A Historical Evaluation of High Molecular Weight Glutenin Subunit Frequencies

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Introduction
The incidence of celiac disease and sensitivity to gluten appears to have increased in recent years in the United States, leading to questions regarding changes over time in the composition of gluten (gliadin and glutenin) in wheat and whether these changes could be the cause for this increased use in gluten sensitivity and celiac disease. These changes would have occurred when new germplasm was introduced into the U.S. wheat breeding programs and/or when there was an increased emphasis on selection for end-use quality in hard and soft winter wheat. These changes could be due to direct genotypic selection for the major glutenin subunits (5+10 – hard wheat, 2+12 – soft wheat) in the D genome or indirect for the minor glutenin subunits on the A and B genome due to phenotypic selection for end-use quality.

Objectives:
1. Determine if there has been any shift in the major and minor glutenin subunits in wheat cultivars grown in the Pacific Northwest (PNW) and United States over the last century.
2. Identify any changes in the glutenin subunits that occurred during the last twenty years that match the proposed timeline for the increase in the incidence of gluten sensitivity and celiac disease in the U.S. population.

Materials & Methods:
122 top U.S production varieties dating from the 1900’s to 2011 (see Table 1.) were collected and grown in a greenhouse. Germlasm was chosen by top production acreage (Borjenaan and Angus 2001) in the U.S. Plants were grown to maturity and grain was harvested and milled using a CEMOTEC 1090 sample mill. High molecular weight glutenin subunits were extracted using a modified 4 step extraction protocol (Uthayakumaran, Listiohadi et al. 2006) using 100 mg of sample flour. Extraction supernatant was analyzed using an Agilent Bioanalyzer 2100 and Protein 230 kDa. Protein bands were analyzed and identified according to Jonnala, Ramakanth S, et al. (Jonnala, Ramakanth S, et al. 2010;Marchetti, Adam Heesacker¹ and Robert Zemeta¹).

Discussion/Conclusion
1. In cultivars grown after 2000 there was a shift in the major glutenin subunits observed in both the hard and soft wheat cultivars with 5-10 subunits being the primary subunits found in hard wheat and 2-12 subunits being the only D genome subunits found in soft wheat. This is most likely due to increased use of genomic selection for these sub-units and the increased emphasis on selection for end-use quality, especially in the soft white winter wheat breeding programs.
2. Variation was observed for the minor glutenin subunits over time in both hard and soft wheat cultivars with some minor subunits increasing or decreasing during various decades. Some of the minor subunits that increased in the 1990s and 2000s cultivars may warrant further study in relationship to glutenin sensitivity.

Future Research
Research is currently underway to determine if there has been a change in the presence and amount of the gliadin epitopes in wheat that induce celiac disease.

References
"National Agricultural Statistics Service," Oregon State Department of Agriculture 2012
Marchetti, Adam Heesacker¹, et al. “Protein quality characterization by replicating protein subunits on to single copy one gram high molecular weight glutenin extraction.” Analytical and bioanalytical chemistry 403.6 (2011): 2493-2494.

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