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ASSESSING THE FIDELITY OF WHOLE GENOME AMPLIFIED SAMPLES FOR HIGH VARIABILITY STR GENOTYPING.

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With the availability of several whole genome amplification (WGA) kits it is now possible to genotype DNA samples for which only minute amounts are available and to replenish depleted rare or valuable DNA samples. Pinard *et. al*. (2006) tested four methods of WGA and observed that multiple displacement amplification maintained the highest level of fidelity and produced the highest yield. Additionally, Paez *et. al*. (2004) observed a 99.82% representative genome in WGA samples using a single nucleotide polymorphism (SNP) approach. Subsequent to WGA, when genotyping short tandem repeats (STRs) which arise from the inherent "copying errors" of DNA polymerase, a check for the accurate amplification of these loci with accelerated rates of mutation is crucial.

We performed WGA on DNA samples representing two species, humans and desert tortoises (*Gopherus agassizii*), using two Phi29 based kits (G.E. Biosciences' GenomiPhi v2 DNA amplification kit and Qiagen's REPLI-g service kit). We then tested the human samples for 67 non-recombining Y-chromosome (NRY) and the desert tortoise samples for 14 autosomal (recombining) loci. These loci span a variety of repeat motifs (di- to hexa-nucleotide repeats), allelic ranges (3 to 44), and mutation rates (0.0009 to 0.3333 for 30 loci). The four human DNA samples yielded an over 10^3-fold increase, consistent with results of Holbrook *et. al*. (2005). Finally we compared STR genotyping results between the original sample genotypes and the WGA samples and across both the Qiagen REPLI-g and the G.E. Biosciences GenomiPhi kits.

References

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