B54 Customizing Genotyper® Macros to Individual Laboratory Specifications

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The goal of this presentation is to present the audience with sufficient background knowledge and information so that the individuals would be capable of returning to their own laboratory and making modifications to their macros to better suite their analytical needs.

When analyzing short tandem repeats (STRs) utilizing the ABI Prism 310 Genetic Analyzer, Genotyper® software is commonly used to assist in allele calls following an electrophoretic run. The macros that are provided along with the software, normally Kazam and Kazam 20%, can aid in this process. During this presentation, some of the basics of the macros supplied with Genotyper® will be explained for fundamental understanding, then the presenter will delve into the details of making alterations to the default macros in order to better serve the user based on the stutter and -A values of each individual laboratory.

Three different types of macro modifications will be discussed. The first will be a simple modification to change the value of a global filter (e.g., changing the Kazam 20% to a 4% filter level). The second modification to be discussed will "Focus" the basic Kazam macro so that only targeted areas (where stutter and -A would be present) will be filtered. This allows for specific peak height or peak area values to be used in filtering the stutter and -A without fear of filtering true off-ladder alleles. The final modification will combine both a low level global filter to aid in the removal of baseline noise, and will make use of the "Focus" principals to target the areas being filtered based on stutter and -A values.

DNA Analysis, STRs, Genotyper

 ** Presenting Author*