

**“PLANT PREBIOTICS AND HUMAN HEALTH: BIOTECHNOLOGY TO BREED
PREBIOTIC-RICH NUTRITIOUS FOOD CROPS”
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ABSTRACT

Microbiota within the gut plays essential roles in human health. Prebiotics are non-digestible complex carbohydrates that are fermented within the colon, yielding energy and short-chain fatty acids, and selectively promote the expansion of Bifidobacteria and Lactobacillus within the digestive tract. Fructans and inulin are the best-characterized plant prebiotics. Many vegetable, root, and tuber crops similarly as some fruit crops are the best-known sources of prebiotic carbohydrates, while the prebiotic-rich grain crops include barley, chickpea, lentil, lupin, and wheat. Some prebiotic-rich crop germplasm has been reported in barley, chickpea, lentil, wheat, yacon, and Jerusalem artichoke. Some major quantitative trait loci and gene-based markers related to high fructan are known in wheat. More targeted search in genebanks using reduced subsets (representing diversity in germplasm) is required to spot accessions with prebiotic carbohydrates. Transgenic maize, potato, and sugarcane with high fructan, with no adverse effects on plant development, are bred, which suggests that it's feasible to introduce fructan biosynthesis pathways in crops to supply health-imparting prebiotics. Developing prebiotic-rich and super nutritious crops will alleviate widespread malnutrition and promote human health. A paradigm shift in a very breeding program is required to realize this goal and to confirm that newly-bred crop cultivars are nutritious, safe, and health-promoting.

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1. Introduction

The microbial genome or microbiome includes complex microorganism mixtures that

have co-evolved with their human hosts. Humans harbor over 100 trillion cells of microbial communities that populate various sites in their anatomy [1]. Many species of bacteria are found within the channel especially within the colon, where this flora is basically anaerobic. Diet variation modulates the composition of gut microbiota. The composition of gut microbiota and therefore the metabolic interactions among its species may affect food digestion and energy harvest. An increased understanding of the mechanisms involved within the interactions involving gut microbiota, host, and diet will open up the avenues to treat complex human diseases [2,3,4,5].

Prebiotics has been characterized as a gaggle of carbohydrates that resist digestion and absorption within the duct (small intestine); which are fermented by the gut (large intestine) microbiota, selectively promote the expansion and activity of a limited number of colonic bacteria, and alter the colonic microflora balance towards a healthier composition [6,7,8]. Prebiotics consumption may enhance immune function, improve colonic integrity, decrease both incidence and duration of intestinal infections, down-regulate allergenic response, and improve digestion and elimination [9]. Some cereal grain oligosaccharides may function as prebiotics and increase the amount of beneficial bacteria within the large bowel [8,10,11]. Likewise, prebiotics also can improve uptake of calcium, iron, and zinc, and significantly decrease carcinoma, the amount of triglycerides and cholesterol [8,12,13,14,15,16].

Overweight and obesity cause 3.4 million deaths, 3.9% of years of life lost, and 3.8% of disability-adjusted life-years (DALYs) worldwide. Populations with a body mass index (BMI) of 25 or greater are more within the developed (up to 38%) than within the developing (up 13.4%) world. Children and adolescents within the developed world are the foremost affected. Overweight and obesity have therefore become a serious global health challenge [17]. Individuals with BMI above 25 are at increased risk of diabetes, cardiovascular diseases, liver disease (non-alcoholic), and hypertension [18,19], which significantly impact public health costs. The evidence to this point suggests that gut microbiota are involved within the pathogenesis of obesity

[19,20,21]. Obese and lean individuals present different microbiota composition profiles [22,23,24]. Obese people use more energy from the diet [22,23,25,26]. The dietary intervention (prebiotics) impacts gut microbial diversity and human health, including obesity [19,22,27,28,29].

Higher intake of dietary fibers plays a crucial role in reducing the chance of disorder, regulating weight management and immune function, and shaping microbial diversity within the human canal [30,31,32]. Whole grains are concentrated sources of dietary fiber, resistant starch, oligosaccharides, and carbohydrates that escape digestion within the gut and are fermented within the gut. The fibers that escape digestion within the gut are fermented within the gut to supply short-chain fatty acids (SCFAs), which are rapidly absorbed within the colon to produce additional energy to the host [30] and stop the establishment of doubtless pathogenic intestinal microbes [33]. SCFA production indicates microbiota metabolic activity. The shift within the gut microbiome of humans consuming noble fibers like polydextrose and soluble corn fiber significantly affects the relative abundance of bacteria at the category, genus, and species level [34] as noted in humans who consume a high vegetable diet versus those fed with a refined grain diet without vegetables [35]. This finding shows the dominant role of the diet in shaping the gut microbial diversity [30,33,34,35] and provides means for elucidating the role of gut microbiota on the subtle balance between health and disease [30].

This short critique provides an summary on plant prebiotics sources and variability; the genotype x environment interaction effects, the genetic and molecular basis of synthesis of fructans, and progress towards designing prebiotics-rich and nutritionally-dense food crops need an interdisciplinary approach among food science, nutrition, and genomics-led crop breeding to tap microbiota and plant genetic resources diversity.

2. Prebiotic carbohydrates in plants

To date, fructooligosaccharides (FOS), inulin, and galactooligosaccharides (GOS) from plants are the best-known sources of prebiotics. additionally, the raffinose family of oli-

polysaccharides and resistant starch (the type that's not absorbed within the gastrointestinal tract) has also been recognized as prebiotic carbohydrates because these aren't absorbed within the intestine and promote the expansion of beneficial bacteria within the gut [36,37]. additionally, some polysaccharides found in plant cell walls, like xylans and pectins, have also been recognized because the potential sources for diverse polysaccharides to supply new prebiotics [38].

Table 1. Genetic variation for prebiotic carbohydrates reported in cereal and legume, root and tuber, and fruit and vegetable crops.

Crop species	Summary of variation reported	Referen
Cereal and legume crops		
Barley (20)	Grain fructan, 0.9 to 4.2 g 100 g ⁻¹ , KVL 1113 and KVL 1112 being highest	[48]
Lentil (10)	Sorbitol, 1039 to 1349 mg 100 g ⁻¹ ; mannitol, 160 to 294 mg 100 g ⁻¹ ; raffinose and stachyose, 2319 to 2793 mg 100 g ⁻¹ ; verbascose, 922 to 1968 mg 100 g ⁻¹ ; and nystose, 52 to 79 mg 100 g ⁻¹	[57]
Durum wheat (10)	Insoluble dietary fiber, soluble dietary fiber and total dietary fiber 102–181, 18–37 and 127–199 g kg ⁻¹ dry weight, respectively	[44]
Lentil (22)	Raffinose, stachyose, and verbascose 1.6 to 2.4 g, 1.7 to 2.9 g, and 1.2 to 1.9 g 100 ⁻¹ dry matter, respectively	[89]
Chickpea (19)	α-galactooligosaccharide (α-GOS), 6.35 to 8.68%, Ciceritol the main sugar	[54]
Wheat (62)	Grain fructan in cultivars 0.66 to 2.27% dry weight; germplasm 0.7 to 2.9% dry weight; advanced lines > 2% dry weight	[43]
Einkorn wheat, maize and rice	Inulin 55–85, 24–27, and 1.7 to 8.4 g kg ⁻¹ in einkorn wheat, maize and rice, respectively	[47]
Rye (19)	Arabinoxylans 26 to 41 and fructan 45 to 64 g kg ⁻¹ dry matter	[49]

Fruit and vegetable crops

- Jerusalem artichoke (79) Inulin, 55.3 to 74.0% dry weight, JA 37 and CN 52867 promising for both yield and inulin [40]
- Fruits (32) and vegetables (41) Most fruits, except nectarine (0.89 mg g^{-1} fresh weight), contain low amount of FOS; vegetables with high FOS: scallion 4.1 mg g^{-1} , onion 2.24 mg g^{-1} , garlic 1.76 mg g^{-1} , and Jerusalem artichoke 1.6 mg g^{-1} fresh weight [94]
- Varieties of plant foods (47) Garlic and Jerusalem artichoke had high inulin-type fructan (19.4 to $29.2 \text{ g } 100 \text{ g}^{-1}$ fresh weight) than shallot and red onion (3.6 to $8.8 \text{ g } 100 \text{ g}^{-1}$ fresh weight); FOS highest in Jerusalem artichoke ($5.2 \text{ g } 100 \text{ g}^{-1}$ fresh weight) [95]
- Bulb (3) and roots/tubers (7) Inulin type fructan 27 to 42% dry weight in garlic, shallot and onion; sweet potato, white radish, cassava and yam bean contain 0.42 to 2.14% [96]
- Fruits and vegetables (13) Jackfruit (flesh, 98 mg g^{-1} ; seeds, 29 mg g^{-1} dry extract), okra (49 mg g^{-1} dry extract), and palm fruit (pericarp, 14 mg g^{-1} ; flesh, 47 mg g^{-1} ; embryo, 34 mg g^{-1} dry extract) rich in oligosaccharides [97]
- Pitaya (dragon) Red-fleshed dragon fruits contain more oligosaccharides 89.6 g kg^{-1} than white-fleshed types, 86.2 g kg^{-1} fresh fruit weight [98]

Onion (15)	Fructan 0.84 to 3.04%, San Juan de la Rambla being highest in fructan	[99]
Fruits (43) and vegetables (60)	High fructan vegetables: garlic, artichoke, shallots, leek bulb, and onions (1.2 to 17.4 g 100 g ⁻¹ fresh weight); fruits with detectable fructan: longon, peach, persimmon, and melon (0.21 to 0.46 g 100 g ⁻¹ fresh weight)	[100]

Figure in bracket within the first column refers to either the number of accessions within a crop or number of different crop species evaluated for prebiotic compounds.

3. Novel sources of variation

A literature search (2003–2014) revealed the presence of prebiotic carbohydrates in a very number of food crops, with vegetable and root and tuber crops being the predominant sources (Table 1). as an example, garlic (*Allium sativum* L.), Jerusalem artichoke (*Helianthus tuberosus* L.), leek (*A. ampeloprasum* L.), okra (*Abelmoschus esculentus* L. Moench), onion (*Allium cepa* L.) and shallot (*A. cepa* L. var. *aggregatum*) among vegetables; dragon fruit (*Hylocereus* species), jack fruit (*Artocarpus heterophyllus* Lam), nectarine (*Prunus persica* L. Batsch), and palm fruit (*Borassus flabellifer* L.) among fruits; chicory (*Chicorium intybus* L.) and yacon [*Smallanthus sonchifolius* (Poepping and Endlicher) H. Robinson] among root crops; or the tuber crops dahliya (*Dahlia* species) and gembili (*Dioscorea esculenta* (Lour.) Burk.) are the most important sources of fructans. Yacon accessions with high fructans include AJC 5189, ASL 136 and MHG 923 [39], while those from Jerusalem artichoke are JA 37 and CN 52687 [40]. More recently, the dicot family of vegetables, which incorporates *Benincasa hispida*, calabash, balsam pear, *Trichosanthes anguina*, and *Cucurbita maxima* has been reported nearly as good source of digestible and indigestible fibers, with significant prebiotic properties [41]. additionally, mushroom [*Agaricus bisporus* (J.E. Lange) Emil J. Imbach] has also been reported as potential source of prebiotic carbohydrates [42].

Barley (*Hordeum vulgare* L.), chickpea (*Cicer arietinum* L.), lentil (*Lens culinaris* Medikus), and wheat (*Triticum aestivum* L.) show genetic variability for prebiotic carbohy-

drates in grain crops (Table 1). Huynh et al. [43] evaluated in glasshouse and within the field 62 bread wheat cultivars and breeding lines of diverse origin for grain fructan. They detected significant genotypic variation for grain fructan, with no evidence of strong genotype \times environment interaction. The fructan contents of field-grown grain samples were positively correlated ($r = 0.83$) with those of glasshouse-grown samples of the identical cultivars. The grain fructan content among 19 cultivars varied from 0.66 to 2.27% grain dry weight, while in a very set of diverse germplasm it ranged from 0.7 to 2.9%. Cultivars like Sokoll, Halberd and Cranbrook had the best levels of grain fructan (glass house: 1.24 to 1.58%, field: 2.2 to 2.27%). Advanced lines had grain fructan above 2%. Marotti et al. [44] detected large differences in dietary fibers among modern and ancient corn cultivars. The insoluble dietary fiber (IDF), soluble dietary fiber (SDF) and total dietary fiber ranged from 102 to 181, 18 to 37, and 127 to 199 g kg⁻¹ dry weight, respectively. Colon bacteria ferment SDF easily, rapidly and completely. In vitro research further revealed that SDF selectively proliferate microbial growth, with fibers from the Kamut®Khorasan (ancient durum wheat) and Solex (modern durum wheat) promoting maximum growth of *Bifidobacterium pseudocatenulatum* B7003 and *Lactobacillus plantarum* L12 strains within the channel [44]. Sweet wheat [45] – a double mutant lacking GBSSI and SSIIa genes – had about twice the maximum amount total dietary fiber and 7-fold higher concentration of low-molecular-weight soluble dietary fiber, largely fructan, as compared to parental or wild-type line [46]. Sweet wheat germplasm is a wonderful source that will be wont to raise fructan levels by crossing it with other high fructan lines [45]. Some einkorn wheat (*Triticum monococcum*) germplasm contain 2 to three times greater inulin than maize (24–27 g kg⁻¹) [47]. Likewise, barley cultivars like KVL 1113 and KVL 1112 are reported to contain grain fructan as high as 3.9 to 4.2 g 100 g⁻¹ [48]. Rye (*Secale cereale* L.) grains are another source of rich dietary fiber. the full dietary fiber among 19 cultivars varied from 147 to 209 g kg⁻¹ dry matter, of which 26 to 41 and 45 to 64 g kg⁻¹ dry matter were arabinoxylans and fructan, respectively [49].

Resistant starches (RS 1, RS 2, RS 3 and RS 4), which escape digestion in gut but fer-

ment within the colon by the resident microflora to supply SCFAs, are receiving greater attention because of their potential role in promoting human health [50]. RS 2 and RS 4 promote distinct microflora, impacting colon health [51]. Their content ranges from 12 to 45 g kg⁻¹ dry weight, among ancient and modern *Triticum turgidum* cultivars.

Grain legumes are rich sources of dietary fiber. Lupin and chickpea kernel-derived fiber stimulates colonic bifidobacteria growth and contributes to colon health [52,53]. Chickpea grains are an honest source of α -galactooligosaccharide (α -GOS), which varied from 6.35% to 8.68% dry matter among 19 chickpea cultivars, with ciceritol and stachyose, respectively, accounting for 50% and 35% of the whole α -GOS [54]. Chickpea accession '171' had the very best α -GOS (8.68%) and lowest sucrose (2.36%), which can be accustomed obtain α -GOS to be used as a prebiotic in functional foods. Chickpea raffinose, another α -GOS was demonstrated to modulate the intestinal microbial composition to push intestinal health in humans [55,56]. Johnson et al. [57] reported significant variation for prebiotic carbohydrates, with raffinose, stachyose, sorbitol, and verbascose being predominant sources of prebiotic carbohydrates in lentil. Other plant products with significant prebiotic properties include almond (*Amygdalus communis* L.) seeds and bamboo [*Gigantochloa levis* (Buluh beting)] shoot crude polysaccharides (BSCP), both promote the expansion of beneficial microbes within the gut [58,59].

Research on identifying genetic variation for prebiotic carbohydrates in most of those crops is in its infancy. However, there's a growing awareness to develop "whole-some" functional food for improving human health. Core [60] and mini core [61] collections that represent diversity of the complete collection of a given species preserved in an exceedingly genebank are reported in most of the grain crops [62,63]; thus suggesting that these may well be used as resource to spot prebiotic-rich germplasm to be used in crop breeding. Likewise, many genebanks have large germplasm collections of fruits, vegetables, and root and tuber crops (Fig. 1 and Table 2), which were previously reported as source of high fructans (Table 1). there's a requirement to develop repre-

sentative subsets in these crops, which might be systematically evaluated for prebiotic carbohydrates.

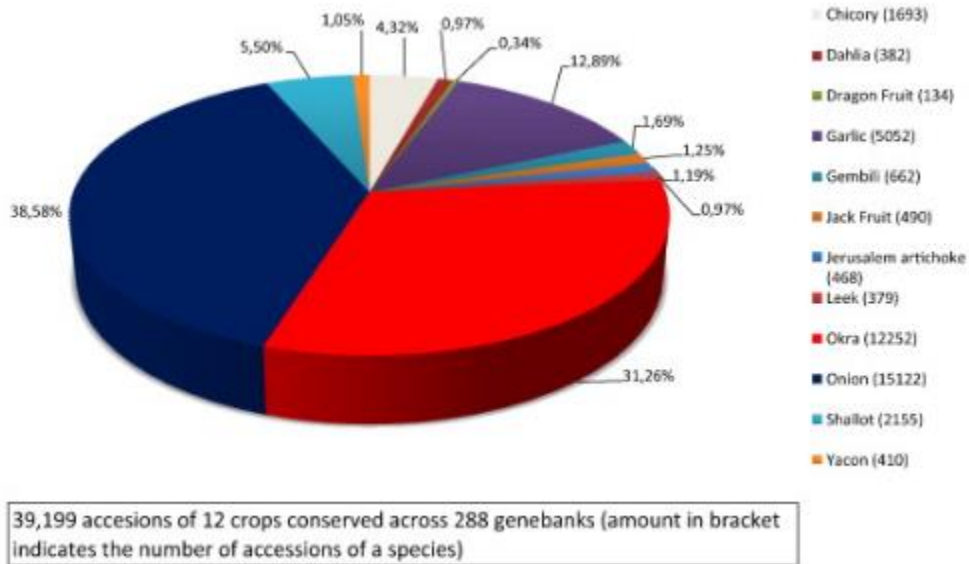


Fig. 1. Proportion of accessions representing 12 fruit, vegetable, root and tuber crops preserved across 288 genebanks globally (Source: <http://apps3.fao.org/views/>).

Table 2. Select genebanks holding major **germplasm** collections of chicory, dahlia, dragon fruit, gembili, garlic, jack fruit, Jerusalem artichoke, leek, okra, onion, shallot and yacon.

	Accession number
Jerusalem artichoke	
Institute of Field and Vegetable Crops Novi Sad, Serbia	120
North Central Regional Plant Introduction Station, USA	107
Leibniz Institute of Plant Genetics and Crop Plant Research, Germany	102
Onion	
National Res. Centre for Onion and Garlic, India	1300
Northeast Regional Plant Introduction Station, Cornell University, USA	1156
Royal Botanic Gardens, Kew, United Kingdom	976
Garlic	
National Res. Centre for Onion and Garlic, India	750
Vegetable Section Olomouc, Czech Republic	623
Asian Vegetable Research and Development Center, Taiwan, China	505

Jack fruit

Laboratoire d'Ecologie Moléculaire, Université de Pau, France 81

Regional Station Thrissur, NBPGR, India 72

Department of Agriculture Sabah, Malaysia 57

Dragon fruit

Programa de Recursos Genéticos Nicaragüenses, Nicaragua 50

Southern Fruit Research Institute, Viet Nam 24

Departamento Nacional de Recursos Fitogenéticos y Biotecnología, Ecuador 18

Yacon

Estación Experimental Agraria Baños del Inca, Perú 123

Universidad Nacional de Cajamarca, Perú 110

Estación Experimental Agraria Andenes, Perú 89

Shallot

Science and Advice for Scottish Agriculture, United Kingdom	707
Leibniz Institute of Plant Genetics and Crop Plant Research, Germany	329
Station d'Amélioration Pomme de Terre et Plantes à Bulbes, France	319

Leek

Agriculture and Food Research Council, United Kingdom	128
Leibniz Institute of Plant Genetics and Crop Plant Res., Germany	95
The Netherlands Plant Research International, Netherlands	88

Okra

Regional Station Akola, NBPGR, India	2286
University of Georgia, USA	2220
University of the Philippines, Los Baños College, Philippines	942

Dahlia

Research Institute of Landscaping and Ornamental Gardening, Czech Republic	224
Vytautas Magnus University, Lithuania	115
National Plant Material Center USDA/SCS, USA	15

Gembili

Dry-lowlands Research Programme, Papua New Guinea	149
Dodo Creek Research Station, Solomon Islands	112
University of the Philippines, Los Baños College, Philippines	73

Chicory

Station de Génétique/Amélioration des Plantes, INRA, France	400
Unité Expérimentale d'Angers, Groupe d'Étude et de contrôle des Variétés et des Semences (GEVES), France	251
Leibniz Institute of Plant Genetics and Crop Plant Res., Germany	223

4. Genotype × environment interaction

Research thus far suggests that almost all of the nutritional traits are highly influenced by environment (location) and genotype × environment interaction effects, with environments having major effects [64]. In a very trial involving 10 lentil cultivars evaluated at two locations for 2 years, Johnson et al. [57] reported significant year and site effects for sorbitol, mannitol, and verbascose, and year × location × cultivar effects for sorbitol, while Putta et al. [40] detected genotype × environment interaction for inulin content in Jerusalem artichoke. The environmental effects in both trials were the foremost significant. Genotype × environment interaction ($P \leq 0.001$) is additionally reported for the raffinose family of oligosaccharides [65]. These results reinforce the requirement for multilocation evaluation of germplasm/cultivars to identifying those with high prebiotic carbohydrates to be used in plant breeding.

5. Genomic regions related to prebiotics

Quantitative trait loci (QTL) related to fructan and inulin is thought in wheat [66]. QTL on chromosomes 2B, 3B, 5A, 6D, and 7A are related to high fructan in an exceedingly doubled haploid (DH) mapping population involving a high-fructan breeding line (Berkut) and also the low-fructan cultivar Krichauff [66]. QGfc.aww-6D.2 and QGfc.aww-7A.1 had the biggest effects (17 and 27% of the full phenotypic variation, respectively). Validation in another mapping population involving Sokoll and Krichauff confirmed that QGfc.aww-6D.2 and QGfc.aww-7A.1 show similar effects. Gene-based single nucleotide polymorphism (SNP) markers have successfully been mapped to a serious QTL (QGfc.qww-7A.1) [66], which affects the buildup of fructan in wheat grains [68]. Furthermore, the alleles controlling high- and low-fructan were related to fructan production in a very diverse set of 128 wheat lines [67]. Stem-water soluble carbohydrate (SWSC) in wheat consists mainly of fructans and sucrose and may function a source for grain development and fructan synthesis [68]. Genes affecting SWSC [69] could likely affect grain fructan accumulation. Likewise, two major QTL for inulin content, Xgcag9 on chromosome 2BL-2 and Xgwm499 on chromosome 5BS contributed respectively 20 and 15% of the phenotypic variation during a DH population involving AC Reed and Grandin [66]. There are QTL with major effects on the fructan level of the vegetative tissues of barley, onion, and ryegrass [70,71,72].

Arabinoxylans represent the main dietary fibers present in wheat bran and its hydrolysis ends up in the formation of arabinoxylan oligosaccharides (AXOS) [73], which incorporates a strong prebiotic effect [74]. QTL mapping and validation revealed that QGax.aww-2A.1 and QGax.aww-4D.1 had a serious effect on wheat grain arabinoxylan accumulation [75], which are apparently different at two QTL with large effects on grain fructan that are in chromosome 6D and 7A [66].

Fructans, the most important component of water-soluble carbohydrate temporarily reserved within the stem are used for grain filling by temperate cereals. Research shows

that sucrose: sucrose 1-glucosyltransferase (1-SST), sucrose: fructan 6-glucosyltransferase (6-SFT), and fructan–fructan 1-fructosyltransferase (1-FFT) enzymes are involved in fructan synthesis in barley and wheat [76,77,78]. More recently, Kooiker et al. [79] investigated the effect of the TaMYB13-1 gene and its influence on fructan synthesis in transgenic wheat. TaMYB13-1 overexpression resulted in up-regulation of all three families of fructosyltransferases and γ -vacuolar processing enzyme (γ -VPE-1) involved within the maturation of fructosyltransferases within the vacuole. The overexpression of those target genes was highly correlated in recombinant inbred lines and through stem development similarly because the transgenic and non-transgenic wheat, supporting an immediate regulation of those genes by wheat transcription factor TaMYB13-1. Further TaMYB13-1 overexpression in wheat led to enhanced fructan accumulation within the leaves and stems and also increased spike weight and grain weight per spike in transgenic plants under water-limited environments. This finding suggests that TaMYB13-1 plays a vital role within the coordinated up-regulation of genes necessary for fructan synthesis and may be used as a molecular tool to enhance the high fructan trait.

6. Designing prebiotic-rich and super-nutritious crops

Marker-assisted selection (MAS) is employed in plant breeding to hurry and increases the precision of genetic progress; and when integrated into optimized molecular breeding strategies, it also can lower the price of selection [63]. As noted above few validated QTL with major effects and related to grain fructan or arabinoxylans are known in wheat. Nguyen et al. [75] identified microsatellite marker gpw-95001-4D nearest at grain arabinoxylans QTL (QGax.aww-4D.1), while Huynh et al. [66] reported microsatellite marker gwm681-7A, closely related to a serious grain fructan QTL (QGfc.aww-7A.1). Huynh et al. [67] successfully mapped gene-based SNPs, Ta1-FFT, Ta6-SFT, and TaWIVRV, co-located with one another and with the grain fructan QTL, QGfc.aww-7A.1 [66]. SNP alleles controlling high or low fructan are related to fructan production in diverse 128 wheat lines [66]. These markers are available for the indirect selection of segregants with high grain fructan or arabinoxylan concentrations in wheat. as an example,

the validated QTL QGfc.aww-7A.1 with a significant effect and SNP-based markers could also be used for targeted enhancement of grain fructan in wheat.

Chicory, artichoke, and onion are good sources of inulin molecules, which are synthesized by two enzymes, sucrose: sucrose 1-SST and fructan: fructan 1-FFT [80] with a series length of up to 200° of polymerization [81]. Tubers of transgenic potato (*Solanum tuberosum* L.) containing 1-SST and 1-FFT genes had the total spectrum of inulin molecules present in globe artichoke, with no adverse effect on plant growth or tuber yield [82]. The insulin-containing tubers however display a discount in starch content, which suggests that the synthesis of inulin doesn't increase tuber storage capacity. Hellwege et al. [82] found that inulin produced in potato tubers is indistinguishable from inulin isolated from artichoke roots. More recently, Stoop et al. [83] produced transgenic maize and potato containing 1-SST and 1-FFT from Jerusalem artichoke. Transgenic maize expressing 1-SST or 1-SST and 1-FFT driven by endosperm-specific promoter produced 3.2 mg g⁻¹ kernel inulin-type fructan, with no adverse effect either on kernel development or in germination. Potato tubers expressing 1-SST accumulated 1.8 mg inulin g⁻¹ tuber, while the tubers with a combined expression of 1-SST and 1-FFT accumulated 2.6 mg inulin g⁻¹ tuber. The introduction of a fructan biosynthetic pathway in a very high-sucrose maize background increased inulin accumulation to 41 mg g⁻¹ kernel, indicating that sucrose availability is limiting fructan production in transgenic maize.

Sugar beet (*Beta vulgaris* L.) is an economically important crop but lacks enzymes to supply fructans. it's a chic source of sucrose that accumulates within the vacuole of its taproot cells. Transgenic sugar beet containing onion fructosyltransferases 1-SST and 6G-FFT had an efficient conversion pathway of sucrose into complex, onion-type fructans, with none adverse effect on taproot growth or the loss of storage carbohydrate content [84,85]. More recently, Hanlie Nell succeeded in introducing the 1-SST and 1-FFT from artichoke in sugarcane (*Saccharum officinarum* L.). Transgenic sugarcane plants accumulated inulin up to 165 mg g⁻¹ fresh weight, which is appreciate that found in native plants; therefore, exhibiting great potential as a future industrial inulin source. It

seems therefore feasible to introduce fructan biosynthesis pathways in both staple and industrial crops, as already noted in transgenic maize, potato, sugar beet, and sugarcane health-imparting prebiotics to be used in functional food to market human health.

Malnutrition is widespread and casts enormous negative socio-economic impact at the individual, community, and national levels [86]. The planet population by 2050 is anticipated to be around 9 billion, and providing enough nutritious food (protein and prebiotic-rich and micronutrient dense) and safe (free from toxic compounds and microbial toxins) to humankind is that the greatest challenge within the 21st century. To date, the research has shown that nutritional traits are often combined into the improved genetic background using both conventional and nonconventional plant breeding. For instance, seed iron-dense beans and rice, maize with high tryptophan and lysine, or β -carotene-rich maize and sweet potato cultivars are developed and are commercially grown in some areas of Africa, Asia, Central, and South America, while “Golden Rice 2” variants (containing high β -carotene) are developed using transgenic breeding and are being introgressed into several Asian rice cultivars [64].

Advances in prebiotic research have conclusively demonstrated that fructans, and therefore the fructooligosaccharides – including inulin – are nondigestible fibers promoting the expansion of beneficial microbiota within the gut, which positively impact micronutrient absorption and utilization in humans [7,8,11,13,16]. Exploratory research to this point suggests that it's possible to spot prebiotic-rich genetic resources, as evidenced in barley, wheat, chickpea, and lentil among grain crops. Likewise, some fruit, vegetable, root, and tuber crops have also been identified as rich sources of prebiotic carbohydrates. A worldwide search of genebank data repository revealed that a lot of the latter groups of crops (fruit, vegetable, root, and tuber) have large germplasm collections (Fig. 1 and Table 2), which has to be scientifically scrutinized to create representative subsets and evaluated for prebiotic carbohydrates. A paradigm shift in plant breeding is required to include nutritional quality (prebiotic-rich and nutrient-dense) as a very important objective that ensures that newly developed cultivars aren't nutritionally inferior

[64].

7. Perspectives

Humans are confronted today with diet-related health problems that in history were of minor importance [87]. Human gut microbiota is populated by an array of bacterial species, which have established multiple mechanisms to influence human health. Diet encompasses a dominant role in shaping gut microbial diversity and human health. Inulin and fructan are the best-characterized prebiotics obtained from plants. Limited search has revealed sufficient genetic variation for inulin and fructan in barley and wheat grains. Prebiotic compounds are abundant in vegetable, root, and tuber crops additionally in some fruit crops. The targeted look for identifying genetic variability for prebiotics is yet to start. Genebanks are the repository of an outsized collection of plant germplasm. Reduced subsets representing a diversity of entire germplasm collection of a given species preserved within the genebanks are available in most of the grain crops, which require evaluation to spot novel germplasm rich in prebiotic carbohydrates to be used in plant breeding. Crops lacking such representative subsets require developing these germplasm samples to capture the variety available within the genebank.

Chicory, artichokes, and onion are good sources of fructan. Transgenic maize and potato containing 1-SST and 1-FFT genes from Jerusalem artichoke, transgenic sugar beet containing 1-SST and 6G-FFT genes from onion, and transgenic sugarcane containing 1-SST and 1-FFT from globe artichoke have shown high fructan with no adverse effect on plant development, which clearly indicates that it's feasible to introduce fructan biosynthesis pathways in both staple and industrial crops, to provide health-imparting prebiotics to push human health.

The evidence up to now strongly suggests that manipulation of gut microbiota represents a unique approach in treating obesity and related metabolic disorders. Culture-independent assays and modern high-throughput sequencing and bioinformatics tools

(not the topic of this review) provide opportunities to research the taxonomic and functional diversity of the gut microbiota. These developments are powerful means of understanding the contribution of the human microbiome to health and its potential as a target for therapeutic interventions [88]. The dietary interventions (prebiotics) to induce microbial change offer an excellent opportunity towards improved human health [20,21,22,27]. Increasing the degree of prebiotics along with other quality traits (fat, protein, minerals, and vitamins) in staple food crops is, therefore, a crucial strategy to reinforce the nutrition and health of malnourished people worldwide.

Research thus far suggests that it's feasible to develop nutritionally dense crop cultivars to fight widespread malnutrition, more specifically within the developing world. It's encouraging to notice that plant breeders are aware that other quality traits like micronutrients, vitamins, and now prebiotics are equally important as are oil and protein. They're progressively taking a holistic approach to breed crops that provide wholesome food promoting human health at large. A multidisciplinary approach involving all stakeholders is required to develop nutritionally dense and prebiotic-rich cultivars adapted to diverse agro-ecosystems.

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