

Structural and functional genomics: resources and uses related to quality.

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The applications of genomics to wheat quality are only now starting to be realized, and a review of current and projected future bioinformatics resources will include examples of contributions of genomics to understanding and improving wheat quality. Such examples will involve structural genomics to understand the chromosome organization of wheat quality loci, use of ESTs to gain structural and functional insights into gene structure and expression, uses and limitations of array platforms, and the development of markers for high-throughput mappings. Projections on the ongoing change in DNA sequencing capacity will be reviewed, along with issues related to data load, such as problems associated with single experiments producing gigabytes of data. How such data can be stored, accessed, analyzed, and useful information extracted will become increasing problematical.

Identifying quantitative end-use quality traits through marker-trait associations.

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End-use quality traits (grain, milling, and baking) are generally expensive and difficult to measure. We are in the process of estimating phenotypic trait values for a wide range of Pacific Northwest wheat genotypes, including soft white spring, winter, and club; hard red winter and spring; and hard white winter and spring. Phase 2 of the research will attempt to associate molecular markers with quantitative variation in end-use quality phenotypes.

We currently have assembled four large data sets derived from a long-term (~10 years) study known as the 'G&E' (Genotype and Environment). The G&E study utilizes grain samples produced from the Washington State University Cereal Variety Testing Program, a multi-location replicated trial of advanced breeding lines and current cultivars. The G&E uses single-rep grain samples from 4–6 locations each year. Most lines and cultivars are included in the study for three years; long-term checks are included for the entire life of the program. The four nurseries are soft spring, soft winter, hard spring, and hard winter. For soft spring, the long-term checks are Alpowa and Zak and for soft white winter, they are Eltan, Madsen, Stephens, Hiller, and Rely. The soft spring data set is comprised of approximately 340 samples; the soft winter set has about 970 samples. The traits under study are grain yield, test weight, grain protein, NIR grain hardness, SKCS single kernel hardness, weight and size and their standard deviations, break flour yield, flour yield, milling score, flour ash, flour protein, Mixograph water absorption, flour SDS sedimentation volume, flour-swelling volume, rapid ViscoAnalyzer peak hot paste viscosity, cookie diameter, sponge cake volume, and polyphenol oxidase L-DOPA absorbance. Currently, the issue at hand is to determine what the best estimate is for each genotype's phenotype. The first two approaches involve i) simple calculations of arithmetic means and ii) calculation of least squares means. The latter has the advantage of accommodating year-to-year variation to adjust the marginal means. As an example, differences between means and LS means for milling score ranged from -2.0 to +1.1 (soft winter) and -3.3 to +3.6 (soft spring) and for cookie diameter -0.14 to +0.13 (soft winter) and -0.17 to +0.11 (soft spring) (see figure at right). Overall means for milling score for soft winter and spring wheats were 84.1 and 83.7, respectively. Cookie diameters of 9.37 and 9.47 cm diameter were obtained for soft winter and spring wheats, respectively.

