THE USE OF SYNCHRONOUS COEFFICIENT OF DRAG ALTERATION (SCODA) TECHNOLOGY TO
EXTRACT, PURIFY AND CONCENTRATE DNA FROM CHALLENGING OR DEGRADED FORENSIC
SAMPLES

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Some forensic samples tend to present many challenges for successful short tandem repeat
(STR) profiling due to degraded and low amounts of template DNA as well as the presence of
inhibitors that can interfere with DNA amplification by polymerase chain reaction (PCR).
Commonly used extraction methods, such as silica-membrane columns and phenol/chloroform,
have been successful in recovering low copy number (LCN) DNA and removing inhibitors.
However, even after the use of such methods some challenged forensic samples still fail to
provide an STR profile. In addition, during sample manipulation with these methods there can
be substantial loss of DNA. Synchronous coefficient of drag alteration (SCODA) is a new
technology, utilized in the Aurora system (Boreal Genomics, Vancouver, BC), that effectively
removes all inhibitors while simultaneously concentrating DNA. SCODA was used to extract,
purify, and concentrate the DNA from challenged forensic samples. Human skeletal remains
(i.e. large bone fragments) from several individuals, which previously failed to generate an STR
profile or only produced a partial profile from a silica-membrane column DNA extraction
method, were selected to be subjected to SCODA. Following bone decalcification and protein
digestion, the large-volume bone lysates were filtered to remove salts and added directly to the
Aurora system. Purified DNA was removed from the cartridge and amplified using the
AmpFSTR® Identifiler® Plus PCR Amplification Kit (Applied Biosystems, Foster City, CA). STR
profiles were generated using the 3500xl Genetic Analyzer (Applied Biosystems) and analyzed
using GeneMapper® ID-X software (Applied Biosystems). SCODA successfully removed
inhibitors and concentrated the low quantity DNA from the bone samples to allow for the
successful amplification of partial to full STR profiles. The Aurora system provides an
automated, minimal-step approach to successfully remove inhibitors and concentrate DNA
from challenged forensic samples.