

Recent Breeding Approaches for Improvement of Quality Traits in Solanaceous Vegetable Crops

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Abstract

Vegetable crops are rich in dietary micronutrients, antioxidants and functional phytochemicals. Among these, solanaceous vegetables are key sources of health-protective dietary constituents such as minerals, vitamins and antioxidants in the human diet. Some of the elements are of public health concern, such as β -carotene, lycopene, anthocyanin, calcium and folic acid, which attract breeders' interest to improve their content in vegetable crops so that their dietary intake could be increased. The attempts through conventional breeding methods have been slow and inadequate to fulfil the mentioned traits. Hence new developments in molecular and biochemical diagnostic tools and techniques have been used to improve the nutraceutical content and other quality traits (Behera and Singh, 2019).

Introduction

Breeding for improved nutritional quality is an important objective of plant breeding in food, fodder and vegetable crops. The important nutritional traits include protein, oil and vitamin contents; some nutraceutical compounds such as anthocyanin, β -carotene, lycopene and glucosinolates have been reported to play an active role in health and their contents have been found more in beetroot, cauliflower, carrot and broccoli, respectively. The attempts through conventional breeding methods have been slow and inadequate. Hence new developments in molecular and biochemical diagnostics tools and techniques showed promise in improving the nutraceutical contents and other quality traits. Molecular markers, next-generation sequencing, RNA interference (RNAi) and genetic engineering have great promise in reducing the time and cost involved in quality breeding. The present review summarizes attempts and potential of improving the nutraceuticals and quality traits in vegetable crops.

- Improving the quality of food crops provides nutrient security.
- Solanaceous vegetables are cheaper sources of nutrients and can easily meet dietary requirements.
- The study of genetic behaviours helps the breeder formulate an effective breeding plan for its improvement.

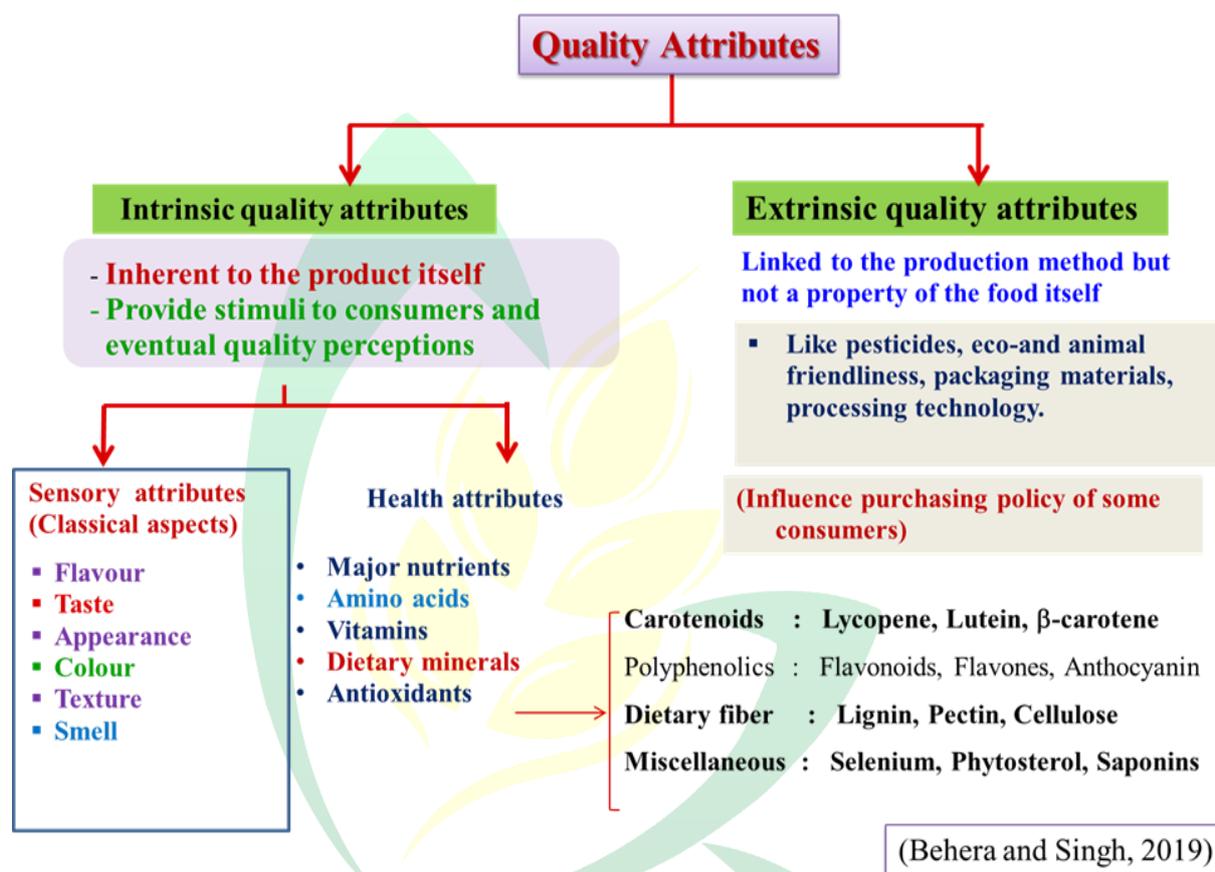


Figure 1. Classification of quality attributes

Advanced breeding methods

Advanced quality breeding needs a combination of genetic sources, modern genomic tools and biochemical diagnostic techniques.

The Recent breeding methods include,

1. Mutation breeding
2. Molecular breeding
3. SNP's discovery
4. RNA interference
5. Targeted genome editing

6. Transgenic approach

A. Mutation breeding

The genetic improvement of crop plants for various economic traits through induced mutation (mutations that mutagenic agents induce: gamma rays, E.M.S., etc.) is called mutation breeding. Important steps to know before mutation breeding are,

- Selection of variety for mutation breeding: Generally variety selected for mutagen treatment should be the best commercial variety of the crop.
- Part of the plant to be treated: In a sexually propagated plant, seeds are most commonly used for mutagen treatment. Pollen grains may be used in some cases.
- Dose of the mutagen: The dose of the mutagen should be such that it induces a maximum frequency of mutations while it causes minimum killing.
- Mutagen treatment: Seeds treated with chemical mutagen are first soaked in water for a few hours. This initiates some metabolic activities and then seeds are treated with the desired dose of chosen mutagen.

B. Molecular breeding for quality traits

Molecular markers enable the unambiguous identification of lines/individuals in segregating populations to handle quality traits. Marker-assisted selection refers to indirect selection for a phenotype based on the banding pattern of linked molecular markers. Molecular breeding is effective in the introgression of desirable genes from the wild into cultivated genotypes.

Table 1. Molecular breeding for quality traits

Reference	Marker	Trait	Crop
Lixiaet <i>et al.</i> , 2011	SCAR	high-lycopene	Tomato
Tanaka <i>et al.</i> , 2016	CAPS	High Pungency in <i>C. Chinense</i>	Chilli
Fischer <i>et al.</i> , 2013	SSR	Cold-induced sweetness	Potato

C. Single nucleotide polymorphism

- It is the most common form of DNA sequence variation between alleles in several plant species.
- SNP have become choice markers due to their abundance, stability, amenability to automation, and cost-effectiveness.

- The selection of SNP enables the selection of desired lines in large-scale populations. SNPs can also discover new genes and their functions by affecting gene expression. The advantages of SNP are that they are abundant in number and SNP detection is more rapid because it is based on oligonucleotide hybridization analysis, with one disadvantage being that there is a high possibility that a SNP does not display any variability in the family that is being studied.

D. RNA interference (RNAi)

- RNA silencing is a gene regulatory mechanism that limits the transcript level by suppressing transcription. This approach was effectively used to alter the gene expressions to improve quality traits.
- The first transgenic cultivar, the 'Flavr-Savr' variety of tomatoes developed in 1994 by Cal gene Company.
- The development of transgenic plants has continued mainly with the introgression of genes-disease resistance and fruit quality.

E. Genome editing

- Genome editing refers to altering DNA sequences to modify gene function to obtain desirable traits.
- Genome editing can effectively induce targeted mutations in plant genomes at a precise location, Reduces non-specific off-target cleavage, and provide highly efficient and site-specific performance observed. Final products- Identical to the mutants obtained by 'conventional' mutagenesis.

F. Transgenic approach

Sequence-specific nucleases enable efficient genome engineering

1. Zinc finger nucleases

- Zinc finger nucleases consist of two DNA binding domains and a DNA cleavage domain attached by linker sequences. DNA binding domain has the specificity to recognize 3 to 6 amino acids.
- First, engineered endonucleases are used to edit genes.

2. Talen- transcription activator-like effector nucleases

- Transcription Activator like Effector nuclease fused with a catalytic nuclease domain

- It is easier to engineer than ZFNs as TALEN protein can bind to a single nucleotide instead of binding into a set of 3 nucleotides.

3. CRISPR/Cas9

- Cas9 is the nuclease protein that cuts the DNA. The site specificity comes from the guide RNA, which can be designed and synthesized easily.

Table 2. Wild Sources for improvement of quality traits

CROP	Wild species	Trait
TOMATO	<i>Solanum pimpinellifolium</i> , <i>Solanum peruvianum</i>	Ascorbic Acid
	<i>Solanum Chmielewski</i>	Total soluble solids
	<i>Solanum cheesmaniae</i>	β -Carotene
BRINJAL	<i>Solanum torvum</i> <i>Solanum khasianum</i> <i>Solanum aviculare</i>	Phenols
	<i>S. vernei</i>	Starch
	<i>S. phureja</i> spp. phureja	Carotene
CHILLI	<i>Capsicum frutescens</i>	Capsaicin

Table 3. Varieties released with improved quality traits

Varieties	Attributes	Method
TOMATO: FlavrSavr	Increased shelf life	Gene silencing
Co-3	Vitamin C (25 mg/100g), TSS (5.2° brix).	Mutation
COTH.1 (1998)	Acidic (0.61%) with a TSS of 4.43° brix.	Hybridization
PKM.1 (1978)	TSS 5.6° brix and acidity is 0.99% and 23.7 mg/100g vitamin C	Mutant of Annaji
BRINJAL: COBH.1 (2001)	Ascorbic acid (16.65 mg/100 g)	Hybridization
PKM.1 (1984)	0.29% acidity and 14mg of ascorbic acid per 100g of pulp	Mutant
ArkaNavneet	Phenol (0.44 g/100 g)	Hybridization
PusaKranti	Glycoalkaloids (6.25 mg/100g)	Hybridization

CHILLI: PMK 1 (1993)	0.36 per cent capsaicin content	Hybridization
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Table 4. Biotechnological and transgenic approaches for quality traits in vegetable crops

Crops	Genes	Improved quality traits
Tomato	<i>Psy-1, Crt B, CYC-B, LCY-B,</i>	Carotenoid rich tomato
	<i>Ros1 and Del</i>	Anthocyanin-rich tomato
	<i>CHI, CHS</i>	Flavanols rich tomato
	S-adenosylmethionine decarboxylase gene	Folate-rich tomato
Potato	<i>AmA1 (Amaranthushypochondriacus)</i>	Protein-rich potato
	<i>Tar1</i> (tarin) gene	
	<i>ZEP</i> gene	Enhanced Zeaxanthin
	<i>xyIA (glucose isomerase)</i>	High tuber fructose

Conclusion

Molecular tools and genome sequencing techniques showed effectiveness in speeding up the classical breeding methods for quality traits of complex pathways. Utilization of conventional breeding techniques and powerful biotechnology tools to pace the development program for redesigning crops. Molecular markers, next-generation sequencing, RNA interference (RNAi) and genetic engineering have great promise in reducing the time and cost involved in breeding to improve quality traits in solanaceous vegetables.

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