The influence of wheat genetics on the development of celiac disease

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During the last decades, an increase has been observed in the prevalence of Celiac Disease (CD). This may partly be attributed to a raise in awareness of the disease and improved diagnostic techniques. But in the meantime, a higher wheat and gluten consumption may also be a major cause. In addition to these aspects, the genetics of wheat may also play an important role on the development of CD (Van den Broeck et al., 2010). For Centuries, grains have been domesticated (Kasarda, 2013) to improve different properties, for example to increase yield, to change kernel size or shape, or to improve disease or insect resistance. The domestication of *Triticum monococcum* which has only the A genome resulted in a hexaploid wheat called *Triticum aestivum* which consists of three genomes designated A, B, and D (Kasarda, 2013). It has been speculated that the changes in wheat proteins that resulted from wheat breeding has increased the incidence of CD. Normally for developing the disorder people must have a genetic predisposition for CD. Depending on the wheat genetics different contents of T-cell stimulatory gluten sequences are available (Molberg et al., 2005). The results of different studies show that especially the sequences of the α-gliadin react with an increased production of antibodies (Molberg et al., 2005). One of the major immunodominant epitopes is the Glia-α9 epitope which can be recognized by the T-cells or Antibodies of most CD patients (Van den Broeck et al., 2010). Furthermore, the sequence of the Glia-α9 epitope is a part of the proteolytic-resistant 33-mer which is also known to have a strong T-cell stimulatory effect (Van den Broeck et al., 2010). Molberg et al. (2005) found that the fragments identical or equivalent to the immunodominant 33mer fragment are particularly encoded by α-gliadin genes on the wheat chromosome 6D. Thus, the D genome contains more active epitopes than the A and B genome, making it more toxic for celiac patients (Molberg et al., 2005; Kasarda, 2013). Van Herpen et al. (2006) also investigated the presence of active epitopes on the different genomes. They have found a majority of T-cell stimulating epitopes on the D-genome, but T-cell stimulating epitopes have also been present on the A-genome. Nevertheless, it is supposed that the D genome is more toxic for celiac patients than other genomes. The results of the different studies lead to the conclusion that ancient wheat varieties should have fewer celiac disease-inducing epitopes. For this purpose, Van den Broeck et al. (2010) and Gregorini et al. (2009) analysed the incidence of epitopes on ancient and modern wheat varieties. Van den Broeck et al. (2010) found that the presence of the Glia-α9 epitope was higher in the modern varieties as compared to the landraces. On the other hand, some modern varieties and landraces have been identified that have relatively low contents of epitopes and can thus be used for the cultivation of less

celiac disease-inducing varieties. Gregorini et al. (2009) also found epitopes on ancient wheat varieties. In conclusion, this leads to the assumption that the toxicity of wheat for CD differs strongly between varieties (Gregorini et al. 2009). A selection of varieties and landraces low in T-cell stimulatory α-gliadin epitopes and other major epitopes can be used for wheat breeding and finding wheat varieties, which are safe for consumption by CD patients.

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