

Genetic improvement for improving nutritional quality in vegetable crops: A review

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Abstract

Nutritional deficiency is one of the major problems globally, especially in resource poor developing countries distressing the economical, social and personal growth simultaneously. Vegetables are an indispensable component of balanced diets as they provide different vitamins, minerals, dietary fiber and phytonutrients required for growth and development of human beings; and are the best and cheapest sources of nutrients particularly to the vegetarians. During last century, the ever increasing population compelled agriculturists and plant breeders for intensive agriculture and development of high yielding varieties, respectively to increase productivity to feed the people. Presently, improving the nutrient concentration in edible plant parts has become a goal of plant/vegetable breeding because of the increasing public awareness towards human nutrition and health. Some land races, old varieties, pre-breeding lines and wild relatives are very good source of nutrients, generally governed by poly-genes and have ability to transfer the traits in elite background. Suitable poly-cross breeding approaches along with evaluation of large number of population would be the best to enhance the nutrient concentration in vegetables. Complementarily, the use of biotechnological tool and molecular marker-assisted selection will certainly expedite the pace and prospects of success for “nutrient biofortification” of vegetable crops.

Keywords: Vegetable, Nutrient, Breeding, Genetic resources, Biofortification, Minerals, Vitamins

Introduction

Vegetables have tremendous potential to alleviate malnutrition, hidden hunger and degenerative disease like

cancer; Alzheimer and cardiovascular disease. Large part of global population, especially developing countries, lack adequate access to vegetables required for building and maintaining good health. Insufficient intake of nutrients is considered among the top 10 causes responsible for the mortality and accounted for 2.7 million deaths per annum globally (Ezzati *et al.* 2002). Malnutrition is more prevalent in the tropical countries because per capita availability and consumption of vegetables is lacking behind of the minimal standard of 73 kg/person/annum. The International Food Policy Research Institute predicts an 18% rise in the number of malnourished children from 2001–2020 (IFPRI 2001). Vegetable crops are recognized as the principal source of micronutrients, both macro and micro elements and loaded with phytonutraceuticals. This insight regarding the distinguished role of vegetables in nutritional security has steered to some efforts for improving nutritive quality further. There are so many vegetables which regarded as noteworthy sources for various minerals, vitamins, and as well as for valuable nutraceutical compounds of plant origin.

For intensive farming, the prime objective of genetic improvement of crop plant was to upsurge the productivity of crops by altering the primary morphological and physiological attributes (Moore and Janick 1983). Nevertheless, during recent times, the requirement in farming has altered towards the importance of crop varieties with improved nutritional and quality traits. During the last three decades, breeding objectives have prioritized for the growing attention for obtaining new standard of quality traits, more particularly nutritive and nutraceutical value (Kumar *et al.* 2009). Improving quality parameters of food has become one of the main objectives of vegetable breeding as the public awareness related to nutraceutical compounds on human nutrition and health increasing day by day. During the course of domestication and genetic improvement of crop plants, several characters were left behind in the wild relatives, primitive, old and obsolete varieties.

Extensive screening of germplasm to find out genetic variation, together with conventional breeding and effective selection procedures is prerequisite to breed novel genotypes with improved nutritional quality. Furthermore, elaborative research is essential to estimate the influence of growing environment and agronomic packages on these newly developed nutritionally enriched genotypes with standard cultivars. Different techniques based on molecular biology can be efficiently exploited to identify, map and clone the gene(s) that regulate the synthesis pathways of carotenoid, ascorbic acid and flavonoid. Biofortification at the crop level can be achieved through the transfer of genes conferring enhanced nutritional traits directly into elite breeding lines and generating transgenic plants. Transgenic plants have been developed in several plant species for producing enhanced levels of beta carotene. Unlike traditional breeding, genetic engineering has the unique benefits to speed up, straight forward development of genotypes, simplicity, make possible for multiple and concurrent biofortification for various phytonutrients, and unlimited admittance to genetic diversity (gene from bacterium, animal and even totally synthetic gene or gene which is artificially tailored that do not present in nature).

Nutritional quality of vegetables

Vegetables are recognized as an indispensable component of balanced diets because they provide different vitamins, minerals, dietary fiber and phytochemicals in food we consume. Vegetables constitute a main part of the human diet across the globe and occupy crucial role in human nutrition by acting as sources of phytonutrients which includes different vitamins (*viz.*, C, A, B1, B6, B9, E), minerals, dietary fiber and phytochemicals (Craig and Beck 1999; Wargovich 2000). Consumption of vegetables in the daily diet improves digestive system, vision, and decreased risk various heart related ailments, diabetes, and cancer. Some phytochemicals found in vegetables are well known antioxidant and reduce the threat of chronic disease by neutralizing free radicals, detoxification of carcinogens, changing metabolic activation, and manipulating processes that alter the course of tumor cells. Each vegetable group has a distinct combination of phyto-nutrients which differentiate them from other groups and crops within same group (Dias 2012).

Crops of the Apiaceae family like carrot, celery and parsley are rich in flavonoids, carotenoids, ascorbic acid and vitamin E (Nielsen *et al.* 1999, Ching and Mohamed 2001, Horbowicz *et al.* 2008). In carrot, the levels of carotenoid have improved spectacularly during last forty years through traditional breeding and reached up to a

level of 1000 ppm on the basis fresh weight (Simon and Goldman 2007). The vegetables belonging to Compositae family i.e. lettuce and chicory are enriched with flavonoids, tocopherols and conjugated quercetin, (Crozier *et al.* 2000, Almeida 2006). The Cucurbitaceae vegetables (pumpkin, squash, melon, cucumber) are good source of vitamin C, carotenoids and tocopherols (Dhillon *et al.* 2012). All the legumes like bean, pea and soybean are rich in isoflavonoids and dietary fiber (Mishra 2012). Cruciferous vegetables including cabbage, broccoli, cauliflower, Brussels sprouts, kales, Chinese cabbage etc., are the richest sources of glucosinolates, minerals and carotenoids (Dias 2012, Singh *et al.* 2012). The glucosinolates of crucifers have been demonstrated to protect from cancer of lung, prostate, breast, and chemically induced cancers (Verhoeven *et al.* 1996, Traka 2010).

The utilization of solanaceous vegetables in traditional therapy is reported from prehistoric times. There are substantial variations in the phytonutrient content among the vegetables of solanaceae family (Dias 2012). As far as food composition concerned, the tomato has a distinctive nutritional and phytochemical composition. It contains noteworthy quantities of various type carotene (α -, β -, γ -, δ -carotene) varying in concentrations from 0.6 to 2.0 mg/kg (Albushita *et al.* 2000, Leonardi *et al.* 2000). Fresh peppers are considered as excellent sources of carotenoids, dietary fibre, ascorbic acid, vitamin K, and flavonoids (Bosland 1996). Red peppers also contain appreciable amount of lycopene and β -cryptoxanthin. The most important phytonutrients in chilli peppers are various capsaicinoids. More than twenty types of capsaicinoids either belong to capsaicin or dihydrocapsaicin were reported in chilli pepper (Nelson 1919). Phytonutrients present in brinjal include various phenolic compounds like chlorogenic acid and caffeic; and flavonoids like nasunin. Delphinidin- 3-(coumaroylrutinoside)-5-glucoside is also known as nasunin is predominant compound in brinjal. It is the component of the anthocyanin responsible for purple pigmentation in the peel of brinjal (Noda *et al.* 1998 and 2000). It is also considered as a decent source of vitamin K, magnesium, heart healthy copper, ascorbic acid, niacin vitamin B6 and folic acid (Ensminger *et al.* 1986, Wood 1988).

The breeding strategy

Improving the nutritional qualities of food crops were discussed before by Munger (1988), and Quebedeaux and Eisa (1990). Moreover, traits related to nutritional quality could be changed through hybridization followed

by selection. However, successes of breeding for nutritional quality might not always have an optimistic influence on nutritionally lacking populations as other limiting factors also involved. To circumvent the disappointment of realizing the genetic alterations only to find out, that the nutritionally improved varieties are inappropriate or unproductive for improving nutritional condition. Therefore the feasibility or operability of genetic improvement for nutritional quality as a realistic approach must be cautiously determined before it is started (Bliss 1999). The worth of any improvements must be calculated by the transformation in nutritive status and health condition of the folks consuming food stuffs obtained from nutritionally improved genotypes of crop plants. To undertake a breeding program for developing new genotypes of crop plants with enhanced nutritional quality, Welch and Graham (2004) recommended certain norms for the consumer acceptance of new genotypes like (a) productivity of the crop must be preserved or enhanced to guarantee extensive grower acceptance (b) the level of micronutrient enhancement obtained must have noteworthy influence on human health (c) the traits related to micronutrient enrichment essentially be relatively constant thru the growing condition (d) finally, the bioavailability of micronutrients in enriched genotypes certainly be verified (e) consumer acceptance must be verified to guarantee maximum influence on nutritional wellbeing. In breeding programs, a significant role is dedicated to the procedures utilized for the artificial selection of the preferred combination of characters, which comprises the association of genes controlling a number of linked traits in developing a completely balanced phenotype. Plant Breeders develop their selection procedure based on the assessment of phenotypic traits of the parental lines and on the hypothesized imminent outcomes. To circumvent the occurrence of breeding lines with negative effects, plant breeders generally reject all the genotypes with undesirable traits (Diamanti *et al.* 2011).

To breed nutritionally superior genotypes, vegetable breeders must plan their breeding work systematically. In planning a breeding program to breed nutritionally improved genotypes of vegetable crops, it is first essential to recognize genetic resources that breeders can utilize to enhance the nutritive value of vegetable crops. Mode of inheritance of the nutritional trait is also an important criterion to select an efficient breeding method. After the determination of the inheritance pattern of the nutritional trait breeder has to select the breeding methodology accordingly, which may be conventional or integrating modern marker technology or transgenic.

Germplasm characterization for nutritional traits

For the development of phytonutrient rich variety, characterization of the vegetable germplasm is considered as primary step to achieve the goal. High nutrient content can be found in cultivated variety, obsolete variety, and landraces or in wild related species. All the available genetic resources, even the wild relatives will have to thoroughly analyze for phytonutrient like micro and macro nutrient, vitamins, pigment and antioxidants. The data related to nutrient and phytonutrient will be used for genetic diversity analysis. It will lead to identification of high nutrient content lines, which may be used for the development of nutritionally improved vegetable varieties. Tomato shows genetic variability for beta carotene content that had been utilized to breed varieties with high carotene content. The highest levels of lycopene, vitamin C, phenolics and solids contents were found in the small fruited wild relative *Lycopersicon pimpinellifolium* (Hanson *et al.* 2004). Nuez *et al.* (2004) reported that *L. cheesmanii* contain high sugar and β -carotene; and has great potential for quality improvement breeding of tomato. Genotypic potential of fifteen genotypes of *S. lycopersicon* and *S. pimpinellifolium* for L- ascorbic acid content was evaluated in three growing conditions. The effect of growing conditions for the accumulation of L-ascorbic acid is reported to be highly genotype dependent (Leiva-Brondo *et al.* 2012). Adalid *et al.* (2008) characterized some *lycopersicon* accessions for high carotenoid and vitamin C content and identified the superior accessions for using in a breeding program design to improve carotenoid and vitamin C content in tomato fruit. Guil-Guerrero and Reboloso-Fuentes (2008) classified eight tomato varieties on the basis of moisture, crude protein, carbohydrates, total lipids, dietary fiber, ash, energy, vitamin C, fatty acids, carotenoid profiles, mineral elements, nitrate and oxalic acid. Twenty five totally dissimilar tomato cultivars and local tomato genotypes were evaluated to study the genetic variability for ascorbic acid and carotene content in mature fruits and reported that the highly significant genotypes could be effectively utilized in cultivars with high content of both compound (Markovic *et al.* 2007). Rosello *et al.* (2000) characterized twenty accessions of *L. pimpinellifolium* collected in Ecuador and Peru and tested for nutritive quality and were found suitable source material to develop varieties with high vitamin and TSS. Fifty three tomato genotypes were screened for their skin firmness, pericarp thickness, TSS, phosphorus, potassium, iron, zinc, copper, manganese, titratable acidity, β -carotene, lycopene and ascorbic acid. Considerable genetic diversity observed for most of the parameters, which

can be utilized for quality improvement of tomato varieties (Saha *et al.* 2009). Characterization of 49 accessions of underutilized tomato or related species revealed plenty genetic diversity; and BGV008057, BGV006863, BGV008060, BGV008365, BGV012627 and BGV008166 lines were found suitable for lycopene, β -carotene and ascorbic acid (Adalid *et al.* 2010). Kuti and Konuru (2005) reported significant genetic diversity for lycopene content in forty tomato varieties which includes F_1 hybrids, round fruited breeding line and cherry tomato types. The quality and health promoting effect of tomato fruits is directly associated to the composition of fruits. The characterization of *Solanum* genetic resources for nutritive value is important to select appropriate donor parental lines and wild species could be very useful in genetic improvement of tomato for fruit quality. Twenty varieties of *S. lycopersicum* and ten genotypes of related wild species were examined for sodium, potassium, calcium, magnesium, copper, iron, zinc and manganese. The wild genotypes belong to *S. cheesmaniae*, *S. pimpinellifolium*, and *S. habrochaites* were reported to have immense potential in improving mineral content of traditional tomato cultivars (Fernandez-Ruiz *et al.* 2011).

Hanson *et al.* (2006) reported very high diversity for superoxide scavenging activity, total phenolics, and ascorbic acid in eggplant (*Solanum melongena*). Pepper has significant role in human diets across the Globe and reported as a key source of many antioxidant compounds like vitamin C, phenolics, carotenoids and tocopherols. Sufficient information related to genetic divergence for the content and activity of antioxidant in *Capsicum* spp. Might contribute toward better human health. Evaluation of forty genotypes of *Capsicum* from core collection of AVRDC performed for five different carotenoids, vitamin C, alpha tocopherol and gamma tocopherol and total phenolics; and two assays for antioxidant activity. Sufficient divergence presents within *C. annuum* testified to upsurge the antioxidant content. Non-pungent *C. annuum* genotypes were reported to have significantly more β -cryptoxanthin, ascorbic acid, total phenolics and α -tocopherol content than pungent genotypes. Brown fruited genotypes reported to have ascorbic acid capsanthin, zeaxanthin, β -cryptoxanthin, β -carotene, α -tocopherol and lutein. Highest amount of ascorbic acid, carotenoids, and α -tocopherol were reported in red fruited 'Verdano Poblano' and 'Guajillo Ancho' (Hanson *et al.* 2004). *Capsicum baccatum* and *C. pubescens* known as Aji and rocoto, respectively and are originated in the Andean region. Till date these two species were not utilized in systemic breeding programme for *Capsicum*.

Composition and amount of content for red and yellow carotenoids, total phenolics and vitamin C analyzed in twenty three Aji genotypes, eight rocoto accession, and three *C. annuum* genotypes. In two different environments *C. baccatum* exhibits substantial variability for all the nutritional parameters studied. The antioxidant content in most of the Aji genotypes is either similar or higher than common chilli indicated that *C. baccatum* can be used as source for antioxidant compounds (Rodriguez-Burruezo *et al.* 2010).

Crude protein, true protein, lysine, methionine and tryptophan content were studied in four pea varieties and variation was observed in the composition of protein among the varieties (Saharan and Khtrapaul, 1994). Holasova *et al.* (2009) reported sufficient genetic variation for Lutein Content. Evaluation of CIAT bean core collection for micronutrient content showed sufficient genetic diversity for micronutrient content (Tohme *et al.* 1995). Graham *et al.* (1999) reported that highest degree of genetic variability that exists for Fe and Zn content in seeds of common beans which can be employed in breeding program. Pinheiro *et al.* (2010) reported high degree of variability for P, Fe, Zn, Cu, Mn and Ca in 155 bean collections.

Kushad *et al.* (1999) conducted an experiment with sixty five broccoli varieties observed the glucoraphanin as most important glucosinolate and there were twenty seven fold variations observed between the variety with highest and lowest concentrations. In cabbage, considerable variation have been reported for glucosinolates (Hansen *et al.* 2010), minerals (Singh *et al.* 2010c, 2013), carotenoids and vitamin C (Singh *et al.* 2010d, 2010e, 2011b) and antioxidant enzymes (Singh *et al.* 2010a). The variability for hydrophilic and lipophilic antioxidant capacity found among different broccoli genotypes suggested that potential efficacy from antioxidants will vary considerably from genotype to genotype (Kurilich *et al.* 2002). Feng *et al.* (2010) identified a carotenoid rich variety in Chinese cabbage having orange colour leaves contain seven fold more carotenoid compounds than white cabbage.

Murkovic *et al.* (2002) evaluated twenty two diverse genotypes varieties of pumpkin belong to either *Cucurbita pepo* or *Cucurbita maxima* and or *Cucurbita moschata*, including a cross between *C. maxima* \times *C. moschata* for carotenoid content and its composition and reported workable genetic diversity for the said traits. Yoo *et al.* (2012) reported variation of carotenoid, sugar, and ascorbic acid concentrations in watermelon. Genetic variability for valuable fruit quality traits like sucrose content as well as high carotenoid and ascorbic

acid contents in *Cucumis melo* was reported by [Burger et al. \(2006\)](#), and for minerals in ridge gourd ([Karmakar et al. 2013](#)).

Mode of inheritance of the nutritional trait

It is noteworthy to understand the inheritance pattern of the nutritional traits and their ability to combine with the yield and inherit to off-springs, as these will, define the breeding methodologies to be effective for enriching the traits in high yielding genotypes and varieties. It is prerequisite to generate extensive data regarding nutritional traits that could be used to determine the mode of inheritance. Concurrently there must have physiological and biochemical approach to determine the expression of the nutritional traits, that will directly lead to effective selection of breeding programs. Side by side, identification and development is the requirement of the time for molecular marker aided breeding programme of traits related to nutritional quality ([Graham et al. 1999](#)).

TSS, titratable acidity, vitamin C, reducing sugar, dry matter and carotenoids including lycopene and carotene are important quality parameters of tomato and showed non-additive and over-dominance inheritance pattern ([Kalloo, 1986](#)). The anthocyanin content in brinjal inherited through both additive and non-additive genes and reciprocal recurrent selection recommended for this trait ([Chadha et al. 1988](#)). Existence of epistasis, overdominance, or dominance complementation was reported for capsaicin and dihydrocapsaicin contents in chilli fruits ([Garces-Claver et al. 2007](#)). Segregation ratios for anthocyanin expression in F_2 and BC_1 populations of a cross between the processing tomato UC82B and LA1996 were consistent with a single dominant gene hypothesis ([Jones et al. 2003](#)). [Stommel and Haynes \(1994\)](#) reported inheritance of beta-carotene in tomato. Inheritance of pigmentation on fruit and beta-carotene content in segregating population fitted for single dominant gene model of inheritance and dominant genotype produced orange coloured fruits having high beta carotene. In carrot carotenoid type and amount are controlled by at least three genes. Degree of orange colour intensity seems to be a typical polygenic trait. Gene action studies for beta carotene content indicated additive and dominance effect as well as additive \times dominance and dominance \times dominance inter action as being significant ([Simon, 1992](#)). The savoy type genotypes of cabbage exclusively expressed the higher magnitude of heterosis for ascorbic acid which could be improved through heterosis breeding ([Singh et al. 2009a, 2011a](#)).

[Gupta et al. \(1984\)](#) reported the influence of additive

and non-additive genes for the inheritance of protein and potassium content in pea. Dominance variance was more important than additive variance for protein content in cow pea ([Tchiagam et al. 2011](#)). Only one dominant gene responsible for the inheritance of high Zn concentration in common bean seed ([Cichya et al.](#)). Segregation of seed coat color in F_2 confirmed significant of additive, dominance, and epistatic component and about five genes responsible for antioxidant activity in cowpea. Factors governing high antioxidant activity seemed to be the identical as those accountable for seed coat color with pleiotropic effect ([Nzaramba, 2004](#)).

The content of chlorophyll and carotenoid in muskmelon segregate together in an F_2 population of Yellow canary line \times line with green rind. On the other hand monogenic segregation is reported for the naringenin chalcone content and independent to former two pigments ([Tadmor et al. 2010](#)). [Hedau \(2002\)](#) reported dominant effect was more prominent than additive for phosphorus and calcium content in *Luffa acutangula*. [Sit and Sirohi, \(2000\)](#) analyzed forty five F_1 hybrids and ten parents of bottle gourd and observed over-dominance effect for phosphorus, calcium, iron and ascorbic acid content in fruits. Non-additive gene action was predominant for the inheritance of these traits. Predominantly the non-additive genetic component is responsible for the inheritance of antioxidants and mineral content in ridge gourd fruits and hybrid breeding might be useful to develop genotypes with high antioxidants and minerals content ([Karmakar, 2011](#)). The nutritive composition of cucumber can be enhanced through the incorporation of β -carotene genes from "Xishuangbanna gourd" into pickling cucumber. In F_2 generation 3:1 segregation ratio suggested single recessive gene responsible for β -carotene content ([Cuevas et al. 2010](#)).

Breeding methods

After identification of superior breeding lines or parental material and determination of mode of inheritance breeder have to decided the suitability of different breeding method for the development of varieties with very high nutrient content in vegetable crop. If the dominant component or dominant \times dominant components are more pronounced then they may go for hybrid breeding, otherwise selection would be efficient tools for the improvements nutritional traits. Some time biotechnological tool like genetic engineering is also help full in this respect.

Conventional breeding to improve nutritional quality of vegetable crops: Conventional breeding methods basically based on alone selection and

hybridization or in combination, have demonstrated as a high potential tool for enriching the nutritional quality in array of crop plants (Balyan *et al.* 2013; Farneti *et al.* 2015). Genetic improvement of nutritional quality can be achieved through mass selection or single plant selection targeting desirable traits or through intra specific or inter specific hybridization to produce new genotypes with enhanced nutritional quality. Genetic variability is essential for competent for successful selection of breeding strategy for enhancing nutraceuticals, and genetic variation for nutritional traits basically quantitative in nature (Parr *et al.* 2000; Stommel *et al.* 2015). Thus the traditional breeding method as well as conventional selection strategies may be employed for increasing the phytonutrients content in vegetables specially those of quantitative traits. For diversifying and increasing phytonutrients like carotenoids and flavonoids, in tomato fruits systematic and intensive research is going on worldwide. These efforts rely on the use of either single point mutations or quantitative trait loci (QTL) influencing the levels of these phytonutraceuticals. In tomato *hp* or *high pigment* mutants are appropriate example of the point mutation. In tomato *hp* mutants were incorporated in important genetic resources to enhance lycopene content (Levin *et al.* 2006).

Singh *et al.* (2009c and 2012) observed considerable parental and hybrid mean square for various mineral elements indicated significant genetic variability in cabbage. The multiple crossing breeding techniques like double hybridization, three way crossing, population improvement scheme like synthetics and composites breeding could be useful for increasing the mineral concentration in cabbage head. The cabbage genotypes CMS-GA and Red Cabbage excelled as good general combiners for enzymatic antioxidants, responsible for stress tolerance, longer stay-green character and longer shelf-life (Singh *et al.* 2009b, 2010b). Karmakar *et al.* (2013) conducted combining ability study for antioxidant properties in ridge gourd using hermaphrodite inbreds. Hedau (2002) studied heterosis, combining ability and gene action for calcium and phosphorus content in ridge gourd and reported that range of heterosis for calcium and phosphorus content varies from 0.54 to 21.30% and 3.29 to 22.74%, respectively. Geleta and Labuschagne (2006) used hybrid breeding to improve the vitamin C content in chili. Introgressions of segments of a chromosome from a wild relative, *Brassica villosa*, enhance glu-cosinolate levels in broccoli (Juge *et al.* 2007). Interspecific hybridization improved the protein content of cowpea (Hazra *et al.* 2006). For genetic improvement of vegetable soybean mutation breeding

has great potential. High protein content and low fibre content mutants identified for further evaluation (Kavithamani *et al.* 2010). Rosati *et al.* (2000) identified *Beta* mutant in tomato which reported for higher LYCB activity as compare to normal fruits.

Molecular breeding of healthy vegetables: Consumer interest in food materials having superior nutritive value is now all-time high, and most of them selecting diets based on the health promoting characteristics of the food. Investigation on the metabolic profile of *Or* gene mutants was enumerated and reported that β -carotene is the principal carotenoid compound in edible portion and synthesizing 100-fold more as compare to normal line (Li *et al.* 2001). Li and Garvin (2003) identified ten AFLP markers, tightly linked with *Or* locus and developed functional SCAR markers to simplify positional cloning of *Or* gene. Santos and Simon (2002) mapped QTL for beta carotene content in carrot utilizing the intercross population of domesticated orange and wild type genotypes; and medium orange (Brasilia) \times dark orange (HCM). Identification of three dominant loci namely *Y*, *Y1* and *Y2* had done which control differential distribution of alpha and beta carotene especially in xylem/phloem level in carrot. AFLP molecular marker for *Y2* in carrot has been successfully converted to PCR based co-dominant marker and can now be employed as a tool for MAS programs (Simon, 1992).

Hamid *et al.* (2012) identified novel quantitative trait loci for increased lycopene content and other fruit quality traits in a tomato recombinant inbred line population. Among the QTL identified for lycopene content two QTL which located on chromosomes 7 and 12, had very large effects and were consistent across generations. QTL analysis of fruit antioxidants in tomato using *L pennellii* introgression lines detected a total of 20 QTL including five for TACW, six for ascorbic acid, and nine for total phenolics (Rousseaux *et al.* 2005). In broad bean a *zt 2* gene specific SCAR marker identified that increased protein content and reduced fiber content in the seeds. In future it should help to identify tannin free broad bean varieties (Gutierrez *et al.* 2008).

Evaluation of RIL populations may be use full for the development of variety with high β -carotene content. Eight quantitative trait loci which influencing the β -carotene content in melon flesh were identified and each responsible for sufficient phenotypic variation ranging from 8-31%. One recognized gene in melon that encrypting β -carotene hydroxylase also mapped as a QTL. Six quantitative trait loci which responsible for noteworthy level of variation for β -carotene content and are potentially beneficial for marker aided selection

(Cuevas *et al.* 2008). The gene regulating b-carotene content was incorporated into cultivated background of cucumber from *Cucumis sativus* var. *xishuangbannanensis* known as Xishuangbanna gourd. Inheritance pattern of b-carotene in endocarp shown that the trait is controlled a single recessive gene. Seven SSR makers specific to endocarp carotene content were identified on linkage group three and mapped in cucumber chromosome along with the putative candidate gene. Furthermore, these SSR makers should be utilized in marker assisted breeding for developing cucumber germplasm with high beta carotene content in the fruits (Bo *et al.* 2011). Sinclair *et al.* (2004) identified two QTL affecting Vitamin C in melon and they were responsible for 14 and 12 percent phenotypic variation, respectively. Four out of the nine molecular markers reported steadily linked with sweetness of fruits.

Song *et al.* (2010) reported that the common cucumbers have low level of carotenoid *i.e.*, only 22 to 48 $\mu\text{g}/100\text{ g}$, but Xishuangbanna gourd has high level of carotenoid quantified as 700 $\mu\text{g}/100\text{ g}$ on flesh weight basis. Thus Xishuangbanna gourd has unique advantage as a germplasm to be used for enhancing nutritive value of the cucumber. Till date, there is lacking of information related to molecular understanding for the carotenoid content in cucumber. QTL linked with orange fruit flesh colour identified in two F_2 populations and could be further used in the marker assisted breeding for incorporation of the gene responsible for orange flesh colour of the commercial cucumber cultivars.

Genetic engineering for nutritional enrichment of vegetable crops: Genetic engineering facilitates vegetable breeders to integrate preferred transgene(s) into desirable back ground which may be well established varieties for enhancing their nutritive value significantly. Nevertheless it offers distinctive prospects to improve nutritive quality and bringing various health benefits. Different vegetables were genetically transformed to enhance their nutritional quality by increasing nutritive composition or improve flavour, and by reducing antinutritional factor including bitterness. Genetically transformed or engineered vegetables have unique advantage as edible vaccine for drug delivery. It can also increase the carotenoid content of crop plant by manipulating the metabolic sink through transgenic approach in vegetables. Transgenic carrots with increase Ca content have possibility to improve the uptake of Ca. Zinc fortified lettuce developed through genetic engineering will overcome the Zn deficiency. Deficiency of folic acid considered as an international health issue, could be solved with genetically engineered tomato having folic acid content. Coronary heart disease and

arteriosclerosis might be prevented with transgenic lettuce having increased tocopherol and resveratrol content (Dias and Ortiz 2012).

Characteristic colour of some vegetables is due to carotenoid pigments more specifically lycopene and beta carotene. Carotenoid pigments reported to have excellent antioxidant activities and beta carotene as precursor of vitamin A. Carotenoids are the product of the isoprenoid biosynthetic pathway. Therefore tinkering this pathway using genetic transformation might be improved the nutritive and organoleptic properties of vegetables. Transformation with bacterial gene encoding phytoene desaturase enzyme, which converts phytoene into carotenoid pigments in transformed plants could increase beta carotene content of tomato more than three times than normal control (Roemer *et al.*, 2000). Flavonoids are another class of polyphenolic secondary metabolites of plant origin, extensively reported for their antioxidant activities and reduced the threat of heart disease in humans. In tomato it is generally found in the fruit peel. Genetic variability for flavonoid content in the gene pool is very limited. The flavonoid profile of tomato fruit could be altered toward increasing pattern utilizing genetic engineering to over express enzymes responsible for the biosynthesis of flavonoid and transcription factors which control the genes in the pathway of synthesis. Substantial increase in the flavonoid content was reported in tomato genetically transformed with petunia *CHI-A* gene, that encoding chalcone isomerase (Muir *et al.* 2001). In tomato ten time enhanced flavonoid content reported through ectopic expression of the transcription factors *LC* and *CI* from corn (Le Gall *et al.* 2003). Cloning of *psy* gene from Arabidopsis to carrot enhance beta carotene content. Transformation of carrot with bacterial *crtB* gene reported ninety three time rise in carotenoid content (Maass *et al.* 2009). *Agrobacterium* mediated genetic transformation of lettuce with a mouse metallothionein mutant \hat{a} -cDNA reported to increase zinc content up to 400 $\mu\text{g}/\text{g}$ on dry weight basis (Zuo *et al.* 2002).

Conclusion

Sufficient consumption vegetables protect human body from different degenerative chronic diseases as are regarded as universal sources of phytonutrients. Nowadays consumers are very health conscious and they well understood the nutritional quality of vegetables; and when available at reasonable price may increase its inclusion in daily diet, in this manner conferring motivation to vegetable breeder for developing genotypes with enhanced nutritional quality. Therefore vegetable breeders have an exceptional chance to fulfil human

nutritional requirements by making available vegetable cultivars rich in nutrients and nutraceuticals. For most vegetables adequate genetic variability undoubtedly exists may be created through genetic engineering which may be useful in the breeding programme exclusively devoted to enhance nutritional quality. Vegetable breeder need to continue the evaluation of phytonutrient content among older as against newer cultivars of crop plants to identify the genetic mechanisms which control the production of phytochemicals (glucosinolates, thiosulfides and flavonoids) to identify genotypes loaded with diverse group of phytochemicals. A multidisciplinary research approach is more appropriate to execute a genetic improvement program utilizing conventional breeding as well as molecular marker aided breeding methods for cultivar development. Socioeconomic issues may be greater obstructions than biological limitations for effective alleviation malnutrition using strategies based on plant breeding.

सारांश

विश्व स्तर पर विशेषतः विकासशील देशों में पोषकीय कमी सबसे प्रमुख समस्या है जो आर्थिक, सामाजिक तथा व्यक्तिगत वृद्धि एक साथ मिलकर संकट उत्पन्न करते हैं। सब्जियाँ सन्तुलित आहार की अपरिहार्य घटक हैं क्योंकि मानव विकास के लिये ये विटामिन्स, खनिज लवण, खाद्य रेशा तथा पोषक तत्व प्रदान करते हैं तथा शाकीय लोगों के लिए उत्तम एवं सस्ते पोषक तत्वों के स्रोत हैं। एक शतक से लगातार बढ़ती जनसंख्या कृषकों तथा पादप प्रजनकों को क्रमशः लोगों के पेट भरने एवं उत्पादकता बढ़ाने के लिए मजबूर करते हैं। क्योंकि लोगों में मानव पोषण व स्वास्थ्य के प्रति वर्तमान में पोषक सान्द्रता वृद्धि एवं उन्नयन पौध/सब्जी प्रजनन का मुख्य उद्देश्य बन गया है। कुल स्थानीय किस्मों, पुरानी प्रजातियाँ, पूर्व प्रजनित लाइन एवं जंगली प्रजातियाँ पोषक तत्वों की अच्छी स्रोत हैं जो बहुजीनी प्रकृति के होते हैं। जिनमें उत्कृष्ट पृष्ठभूमि में स्थानान्तरित होने की क्षमता होती है। उपयुक्त बहुसंकरण प्रजनन पद्धति के साथ ज्यादा संख्या में समूह मूल्यांकन सब्जियों में पोषक तत्वों की सांद्रता वृद्धि में सहायक होंगे। सम्पूर्ण रूप में जैव प्रौद्योगिकी उपकरणों तथा आण्विक चिन्हक आधारित चयन विधि निश्चित तौर पर कार्य को गति प्रदान करेगा और सब्जियों में न्यूट्रीएन्ट बायोफोर्टिफिकेशन की सम्भावनाओं को सफलता प्रदान करेगा।

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