Complete Genotype with Project Merge Tool

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Introduction

Obtaining a complete genetic profile for wildlife and plant research or medical research is often complicated by overlapping marker ranges and/or incompatible chemistry; making it necessary to amplify the same samples multiple times using different sets of markers or locus specific primers. Traditionally, researchers export the genotyping results from several multiplexes into a spread sheet and manually combine allele calls for each individual.

GeneMarker 1.90 addresses this problem with a new tool: Merge Projects. Researchers can conveniently combine two or more GeneMarker projects (each project using a panel containing a unique set of markers or loci) into a single, comprehensive report. This report represents a single view of multiplexes (a super panel) of markers/loci from the individual projects, providing a complete genotype for each sample. This merged report may be saved in a spread sheet as a genome-wide genotype, or imported into other special applications, such as, Clustering Analysis or Relationship Testing and Kinship Analysis, improving the robustness of these analyses by including information from a greater number of markers.

Procedure – Merge Projects

1. Import data files (fsa, abi, ab1, scf) or open a saved GeneMarker Project file
2. Select the Run icon to launch the Run Wizard – using a panel with uniquely named markers
3. Repeat with data files amplified with a second multiplex of uniquely named markers
4. Save each project for a set of individual files
5. Select Tools →Merge Project →Open Merge Project →Add project files →OK
6. Select File Name Group icon →Match Files by group identifier or character position →Match →OK
7. Click Report Settings Icon to activate the Allele Report Settings dialog
8. Save the merged project report as a .txt file.

Figure 1: Three different multiplexes were used to amplify 30 DNA samples. Each multiplex contained primers for 4 or 5 independently assorting loci. The merge project tool in GeneMarker provided a single genotype for each individual with 14 markers. Allele drop out is indicated by **. The report style pictured here is a Marker Table suitable for further analysis in Relationship Testing or Kinship Analysis. Saving as a Peak Table would provide a spread sheet with marker and allele name, fragment size (MW), peak height, height ratio, peak area, area ratio. The Bin Table format would be selected for further analysis using clustering algorithms for phylogeny.

Results and Discussion

Figure 1 illustrates a three-fold increase in the number of loci in one report made possible by merging projects. The .txt tab delimited format of the saved report provides the ability to save any number of loci and samples into one merged report.
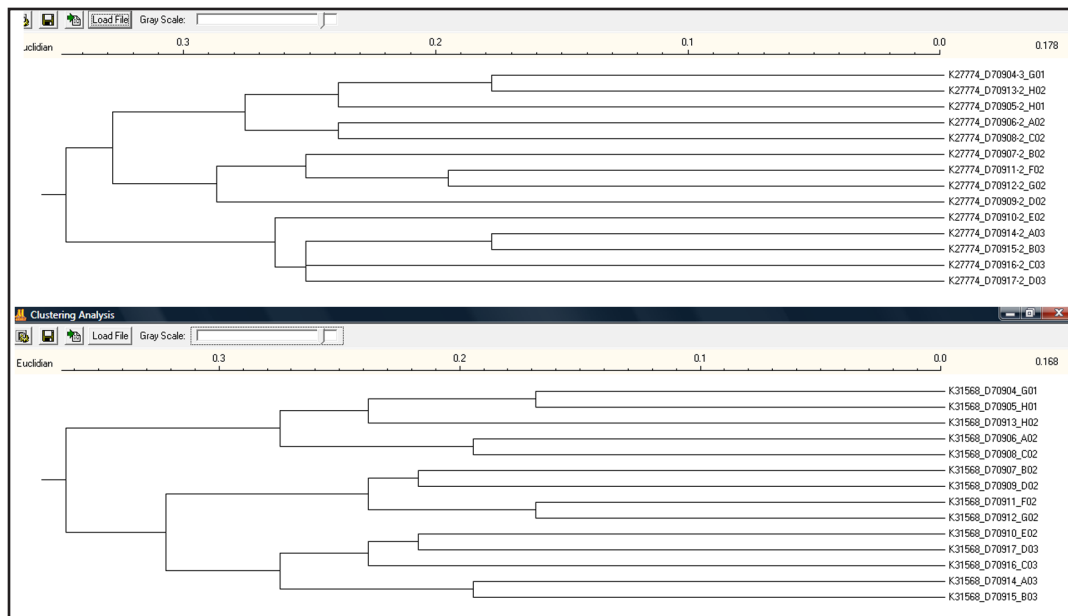
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Figure 2. Expanded discriminatory power is possible by including 9 loci from two projects (upper dendrogram) in contrast to the lower dendrogram that is based on the 4 loci of one multiplex.

Overlapping marker ranges or incompatible chemistries are common challenges in microsatellite analysis. GeneMarker's Merge Project tool enables researchers to combine genotype information on the same samples analyzed with different multiplexes. The result is a master report that provides genotype information from multiple kits or multiplexes with the flexibility to be saved in a variety of formats: Marker Table, Peak Table or Bin Report.

Examples of clinical research applications with Merge Project include pathogen and genetic disorder research. Often several PCR kits are used to screen individuals for a variety of pathogens that cause similar symptoms, such as influenza strains or drug resistant tuberculosis strains. Results from these multiple kits are presented in one report table, providing more complete information for each patient in a single report. Multiple kits are also required for complete genetic profiles for genetic disorders, such as breast cancer or Duchenne muscular dystrophy (DMD). Merged projects provides complete genotypes, allowing combination of kit results for one disorder, or combining results from kits for different disorders on one report for each individual.

Ecology and agriculture applications include compilation of a genome-wide report for each individual in one table. The table can be saved as a spread sheet for import into other statistics packages, or used with GeneMarker applications; providing greater discriminatory power for kinship analysis and relationship testing, and expanded rigor for clustering algorithms used in phylogeny, lineage and evolution studies.

GeneMarker has been designed to provide genetic researchers with a biologist friendly genotyping tool; with unique pattern recognition and sizing technology providing >99% accuracy, easy linked navigation, management control and tracking, exportable LIMS reports, bulk printing capabilities, instrument compatibility with ABI®, MegaBACE™ and Beckman Coulter™. Unique post-genotyping applications in GeneMarker of interest to ecology and population genetics research include: cluster analysis and phylogeny, relationship testing and kinship analysis, microsatellite instability, and TILLING®.

Acknowledgements

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