DNA INFORMATION SHEET

PREAMBLE

Deoxyribonucleic acid (DNA) contains the genetic instructions used in the development and functioning of living organisms, including humans. DNA is often referred to as a blueprint or a recipe since it contains the instructions needed to construct other components of cells, such as proteins.

The same DNA is found in all nucleated cells throughout the body. Half of this DNA is contributed by one's father while the other half is contributed by one's mother. Everyone, with the exception of identical twins, has different DNA and these differences are the basis for forensic DNA analyses.

This information sheet pertains to nuclear DNA only. Please review the DNA Glossary (available at www.wyndhamforensic.ca) for a description of commonly encountered terms used in forensic DNA analysis.

TESTS

Forensic DNA analysis is a series of analytical processes designed to generate and compare DNA profiles. Analysis may be attempted on any bodily source of cells, including but not limited to blood, semen and saliva.

- **Extraction** — Extraction is the process by which 1) cells are removed from their substrate (e.g. fabric) and by which 2) DNA is removed from cells and purified. Wfg utilizes the commercially produced PrepFiler™ Forensic DNA Extraction Kit to perform these processes.

- **Quantitation** — Quantitation is the process used to estimate the amount of human DNA in a sample and to determine whether sufficient DNA exists to continue with the analysis. Wfg utilizes the commercially produced Plexor® HY system to perform the quantitation process. This system quantifies both the total amount of human DNA present in a sample as well as the amount of male DNA, if any, present.

- **Profiling & Analysis** — Following quantitation, and provided sufficient DNA is detected (Wfg has thresholds below which subsequent analysis processes do not proceed) a portion of the DNA extract is used to generate and tag multiple copies of specific STR locations. These tagged copies of DNA are then sorted to generate a DNA profile for the sample in question. Wfg utilizes one or both of two commercially produced typing systems to perform the profiling and analysis processes.

  The PowerPlex® 16 HS system (PP16) types autosomal DNA at 15 STR loci plus the gender determining Amelogenin locus, and is used as the default testing system in most cases. The PowerPlex® Y23 (PPY23) system types 23 STR loci located on the Y-chromosome, which is found exclusively in males, and is used in select cases where the value of autosomal STR typing of male DNA may be limited.

- **Direct Amplification** — Samples from a known single-source (comparison or reference sample) may be processed without the need for extraction or quantitation. Following a brief chemical pre-treatment, samples may undergo profiling and analysis.

- **Interpretation & Comparison** — The final step of the process involves the interpretation of DNA profiles and the comparison of profiles to determine, depending on the application, whether particular individuals can be excluded as their source or whether different samples come from the same source or whether individuals may be related.

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When an individual cannot be excluded as the source of a DNA profile, the strength of the association is expressed as a random match probability. In certain cases, including in relationship tests, it may be expressed as a likelihood ratio or probability of relatedness. In any case, calculations of probabilities are based on DNA frequency data contained in databases of relevant populations.

APPLICATIONS

Forensic DNA analysis may be applied in a number of different circumstances, including in criminal or other official investigations as well as in civil and private matters.

LIMITATIONS

- Numerous limitations exist, and are different from case to case, with respect to the significance of DNA test results.
- The quality of DNA in forensic samples can vary significantly. Degraded biological samples may yield little to no DNA and either partial or no profiles. Additionally, inhibitory substances (e.g. certain types of fabric dyes) are sometimes co-extracted with DNA, leading to partial or no profiles.
- When it has been reported that 'insufficient' DNA was detected from a sample and that it was therefore not further processed, this may mean that DNA is present at a very low level or is not present at all.
- A mixture of DNA from more than one person can sometimes limit a scientist's ability to unambiguously establish individual contributing profiles and can thus decrease the ability to exclude a particular individual as a contributor to the mixture.
- While DNA results may provide strong support for the assertion that a particular individual is the source of a DNA profile, they do not in and of themselves provide any information as to how or when the DNA was deposited where it was found. Other test results (e.g. body fluid test results) in combination with DNA test results may provide sufficient information upon which a qualified opinion may be formulated with respect to such questions.
- While Y-STR testing can have significant advantages over autosomal STR testing (e.g. it is far more sensitive in detecting male DNA in female-male mixtures and can be very useful in certain types of familial analyses), there are distinct limitations pertaining to this technology relative to autosomal testing systems.
    - All males in the same paternal lineage will share the same Y-STR DNA profile. Therefore, when it is reported that a particular male individual cannot be excluded as the source of a Y-STR profile, his paternal male relatives also cannot be excluded. These include, but are not limited to, his brother(s) from the same father as well as their sons, his father, his grandfather on his father's side, his uncles on his father's side as well as their sons.
    - Match probabilities with Y-STR profiles are higher (i.e. more common), even in terms of unrelated persons, than they generally are with autosomal STR profiles.