"Individual" (Ind) was the handler's genotype.

	1CE1		1CE2		1CE3		1CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	11, 12, 13	C	8, 9, 11, 12, 13	C	10, 11, (12, 13)	C	-	F
D7S820	9, 10, 11	D	(8), 9, 10, 11, 12	C	8, (9, 10, 11), 12	C	-	F
AMEL	X(Y)	B	X(Y)	B	X	A	-	F
D2S1338	17, (18, 19, 20, 25)	B	17, (18), 19, (20)	C	17, (18, 19), 23	C	-	F
D21S11	28, 29, (30, 31.2), 32	C	28, 29, 30, 31, 32.2	C	(28, 29, 30), 31, (32, 37)	C	-	F
D16S539	10, 15, 16, 17	D	9, 11	D	11, 13	D	-	F
D18S51	9, 11, 15	D	(14, 15), 16, (7, 18)	C	15, 17, (18)	C	-	F
CSF1PO	10, (11), 12	B	(8, 10, 11), 12, (13, 14)	C	9, 12, (13, 14)	C	-	F
FGA	21, (22), 23, (24, 25, 27)	B	(21, 22), 23, (26)	C	(21), 22, 23, (24, 28)	C	-	F

Table 9: Alleles for pipe bomb 1C

	1CP1		1CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	11, 12, 13	C	(10), 11, (12, 13, 14)	C	11,12,13	3	**12, 13**
D7S820	(8), 9, 10, 11, (12)	C	9, 10, 11, (12, 13)	C	-	4	**9, 12**
AMEL	X(Y)	B	X(Y)	B	X	2	**X**
D2S1338	17, (19, 20), 23	C	17, (19, 20, 24, 25)	B	17	2	**17**
D21S11	(26, 28), 29, 30, (31, 31.2), 32	C	28, 29, 30, 31.2, (32)	C	-	4	**29, 32**
D16S539	(9), 11, 13	B	9, 11, 13	C	9,11,13	3	**11, 13**
D18S51	(10.2, 13), 17, 18	B	14, 15, 17, 18	C	15,17,18	3	**17, 18**
CSF1PO	10, 12, (13)	B	10, 12	A	10,12	2	**10, 12**
FGA	(16, 19, 21, 22), 23, (24)	C	(18, 20), 21, 22, 23, 24	C	22,23	3	**21, 23**

Table 10: Alleles for pipe bomb 1C continued

	1FE1		1FE2		1FE3		1FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	(8, 12), 13	C	10, 11, 12	C	9, 11, 12, 13	C	(9), 11	C
D7S820	9, 10, (11, 12)	C	9, 10, 11, (12)	C	8, 11	E	9, 11, 12	C
AMEL	X	A	X(Y)	B	X	A	XY	C
D2S1338	17	A	17	A	17, 18, 20, 28	C	17, (19)	B
D21S11	29, 32	A	29, 32	A	29, 32	A	-	F
D16S539	11, 13, 14	C	(5), 8, 12, 13	C	(10), 11, (12)	D	(8), 9, 11, 12, 12.2, (13)	C
D18S51	10.2, 17, 18	C	17, 18	A	(8), 13, (17), 18	C	13, 14	E
CSF1PO	10, 12	A	10	D	10, 12	A	12, 13, 14	D
FGA	21, 22, 23, 26	C	(20, 20.2), 21, (22), 23, 24	B	(21), 22, 23	B	23	D

Table 11: Alleles for pipe bomb 1F

	1FP1		1FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	11, (12, 13)	C	11, (12), 13	C	11, 12, 13	3	**12, 13**
D7S820	(8, 9), 10, (11), 12	C	(8, 9), 10, (11, 12)	C	-	4	**9, 12**
AMEL	X	A	X(Y)	B	X	2	**X**
D2S1338	(15), 17, (19), 20, 22, (24)	C	17, 19, (20, 28)	C	17, 19, 20	3	**17**
D21S11	27, 28, 29, 30, 32, 33	C	(28), 29, 31.2, 32	C	29, 32	1	**29, 32**
D16S539	11, 12, 13	C	8, (9), 11	D	11, 12	2	**11, 13**
D18S51	14, 16, 17, 18	C	(16, 16.2), 17, 18	B	17, 18	1	**17, 18**
CSF1PO	10, 11, 12, 13	C	10, (11), 12, (13)	B	12	3	**10, 12**
FGA	17.2, 21, 22, 23, 24, 25	C	(19, 20), 21, (22), 23(25)	B	21, 23	3	**21, 23**

Table 12: Alleles for pipe bomb 1F continued

	2CE1		2CE2		2CE3		2CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	8	E	12	A	12	A	8, 12	C
D7S820	8	D	(8), 10	C	8	D	8, (10), 12	C
AMEL	X	A	X(Y)	B	X	A	XY	C
D2S1338	19, (21), 23	C	(18), 19, (21)	C	17, 19, 21	C	19, 920, 21)	C
D21S11	30, 31.2, 32.2	D	27, 30, 32.2	C	32.2	D	27, (32.2)	C
D16S539	10, 11	A	10, 11	A	10, (11)	C	(9), 10, 11, (15)	B
D18S51	18	D	17, 18, 20	C	(15), 18, 20	B	(14), 15, 18	D
CSF1PO	10, 11	A	10, 11	A	10, (11, 12, 14)	C	10, (11, 14)	C
FGA	21	E	(21), 22, 23, 24	C	22, 23, 24, (25)	C	22, 23, 24	C

Table 13: Alleles for pipe bomb 2C

	2CP1		2CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	8, (10), 11, 12	C	(11), 12	B	12	2	**12**
D7S820	(8), 10	C	8, 10	A	8, 10	1	**8, 10**
AMEL	X(Y)	B	X(Y)	B	X	2	**X**
D2S1338	17, 18, (19, 21)	C	(17, 18), 19, (24)	E	19, 21	3	**19, 21**
D21S11	29, 32.2	D	27, 32.2	A	27, 32.2	3	**27, 32.2**
D16S539	-	F	10, 11, 13	E	10, 11, 12	3	**10,11**
D18S51	13, 15, 17, 20	E	(15, 16, 16.2), 18, (19, 20)	C	-	4	**18, 20**
CSF1PO	(6, 8), 10, (11, 14)	C	10, 11, 12	C	10	3	**10, 11**
FGA	18, 21, 22, 23	E	19, (21), 22, 24	C	22, 23, 24	3	**22, 24**

Table 14: Alleles for pipe bomb 2C continued

	2FE1		2FE2		2FE3		2FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	(8), 12	B	(10), 12	B	(8), 11, 12	C	8	E
D7S820	8, 10, (13)	B	8, (9), 10	B	(8), 10	C	8, 10, (12)	B
AMEL	X(Y)	B	X, (Y)	B	X(Y)	B	X	A
D2S1338	(16, 17, 18), 19, (20), 21, (22, 24, 29	B	(17), 19, (20), 21, (29)	B	19, 21, (25, 29)	B	19, 21	A
D21S11	27, (29, 30, 30.2, 31.2), 32.2	B	27, (31), 32.2, (31, 33, 33.2)	B	27.32.2	A	27, 32.2	A
D16S539	(9), 10, 11	B	(9), 10, 11	B	10, 11	A	10, 11	A
D18S51	(13, 14, 15), 18	D	(14, 16), 18, (18.2, 19, 20)	C	(17.2), 18, (19, 19.2), 20	B	18, 20	A
CSF1PO	10, 11, (12, 13, 14)	B	10, 11, (14)	B	(6), 10, 11, (13, 14)	B	10, 11, 14	C
FGA	(21), 22, 24, (26)	B	(21), 22, 24	B	(21), 22, 24	B	21, 24	E

Table 15: Alleles for pipe bomb 2F

	2FP1		2FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	12	A	12	A	12	1	**12**
D7S820	8, 10	A	8, 10	A	8, 10	1	**8, 10**
AMEL	XY	C	X(Y)	B	X	1	**X**
D2S1338	19, 21, (29)	B	19, 21, (29)	B	19, 21	1	**19, 21**
D21S11	27, (28, 29, 31.2), 32.2	B	27, (30), 32.2	B	27, 32.2	1	**27, 32.2**
D16S539	8, 10, 11	C	10, 11	A	10, 11	1	**10,11**
D18S51	18, (18.2, 19), 20	B	18, (19, 19.2), 20	B	18, 20	2	**18, 20**
CSF1PO	9, 10, 11, (12, 14)	C	9, 10, 11, (12, 14)	C	10, 11	1	**10, 11**
FGA	(21), 22, (23), 24	B	22, 24	A	22, 24	1	**22, 24**

Table 16: Alleles for pipe bomb 2F continued

	3CE1		3CE2		3CE3		3EC4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	11	E	11	E	11, 13, 14	C	11, 13, 14	C
D7S820	-	F	-	F	11, 12	A	11	E
AMEL	XY	B	-	F	XY	C	X	A
D2S1338	16, 21	A	16, 21	A	16, 17, 19, 20, 21	C	16, 19, 20, 21	C
D21S11	28, 30	E	-	F	28, 29, 31, 31.2	E	29, 30, 32.2	C
D16S539	11	D	5	E	9, 10, 11	C	8, 9, 10, 11	C
D18S51	-	F	-	F	12, 15, 16	C	12, 16	A
CSF1PO	-	F	-	F	(10), 11, (12)	C	11, (12)	C
FGA	20, 22	E	21	E	20, 21, 23	C	21, 23	E

	3CP1		3CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	13, 14	A	-	F	11, 13, 14	3	**13, 14**
D7S820	11	E	-	F	11	3	**11, 12**
AMEL	X	A	X	A	X	2	**X**
D2S1338	17, 19, 20, 21, 24	E	16, 19, 23, 24	E	16, 19, 21	3	**16, 21**
D21S11	32.2	E	32.2	E	-	4	**29, 32.2**
D16S539	10, 11	A	11	E	11	3	**10, 11**
D18S51	16	E	12, 16	A	12, 16	3	**12, 16**
CSF1PO	10, 11, 12	C	10, 11, 12	C	10, 11, 12	3	**11, 12**
FGA	21, 23	E	21	E	20, 21, 23	3	**20, 21**

Table 17: Alleles for pipe bomb 3C

	3FE1		3FE2		3FE3		3FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	-	F	-	F	12	E	13	D
D7S820	-	F	-	F	8, 10, 11	D	-	F
AMEL	-	F	XY	C	-	F	X	A
D2S1338	19	E	25	E	-	F	(16), 19, 23	E
D21S11	-	F	-	F	-	F	28	E
D16S539	11	D	11	D	7	E	11, 11, 13	C
D18S51	-	F	17	E	-	F	12, 15	E
CSF1PO	6	E	-	F	12	E	(10, 12), 11	C
FGA	-	F	-	F	-	F	20(21)	C

	3FP1		3FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	12, 14	D	9, 13, 14	C	-	4	**13, 14**
D7S820	11	D	13	E	-	4	**11, 12**
AMEL	XY	C	-	F	XY	2	**X**
D2S1338	21	D	16, 19, 21	C	19, 21	3	**16, 21**
D21S11	29, 32.2	A	-	F	-	4	**29, 32.2**
D16S539	9, 11	D	(10), 11	C	-	4	**10, 11**
D18S51	-	F	-	F	12, 15	3	**12, 16**
CSF1PO	(10), 11, 12	B	13	E	11, 12	3	**11, 12**
FGA	21, 24	E	20, 21, 24	C	20, 21, 24	3	**20, 21**

Table 18: Alleles for pipe bomb 3F

	4CE1		4CE2		4CE3		4CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	11, 12	A	8, 11, 12	C	(8, 9), 11, 12	B	11, 12	A
D7S820	11, 13	A	10, 11	E	11, 13	A	11, (12), 13	B
AMEL	XY	A	XY	A	XY	A	XY	A
D2S1338	24	A	(17, 19), 24	B	(17, 23), 24	B	(19, 22), 24	B
D21S11	29, 30, 31.2	C	31.2	E	-	F	(28), 30, 31.2	B
D16S539	(8), 9, 11, (15)	B	9, 11, 12	C	9, 11, 12	C	9, 11	A
D18S51	13, 19	A	13, 19	A	19	E	13, 19	A
CSF1PO	(10), 12	B	(10, 11), 12	B	12, (13, 14)	B	12	A
FGA	21, 34.2	C	21, (25, 34.2)	B	21, (22)	B	21, (34.2)	B

	4CP1		4CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	11, 12	A	11, 12	A	11, 12	1	**11, 12**
D7S820	11, 13	A	(8), 11, 13	B	11, 13	1	**11, 13**
AMEL	XY	A	XY	A	XY	1	**XY**
D2S1338	(23), 24	B	(19, 20), 24	B	24	1	**24**
D21S11	29, 30, 31.2	C	30, 31.2	A	30, 31.2	1	**30, 31.2**
D16S539	9, (10), 11	B	9, 11	A	9, 11	1	**9, 11**
D18S51	13, 19	A	13, 19	A	13, 19	1	**13, 19**
CSF1PO	(11), 12, (13)	B	(10), 12	B	12	2	**12**
FGA	21, 34.2	C	21, 34.2	C	21	3	**21**

Table 19: Alleles for pipe bomb 4C

	4FE1		4FE2		4FE3		4FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	-	F	-	F	-	F	11, 12	A
D7S820	-	F	11	D	-	F	11	D
AMEL	-	F	X	D	XY	A	XY	A
D2S1338	17	E	24	A	24	A	24, (25)	B
D21S11	31.2	E	31.2	E	31.2	E	30, 31.2	A
D16S539	6, 7	E	9, 11	A	9, 11	A	(8, 9), 11, (12)	C
D18S51	16	E	13	D	13	D	13, 19	A
CSF1PO	8	E	12	A	10, 11, 12	C	6, 11, 12	C
FGA	27	E	(16.2), 18.2, 21	C	(16.2), 21, (25)	B	16.2, 18.2, 21, 24, 45.2	C

	4FP1		4FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	11, 12	A	11, 12	A	11, 12	2	**11, 12**
D7S820	(8), 11, 13	B	11, 13	A	11, 13	2	**11, 13**
AMEL	XY	A	XY	A	XY	1	**XY**
D2S1338	(19, 20), 24, (29)	B	24	A	24	1	**24**
D21S11	(29), 30, 31.2	B	30, 31.2	A	30, 31.2	2	**30, 31.2**
D16S539	9, 11, (12)	B	9, 11	A	9, 11	1	**9, 11**
D18S51	13, (18), 19	B	13, 19	A	13, 19	2	**13, 19**
CSF1PO	(11), 12	B	12	A	11, 12	2	**12**
FGA	(18.2), 21, (22, 23, 24, 32, 34.2)	B	18.2, 21, (23, 34.2)	C	21	2	**21**

Table 20: Alleles for pipe bomb 4F

	5CE1		5CE2		5CE3		5CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	(9), 11, 12	B	11, 12	A	11, 12	A	11, 12	A
D7S820	(9), 11, 13	E	(8), 10, 13	B	10, 13	A	10, 13	A
AMEL	(X)Y	C	XY	A	XY	A	XY	A
D2S1338	17, 19, (28)	B	17, 19, (20)	B	17, 19	A	17, 19	A
D21S11	30, 30.2	D	30, 32.2	A	30, 32.2	A	30, 32.2	A
D16S539	11, (15)	B	(8, 9, 10), 11	B	11	A	11	A
D18S51	14, (20)	C	14, (15, 15.2), 20	D	14, 20	E	14, 20, (27)	B
CSF1PO	10, (11), 12, (13)	B	10, (11), 12	B	10, (11), 12, (13, 14)	B	10, (11), 12	B
FGA	(21), 22, 23	B	(21), 22, 23	B	(21), 22, 23, (24)	B	(21), 22, 23	B

	5CP1		5CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	11, 12	A	11, 12	A	11, 12	1	**11, 12**
D7S820	10, 13	A	10, 13	A	10, 13	1	**10, 13**
AMEL	XY	A	XY	A	XY	1	**XY**
D2S1338	17, 19, (28)	B	17, 19	A	17, 19	1	**17, 19**
D21S11	(30), 32.2	C	30, 32.2, (33.2)	B	30, 30.2	1	**30, 32.2**
D16S539	11	A	(8, 10), 11	B	11	1	**11**
D18S51	14, 20	A	14, 24	D	14, 20	3	**14, 20**
CSF1PO	10, (11, 12, 13)	C	10, (11), 12, (13)	B	10, 12	2	**10, 12**
FGA	22, 23	A	(20, 21), 22, 23	B	22, 23	1	**22, 23**

Table 21: Alleles for pipe bomb 5C

	5FE1		5FE2		5FE3		5FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	11, 12	A	11, 12	A	11, 12	A	11, 12	A
D7S820	10, 13	A	10, (11, 13)	C	(8), 10, (11), 13	B	10, 13	A
AMEL	X(Y)	B	XY	A	XY	A	XY	A
D2S1338	17, 19	A	17, 19, (24, 28)	B	17, 19, (20, 28)	B	17, 19, (28)	B
D21S11	30, 32.2	A	30, 32.2	A	(28, 30, 31), 32.2	C	30, 32.2	A
D16S539	11	A	11, (8)	B	(9), 11, (15)	B	11, 14	C
D18S51	14	E	14, (20)	C	14, (15, 16, 20)	C	14, (16), 20	B
CSF1PO	10, 12, (13)	B	10, (11), 12, (13)	B	10(11), 12, (13)	B	10, 12	A
FGA	(20, 23), 22	C	(21, 22, 24), 23	C	(21) 22, 23, (24)	B	(21), 22, 23, (24)	B

Table 22: Alleles for pipe bomb 5F

	5FP1		5FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	(9), 11, 12	B	(9), 11, 12	B	11, 12	1	**11, 12**
D7S820	(8), 10, (11), 13	B	(8), 10, (11), 13	B	10, 13	1	**10, 13**
AMEL	XY	A	XY	A	XY	1	**XY**
D2S1338	17, 19(20, 28)	B	17, 19	A	17, 19	2	**17, 19**
D21S11	(26.2), 30, 32.2	B	(28), 30, 32.2	B	30, 30.2	3	**30, 32.2**
D16S539	11, 14	C	(8, 9), 11, (12, 12.2, 13, 15)	B	11	3	**11**
D18S51	(13), 14, (16, 17, 17.2), 20	B	14, 20	A	14, 20	3	**14, 20**
CSF1PO	10, (11), 13	D	10, (11), 12, (13)	B	10, 12	3	**10, 12**
FGA	(20), 22, 23, (24)	B	(21), 22, 23, (24, 25)	B	22, 23	3	**22, 23**

Table 23: Alleles for pipe bomb 5F continued

	6CE1		6CE2		6CE3		6CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	11	D	11, 12	A	11	D	11, 12	A
D7S820	8, 12	A	6, (8, 12)	C	12	D	8, 9, 10, 11, 12	C
AMEL	X(Y)	B	X	A	X	A	X(Y)	B
D2S1338	(18), 20	C	18, 20, 25	C	18, 19, 20, 25	C	16, 17, 18, 19, 20	C
D21S11	-	F	27, 32.2	A	27, 32.2	A	27, 32.2	A
D16S539	-	F	(11), 13	B	10, 13	C	9, 13	C
D18S51	16	E	(14), 17, 18	B	10, 13, 15, 17, 18	C	10, 12, 17	D
CSF1PO	11	A	(10), 11	B	11, (13)	B	5, 11	C
FGA	-	F	17, 20, 22, 30	D	20, 21, 22, 25	C	19, 21, 23, 30	D

	6CP1		6CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	11	D	-	F	11, 12	3	**11, 12**
D7S820	-	F	11	E	8, 12	3	**8, 12**
AMEL	X	A	Y	D	XY	2	**X**
D2S1338	23	E	-	F	18, 20	3	**18, 20**
D21S11	29	E	31.2, 35.2	E	27, 32.2	3	**27, 32.2**
D16S539	-	F	13	A	13	3	**13**
D18S51	-	F	17	D	-	4	**17, 18**
CSF1PO	11	E	10, 11	C	11	3	**11**
FGA	32	A	20, 34.2	D	-	4	**20, 21**

Table 24: Alleles for pipe bomb 6C

	6FE1		6FE2		6FE3		6FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	11, 12	A	8, 11	D	11, 12	A	11, 12	A
D7S820	8, 12	A	8, 11, 12	C	10	E	8, 12	A
AMEL	XY	C	X(Y)	B	X	A	XY	C
D2S1338	(16, 17), 18, (19), 20	B	17, 20	D	17, 18, 24	D	17, 18, 20	C
D21S11	27, 31.2, 32.2	C	30, 32.2	D	-	F	32.2, 34.2	D
D16S539	(8), 13	B	(9), 13, (15)	B	11, 13	C	13	A
D18S51	10, 15, 18	D	18	D	14	E	12, 17	D
CSF1PO	(6, 10), 11	B	(9, 10), 11, (13)	B	11	A	11	A
FGA	20, 21, (22, 30, 34.2)	A	20	D	20	D	(19), 20, 21	B

	6FP1		6FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	9, 11, 12	C	11, 12	F	11, 12	1	**11, 12**
D7S820	12, 13	D	8, 10, (11), 12	F	8, 12	1	**8, 12**
AMEL	XY	C	XY	A	XY	1	**X**
D2S1338	18, 20	A	19, 20, 24	D	18, 20	2	**18, 20**
D21S11	27, 29, 30, 31, 32.2	C	28, 31	F	32.2	3	**27, 32.2**
D16S539	9, 12, 13	C	9, 12, 13	D	11, 13	3	**13**
D18S51	13, 15, 17, 18	C	(14, 15), 16, 17, 18	F	17, 18	3	**17, 18**
CSF1PO	11, 12, 13	C	10, (11, 12)	B	11, 12	3	**11**
FGA	20, 21, 22, 20, 32	C	21, 22, 23, 26	E	20, 21, 22	3	**20, 21**

Table 25: Alleles for pipe bomb 6F

	7CE1		7CE2		7CE3		7CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	(9), 12	B	(9), 12	B	-	F	-	F
D7S820	(7), 8, 9	B	8, 9, 11	C	8, 9	A	-	F
AMEL	X(Y)	B	X	A	X	A	-	F
D2S1338	16, 19, (23, 29)	B	16, 19, (24, 29)	B	16	E	16, 19	A
D21S11	29, (30, 30.2), 31.2	B	(27), 29, (31.2)	C	29	D	31.2	D
D16S539	9, 10, 11	C	10, (11)	C	-	F	10	D
D18S51	14, 15, 17	C	14, 15	A	-	F	-	F
CSF1PO	10, 12, (14)	B	10, 11, 12	C	10	D	-	F
FGA	24, (25), 32, (34.2)	C	20, 24, 25, 32, 34.2	C	25, 32	D	-	F

	7CP1		7CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	12	A	(9, 11), 12	B	12	2	**12**
D7S820	11	E	8, 9	A	8, 9	3	**8, 9**
AMEL	X	A	X(Y)	B	X	1	**X**
D2S1338	16, 18, 19, 29	C	16, 19	A	16, 19	2	**16, 19**
D21S11	29, 31.2	A	28, 29, 31.2	C	29, 31.2	1	**29, 31.2**
D16S539	10, 11	A	9, 10, 11, (15)	C	-	4	**10, 11**
D18S51	15	D	14, 15	A	14, 15	3	**14, 15**
CSF1PO	9, 10, 12	C	9, 10, 11, 12	C	-	4	**10, 12**
FGA	20, 24, 25, (34.2)	C	24, 25, (34.2)	B	20, 24, 25	3	**24, 25**

Table 26: Alleles for pipe bomb 7C

	7FE1		7FE2		7FE3		7FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	-	F	-	F	-	F	11, 12	C
D7S820	-	F	8	D	8, 11	D	10, 11, 12	D
AMEL	X	A	X	A	X	A	X(Y)	B
D2S1338	16	D	16, 19	A	19	D	16, 19, (20)	B
D21S11	-	F	-	F	31.2	D	28, 29, 31.2	C
D16S539	11	D	-	F	8, 10	D	10, 11	A
D18S51	-	F	-	F	-	F	14, 15	A
CSF1PO	9, (10), 12	B	-	F	10	D	10, 11, 12	C
FGA	21, 22	E	-	F	19, 24	D	(21, 23, 24), 25, (34.2)	C

	7FP1		7FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	11, 12	C	-	F	11, 12	3	**12**
D7S820	-	F	-	F	-	4	**8, 9**
AMEL	X	A	X	A	X	1	**X**
D2S1338	16, 18	D	16, 18, 20	D	16	2	**16, 19**
D21S11	-	F	32.2	E	31.2	3	**29, 31.2**
D16S539	11, 12, 13	D	10, 12	D	-	4	**10, 11**
D18S51	-	F	14, 16.2, 18	D	-	4	**14, 15**
CSF1PO	10, (12)	C	8, 12	D	-	4	**10, 12**
FGA	21	E	20, 21, 23	E	-	4	**24, 25**

Table 27: Alleles for pipe bomb 7F

	8CE1		8CE2		8CE3		8CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	8, 11	D	11	D	(9), 10, 11	B	9, 10, 11	C
D7S820	11	D	8	D	8, (9), 11	B	8, 9, 11	C
AMEL	-	F	X	A	X(Y)	B	X	A
D2S1338	17, (19)	C	(17), 19	C	17, 19	A	17, 19	A
D21S11	31.2	E	30	D	-	D	20, 30, 31.2	C
D16S539	11	D	9, 11	A	(8, 9), 11	C	(8), 9, 11	B
D18S51	-	F	12, 16, 17	C	12, 15	D	10, (11)	E
CSF1PO	-	F	10, 13	C	10, (11, 12)	B	14	E
FGA	-	F	21, 25	E	18, 19, (20, 21, 22)	B	18, 19, (20), 21, (32)	B

	8CP1		8CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	10, 11	A	10, 11	A	10, 11	2	**10, 11**
D7S820	8, 11	A	8, 11	A	8, 11	2	**8, 11**
AMEL	X	A	X	A	X	1	**X**
D2S1338	17, 19	A	(17), 19	B	17, 19	2	**17, 19**
D21S11	29, 30	A	29, 30	A	29, 30	2	**29, 30**
D16S539	9, 11	A	9, 11	A	9, 11	2	**9, 11**
D18S51	14	E	16, 17	D	16, 17	3	**12, 17**
CSF1PO	10	A	10, 12	C	10	3	**10**
FGA	18, 19, (21)	B	18, 19, (19.2), 20.2, 25	C	18, 19	3	**18, 19**

Table 28: Alleles for pipe bomb 8C

	8FE1		8FE2		8FE3		8FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	10, 11	A	10, 11	A	11	D	(10), 11	B
D7S820	8, 11	A	11	D	8, 12	D	11	D
AMEL	X	A	X	A	X	A	X	A
D2S1338	17, 19	A	17, 19	A	17	D	17, (19, 23)	C
D21S11	29	D	28, 29	D	29	D	29	D
D16S539	9, 11, 12	C	9, 11	A	9, 11	A	9	D
D18S51	11.2, 14	E	11.2, (13.2), 14	E	17	D	14, 15	E
CSF1PO	10	A	10	A	10	A	10	A
FGA	18, 19, 32	C	(18), 19, 19.2,	C	18, 19	A	18, 19	A

	8FP1		8FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	10, 11	A	10, 11	A	10, 11	1	**10, 11**
D7S820	8, 11	A	8, 11	A	8, 11	1	**8, 11**
AMEL	X	A	X	A	X	1	**X**
D2S1338	17(18, 19)	C	17, 19	A	17, 19	1	**17, 19**
D21S11	29, 30	A	29, 30	A	29	2	**29, 30**
D16S539	(8), 9, 11	B	9, 11	A	9, 11	1	**9, 11**
D18S51	(9.2), 11.2, (13.2), 14	E	(11.2), 13, 14	E	11.2, 14	1	**12, 17**
CSF1PO	10, (12)	B	10	A	10	2	**10**
FGA	18, 19, (32)	B	18, 19, (32)	B	18, 19	1	**18, 19**

Table 29: Alleles for pipe bomb 8F

	9CE1		9CE2		9CE3		9CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	8	D	13	D	8, (11, 12)	D	8, 11, 12, 13	C
D7S820	9, 10	E	12	A	9, 12	C	(8), 12	B
AMEL	X(Y)	C	Y	D	X	D	Y	D
D2S1338	24	D	24, 25	A	(20), 23, 24, (25, 29)	B	17, (19, 22), 24	D
D21S11	(28, 29), 30.2, 31.2	C	28, 30	C	28, 31.2	C	28	A
D16S539	9, (10), 11, 12	C	9, 12	A	8, 12	D	9, 12	A
D18S51	13	D	10, 12, 13	C	12, 13, 19.2	C	12, 13	A
CSF1PO	10, 11	A	10	D	10, 12	D	10, 11	A
FGA	20, 22, 24	D	24, 25	A	24, 25	A	20, 24, 25, 31	C

	9CP1		9CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	-	F	8, (12), 13	B	8, 13	2	**8, 13**
D7S820	12	A	8	E	9, 12	3	**12**
AMEL	XY	A	XY	A	XY	2	**XY**
D2S1338	17	E	(17), 24, 25	B	17, 24, 25	3	**24, 25**
D21S11	29	E	28	A	28	2	**28**
D16S539	-	F	9, 12	A	9, 12	1	**9, 12**
D18S51	(10), 12, (15)	D	(12), 15, (16)	D	12, 13, 15	3	**12, 13**
CSF1PO	10, 13	D	10, 11	A	10, 11	2	**10, 11**
FGA	21, (23) 24, 25, (32)	C	19.2, 25, 31	D	24, 25	2	**24, 25**

Table 30: Alleles for pipe bomb 9C

	9FE1		9FE2		9FE3		9FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	11	E	8, 13	A	8, (11, 12), 13	B	8, 13, 14	C
D7S820	10	E	12	A	9, 11, 12	C	(9), 12	C
AMEL	XY	A	Y	D	X(Y)	C	XY	A
D2S1338	20, 24	D	25	D	(19), 24, 25, (29)	B	(17, 23, 14), 25, (29)	D
D21S11	28, 31	C	28	A	28	A	28, 30, 30.2	C
D16S539	9, 12, 15	C	9, 11, 12	C	12, 13, (14), 15	D	9, 12	A
D18S51	12, 13, 16	C	13	D	9, 11, 12	D	12, 13, 18	C
CSF1PO	10, 11, (12)	B	(9), 10, 11	B	10, 11	A	10, 11, (13)	B
FGA	20, 21, 24, 25, 31	C	19.2, 24, 25, 31	C	24, 25, 31	C	22, 24, 25, 31	C

	9FP1		9FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	(8, 9), 11, 13	C	8, (13)	C	8, 13	1	**8, 13**
D7S820	(9), 10, 11, (12)	C	12	A	9, 12	2	**12**
AMEL	XY	A	X(Y)	C	XY	1	**XY**
D2S1338	17, 20, 24	D	(17, 24), 25, (29)	C	24, 25	2	**24, 25**
D21S11	28, 29, 30	C	28, (31, 32.2)	B	28	2	**28**
D16S539	9, 12	A	9, 12	A	9, 12	1	**9, 12**
D18S51	(10), 12, (13, 15, 16, 18)	C	12, 13	A	12, 13	1	**12, 13**
CSF1PO	10, (11, 12, 15)	C	(6), 10, 11	B	10, 11	1	**10, 11**
FGA	25, 31	D	24, 25, 31	C	24, 25	1	**24, 25**

Table 31: Alleles for pipe bomb 9F

	10CE1		10CE2		10CE3		10CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	8, 11	D	8, (11), 12	B	11	E	8, 12	A
D7S820	10, 12	A	10, 12	A	-	F	10	D
AMEL	X(Y)	B	XY	C	X	A	X	A
D2S1338	16, 20, (23)	B	16, 20	A	-	F	16, 17, 20	C
D21S11	28, 29, 30.2	C	28, 30.2	D	-	F	28	D
D16S539	9, 10, (12)	D	11, 12	A	9	E	8, 11, (12)	C
D18S51	14	D	14, (15, 18)	C	14	D	14	D
CSF1PO	10, 12	D	(11, 13), 12	C	13	E	11, (12)	C
FGA	21, 23	D	21, 24	D	-	F	22, 23, 24	C

	10CP1		10CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	8	D	8, 12	A	8, 11, 12	3	**8, 12**
D7S820	10, 12	A	10, 12	A	10, 12	1	**10, 12**
AMEL	XY	C	X	A	X	2	**X**
D2S1338	16, (20)	C	20	D	16, 20	2	**16, 20**
D21S11	-	F	-	F	-	4	**28, 29**
D16S539	11, 12, (14)	B	11, 12	A	11, 12	1	**11, 12**
D18S51	13, 14, 18	C	10, 17, 18	D	14, 18	3	**14, 18**
CSF1PO	11, 12, 13	C	11, 12, 13	C	11, 12	2	**11, 12**
FGA	23, 24	A	23	D	-	4	**23, 24**

Table 32: Alleles for pipe bomb 10C

	10FE1		10FE2		10FE3		10FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	(8, 12), 11	C	11, 12	D	8, 12	A	-	F
D7S820	9, 10, 12	C	10	D	10	D	-	F
AMEL	XY	C	XY	C	X	A	-	F
D2S1338	16, 17, 19, 20	C	16, 17, 20	C	16	D	16, 20	A
D21S11	28, 29, (30), 31	C	28, 31.2	D	28, 29, 31	C	29	D
D16S539	9, 11, 12, 13, 15	C	6, 11, 12	C	(11), 12, (13)	C	11, 12, 13	C
D18S51	(14), 15, 18	C	-	F	-	F	-	F
CSF1PO	(10, 11), 12	C	11, 12	A	11, 12	A	11, 12	A
FGA	21, (22), 23, 25, (31)	D	23, 24, 31	C	24	D	32	E

	10FP1		10FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	9, 11	E	-	F	8, 11, 12	3	**8, 12**
D7S820	11	E	-	F	-	4	**10, 12**
AMEL	Y	E	X	A	XY	1	**X**
D2S1338	16, 17, 19, 20	C	19, 23	E	16, 20	3	**16, 20**
D21S11	28, 29	A	29, 31	D	28, 29, 31	3	**28, 29**
D16S539	8, 11, 12,	C	-	F	11, 12, 13	3	**11, 12**
D18S51	15, 18	D	-	F	15, 18	3	**14, 18**
CSF1PO	10, (11, 12, 13, 14)	C	10, 11, 12	C	10, 11, 12	3	**11, 12**
FGA	-	F	-	F	-	4	**23, 24**

Table 33: Alleles for pipe bomb 10F

	11CE1		11CE2		11CE3		11CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	-	F	11 (12, 13)	D	12	D	12, 13	D
D7S820	9, 11	E	(8) 10, 12	B	8	E	-	F
AMEL	-	F	X, Y	A	-	F	-	F
D2S1338	-	F	(17, 19, 20) 22, 23	E	18, 23, 24	C	(17, 19) 18	D
D21S11	28	E	(28, 30, 31.2) 29	D	30	E	-	F
D16S539	-	F	9	E	11	E	11	E
D18S51	20	E	14, 15, 22	E	13, 17, 18, 20	D	12	E
CSF1PO	-	F	12	D	10, 12	A	12	D
FGA	26	E	19, 20, 24	D	22	D	-	F

	11CP1		11CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	11, 12	D	(9, 11) 12	C	11, 12	3	**9, 12**
D7S820	10, 13	D	-	F	-	4	**10, 12**
AMEL	XY	A	X	D	XY	1	**XY**
D2S1338	18, 20 (24)	C	24	D	-	4	**18, 24**
D21S11	30	E	29	D	-	4	**29, 31**
D16S539	8, 9, 11, 12, 15	C	11, 12	D	11	4	**8, 12**
D18S51	16, 17	D	14, 17	D	17	3	**12.2, 17**
CSF1PO	10	D	(10, 11) 12	C	10, 12	2	**10, 12**
FGA	20, 21	D	22	D	-	4	**20, 22**

Table 34: Alleles for pipe bomb 11C

	11FE1		11FE2		11FE3		11FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	11	E	9, 11	D	12	D	11	E
D7S820	-	F	-	F	-	F	8, 10 (9, 11)	D
AMEL	-	F	X	D	XY	A	XY	A
D2S1338	20	E	18, 19	D	19, 24 (20, 23)	D	17, 19, 20, 24	D
D21S11	29	D	29, 31	A	-	F	28	E
D16S539	-	F	8, 12, 13	C	11, 14, 15	E	13	E
D18S51	13, 17	D	13, 15, 17	D	10, 15, 16, 18	E	10, 16	E
CSF1PO	10, 12	A	10, 11	D	10, 12	A	10	D
FGA	22, 24	D	20, 23, 24	D	21, 23	E	-	F

	11FP1		11FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	9, 12	A	(8) 9, 12	B	9, 11, 12	3	**9, 12**
D7S820	10	D	9, 10, 12	C	-	4	**10, 12**
AMEL	X	D	XY	A	XY	1	**XY**
D2S1338	17, 19, 24 (18)	C	18, 19, 24	C	19, 24	3	**18, 24**
D21S11	28, 29, 31.2	D	29, 31, 32.2	C	29	4	**29, 31**
D16S539	8, 11, 12	C	8, 9	D	-	3	**8, 12**
D18S51	14, 17	D	(14, 15) 17	D	17	3	**12.2, 17**
CSF1PO	10, 12	A	10	D	10, 12	2	**10, 12**
FGA	20, 24	D	18, 20, 23, 24	D	-	4	**20, 22**

Table 35: Alleles for pipe 11F

	12CE1		12CE2		12CE3		12CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	(8), 9, 11	B	9, 13	D	(9), 11	C	8, 9	D
D7S820	9	D	(7), 8	D	8, 9, 10, 11	C	8, 9, 10	C
AMEL	X	A	X(Y)	B	X(Y)	B	X(Y)	B
D2S1338	(23, 25), 26	C	17, 24, 25	D	25, 26	A	(23, 24), 25, 26	B
D21S11	28, 32.2	D	28, 29, 33.2	C	28, 31	D	28, (29)	D
D16S539	(5), 9, (11)	C	9, 11, 13	C	9, 11, (14)	B	9, (10), 11	B
D18S51	14.2(15), 16	D	13.2, 14.2, 15	E	13, 13.2	E	10, 15	E
CSF1PO	11, 12	A	(9), 11	D	12, 13	D	11, 12	A
FGA	20.2, 22, 24	C	21, (22), 24	C	20.2, 23	E	(22), 24, (26)	C

	12CP1		12CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	9, 11	A	11	D	9, 11	3	**9, 11**
D7S820	8, 9	A	8, 9	A	8, 9	3	**8, 9**
AMEL	X(Y)	B	X	A	X	2	**X**
D2S1338	17, 20, (23), 25, 26	C	19, 25, 26	C	25, 26	2	**25, 26**
D21S11	28, 33.2	A	29, 30	E	28, 33.2	3	**28, 33.2**
D16S539	11, 12, 19	D	(6), 9, 11	B	9, 11	3	**9, 11**
D18S51	13, 14.2, 15	E	-	F	14.2, 15	3	**16, 17**
CSF1PO	(10), 11, 12	B	10, 11	A	11, 12	2	**11, 12**
FGA	(19, 20), 22, 23, 24	C	24	D	22, 24	1	**22, 24**

Table 36: Alleles for pipe bomb 12C

	12FE1		12FE2		12FE3		12FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	9, 11	A	9, 11	A	8, 9, 11	C	9, 11	A
D7S820	7	E	12	E	8, (9), 10	C	-	F
AMEL	X(Y)	B	Y	D	X(Y)	B	X	A
D2S1338	(17), 19, 25, 26	C	20, 23, (25, 26)	C	25, (26)	C	(24), 25	D
D21S11	(28, 29, 30), 33.2	C	-	F	29, (30)	E	-	F
D16S539	9, 11, 12	C	9, 11	A	(9, 11), 12	C	12	E
D18S51	15, 16	D	16, 17, (17.2, 18)	B	10, 14, 16, 17	C	10, 17	D
CSF1PO	10, 11, 12	C	11, 12	A	11, (13)	D	12	D
FGA	(20.2), 21, 24	D	20.2, 21, 22, 26	D	21, (22), 24	C	-	F

	12FP1		12FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	11	D	11	D	9, 11	2	**9, 11**
D7S820	8, 9	A	8	D	8	3	**8, 9**
AMEL	X	A	X	A	X	2	**X**
D2S1338	20, (25), 26	C	18, 26	D	25, 26	2	**25, 26**
D21S11	28, 30, 31	D	33.2	D	-	4	**28, 33.2**
D16S539	9, 11	A	11, 12	D	9, 11, 12	3	**9, 11**
D18S51	16, 17	A	16	D	16, 17	3	**16, 17**
CSF1PO	10, (11), 12, (13)	C	11, 12, 13	C	11, 12	3	**11, 12**
FGA	20, 22	D	22, 23	D	21, 22	3	**22, 24**

Table 37: Alleles for pipe bomb 12F

	13CE1		13CE2		13CE3		13CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	12	A	(8, 9) 11, 12	C	12	A	(11) 12	B
D7S820	8, 10	A	8	D	8, 10	A	8, 10	A
AMEL	X(Y)	B	X(Y)	B	X	A	X	A
D2S1338	19, 25 (20)	B	19, 25	A	19, 25	A	(17) 19, 25	B
D21S11	30, 30.2	A	(29, 30) 30.2	C	30, 30.2	A	(29) 30, 30.2	B
D16S539	(8, 12) 11	B	11	A	11	A	11 (13)	B
D18S51	(10, 17) 14, 16	B	14 (16, 17)	C	14, 16	A	10, 14, 16	C
CSF1PO	11, 12	A	(10, 12) 11	C	11, 12	A	(10) 11, 12	B
FGA	(20, 21, 24) 22, 25	B	21 (22, 25)	C	22, 25	A	(20, 23) 22, 25	B

	13CP1		13CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	12	A	-	F	12	1	**12**
D7S820	8, 10 (11, 12)	B	8, 10	A	8, 10	1	**8, 10**
AMEL	X	A	X	A	X	1	**X**
D2S1338	(16, 17, 22) 19, 25	B	(17), 19, 25	B	19, 25	1	**19, 25**
D21S11	(28, 29, 31.2, 32.2) 30, 30.2	B	(29), 30, 30.2	B	30, 30.2	1	**30, 30.2**
D16S539	(6, 9), 11	B	11	A	11	1	**11**
D18S51	(10, 12), 14, (15), 16, (17, 18)	B	(12), 14, 16	B	14, 16	1	**14, 16**
CSF1PO	11, 12	A	11, 12	A	11, 12	1	**11, 12**
FGA	(20), 22, 25, (26)	B	(20, 21), 22, 25	B	22, 25	1	**22, 25**

Table 38: Alleles for pipe bomb 13C

	13FE1		13FE2		13FE3		13FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	(9, 10, 12) 11	C	12	A	(9, 11) 12	B	12	A
D7S820	8, 11 (10, 12)	C	8, 10	A	8, 10	A	8, 10	A
AMEL	XY	C	X	A	X(Y)	B	X	A
D2S1338	(17, 20, 25) 19	C	19, 25 (23)	B	19, 25 (20)	B	19, 25	A
D21S11	29, 30.2 (27, 30, 31)	C	(29) 30, 30.2	B	(28, 29, 31, 31.2) 30, 30.2	B	30, 30.2	A
D16S539	(9, 15) 11	B	11 (6, 13)	B	(6, 7, 9, 12, 13, 15) 11	B	(9, 13) 11	B
D18S51	14, 16, 17	C	14, 16	A	(10, 15) 14, 16	B	14, 16	A
CSF1PO	(9, 10) 11, 12	B	11, 12	A	(10) 11, 12	B	11, 12	A
FGA	(20, 22) 21, 25	C	22, 25	A	(21), 22, 25	B	22, 25	A

	13FP1		13FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	12	A	(8), 11, 12	C	12	1	**12**
D7S820	8, 10	A	8, 10 (11)	B	8, 10	1	**8, 10**
AMEL	X(Y)	B	X(Y)	B	X	1	**X**
D2S1338	19, 25 (20, 23)	B	19, (20, 25)	C	19, 25	1	**19, 25**
D21S11	(27, 29, 32.2) 30, 30.2	B	28, 30, 30.2 (29, 31)	C	30, 30.2	1	**30, 30.2**
D16S539	(5, 6, 7, 12, 13) 11	B	(5, 6, 7, 9, 15) 11	B	11	1	**11**
D18S51	12, 14, 16	C	(12) 14, 15, 16	C	14, 16	1	**14, 18**
CSF1PO	11, 12	A	10, 11, 12	C	11, 12	1	**11, 12**
FGA	22, 25	A	21, 22, 23, 25	C	22, 25	1	**22, 25**

Table 39: Alleles for pipe bomb 13F

	14CE1		14CE2		14CE3		14CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	9, 11	D	11	D	(10), 11	D	12	D
D7S820	8, 9, (11)	C	8, 9	D	9, 11	D	8, (9), 10, 11	C
AMEL	XY	A	X	D	X	D	X(Y)	C
D2S1338	(17, 19), 20, (22)	C	19, (22), 23	C	22, 23	C	(19, 22), 27	C
D21S11	(28, 29), 31, 31.2, (32.2)	D	30	D	-	F	32.2	D
D16S539	(8), 9, 12, 13, (15)	C	9, 12	D	9, (11, 12, 13), 15	C	(8), 12, 13, (15)	B
D18S51	15, (16, 17)	C	15, 17, 18	C	15, 17	A	13, 17, 18	D
CSF1PO	(9), 10, 11, (12)	B	10, 11, 12	C	(10), 11, (12)	C	(9), 10, (11)	C
FGA	21, (23, 24)	C	(21), 23, (24)	C	(23), 24	C	21, (23, 24)	C

	14CP1		14CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	11, 12	A	(9), 11, 12	B	11, 12	2	**11, 12**
D7S820	8, 11	A	8, 10	D	8	3	**8, 11**
AMEL	XY	A	XY	A	XY	1	**XY**
D2S1338	(17, 20), 22	B	20, 22, (23, 24)	C	22	3	**22**
D21S11	32.2	D	28, 32.2	D	-	4	**30, 32.2**
D16S539	(11), 12	D	12	D	-	4	**12, 13**
D18S51	17	D	13, 15, (16, 17)	C	15, 17	2	**15. 17**
CSF1PO	(9), 10, (11, 12)	C	10, (11, 12)	C	10, 11, 12	3	**10, 11**
FGA	19, 21, 23	D	22, 23, 24	C	21, 23, 24	3	**23, 24**

Table 40: Alleles for pipe bomb 14C

	14FE1		14FE2		14FE3		14FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	11, 12	A	11, 12	A	11, 12	A	(9, 11) 12	B
D7S820	8 (10, 11)	C	5.2, 8, 11	C	(8, 13) 11	C	8, 10, 11	C
AMEL	X(Y)	C	XY	A	X(Y)	C	XY	A
D2S1338	(17, 25) 19, 22	C	22	A	(20) 22	B	22	A
D21S11	30 (32.2)	C	(28), 30, 32.2	B	29, 31	E	31.2	E
D16S539	11, 12	D	(11) 12, 13	C	12, 13	A	12, 13	A
D18S51	(10) 14, 15, 17	C	15, 17	A	15, (17, 19)	C	(10, 17) 15	C
CSF1PO	10, 11 (12)	B	10, 11	A	10, 11	A	10, (11)	C
FGA	22, 23 (24, 25, 29)	C	23, 24	A	23, 24	A	(22), 23	D

	14FP1		14FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	(9) 11, 12	B	(8, 9) 11, 12	B	11, 12	1	**11, 12**
D7S820	8, 11	A	8, 11	A	8, 11	1	**8, 11**
AMEL	XY	A	XY	A	XY	1	**XY**
D2S1338	22 (25)	B	(20) 22	B	22	1	**22**
D21S11	30, 32.2	A	(28, 30, 31) 32.2	C	30, 30.2	2	**30, 32.2**
D16S539	(9, 11) 12, 13	B	(9) 10, 12, 13	C	12, 13	1	**12, 13**
D18S51	15, 17 (19)	B	15, 17 (16)	B	15, 17	1	**15. 17**
CSF1PO	10, 11	A	10, 12 (11)	C	10, 11	1	**10, 11**
FGA	23, 24 (25)	C	(21, 22, 24) 23	C	23, 24	2	**23, 24**

Table 41: Alleles for pipe bomb 14F

	15CE1		15CE2		15CE3		15CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	10, 11	A	10, 11	A	10, 11	A	10, 11	A
D7S820	8, 9	A	8, 9	A	8, 9, (11)	B	8, (9)	C
AMEL	X(Y)	B	X(Y)	B	X(Y)	B	X(Y)	B
D2S1338	(15), 17, 20, (22)	B	17, 20	A	17, (19), 20	B	17, 20	A
D21S11	29, 35.2	A	29, 35.2	A	(27), 29, 35.2	B	29, (34.2), 35.2	B
D16S539	11, 12	A	(9), 11, 12	B	11, 12	A	11, 12	A
D18S51	16, 17	A	(10, 13), 16, 17	B	16, 17	A	16, 17	A
CSF1PO	10, 11, (12, 13)	B	10, 11, (12, 13)	B	10, 11, (12, 13)	B	(6), 10, 11, (12, 13)	B
FGA	19, (20, 21)	B	19, (19.2, 20.2)	B	19, (23)	B	19	A

	15CP1		15CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	10, (11)	C	10, 11, (13)	B	10, 11	1	**10, 11**
D7S820	8, 9	A	8, 9	A	8, 9	1	**8, 9**
AMEL	X	A	X(Y)	B	X	2	**X**
D2S1338	17, (19, 20, 23)	C	17, 20	A	17, 20	1	**17, 20**
D21S11	29	D	29, 35.2	A	29, 35.2	1	**29, 35.2**
D16S539	(9), 11, 12	B	(9), 11, 12	B	11, 12	1	**11, 12**
D18S51	(15), 16, 17	B	(15), 16, 17	B	16, 17	1	**16, 17**
CSF1PO	10, 11	A	10, 11, (12, 13)	B	10, 11	1	**10, 11**
FGA	19	A	19	A	19	1	**19**

Table 42: Alleles for pipe bomb 15C

	15FE1		15FE2		15FE3		15FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	10, 11, (12)	B	10, 11	A	(10), 11, 12	C	10, 11	A
D7S820	8, 9, (11)	B	8, 9	A	(8, 9), 10, 11	C	8, 9, (10, 13)	B
AMEL	X(Y)	B	X(Y)	B	X(Y)	B	X(Y)	B
D2S1338	17, 20	A	17, (19), 20	B	17, 19, 20, 24	C	17, 20, (23)	B
D21S11	29, 35.2	A	29, 35.2	A	28, (29), 33, (34), 35.2	C	(28), 29, (30), 35.2	B
D16S539	(6, 8, 9), 11, 12	B	11, 12	A	11, 12	A	(8), 11, 12	B
D18S51	(10), 14.2, 15	E	14.2, 15	E	13.2, (14, 15), 18	E	14.2, 15, 16	D
CSF1PO	10, 11, (12, 13)	B	10, 11, (12, 13)	B	11, 12, (13, 14)	D	10, 11, (12, 13)	B
FGA	19, 24	C	19	A	(17.2, 18.2, 19), 23, 25	C	19	A

	15FP1		15FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	10, 11	A	10, 11, (12)	B	10, 11	1	**10, 11**
D7S820	8, 9, (10, 11, 12)	B	8, 9	A	8, 9	1	**8, 9**
AMEL	X(Y)	B	X(Y)	B	X	2	**X**
D2S1338	17, 20	A	17, 20	A	17, 20	1	**17, 20**
D21S11	(28), 29, (31, 31.2), 35.2	C	29, 35.2	A	29, 35.2	1	**29, 35.2**
D16S539	(9), 11, 12	B	(11), 12	C	11, 12	2	**11, 12**
D18S51	(14), 14.2, 15, (26)	E	14, 14.2, 15	E	14.2, 15	2	**16, 17**
CSF1PO	10, 11, (12, 13)	B	10, 11, (12, 13)	B	10, 11	2	**10, 11**
FGA	12.2, (18.2), 19	C	19, 19.2	C	19	2	**19**

Table 43: Alleles for pipe bomb 15F

	16CE1		16CE2		16CE3		16CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	12	D	8, 12	A	8, 11, (12)	C	11, (12)	D
D7S820	8, 9	D	9	D	(8), 9, 11, (13)	D	10, 11, (13)	D
AMEL	-	F	X	A	X(Y)	B	XY	C
D2S1338	25	D	15, 19, 20	D	19, 20, 23, (24), 25	C	19, 20	D
D21S11	-	F	-	F	29, 31	D	27, 28	E
D16S539	12	D	9, 12	A	9, 12, 14, 15	C	9, 11, 12	C
D18S51	13	D	13	D	13, 14.2, 18	D	13, 13.2, (14), 14.2	C
CSF1PO	11	A	7, 11	C	11, (12), 13	C	10, 11, 13, 14	C
FGA	-	F	19, (23), 24	D	19.2, 21, (22), 23, 25	E	(21), 22, 23, 25, 26	D

	16CP1		16CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	8, 11, 12	C	8, 11, 12	C	8, 11, 12	3	**8, 12**
D7S820	9, 10, 11	C	8, 9, 10	C	-	4	**9, 10**
AMEL	X(Y)	B	XY	C	XY	3	**X**
D2S1338	17, 19, 20, 25	C	17, 19, 23, 25	C	19, 20	2	**19, 25**
D21S11	28, (29), 31, (31.2, 32)	C	24.2, 28, 29, 31, 31.2	C	-	4	**29, 31.2**
D16S539	9, (10), 12, 15, (19)	C	9, 11, 12	C	9, 12	3	**9, 12**
D18S51	(13, 13.2), 14, 14.2	C	10, 13, 13.2, 15, 16	D	-	4	**13, 14**
CSF1PO	10, 11, (12, 14)	C	(10), 11, 12	C	11, 12	3	**11**
FGA	(20), 21, (22), 23, (24), 26	C	24, 26	A	-	4	**24, 26**

Table 44: Alleles for pipe bomb 16C

	16FE1		16FE2		16FE3		16FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	(8), 11, (12)	C	(8, 9, 12), 11, (13)	C	(8, 9, 10), 11, (12, 13)	C	(8, 9), 11	D
D7S820	8, 9, 10, 12, 15	C	7, (8), 9, 10, (11), 12	C	(6, 7, 8, 9, 10), 11, (12)	C	(6, 7, 8), 9, 10, (15)	B
AMEL	X	A	X(Y)	B	XY	C	X	A
D2S1338	(17), 19, (20, 21, 23, 24, 25	C	(16, 17, 18), 19, 20, (21, 22, 23, 24, 25)	C	(17), 19, 20, 21, (22, 23, 24, 25, 26)	C	(16, 17, 18), 19, 20, (21, 22, 23, 24, 25, 26, 27, 28)	C
D21S11	28, 28.2, 29, 20, 31, 31.2, 32, 32.2, 34.2, 36, 38	C	27, 28, 29, 29.2, 30, 30.2, 31, 31.2, 32.2	C	(27, 28), 29, 30, 30.2, 31, 31.2, 34	C	27.2, 28, 28.2, 29.2, 30, 30.2, 31, (32)	E
D16S539	9, 10	D	(5, 8), 9, (10, 11)	D	7, 9, 11	D	-	F
D18S51	13, 15, 16, 17	D	9, 10	E	(7, 8), 9, 10,	E	-	F
CSF1PO	6, 10, 11, 12, 13, 14, 15	C	(10), 11, 12, (13)	C	(9, 10), 11, 12, (13)	C	(5, 6, 7, 8), 9, 10, 11, (12, 13, 14, 15, 16)	C
FGA	(18, 19, 20), 21, (22, 23), 24, 25, (26, 27, 28)	C	17, 20, 22, 23, 24, 25, 26	C	(20), 21, 22, 23, (24, 25, 26)	C	24.2, 25.2	E

Table 45: Alleles for pipe bomb 16F

	16FP1		16FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	11	E	11, 12, (15)	D	11	3	**8, 12**
D7S820	9, 10, (12, 13)	B	9, 10, 11, 12, (15)	C	-	4	**9, 10**
AMEL	X(Y)	B	X(Y)	B	X	2	**X**
D2S1338	15, 19, 25, 29	C	(15, 16), 19, 20, 21, 22, 23, 24, 25, 26, 27	C	-	4	**19, 25**
D21S11	24.2, 29, 29.2, 31, 33	E	26, 28, 29, 29.2, 30, 31.2	C	-	4	**29, 31.2**
D16S539	9, 10	D	8, 9, 11, 12	C	9, 11	3	**9, 12**
D18S51	(9, 10), 13, 13.2, 14	C	12, 13, 13.2	D	-	4	**13, 14**
CSF1PO	10, 11, (13, 14)	C	(10), 11, 12, (13, 14)	C	10, 11, 12	3	**11**
FGA	21, (22), 23, (23.2, 24, 25)	D	(20, 21, (22), 23, (24, 25), 26	C	-	4	**24, 26**

Table 46: Alleles for pipe bomb 16F continued

	17CE1		17CE2		17CE3		17CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	(6, 7, 8, 9), 10, 11, 12, 13, 14, 15	C	-	F	11	A	-	F
D7S820	11, (12, 13, 14, 15)	D	-	F	-	F	9, 11, 16	D
AMEL	XY	C	-	F	XY	C	-	F
D2S1338	(16, 17, 18), 19, 20, 21, (22), 23, 24, (25)	C	-	F	17, 19, (24, 25)	B	17, 18, 19, 23, 26	C
D21S11	28, 28.2, 29, 30, 30.2, 31, 31.2, 32, 32.2, 33, 33.2, 34.2, 35, 35.2, 37, 38	C	-	F	28, 33	D	28, 32.2	A
D16S539	6, 7, 8, 9, 10, 11, 12, 15	C	-	F	9, 11, 12, 12.2, 13, 14	C	11	D
D18S51	9, 9.2, 10, 10.2, 11, 12, 13, 14, 14.2, 15, 15.2, 16, 17, 18.2, 19, 19.2, 20, 21, 21.2	C	-	F	15, 16, 17	D	15, 18.2, 21.2, 23	D
CSF1PO	(6, 8, 9), 10, 11, 12	D	11, 12	D	(11), 12, 13	C	10, 12, 14	E
FGA	20, 21, 22, 23, 24, 25, 26	C	-	F	20, 21, 22, 25	C	-	F

Table 47: Alleles for pipe bomb 17C

	17CP1		17CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	9, 11	C	9, 10, 11	C	--	4	**11**
D7S820	9, 10, 13	E	8, 9	D	-	4	**8, 11**
AMEL	X	A	X	A	-	4	**X**
D2S1338	(16, 17), 19, 20	C	17, 18, 19	C	17, 19	3	**17, 19**
D21S11	30.2	E	28, 32.2	A	-	4	**28, 30.2**
D16S539	11, 12	A	11, 12	A	11, 12	3	**11, 12**
D18S51	10, 10.2, 15, 18	D	8, 10, 13, 15, 16	C	15	3	**13, 15**
CSF1PO	10, 12, 15, 18	E	10, 12, 13	D	10, 12	3	**11, 13**
FGA	(17, 18.2), 21, 22	C	22	A	-	4	**22**

Table 48: Alleles for pipe bomb 17C continued

	17FE1		17FE2		17FE3		17FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	8, (9), 10, (11)	C	11	A	11	A	11, (12)	B
D7S820	8, 9, 12	D	11	D	8, 9, 11	C	8, 9	D
AMEL	X	A	X	A	X(Y)	C	Y	E
D2S1338	17, 24	D	17, 19, 22	C	(16), 17, 19	B	(15), 17	D
D21S11	29	D	-	F	28, 29, 30, 30.2	C	28, 30	D
D16S539	10, 12	D	11, 12	A	(9, 11), 12	D	9, 12	D
D18S51	13, 15	A	13	D	16	E	10, 13, 15	C
CSF1PO	10, 11, 12, 13	C	13	D	11, 13	A	11, 13	A
FGA	20, 22	C	16.2, 19, 20	C	22	E	17, 20, 21, 22, 25	C

	17FP1		17FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	-	F	10	E	11	3	**11**
D7S820	8	D	8, 11, (13)	B	8, 9, 11	3	**8, 11**
AMEL	X(Y)	B	X	A	X	3	**X**
D2S1338	17, (18, 19, 23)	C	17, (19)	C	17, 19	3	**17, 19**
D21S11	28, (30, 30.2)	C	20, 30, 30.2	C	28, 30, 30.2	3	**28, 30.2**
D16S539	9, 10, 11	D	(5, 9), 11, 12, (13)	D	11, 12	3	**11, 12**
D18S51	13, 14, 16, 17	D	10, 14, 18	E	-	4	**13, 15**
CSF1PO	(10), 11, 13	B	10, 11, 12	D	11, 13	3	**11, 13**
FGA	(21), 22, (23, 25)	B	(18.2), 21, 22, (24, 26.2)	C	21, 22	3	**22**

Table 49: Alleles for pipe bomb 17F

	18CE1		18CE2		18CE3		18CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	(8), 12	B	(8), 12, (13)	B	(11), 12	B	(11), 12	B
D7S820	7, 11	A	7, (11)	B	7, (9, 11)	C	7, 10, 11	C
AMEL	X(Y)	B	X(Y)	B	X(Y)	B	X(Y)	B
D2S1338	19, 20, (23)	B	(17), 19, 20	B	19, 20, (26)	B	19, 20	A
D21S11	30, (31), 32.2	B	30, 33.2	D	27, 29, 30, 32.2	D	28, 29, 30, 31, 33.2	C
D16S539	9, (10), 12	B	9, 12	A	(8), 9, 12, (15)	B	9, 12, (15)	B
D18S51	13, 14	D	13, 14	D	(9), 13, (14), 16	D	13, 14, (14.2)	D
CSF1PO	11, 12, (14)	B	11, 12, (14)	B	11, 12, (14)	B	11, 12	A
FGA	(22), 23, 25, (28)	B	(20, 21, 22), 23, 25	B	21, (21.2), 23, 25	C	21, 22, 23, 25	C

	18CP1		18CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	(11), 12	B	(8, 11), 12	B	12	1	**12**
D7S820	7, (9, 10), 11, (13)	B	7, (8), 11, (13)	B	7, 11	1	**7, 11**
AMEL	X(Y)	B	X(Y)	B	X	2	**X**
D2S1338	(17), 19, 20, 23	C	(17), 19, 20, (22)	B	19, 20	1	**19, 20**
D21S11	30, (31), 33.2	B	(28, 29), 30, 33.2	B	30, 33.2	1	**30, 33.2**
D16S539	9, 12, (15)	B	9, (12)	C	9, 12	1	**9, 12**
D18S51	13, 14, (14.2)	D	13, 14, (14.2	D	13, 14	1	**13, 15**
CSF1PO	(10), 11, 12, (14)	B	(10), 11, 12, (13, 14)	B	11, 12	1	**11, 12**
FGA	(21, 22), 23, 25	B	(21, 22), 23, 25	B	23, 25	1	**23, 25**

Table 50: Alleles for pipe bomb 18C

	18FE1		18FE2		18FE3		18FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	12	A	11, 12	C	12	A	8, 12	C
D7S820	(7, 9), 11	C	8, (9, 11, 14)	D	(7), 11	C	7, (9), 11	B
AMEL	XY	C	X(Y)	B	X(Y)	B	X(Y)	B
D2S1338	19, 20	A	19, (20, 25)	C	19, 20	A	19, 20	A
D21S11	29	E	(30, 30.2), 33.2	C	(28), 30, (32.2), 33.2	B	30, 33.2	A
D16S539	7, 9, 12	C	8, 12	D	9, 12	A	9, 12	A
D18S51	14, 14.2	E	10, 13, 14	D	13, (13.2, 14, 14.2, 20)	D	13, 15, (16)	B
CSF1PO	11, 12, (14)	B	11, 12	A	11, 12, (14)	B	(9), 11, 12, (14)	B
FGA	20, 22	E	20, 23, 25	C	(22), 23, (25, 26)	C	(22), 23, (25)	C

	18FP1		18FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	12	A	12	A	12	1	**12**
D7S820	7, 8, 11	C	7, (9), 11	B	7, 11	1	**7, 11**
AMEL	X(Y)	B	X(Y)	B	X	2	**X**
D2S1338	(17), 19, (20)	C	19, 20, (22, 26)	B	19, 20	1	**19, 20**
D21S11	30, 31.2	D	30, 33.2	A	30, 33.2	2	**30, 33.2**
D16S539	9, (10), 12	B	9, 12	A	9, 12	1	**9, 12**
D18S51	13(14, 15)	C	13, 14	D	13, 14	1	**13, 15**
CSF1PO	(11), 12, (14)	C	11, 12, (14)	B	11, 12	2	**11, 12**
FGA	(20), 23, 25	B	23, 25	A	23, 25	1	**23, 25**

Table 51: Alleles for pipe bomb 18F

	19CE1		19CE2		19CE3		19CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	8, 9, 11	D	11, 12	A	(10), 11, (12)	C	(8, 10), 11, (12)	C
D7S820	8, 9, 10, 12, 13	C	10, (11), 12	B	10, 11, (12)	C	8, 10, (11), 12	C
AMEL	X(Y)	B	X(Y)	B	X(Y)	B	X(Y)	B
D2S1338	18	D	16, 18, (19, 20), 23	C	18, 19, 20, 23	C	(17, (18, 19, 20), 23, (25)	C
D21S11	24, 30.2, 31.2	D	(30.2, 32), 34.2	C	28, (30.2), 31	C	(28, 29, 30, 30.2), 31, 34.2	C
D16S539	8, 12	A	8, 12	A	8, 9, 10, 11, 12, 15	C	8, 9, 10, (11), 12, (15)	C
D18S51	13, (15), 16	C	13, 15	A	(13), 15, (16, 17)	C	13, 15, 16	C
CSF1PO	(11), 12	B	12, (13, 14)	B	(9, 10, 11), 12, (14)	B	(9, 11), 12, (13, 14)	E
FGA	19, (20, 21), 22, (24)	B	17.2, 19, (21), 22, (23)	C	(17.2, 19.2), 21, 22, 23	C	(19, 19.2, 21), 22, 23	C

Table 52: Alleles for pipe bomb 19C

	19CP1		19CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	(8), 11, 12	B	11, (12)	C	11, 12	3	**11, 12**
D7S820	(8), 10, 11, 12	C	(8), 10, 11, (12)	C	10, 11, 12	3	**10, 12**
AMEL	XY	C	XY	C	X	3	**XX**
D2S1338	16, 18, 19, 23	C	(16), 18, 19, (20, 23, 25)	C	-	4	**18, 23**
D21S11	(28, 29), 30.2, (34.2)	C	28, 31	E	-	4	**30.2, 34.2**
D16S539	8, 9, 12, 15	C	(8), 9, (11), 12, 15	C	8, 12	3	**8, 12**
D18S51	13, (14), 15, 16	C	(13), 15, 16, (20)	C	13, 15	3	**13, 15**
CSF1PO	8	E	10, (11), 12	C	12	3	**12**
FGA	19, (19.2), 21, 22, (23)	C	19, 21, 22, 26	C	-	4	**19, 22**

Table 53: Alleles for pipe bomb 19C continued

	19FE1		19FE2		19FE3		19FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	(8, 9), 11, 12	B	(8), 11, 12	B	11, 12	A	(8)11, 12	B
D7S820	10, (11), 12	B	10, 12	A	10, (11), 12	B	10, 12, (13)	B
AMEL	X(Y)	B	X(Y)	B	X(Y)	B	X	A
D2S1338	18, (19), 20, 23, (24, 25)	C	(16), 18, (19), 23(24)	B	(16, 17), 18, (19, 20), 23	B	18, (19, 20), 23, (24)	B
D21S11	(28, 29, 30), 30.2, 34.2	B	(29, 30), 30.2, 34.2	B	(29), 30.2, (31.2), 34.2	B	(28, 29, 30), 30.2, (31, 31.2), 34.2	B
D16S539	8, (9, 10), 12	B	8, 12	A	8, (11), 12	B	12	D
D18S51	(11), 12	E	13, 15	A	13, 15	A	13, 15	A
CSF1PO	(11), 12	B	12, (13, 14)	B	12, (13, 14)	B	6, (11), 12, (13, 14)	C
FGA	19, (20), 21,22, (23, 24)	C	19, (21), 22, (23)	B	19, (21), 22, (23)	B	19, (21), 22, (23)	B

	19FP1		19FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	8, (11, 12)	B	(8), 11, 12	B	11, 12	1	**11, 12**
D7S820	8, (10), 12, (13)	B	10, 12	A	10, 12	1	**10, 12**
AMEL	XY	C	X	A	X	2	**XX**
D2S1338	(18), 20, 23, 24, 26	C	(16), 18, (19), 23	B	18, 23	1	**18, 23**
D21S11	29, 30, (33.2)	D	30.2, 34.2	A	30.2, 24.2	1	**30.2, 34.2**
D16S539	9, (10), 12	D	8, 12	A	8, 12	1	**8, 12**
D18S51	14, 15, (16),	D	10, 13, 15, (16)	C	13, 15	1	**13, 15**
CSF1PO	10, 11, (12)	C	12, (13, 14)	B	12	1	**12**
FGA	19, (20, 22), 25	C	19, (21), 22, (23, 24)	B	19, 22	2	**19, 22**

Table 54: Alleles for pipe bomb 19F

	20CE1		20CE2		20CE3		20CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	(11), 12, (13), 14	B	9, 10, 11, 12, 14	C	11, 12, 14	C	11, 12, (14)	C
D7S820	9, 11, 12	C	(10), 11, 12	B	8, 10, 11, 12	C	(10), 11, (12)	C
AMEL	X	A	X	A	X	A	X	A
D2S1338	17, (21, 25)	C	17, (19, 20, 24), 25	B	17, 19, (20, 24), 25	C	17, (24), 25, (26)	B
D21S11	(29), 32.2	C	29, 32.2	A	28, 29, (30), 32.2	C	(28), 29, (30, 31.2), 32.2	B
D16S539	11, (12)	C	(9), 11, 12	B	(9), 11, (12)	C	11, 12	A
D18S51	(13), 13.2, (14.2)	E	13.2, (14, 16, 17, 18)	C	(12), 13.2, (14, 14.2)	C	10, 13.2, 17, (26)	E
CSF1PO	9, (12, 14)	C	9, 10, (11), 12, 13, 14	C	(8), 9, 12, (14)	B	9, (10, 11), 12	B
FGA	21, (22), 23, 25	C	(18.2), 21, 25	C	(20, 21), 25	B	(21, 22), 23, 25	C

	20CP1		20CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	(11), 12	D	(10), 11	E	12, 14	3	**12, 14**
D7S820	11	D	10, 11	D	11, 12	3	**11, 12**
AMEL	X(Y)	B	X	A	X	1	**XX**
D2S1338	17, 20, 23	D	(17), 20, 24, 25	C	17, 20, 25	3	**17, 25**
D21S11	32.2	D	(28, 30), 31	E	29, 32.2	2	**29, 32.2**
D16S539	12, (13)	D	9, 11, 15	D	11, 12	2	**11, 12**
D18S51	13.2, (14)	C	13.2, (14), 14.2, (17)	C	13.2	2	**14**
CSF1PO	9, (11), 12, (14)	B	9, 10, (11), 12, 14	C	9, 12	3	**9, 12**
FGA	25	A	21, 22, 26	E	21, 25	3	**25**

Table 55: Alleles for pipe bomb 20C

	20FE1		20FE2		20FE3		20FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	-	F	-	F	12	F	11, 14, 15	D
D7S820	11	D	-	F	-	F	11	D
AMEL	X	A	X	A	-	A	XY	C
D2S1338	19, 25	D	20, 24, 25	D	17, (19, 25)	D	17, 19, 24, 25	C
D21S11	-	F	30	E	29, 31	E	29	D
D16S539	12	D	9, 11, 12, 15	C	9, 12	C	10	E
D18S51	7, 14, 16, 19	C	14, 15, 26	C	13, 15, 19	C	10, (13, 14)	C
CSF1PO	(11), 12	D	9	D	11, 12	D	11, 12	D
FGA	21, 26, 30	E	21, 22	E	-	E	22	E

	20FP1		20FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	-	F	11	E	-	4	**12, 14**
D7S820	11	D	10, 11	D	11	3	**11, 12**
AMEL	-	F	X	A	X	2	**XX**
D2S1338	23	E	(16, 17), 18, 19, (27, 28)	D	-	4	**17, 25**
D21S11	30.2	E	28, 31.2	E	-	4	**29, 32.2**
D16S539	11, 12	A	8, 9, 11	D	-	4	**11, 12**
D18S51	-	F	(13), 14, (15)	C	-	4	**14**
CSF1PO	12	D	10, 12, 13	D	11, 12	3	**9, 12**
FGA	25	A	21, 22, 23	E	-	4	**25**

Table 56: Alleles for pipe bomb 20F

	21CE1		21CE2		21CE3		21CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	(8, 9), 11	B	(9), 11	B	(9), 11	B	11, (12)	B
D7S820	7, 8, (10)	B	7, (8, 10)	C	7, 8	A	7, (8, 9)	C
AMEL	X(Y)	B	X(Y)	B	X(Y)	B	X	A
D2S1338	(19, 21), 23, 24	B	(17, 22), 23, 24	B	(19), 23, (24)	C	(19), 23, 24	B
D21S11	(28, 29), 30.2, 31	D	29, 30.2, 31.2	C	(29, 30), 32.2, (31.2)	C	(27, 29), 30.2, 31.2	B
D16S539	9, 11, (14, 15)	B	9, 11	A	(9, 10), 11, 12	C	9, 11	A
D18S51	(12), 14, (15)	C	(10), 12, 14, 17	C	12, 14, 19	C	12, 14, 17	C
CSF1PO	9, (10), 11, (12, 13)	B	11, (12, 13)	D	(9), 11, (13)	C	9, (10, 11, 13)	C
FGA	17.2, 22, 23, 25	C	(16.2), 17.2, 22, 24, 25	C	22, (23, 24, 25)	C	21, 22, 25	C

	21CP1		21CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	(9), 11	B	(8, 9), 11, (12, 13)	B	11	2	**11**
D7S820	7, 8, 10	C	7, 8, 10, (12)	C	7, 8	1	**7, 8**
AMEL	X(Y)	B	X(Y)	B	X	2	**XX**
D2S1338	(22), 23, (24)	C	(17, 18, 19, 20, 22), 23, (24)	C	23, 24	3	**23, 24**
D21S11	-	F	(28, 30.2), 31.2	C	29, 30.2	1	**30.2 31.2**
D16S539	9, 11	A	(8), 9, (10), 11	B	9, 11	2	**9, 11**
D18S51	12, 13, 14	C	12, 14	A	12, 14	2	**12, 14**
CSF1PO	9, 11, (13)	B	9, 11, (12, 13)	B	9, 11	2	**9, 11**
FGA	22, 23, 25	C	(21), 22, (23), 25	B	22, 25	2	**22, 25**

Table 57: Alleles for pipe bomb 21C

	21FE1		21FE2		21FE3		21FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	9, 11, 13	C	11	A	11	A	(8), 11	B
D7S820	7, 8, (10)	B	7, 8, (10)	B	(6), 7, 8, 10, 13	C	7, (8)	B
AMEL	X(Y)	B	X(Y)	B	X(Y)	B	X(Y)	B
D2S1338	23, 24	A	(19, 20), 23, 24	B	(18, 19, 20), 23, 24	B	23, 24	A
D21S11	30.2, (31, 31.2)	C	29, 30.2, 31.2	C	(30), 30.2, (31), 31.2, (32.2)	B	30.2, 31.2	A
D16S539	9, 11	A	9, 11	A	9, 11	A	8, 9, 11	C
D18S51	12, (13), 14, (15, 16, 18)	B	10, 12, 14	C	12, (15, 16)	D	(10), 12, 14, (19)	B
CSF1PO	9, 11, (12, 13)	B	9, (11, 12, 13)	C	9, (10), 11, 12, (13)	C	9, 11, (12, 13)	B
FGA	(21), 22, (23, 25)	C	(21), 22, (23), 25	B	22, (23, 24, 25)	C	19, 20, 22, 25	C

	21FP1		21FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	11	A	11, (12)	B	11	2	**11**
D7S820	(7), 8, (10, 11)	C	7, 8	A	7, 8	1	**7, 8**
AMEL	X(Y)	B	X(Y)	B	X	2	**XX**
D2S1338	(17, 20), 23, (24, 25)	C	(17, 20), 23, 24	B	23, 24	2	**23, 24**
D21S11	(27, 28, 30.2, 31), 31.2	C	(28), 30.2, 31.2, (32.2, 34.2)	B	30.2, 31.2	2	**30.2 31.2**
D16S539	(8), 9, 11	B	9, 11	A	9, 11	1	**9, 11**
D18S51	12, (13), 14, (16)	B	12, 14	A	12, 14	2	**12, 14**
CSF1PO	9, (10), 11, (12, 13)	B	9, 11, (12, 13)	B	9, 11	2	**9, 11**
FGA	(21), 22, (23), 25	B	(20), 22, 25	B	22, 25	2	**22, 25**

Table 58: Alleles for pipe bomb 21F

	22CE1		22CE2		22CE3		22CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	11	D	11, 12	A	-	F	11, 12	A
D7S820	-	F	-	F	11	D	11, 12	A
AMEL	X	D	XY	A	-	F	X(Y)	C
D2S1338	23	A	23	A	(18), 20, 23	C	19, 23	C
D21S11	-	F	-	F	28	E	28, (30, 32.2)	D
D16S539	11, 13	A	-	F	9, 15	E	9, (13, 15)	D
D18S51	-	F	13, 17	A	13, 16	D	13, 16, 18.2	D
CSF1PO	(10, 11), 12	B	12	A	(10), 12	B	7, 12	C
FGA	22	A	22	A	(20), 21, 22	C	21	E

	22CP1		22CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	-	F	11	D	11, 12	3	**11, 12**
D7S820	11	D	10, (11)	D	11	3	**11, 12**
AMEL	X	D	X	D	X	2	**XY**
D2S1338	19, (22), 23	C	(19), 23	B	19, 23	3	**23**
D21S11	28, 29	E	31	E	-	4	**30, 32.2**
D16S539	9, 10	E	(9, 14), 15	E	9, 15	3	**11, 13**
D18S51	17	D	16, 17	D	-	4	**13, 17**
CSF1PO	12	A	(10), 12	B	12	3	**12**
FGA	-	F	21, 23	E	-	4	**22**

Table 59: Alleles for pipe bomb 22C

	22FE1		22FE2		22FE3		22FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	(8, 9), 11, 12	B	11	D	(9), 11, 12	B	(8, 9), 11, (12)	C
D7S820	(8, 10), 11, 12	B	12	D	11, 12	A	(8), 9, (11)	D
AMEL	X(Y)	C	-	F	Y	D	XY	A
D2S1338	(17, 19, 20), 23	B	20, (23), 25	C	19, 23	C	17, 19, 23	C
D21S11	(28), 30, (31), 32.2	B	30	D	-	F	29	E
D16S539	(9), 11, 13	B	9, 0, 11, 13	C	11, 13	A	8, (9, 11), 14	D
D18S51	13, (15, 16), 17	B	10, 13, 17	C	13, 14	D	10, (13), 15, 16	D
CSF1PO	(6, 10), 12, (13, 14)	B	12	A	12	A	10, (11), 12, (13)	C
FGA	(21), 22, (23, 24)	B	-	F	22	A	(20), 21, 22, (23)	C

	22FP1		22FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	(8, 9), 11, (12)	C	9	E	11, 12	3	**11, 12**
D7S820	(10), 11, (12)	C	12	A	11, 12	2	**11, 12**
AMEL	XY	A	XY	A	XY	1	**XY**
D2S1338	19, 23	C	20, (22), 23	C	19, 23	3	**23**
D21S11	31	E	28	E	-	4	**30, 32.2**
D16S539	(5), 9, 11, 15	C	9, 11, 12, 13, 15	C	11, 13	3	**11, 13**
D18S51	13, 15, 16, 17	C	13, 14, 15, 16, 17	C	-	4	**13, 17**
CSF1PO	10, (11), 12	C	10, 12	C	10, 12	3	**12**
FGA	(21), 22, (23)	B	22, (23)	B	21, 22	3	**22**

Table 60: Alleles for pipe bomb 22F

	23CE1		23CE2		23CE3		23CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	(9), 11	E	11	E	10	D	10, (12, 14)	C
D7S820	(8, 10), 11	B	11	A	(8), 11	B	11	A
AMEL	(X)Y	C	X	D	XY	A	XY	A
D2S1338	20, (24)	C	-	F	24	A	19, (20), 24	E
D21S11	28, (30, 31)	D	29	D	29	D	29, 31	A
D16S539	(8), 9, (11), 15	C	11	E	9, (11)	D	9	A
D18S51	15, 16	E	-	F	10, 12, 16	D	12, 13, 16, 20	C
CSF1PO	11, 12, 13	D	10	D	10, (11, 12)	C	10, 11, 12	C
FGA	21, (22), 23	E	20	E	19.2, (21, 22), 23, 24, 26	C	(21), 24	B

	23CP1		23CP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	10, 11, 12	C	(9), 10, 11, 12	C	10, 11, 12	3	**10, 12**
D7S820	11	A	(8, 9, 10), 11	B	11	2	**11**
AMEL	XY	A	XY	A	XY	1	**XY**
D2S1338	19, (20), 24	C	19, 24	C	19, 24	2	**24**
D21S11	28, 29, (31)	C	(28), 29, (31, 31.2)	C	29, 31	3	**29, 31**
D16S539	9	A	(8), 9, (11), 15	C	9	3	**9**
D18S51	12, 13, (14, 15, 16)	B	(10), 12, 13, 17	C	12, 13	3	**12, 13**
CSF1PO	10, 12, (13, 14)	B	10, (11), 12, (13, 14)	B	10, 12	2	**10, 12**
FGA	21, (22), 23, 24	C	(20), 21, (22, 23), 24	C	21, 24	3	**24**

Table 61: Alleles for pipe bomb 23C

	23FE1		23FE2		23FE3		23FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	10, 11, (12, 14)	C	(9), 11, 12	D	10, 12	A	9, 10, 12	C
D7S820	-	F	11	A	11	A	11, (12)	B
AMEL	-	F	X	D	XY	A	XY	A
D2S1338	17, 20, 24	C	24	A	17, (19, 20, 23), 24	C	(19), 24	B
D21S11	29	D	29	D	29, 31	A	29, 31	A
D16S539	-	F	(6), 9	B	(8), 9, (11)	B	(8), 9	B
D18S51	-	F	12, (13)	C	12, 13	A	12, 13	A
CSF1PO	10, 12	A	10, 12, (14)	B	10, 12, (14)	B	10, (11, 12, 14)	C
FGA	-	F	24	A	(22), 24	B	(22), 24	B

	23FP1		23FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	10, 12	A	10, (11), 12	B	10, 12	2	**10, 12**
D7S820	11, 12	C	11	A	11	1	**11**
AMEL	X(Y)	C	XY	A	XY	2	**XY**
D2S1338	19, 24	B	(19, 20)	C	24	2	**24**
D21S11	(24.2), 29, 31	B	(28), 29, 31, (32.2, 33.2)	B	29, 31	2	**29, 31**
D16S539	9	A	9	A	9	2	**9**
D18S51	12, 13	A	12, 13	A	12, 13	1	**12, 13**
CSF1PO	10, (11), 12, (14)	B	10, (11), 12, (13, 14)	B	10, 12	2	**10, 12**
FGA	(22), 24, (25)	B	(21, 22), 24, (26)	B	24	3	**24**

Table 62: Alleles for pipe bomb 23F

	24CE1		24CE2		24CE3		24CE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	11, (12), 13	B	(10), 11, (13)	C	11	D	11, (13)	C
D7S820	(8, 9), 11, (12)	C	(9, 10), 11, (12)	D	9, 10	E	9, 11	E
AMEL	XY	C	X(Y)	B	X	A	X(Y)	B
D2S1338	(15, 17, 18), 19, 20, (22, 23, 24, 25, 28)	C	(17, 18, 19), 20	D	20, 24	E	19, (20, 24, 25)	C
D21S11	(25), 28, (29, 30), 31	C	28, (29, 30, 31)	C	31	E	29	A
D16S539	(6), 9, (11), 15	D	9, 11	D	9, 11, 15	D	11, 15	D
D18S51	(12, 13), 15, (15.2), 16	E	(12, 13), 15, 16	E	(12), 14, 15, (16)	D	12, 13, 14, 15, (16)	D
CSF1PO	10, (11), 12, (14)	C	10, 11, 12, (13, 14)	C	10, 11, 13	C	10, 11, 12, 13	C
FGA	21, (22), 23, (24, 25)	D	(19), 21, 22, 23	D	21, 22.2	A	(21, 22), 22.2, 23	C

	24CP1		24CP2				
	Alleles	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	11	D	11	D	11	2	**11, 13**
D7S820	(9), 10, 11	E	10, 11	E	9, 11	3	**9, 10**
AMEL	XY	C	XY	C	XY	2	**XX**
D2S1338	(17), 19, 20, (22, 23, 24, 25)	C	(17), 19, 20, (22)	E	-	4	**24, 25**
D21S11	28, (29), 31	C	(25.2), 28, (29, 30), 31	C	28, 31	2	**29**
D16S539	9, (11), 15	D	9, (10), 15	E	9, 15	3	**11, 13**
D18S51	13, 14, 14.2	D	(12), 14, 14.2	D	-	4	**14, 19**
CSF1PO	10, 11, 12, 13	C	10, 11, 12, 13	C	10, 12	2	**10, 11**
FGA	21, (22), 23, (24)	D	21, (22), 23	D	21, 23	2	**21, 22.2**

Table 63: Alleles for pipe bomb 24C

	24FE1		24FE2		24FE3		24FE4	
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**
D13S317	11	D	(9), 11	D	(12), 13	D	11	D
D7S820	(10), 11	D	9, 11, 12	D	-	F	8, 9, 10	C
AMEL	(X)Y	B	X(Y)	B	-	F	X	A
D2S1338	19, 20, (24)	D	19, (20, 23, 24, 25)	C	-	F	17, (19), 24	D
D21S11	28, (30, 31)	E	28, (30), 31, (31.2)	E	-	F	29	D
D16S539	(6), 9, 15	E	9, 15	E	-	F	11, (13)	C
D18S51	(14), 15, 16	D	15, 16	E	-	F	14, 20	D
CSF1PO	10, (11, 12)	C	10, (11, 12, 13)	C	11	D	11	D
FGA	21, (22), 23, (25)	D	(21), 23	D	-	F	20, 21	D

	24FP1		24FP2				
Locus	**Alleles**	**Loc Cat**	**Alleles**	**Loc Cat**	**Con**	**Score**	**Ind**
D13S317	(9), 11	D	11	D	11	2	**11, 13**
D7S820	9, 10, 11	C	8, 11	E	-	4	**9, 10**
AMEL	XY	C	-	F	XY	2	**XX**
D2S1338	19, 20, (22, 24, 25)	C	19, 24	D	-	4	**24, 25**
D21S11	28, (29), 31, (31.2)	C	(29), 31.2	C	-	4	**29**
D16S539	9, 11	D	-	F	-	4	**11, 13**
D18S51	12, 16	E	10.17	E	15, 16	3	**14, 19**
CSF1PO	9, 12, 13	E	12	E	10, 11, 12	3	**10, 11**
FGA	21, 23	D	21	D	21, 23	3	**21, 22.2**

Table 64: Alleles for pipe bomb 24F

Locus	DRBE1	DRBE2	DRBE3	DRBE4	DRBP1	DRBP2
D13S317	9, 11	11, 12, 13	-	-	11,13	-
D7S820	8, 9, 11	10, 11, 12	-	-	10, 11	-
AMEL	XY	XY	-	-	XY	-
D2S1338	(17, 18), 19, (25)	(17, 18), 19, 25	-	-	19, 28	-
D21S11	28, 29	28, 31	-	-	28, 30, 31	-
D16S539	8, 9, 11, 15	9, 11, 15	8	-	9, 15	-
D18S51	10, 15, 17	10, 15, 18	-	-	15	-
CSF1PO	(10, 11), 12	(11), 12	-	-	10, (11), 12	12
FGA	18.2, 20, 23	20, 21, 23	-	-	21, 22, 23	21

Table 65: Alleles for pipe bomb reagent blank

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