

Food science meets plant science: A case study on improved nutritional quality by breeding for glucosinolate retention during food processing

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Nutritional quality of vegetables is affected by several steps in the food chain. Up to now the effects of these different steps are mostly studied separately. We propose the cooperation between plant breeding and food technology by using food technological parameters as breeding traits to identify genetic loci associated with food processing. An example of mechanistic studies of glucosinolate losses during cooking

is used to discuss requirements, possibilities, challenges and benefits of such an integrated approach with the final aim to breed for vegetables with higher retention of glucosinolates, as example for other phytochemicals, during food processing.

Introduction

Food quality, including nutritional quality, is affected by many steps in the food supply chain like cultivation, storage, industrial processing, packaging and domestic preparation (Dekker, Verkerk, & Jongen, 2000). Optimizing the chain for food quality can be done by changing the conditions of handling the food and its ingredients throughout the chain Verkerk *et al.* (2009). Plant-based raw materials for food products are known to often have large variation in initial quality related product properties like the content of certain (micro-) nutrients or phytochemicals. Dekker *et al.* (2000) estimated the variability of phytochemical content at each step in the food chain to 5–10-fold, which can lead to a 100-fold differences at the level of the consumer (Dekker *et al.*, 2000). Insights from plant science, e.g. plant breeding, can be exploited to enhance the initial quality, e.g. by increase the content of a health promoting component in the raw material. In this paper we aim to demonstrate that not only this initial quality can be increased by genetic improvement of the starting material through plant breeding, but also the dynamic behaviour of quality attributes throughout the food supply chain can be optimized by adapting the genotype of the plants through plant breeding. We will give an example of enhancing the nutritional quality of *Brassica* vegetables by breeding for an increased retention of certain phytochemicals, glucosinolates (GLs), during processing and preparation. In order to do this, food scientists have to collaborate with plant scientists to exchange knowledge and information.

In the subsequent sections existing studies on breeding for food quality traits are reviewed, followed by the introduction of phytochemicals as a quality attribute, the GLs as an example of phytochemicals studied in the food chain and the mechanisms and kinetics of glucosinolate (GL) losses during processing. The main point of view of this paper is discussed at the end: how insights from food and plant sciences can be usefully joined by breeding *Brassica* vegetables for GL retention during food processing.

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Breeding for food quality traits

Introduction to principles of marker assisted breeding

Many agriculturally important characteristics of a crop such as yield, disease resistance, sugar or vitamin content are controlled by many genes and are known to breeders as quantitative traits. The regions within genomes that are associated with a particular quantitative trait are known as quantitative trait loci (QTL) (Collard, Jahufer, Brouwer, & Pang, 2005). Phenotypic variation for the trait of interest is the first step to find the associated genetic differences (Koorneef, Alonso-Blanco, & Vreugdenhil, 2004). As illustrated in Fig. 1, two parents, with phenotypic variation for the trait of interest, are used to develop segregating

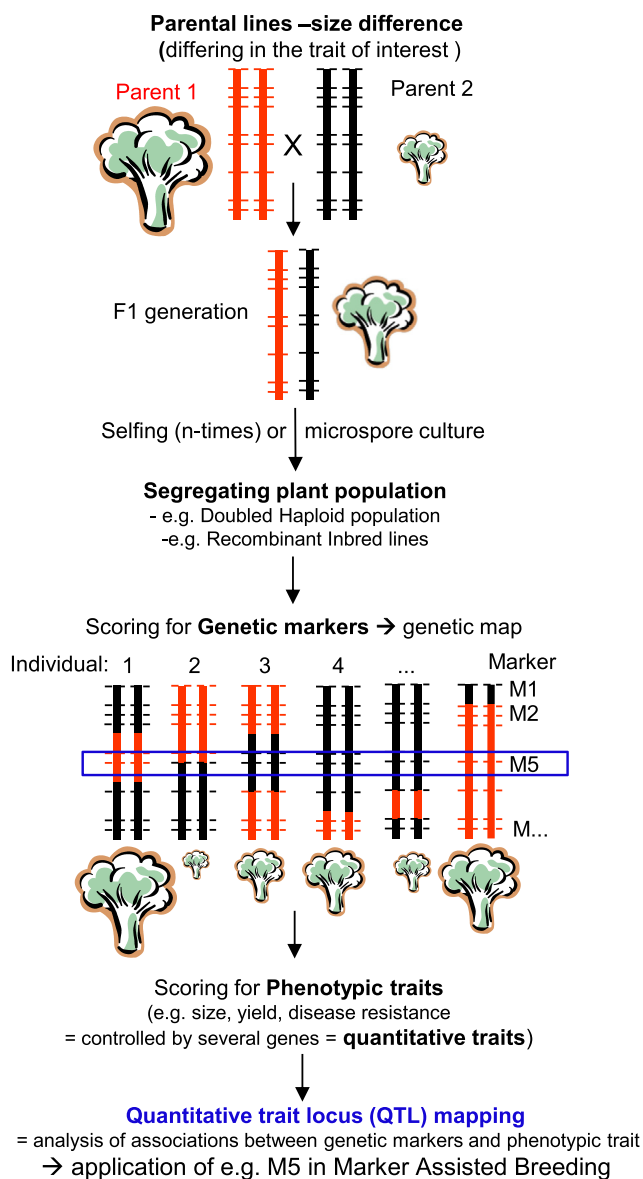


Fig. 1. Introduction to quantitative genetics based on Collard *et al.* (2005) on the example of the quantitative trait “broccoli size” and the application of marker-phenotype-relations in marker assisted breeding.

populations, which are the progeny of the cross with each genotype/line containing different combinations of the parental genomes through genetic recombination. The segregation of parts of the parent genome (containing molecular markers and genes) is caused by chromosome recombination (crossing-over) during meiosis, which is the basis of genetic map construction. Using molecular tools (scoring of molecular markers throughout the segregating population) genetic (linkage) maps can be constructed. By combining these maps with quantitative phenotypic information associations can be detected between the phenotype and molecular markers, the so called QTLs (Collard *et al.*, 2005).

It is important to realize that quantitative traits are not only affected by allelic variation in genes, epigenetic changes which affect the expression of genes, but also by the environmental conditions during growth. By statistical experimental designs, plant breeders quantitatively separate the environmental effects from the genetic effects, with the aim to cross the QTL with beneficial alleles into commercial cultivars. For this purpose, marker assisted selection (MAS) is an efficient, reliable and cost-effective method compared to conventional breeding (Collard *et al.*, 2005).

Genetic studies with prior knowledge of the trait

An example of a breeding strategy for affecting a quality attribute of a processed food product is the breeding for improving the colour of potato chips. QTL for the colour of potato chips after frying were identified by Li *et al.* (2008). A too dark colour of potato chips, a negative quality attribute, is a result of the Maillard reaction, a reaction between free amino groups and reducing sugars occurring at high temperatures. A high amount of reducing sugars results in dark colour during frying and formation of the toxicologically suspect compound acrylamide, whereas a high starch content and a low amount of reducing sugars results in lighter colours. For the genotyping, primers were partly selected based on known genes involved in sugar and starch metabolism. The authors identified several QTL for chip quality and most significant QTL were detected at genetic loci, which encode enzymes involved in carbohydrate metabolism. Another example is given by Simons *et al.* (2012) who studied the genetic effects of bread making quality traits in spring wheat using a segregating population. Gluten, consisting of the main two proteins glutenin and gliadin, affects the rheological (viscoelastic) properties of dough and hence plays a major role in dough strength and baking performance. The authors complemented the genetic map with molecular markers based on the DNA sequences of high and low molecular weight glutenins. A major QTL, explaining 47–63% of the phenotypic variation for three dough mixing time parameters and bread making performance, was identified at the genomic region where also the high molecular weight glutenin gene mapped.

Both studies clearly illustrate the advantage of the use of mechanistic knowledge from food scientists to study the

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