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Deliverable 11 – Agenda for the next 5 years for agronomy and plant breeding research

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Executive Summary

Executive Summary is the introductory chapter of each Deliverable.
This chapter should aim at outlining the main topics of work reported, firstly by giving a brief context analysis and then deepening the work done.
This text should be brief and included in this single page.

Acrylamide (C_3H_5NO) represents one of the potential high risks to human health due to its neurotoxicity and genotoxicity. Acrylamide is a white, odourless and water-soluble molecule, which is rapidly absorbed through the skin and from the gastro-intestinal tract. The main chemical process that causes the formation of acrylamide is known as "Maillard cascade reactions", that are caused by the reaction between reducing sugars, such as glucose, fructose or maltose, and free amino acids, mainly asparagine, which are naturally present in many foods. Over the past 20 years, several studies have used strategies to reduce acrylamide formation in foods, such as minimizing the content of reducing sugars and asparagine, increasing moisture, heating at a lower temperature, and reducing processing time. In wheat derivatives, the asparagine content is one of the key factors for the formation of acrylamide. For this reason, an important recommendation for the food industry is the use of flours characterized by a low content of free asparagine, and then many efforts are made for the reduction of free asparagine level in cereal grains. In recent years an increasing number of studies aimed to compare levels of free asparagine in grains in different cereal species and genotypes and to identify the factors influencing this trait. These studies have shown that free asparagine accumulation in cereal grains varies highly between different genotypes and established that this trait is strongly influenced by environmental factors, such as abiotic and biotic stresses, fertilization, and fungicide treatments. The accumulation of free asparagine in cereal grains is a specific trait that shows good heritability and is influenced by genotype, environment and crop management interaction (GxExM).

The working group WG2 „Agronomy and cereal breeding" in COST ACRYRED Action (CA21149) aims to assess diversity of free asparagine in cereal species and cultivars and to identify those having low content. The understanding of pathways for accumulation of free asparagine and the identification of efficient ways for free asparagine reduction in cereal grains is an important aspect, as well as the development of fast techniques for screening free asparagine level in cereals. Providing recommendations for farmers and food industry is a further target of WG2.

In the previous deliverable of WG2 we defined a "Draft agenda for the next 5 years for agronomy and plant breeding research". Here, we refined and updated the previous document and defined the possible roadmap of the next research aimed to lower free asparagine content in cereal grains. The content of this deliverable is based on the review "Agronomic, genetic and biotechnological approaches to lower free asparagine content in cereals: state of the art and perspectives" (Food Chemistry: X 37 (2026) 104097; https://doi.org/10.1016/j.fochx.2026.104097) written by the same authors of this document.

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Introduction

This chapter will include a recursive section dedicated to ACRYRED Action, to be replicated within each Deliverable.
An additional part should be dedicated to the Working Group in which the Deliverables will be drafted.

ACRYRED COST Action is aimed to "Reducing Acrylamide Exposure of Consumers by a Cereals Supply-chain Approach Targeting Asparagine". ACRYRED's challenge is to establish a multi-disciplinary research and communication network on reducing acrylamide formation, involving the entire value chain from grains to consumer products. ACRYRED brings together plant breeders, the agricultural grain farming community, grain traders, European food processors, toxicologists, public regulators and consumer interest groups to establish research requirements on asparagine formation in plants, as well as investigate new economic models that encompass the full supply chain. The Action will also elaborate new approaches to inform catering/hospitality and consumers about responsible cooking of cereal-based foods. ACRYRED is formed by 5 Working Groups (WG): WG1 "Interdisciplinary Exchange and Integration of Knowledge on Asparagine and Acrylamide"; WG2 "Agronomy and Plant Breeding"; WG3 "Chemistry & Processing"; WG4 "Cereal Supply Chain Economy"; and WG5 "Risk-benefit of MR Products and its Mitigation".

Aims of the working group 2 (WG2) "Agronomy and cereal breeding" is to assess diversity of asparagine in cereal species and cultivars and to identify potential sources of low asparagine cereal species and cultivars. Understanding pathways for the reduction of free asparagine levels in cereals and identification of efficient ways for the reduction of free asparagine levels in cereal grains through plant breeding (including genetics & genomics tools), cereal production and/or field management practices (*e.g.,* N application, resistance to biotic and abiotic stress, organic vs. low input vs. conventional systems etc.) is also an important question to be solved. Furthermore, developing/identifying fast techniques for screening free asparagine level in cereals, providing recommendations for the reduction of free asparagine levels in cereal from breeder's and agronomy point of view for farmers and food industry would also be a crucial achievement.

Objectives of the document

This sub-chapter aims at outlining the objectives of the work reported in the document

To achieve the aforementioned aims, this document (ACRYRED Deliverable n. 11, D2.3) aims to provide an agenda for the next 5 years for agronomy and plant breeding research. The information included in this report comes from the information collected in Deliverable n. 3 (D2.1) "Overview of research activities in Europe to reduce acrylamide in cereal-based foods for the field of agronomy and plant breeding", the discussions made within WG2 in these years of activity, the Deliverable n. 9 (D2.2) "Draft agenda for the next 5 years for agronomy and plant breeding research", and from the available literature data, in particular the review "Agronomic, genetic and biotechnological approaches to lower free asparagine content in cereals: state of the art and perspectives" (Food Chemistry: X 37 (2026) 104097; https://doi.org/10.1016/j.fochx.2026.104097) written by the same authors of this document.

1. The role of free asparagine in the formation of acrylamide in cereal-based foods

Acrylamide (C_3H_5NO) represents a risk to human health due to its neurotoxicity and genotoxicity. Acrylamide is a white, odourless and water-soluble molecule, which is rapidly absorbed through the skin and from the gastro-intestinal tract. Once metabolised in the body, a derivative called glycidamide ($C_3H_5NO_2$) is produced, which in turn forms other derivatives capable of binding to DNA both *in vitro* and *in vivo* in animal and human tissues (EFSA, 2015). Acrylamide is classified as a Group 2A carcinogen, defined as "probable human carcinogens" by the International Agency for Research on Cancer (IARC, 1994). Furthermore, several studies have highlighted that acrylamide can be genotoxic, neurotoxic and toxic to the reproductive system (Chapin et al., 1995; Lopachin, 2004).

Acrylamide is formed in a wide range of foods during normal high-temperature cooking (frying, roasting, baking and grilling), and industrial processing at more than 120°C and low humidity (Tareke et al., 2002). The formation of acrylamide occurs principally in plant-derived foods, whereas acrylamide levels measured in animal-derived foods are very low and do not represent a risk for human health (Tareke et al., 2002). The most important food groups that contribute to acrylamide exposure are fried potato products, coffee, biscuits, crackers, breakfast cereals, crispbreads and soft breads. Cereal-derived products strongly contribute to the intake of acrylamide among the human population, due to the daily quantity and frequency of consumption of these foods, as reported by the EFSA CONTAM Panel (EFSA, 2015). For this reason, there is a strong interest in developing strategies to lower the acrylamide-forming potential in cereal grain. The Food and Agriculture Organization of the United Nations (FAO) and the European Food Safety Authority (EFSA) have analysed various products available on the market and have published related guidelines to minimize the risks related to acrylamide (EFSA, 2015; FAO, 2009). The World Health Organization (WHO) has set the maximum level of acrylamide in drinking water at 0.5 µg/L (WHO, 1993); however, foods such as crisps (US chips), baked crisps and crisp bread may contain acrylamide up to 1000 µg/kg and more. Furthermore, in 2011 a joint FAO/WHO expert committee on food additives established a maximum limit of daily consumption of 180 µg/kg body weight (b.w.), to reduce the risk of cancer development, based on data from dose-response models that evaluated the effects of acrylamide exposure in laboratory animals (WHO, 2011). In the European Union (EU), EFSA lowered the threshold to 170 µg/kg b.w. per day and clarified that it is not a "recommended value", but a reference point for calculating the margin of exposure (MOE) (EFSA, 2015). Furthermore, these agencies recommend dedicating great efforts to the development and implementation of mitigation methods for acrylamide in foods, to reduce the levels of this substance as much as possible, given its probable carcinogenic effects (WHO, 2011; Commission EU Regulation, 2017/2158, https://eur-lex.europa.eu/eli/reg/2017/2158/oj?eliuri=eli%3Areg%3A2017%3A2158%3Aoj&locale=en).

Based on this evidence, Benchmark Levels (BLs) have been defined by the European Commission (EC) for the acrylamide content in some foods: 50–800 µg/kg for baked foods, 750 µg/kg for potato crisps and 400 µg/kg for roast coffee (European Union Regulation (EU) 2017/2158). Recent studies confirmed the effectiveness of BL to lower acrylamide content in some foods. Indeed, a general downward trend in acrylamide content was observed from 2018, indicating that specific initiatives of industry can have an effective role in reducing contaminant levels. However, some products still contained acrylamide above the BL (Mesías et al., 2025). Currently, the European Commission is considering reducing BLs and imposing Maximum Levels (ML) for some foods, including all major

cereal products (https://ec.europa.eu/food/safety/chemical-safety/contaminants/catalogue/acrylamide_en). Therefore, the scientific world focuses on the development of further mitigation strategies for acrylamide in cooked foods, especially those derived from tubers, storage roots, beans and grains.

The main chemical process that causes the formation of acrylamide is known as "Maillard cascade reactions"; the same process gives the fried/toasted appearance to foods and makes them tastier (Mottram et al., 2002; Stadler et al., 2002). Maillard reactions involve reducing sugars, such as glucose, fructose or maltose, and free (soluble, non-protein) amino acids, which are naturally present in many foods. Acrylamide forms when free asparagine ($C_4H_8N_2O_3$) participates in the later stages of the reaction. Over the past twenty years, several studies have described strategies to reduce acrylamide formation in foods, such as minimizing the content of reducing sugars and asparagine, increasing moisture, heating at a lower temperature, and reducing processing time (Anese et al., 2010). Since colour forms from similar pathways to acrylamide, it is now common to use colour as a quality control measure, particularly in potato crisp manufacture.

In cereal grain-based foods, free asparagine concentration is the rate-limiting factor for acrylamide formation (Raffan & Halford, 2019). Indeed, the addition of asparagine markedly increases the acrylamide content of bread (Surdyk et al., 2004). A correlation between free asparagine concentration in wheat flour and acrylamide formation after heating has been demonstrated (Raffan & Halford, 2019). Wheat flour is a highly starchy matrix and has a very variable free asparagine content, between 74 and 664 mg/kg of flour (which corresponds to 0.56 – 5.03 mmol/kg; Claus et al., 2006; Curtis et al., 2018a; Lea et al., 2007; Navrotskyi et al., 2018). In some cases, the levels can be even higher (Corol et al., 2016). Wholemeal flours contain much higher quantities than refined flours, since in grain free asparagine is mainly stored in germ (embryo) and the external layers that form the bran. Consequently, the acrylamide forming potential is higher in cereal foods derived from wholemeal flour (Covino et al., 2024). In the European Regulation (2017/2158), one of the strategies to reduce the formation of acrylamide is the elimination of free asparagine. There are several strategies aimed at this purpose, one of which concerns the use of the enzyme L-asparaginase, which catalyses the hydrolysis of asparagine into aspartic acid and ammonium (Covino et al., 2023). Another strategy for reducing free asparagine in flours is the use of fermentations that use specific microorganisms to reduce the levels of asparagine or reducing sugars in the dough (Bartkiene et al., 2013; Nachi et al., 2018; Wang et al., 2017). The use of fermentations with lactic acid bacteria or the use of sourdough are possible strategies which, in addition to decreasing the level of acrylamide in baked products, improve some of their nutritional properties (Nachi et al., 2018).

These strategies are undoubtedly useful. Nevertheless, they are not feasible for all food matrices and for all processes and difficulties may occur in their implementation. For this reason, an important recommendation for the food industry is the use of flours (and therefore grains) characterized by a low content of free asparagine. In this context, breeding aimed to create low-asparagine varieties could minimize acrylamide-associated risks. The request of new cereal varieties from food industry could intensify if the EU imposes MLs for acrylamide in cereal foods (Kaur & Halford, 2023).

Free amino acids represent approximately 5% or less of the total nitrogen (N) content of the cereal grain, with asparagine representing 10% or less of the total free amino acids (Lea et al., 2007). Consequently, both scientific research and breeding activities have shown little interest in the past regarding the levels of free asparagine in grains, until the demonstration that this amino acid is a

precursor of acrylamide during cooking. For this reason, in recent years an increasing number of studies aimed at identifying specific factors that influence this trait. These studies have shown that free asparagine accumulation in wheat grains varies highly among genotypes (Claus et al., 2006; Corol et al., 2016; Curtis et al., 2018b; Navrotskyi et al., 2018; Tafuri et al., 2023). It is also well proven that this trait is strongly influenced by environmental and agronomic factors, such as abiotic and biotic stresses (Lea et al., 2007), sulphur (S) and/or N availability (Curtis et al., 2016; Martinek et al., 2009; Wilson et al., 2020), and poor disease control (Martinek et al., 2009; Curtis et al., 2016). The accumulation of free asparagine in wheat grains is a specific genetic trait, and related studies reported low or medium heritability values for this trait (Corol et al., 2016; Emebiri, 2014; Rapp et al., 2018; Tafuri et al., 2025). The interaction of genotype and environmental factors (G × E) is also known to influence free asparagine content in cereal grains (Xie et al., 2021; Postles et al., 2013; Corol et al., 2016; Curtis et al., 2018b). Therefore, both agronomy and genetics can play an important role to breed and select cultivars that accumulate low and stable free asparagine levels in different growing environments, to mitigate the risk of acrylamide formation in cereal-based products.

In this document, we summarize the present knowledge useful for decreasing free asparagine levels in cereals grain, considering all the factors that influence this trait, from modification of soil composition through fertilization to the use of biotechnology through genome editing, and present the possible strategies that can be exploited in the future research to reach this goal (Figure 1).

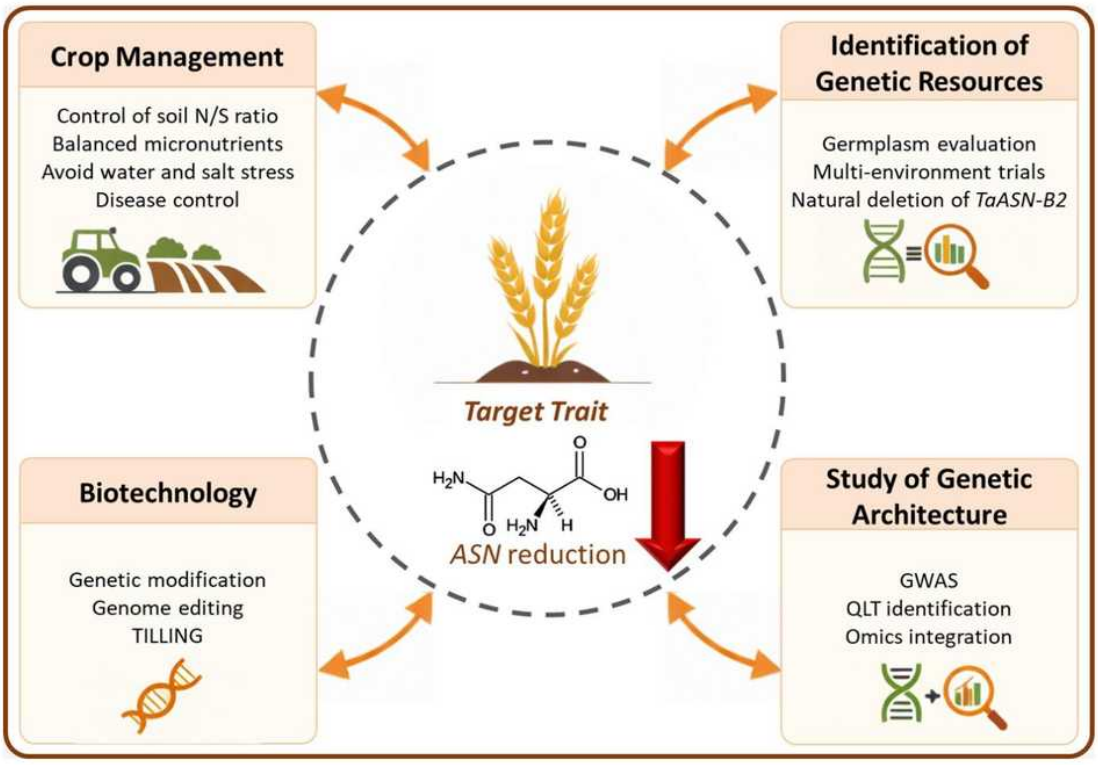


Figure 1. Graphical summary of the strategies adopted to obtain low free asparagine levels in cereal grain.

2. Overview of the relevant strategies present in literature

2.1. Field factors influencing free asparagine content

Asparagine functions as a major N storage and transport compound in plants, largely due to its high nitrogen-to-carbon ratio (Gaufichon et al., 2010). Free asparagine mobilizes N from source to sink tissues during germination, vegetative growth, senescence, and seed filling, and plays a critical role in ammonia detoxification. This detoxification becomes particularly important when N is abundant, such as under high N fertilizer inputs, or during biotic and abiotic stresses that cause ammonia accumulation in plant tissues (Zheng et al., 2018). During senescence or stress induced by pathogens and insects, N remobilization increases ammonia levels. Abiotic stressors can also trigger energy stress and proteolysis, leading to reduced cellular hexose concentrations and increased ammonia, which in turn promotes asparagine synthesis (Beato et al., 2014; Hildebrandt et al., 2015). Asparagine synthetase and asparaginase are the main enzymes regulating this process: the former catalyses the ATP-dependent conversion of aspartate to asparagine, while the latter hydrolyses asparagine to aspartate and ammonia (Oddy et al., 2023a). Asparaginase activity significantly increases as free asparagine concentration increases (Sodek et al., 1980), while it is strongly downregulated by glutamine concentration (Tonin & Sodek, 1990). The expression of these two enzymes is tightly regulated by environmental conditions: asparagine synthetase is typically upregulated by high N, while asparaginase activity is downregulated. Because of its sensitivity to both N supply and stress, free asparagine accumulation represents a critical indicator of N metabolism efficiency and the crop's response to soil and fertilization management. The availability of macro, meso and micronutrients, as well as the occurrence of environmental cues, highly affect free asparagine metabolism, as reported in Table 1 and extensively reviewed in Baldoni et al. (2026).

Table 1. Effects of nutrient availability, abiotic and biotic stresses on free asparagine metabolism in wheat. Arrows indicate the direction and magnitude of the effect on free asparagine: ↑ increase; ↓ decrease; ↑↑ strong increase; ↑↓ variable or context-dependent effect. Modified from Baldoni et al. (2026).

Category	Factor/stress		Effect on free asparagine	Physiological mechanism
Macronutrients availability	Nitrogen (N)	Excess	↑ Increase	Ammonium detoxification via asparagine synthesis
		Adequate	↓ Decrease	Enhanced protein synthesis
		Deficiency	↑ Increase	Reduced protein synthesis
	Phosphorus (P)	Excess	↑ Increase	Induced secondary deficiencies (Ca, Fe, Zn, Cu…)
		Deficiency	↑ Increase	Reduced protein synthesis for low ATP availability
	Potassium (K)	Excess	↑ Increase	Reduced uptake of N, B, Mg
		Deficiency	↑ Increase	Reduced asparaginase activity
Mesonutrients availability	Calcium (Ca)	Excess	↑ Increase	Reduced uptake of P, Zn, Mn, Fe
		Deficiency	↑ Increase	Reduced membrane/cell wall stability
	Magnesium (Mg)	Excess	↑ Increase	Reduced K uptake
		Deficiency	↑ Increase	Reduced photosynthesis

Micronutrients availability	Sulphur (S)	Adequate	↓ Decrease	Enhanced N assimilation and protein synthesis
		Deficiency	↑↑ Strong increase	Enhanced asparagine synthetase activity
	Zinc (Zn)	Excess	↓ Decrease	Inhibition of asparagine synthetase activity
		Deficiency	↑↑ Strong increase	Impaired N assimilation and protein synthesis
	Iron (Fe)	Deficiency	↑ Increase	Impaired nitrate reduction and protein synthesis
	Molybdenum (Mo)	Deficiency	↓ Decrease	Reduced nitrate reductase activity
	Selenium (Se)	Excess	↑ Increase	Possible S-starvation-like response
		Deficiency	Decrease ↓	Enhanced oxidative stress mitigation
Abiotic stresses	Salt (NaCl)	Excess	↑↑ Strong increase	Induced asparagine synthetase activity
	Salt + Nitrate (NO_3^-)	Excess	↑↑ Strong increase	Increased asparagine synthesis
	Drought	Excess	↑ Increase	Increased asparagine synthesis for ammonium detoxification
	Temperature	Excess	↑ Increase	Reduced protein synthesis
Biotic stresses	Fungal infection		↑ Increase	Increased proteolysis
	Arbuscular mycorrhizal fungi		↑↓ Variable effect	Improved nutrient uptake; change in N availability

2.2. Crop management strategies

The average free asparagine content in commonly cultivated cereal species ranged from 426 ± 144 mg kg^{-1} in common wheat to 1179 ± 359 mg kg^{-1} in rye in a study by Žilić et al. (2017). The cereals can be ranked according to increasing mean asparagine concentration as follows: common wheat < durum wheat < hull-less barley < dent maize < hull-less oat < rye (Žilić et al., 2017, Stockmann et al., 2019, Yiltirak et al., 2021; Szafrańska et al., 2025). Reduction of free asparagine in cereal grain can be achieved through various crop management strategies, although these have not been fully optimized (Oddy et al., 2022). The first initiative that was taken in this sense was introduced in the Commission Regulation (EU) 2017/2158, which included certain crop management strategies as a part of the compulsory mitigation measures set out in the Regulation. These involved avoiding excessive N application while maintaining balanced S levels in the soil, as well as implementing good crop practices to prevent fungal infection. Current recommendations for reducing free asparagine in cereals, particularly in wheat, emphasise: i) the application of N fertiliser at the minimum levels to ensure that the optimum yield and required protein content is achieved, ii) the application of S fertiliser to ensure that S deficiency is avoided, and iii) the use of fungicides to control disease (FoodDrinkEurope, 2019). It is important to note that these recommendations do not fully address whether these practices are environmentally or economically sustainable, and their overall sustainability for farmers remains context dependent.

The effects of N and S fertilization on cereal grains are clear and well-established: high N fertilization promotes asparagine synthesis as plants detoxify excess ammonia by incorporating it into asparagine (Fernández-Calvino et al., 2016), leading to an increase in the concentration of free asparagine in the grain (Claus et al., 2006; Martinek et al., 2009; Granvogl et al., 2007; Curtis et al., 2016, 2018a; Wilson et al., 2020; Szafrańska et al., 2024). S fertilization has the opposite effect; indeed, its deficiency leads to a substantial increase in free asparagine content in the grain, especially in wheat and barley (Granvogl et al., 2007; Curtis et al., 2018a). In rye, the effect of S deficiency under field conditions appears less pronounced (Postles et al., 2013), possibly due to greater efficiency of rye in S uptake and its different metabolic response compared to wheat and barley. Consequently, optimizing appropriate amounts of N and S fertilizers, as well as the N:S ratio, is essential to support plant growth and protein synthesis while minimizing acrylamide-forming potential. N application should be synchronized with crop demand through split applications, site-specific nutrient management, and precision fertilization tools. These approaches, including vegetation index-based canopy sensing and variable-rate fertilization, allow farmers to match N availability to crop uptake (Fabbri et al., 2025), minimizing surpluses that drive asparagine synthesis (Wilson et al., 2020; Halford et al., 2022). Field trials demonstrated that applying N and S at a 10:1 kg ha^{-1} ratio was sufficient to prevent large increases in free asparagine concentration in wheat grain (Oddy et al., 2023a). Similarly, physiological studies in maize indicated that N:S ratios within the 10–15:1 range optimize amino acid balance, N assimilation, and redox status (Liu et al., 2020; Zhao et al., 1999).

Environmental factors also influence free asparagine accumulation. As previously stated, the asparagine content in grain is influenced by various abiotic and biotic factors, including drought, soil salinity, pathogen attack, toxicity, solar radiation, and nutrient deficiencies. These stress conditions trigger asparagine synthesis as a biological response to the restriction of protein formation (Lea et al., 2007; Navrotskyi et al., 2018). Biotic stresses have been shown to play an important role in free asparagine accumulation in wheat grain and an efficient fungicide treatment may decrease asparagine concentration (Lea et al., 2007; Martinek et al., 2009). Consistently, a correlation between the onset of serious fungal diseases and the increase in free asparagine concentration in wheat kernel was demonstrated, with the response varying among different wheat varieties (Curtis et al., 2016). Therefore, proper disease control *via* fungicide application is a primary crop management measure for mitigating acrylamide formation in cereal products. Arbuscular mycorrhizal fungi (AMF) inoculation may also be used to prevent fungi infection, although this practice may have side effects on asparagine accumulation due to higher supply of N and other nutrients (Whiteside et al., 2012; Saia et al., 2015).

Another factor that should be taken into consideration is the use of different agricultural practices between organic and conventional farming systems and their influence on the accumulation of free asparagine content. While most research has focused on conventional systems, studies on organic farming have produced inconsistent results. Springer et al. (2003) found higher free asparagine content in organically-produced rye, for example, whereas Stockmann et al. (2019) observed significantly lower levels of this amino acid in wheat cultivated under organic conditions compared with conventional systems. Moreover, the reduction in free asparagine content in spelt and rye was strongly influenced by the crop year (Stockmann et al., 2019).

2.3. Identification and creation of varieties of cereals with low free asparagine levels

Several studies have reported data on the differing propensities of cereal genotypes to accumulate free asparagine in the grain (Žilic et al., 2017; Curtis et al., 2010; Postles et al., 2013; Corol et al., 2016). Most of the attention has been focused on wheat, due to its agronomic and commercial importance (Curtis et al., 2018b; Navrotskyi et al., 2018; Wilson et al., 2020; Xie et al., 2021; Oddy et al., 2023a; Tafuri et al., 2023; Szafrańska et al., 2024; Spanic et al., 2025; Tafuri et al., 2025). Some studies highlighted that certain genotypes maintain low and stable levels of free asparagine in the grain. For instance, eight bread wheat varieties with low free asparagine concentration in the grain, regardless of crop management and growing year, were identified by Curtis and coworkers (2018b). More recently, further bread wheat cultivars, relevant for the Italian market, have been found to exhibit relatively stable free asparagine content across different years and locations, *i.e.*, three Italian locations over two crop years (Tafuri et al., 2023). Interestingly, this study took advantage of the Italian experimental trial network, which evaluates wheat varieties across multiple locations to assess qualitative performance: the 54 analysed bread wheat cultivars were included in the Italian "National Network of Common Wheat Variety Comparison" (In Italian: "Rete Nazionale di Confronto Varietale del Frumento Tenero") coordinated by the Council for Agricultural Research and Economics (CREA).

The cultivars identified in these studies represent valuable donor lines for breeding programs targeting acrylamide mitigation. Despite the strong influence of environmental factors, these studies have pointed out an important role of genetics in determining free asparagine concentration. They also have suggested that the selection of low-asparagine varieties could be a successful approach in breeding to reduce acrylamide-forming potential. Importantly, lowering free asparagine levels does not negatively affect end-use quality or technological performance (Oddy et al., 2022; Tafuri et al., 2023), supporting the feasibility of breeding low-asparagine wheat varieties without compromising product quality.

2.4. Genetic determinants for free asparagine content in cereals

Few genetic studies have been carried out to dissect the genetic bases of free asparagine accumulation in cereal grain so far, and most of them related to wheat. Genome wide association studies (GWAS) conducted on bread and durum wheat have identified 70 and 6 marker-trait associations (MTAs), respectively, linked to free asparagine (Table 2).

Table 2. Number and position of peak markers of the MTAs and QTL identified for free asparagine content in Triticum aestivum and turgidum. From Baldoni et al. (2026).

Species	Reference	Reference Genome	N. of peak markers	Chr	Chromosomic region (Mbp)
T. aestivum ssp. *aestivum*	(Emebiri, 2014)	IWGSCv1.0	9	5A	585.1 - 588.7
	(Rapp et al., 2018)	IWGSCv1.0	1	1A	307.4
			1	4A	743.8
			1	7A	54.9
			1	1B	40.8
			1	6B	164
			1	7B	750.6
			1	2D	19.8

			1	6D	467
	(Oddy et al., 2023b)	IWGSCv1.0	1	4B	601
	(Lavoignat et al., 2024)	IWGSCv2.1	1	1A	464.5
			1	1B	515.2
			1	2B	794.7
			1	2D	610.4
			1	3B	781.3
			1	5B	295.1
			1	7A	706.7
			2	7B	176.2; 177.8
	(Rączka et al., 2025)	IWGSCv2.1	4	1B	468.9 - 495.3
			3	1D	20.5; 368.0; 423.0
			3	2B	31.5; 111.5; 516.7
			2	2D	35.8; 496.8
			1	3A	0.9
			3	3B	2.5; 256.1; 837.2
			1	3D	40.6
			1	4A	698.2
			2	5B	634.2; 697.9
			1	5D	122.2
			7	6B	18.8; 245.3; 313.1; 323.2; 356.0; 375.6; 708.3
			2	6D	181.1; 418.4
			8	7A	25.8; 413.0; 477.5; 549.9; 622.0; 638.9; 656.7; 702.8
			1	7B	756.0
			4	7D	15.4; 77.7; 114.5; 633.0
T. turgidum ssp. *durum*	(Tafuri et al., 2025)	Svevo v1	1	6A	132.5
			1	7A	688.4
			1	2B	405.2
			1	4B	609.4
			2	7B	545.2; 697.6

Multi-environment GWAS analyses have revealed considerable instability in MTAs, with many loci exhibiting environment-specific effects. For example, Lavoignat et al. (2024) observed average increases in free asparagine content of 4% under high N supply and 3% under water-deficit conditions. To date, no major-effect QTL have been identified, with individual markers typically explaining only 6.3% to 12.2% of the phenotypic variance (Rączka et al., 2025). These findings underscore the complex genetic architecture of the trait, which is governed by multiple loci with moderate additive effects. Strong G×E interactions, along with potential pleiotropic effects on agronomic traits, such as yield and grain quality, further complicate breeding strategies. These interactions highlight the need for multi-environment trials and integrative approaches to select genotypes with low free asparagine levels without compromising other key traits. Nevertheless, the heritability of free asparagine content is medium to high (Rączka et al., 2025; Lavoignat et al., 2024; Tafuri et al., 2025), supporting the feasibility of genetic selection, especially when supported by stability analyses and data from diverse growing environments.

Integrative metabolomic analyses have highlighted the involvement of pathways related to amino acid metabolism, aromatic compound biosynthesis, and redox balance in regulating free asparagine accumulation. Tafuri et al. (2025) combined GWAS and metabolomics to identify 40 metabolites correlated with free asparagine variation, demonstrating that such integrative approaches are essential to uncover novel regulatory components and deepening our understanding of the metabolic networks involved.

Thanks to high-quality cereal reference genomes (IWGSC, 2018; Maccaferri et al., 2019), MTAs and some QTL were linked to candidate genes potentially involved in free asparagine regulation in bread (Raffan et al., 2021; Oddy et al., 2021; Rączka et al., 2025) and durum (Tafuri et al., 2025) wheat (Table 3).

Table 3. Candidate genes, and associated markers, potentially involved in free asparagine regulation from literature. Modified from Baldoni et al. (2026).

Species	Candidate gene	Gene name	Metabolic pathway	Chr	Associated QTL	Peak marker position (Mbp)
T. aestivum	*TraesCS3A02G077100; TraesCS3D02G077300*	asparagine synthetase 2 (*TaASN2*)	asparagine synthesis in seed	3A, 3D	-	-
	-	asparagine synthetase 2B (*TaASN-B2*)	asparagine synthesis in seed	3B	-	-
	TraesCS1B03G0736700	H-subunit of mitochondrial NAD(P)H dehydrogenase	mitochondrial electron transport chain	1B	QGfac.rut.1B.1	468.9
T. turgidum ssp. durum	*TRITD4Bv1G182260*	anthranilate phosphoribosyl transferase (*PAT1*)	tryptophan biosynthesis pathway	4B	GENE-4008_418	609.4
	TRITD7Bv1G172590	L-lactate dehydrogenase (*LDH*)	glucose metabolism / asparaginase II pathway	7B	BS00108573_51	545.2
	TRITD7Bv1G172680	L-lactate dehydrogenase (*LDH*)	glucose metabolism / asparaginase II pathway	7B	BS00108573_51	545.2
	TRITD7Bv1G225350	polyamine oxidase (*PAO*)	polyamine metabolism /asparagine-methionine bicycle	7B	BS00062611_51	697.6

Recently, a network describing asparagine metabolism was built using information available in literature and in public databases (Curtis et al., 2018b). This analysis highlighted the complexity of this network, which includes 212 nodes (genes, enzymes, or molecules) and 246 edges (reactions between nodes). The main enzymes involved in asparagine metabolism are: asparagine synthetase, glutamine synthetase, glutamate dehydrogenase, ferredoxin-dependent glutamate synthase, NADH-dependent glutamate synthase, aspartate amino transferase, and glutamate decarboxylase. In addition, specific

kinases and transcription factors were identified as regulators of gene expression within this network (Curtis et al., 2018b). Asparagine metabolism is highly branched and dependent on several factors, and the precise mechanisms regulating its accumulation in grains remain unclear. Notably, many QTL associated to free asparagine levels do not co-localize with known asparagine metabolism genes. This suggests that additional regulatory elements or less obvious pathways, such as transport, degradation, secondary metabolism, or epigenetic control, may contribute to this metabolic network. These observations underscore the need for functionally validating candidate genes *via* expression profiling, mutagenesis, or genome editing.

2.5. Biotechnological approaches for lowering free asparagine content in cereals

Genome editing is the main approach that can be used to reduce free asparagine content in cereal grain, partly because of the relative simplicity of editing based on Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) and CRISPR-associate nucleases (Cas), in particular CRISPR/Cas9.

Bread wheat (*Triticum aestivum*) has five asparagine synthetase genes in each of its three genomes, A, B and D (Xu et al., 2018). These are *TaASN1*, *TaASN2*, *TaASN3.1*, *TaASN3.2* and *TaASN4*. *TaASN2*, highly expressed in embryo and endosperm (Xu et al., 2018, Curtis et al., 2019), is absent on the B genome (*TaASN-B2*) in some cultivars due to a natural deletion, correlating with reduced grain asparagine (Oddy et al., 2021). This remains the only QTL validated across multiple environments to date (see previous section).

The development of lines in which *TaASN2* was knocked out using CRISPR/Cas9 was reported in 2021 (Raffan et al., 2021) and a field trial of an A genome null for *TaASN2*, and a total null for *TaASN2* was carried out in 2021 to 2022 (Raffan et al., 2023; Kaur et al., 2024). Also included were AB genome nulls derived from a selected line of a mutant population of wheat cv. Cadenza seeds that was produced by chemical mutagenesis through ethyl methanesulphonate treatment (Rakszegi et al., 2010), referred to as TILLING lines. The mutated *TaASN2-A2* gene had been backcrossed into the cv. Claire background, which already lacks a B genome *TaASN2* gene (Oddy et al., 2021). The CRISPR lines showed a significant reduction of free asparagine concentration in the grain compared with the Cadenza control, by just over 50% in the total nulls and 14% in the A genome null (Raffan et al., 2023; Kaur et al., 2026). The TILLING lines showed more variable responses when compared to Claire; however, when compared with a TILLING control that had come through the mutagenesis process but did not carry mutations in *TaASN2*, they did show significant reductions of 20-40%, comparable with the 28% reduction that was previously evaluated in A genome TILLING nulls in the Cadenza background and the tetraploid Kronos background (Alarcón-Reverte et al., 2022). Notably, the large reductions in free asparagine concentration in the CRISPR lines was achieved without significant effects on yield (Raffan et al., 2023), although there was evidence of a yield drag in TILLING lines, possibly due to the genetic baggage of additional random mutations that they will inevitably carry.

A second *TaASN2* null line was found to have additional edits in the *TaASN1* genes (Kaur et al., 2024). This line and a total *TaASN2* TILLING line are still being evaluated in the field but are likely to have even greater reductions in free asparagine concentration.

These results show that step reductions in the free asparagine concentration of wheat grain are possible using genome editing or chemical mutagenesis (TILLING), suggesting that these strategies could offer a critical path forward to the development of crop varieties with inherently low

acrylamide-forming potential. In this context, the identification of additional genetic determinants controlling the levels of free asparagine and possibly reducing sugars has become an important target for crop geneticists.

2.6. Available techniques for screening free asparagine level in cereals

Monitoring free asparagine content is essential for both the selection of raw materials and the analysis of raw food ingredients. For this reason, the development of new and improved methods for this measurement is of great interest for all the actors of the supply chain, form breeders to food technologists.

The analytical techniques mostly used for the analysis of free asparagine in biological materials are based on chromatography and mass spectrometry (HPLC, UHPLC, GC, GC-MS or LC-MS, LC–MS–MS) and are performed on partially purified and derivatised amino acid fractions (Palazoğlu et al., 2015; Žilić et al., 2017; Curtis et al., 2018b; Žilić et al., 2020). These conventional chromatographic methods offer high sensitivity but require a long and tedious multi-step sample preparation. Indeed, these techniques are complex, time consuming and expensive, requiring dedicated and expensive devices such as amino acid analysers or special detectors. Optimization of extraction conditions, removal of proteins and other components from the analysed matrix, as well as required derivatization procedures, further complicate this process. Some procedures for these techniques have been updated to decrease the time for the analysis. Phenomenex, for example, has developed the EZ:faast® Amino Acid Analysis Kit (Phenomenex, Inc., Torrance, CA), which requires just 15 min for sample preparation and analysis, for the measurement of free asparagine in potato samples (Farkas & Toulouee, 2003). This procedure requires a simple solid phase extraction (SPE) step, followed by a fast derivatization reaction and GC (FID/NPD) analysis. Alternative kits with simplified procedures are available for either GC/MS or LC/MS analysis (Farkas & Toulouee, 2003).

Another technique that can be adopted for the measurement of free asparagine is ^{1}H-Nuclear Magnetic Resonance (^{1}H-NMR). Corol et al. (2016) described the development and application of a rapid ^{1}H-NMR-based analysis of cereal flour for free asparagine quantification. Tafuri et al. (2025) confirmed the reliability of this analytical method. ^{1}H-NMR is quantitative and does not rely on the use of calibration curves. Extraction of chemical compounds involves simple procedures, with no need for derivatisation. However, accurate quantitation of individual compounds in complex compound fingerprints strictly depends on the presence of molecule-specific resonances nonoverlapping with other signals in the spectra. According to the protocol described by Corol et al. (2016), the characteristic, geminally-coupled signals of the asparagine C-3 hydrogen atoms fall in a relatively clear area of the spectrum and thus are suitable for integration. The cleanest signal of the pair at δ2.95 (dd, J = 17 and 4 Hz) arising from 3-Hb was used by authors for integration and quantitation. The selected peaks were accomplished by comparison to the known concentration of the d4-TSP standard. It is then clear that the use of ^{1}H-NMR requires specific and expensive instruments, as well as high specialized personnel.

Breeders and food manufacturers need more straight-forward and faster methods to analyse raw materials. These methods should ensure that the measurement of free asparagine is easy, instantaneous and reliable. For this reason, in recent years activities have been focused on developing new user-friendly methods, such as enzymatic and spectrophotometric approaches, that would find

application directly in breeding companies, food industries, raw material receiving points, warehouses, etc.

An interesting product is the enzymatic assay "L-Asparagine/L-Glutamine/Ammonia Assay Kit" (K - ASNAM Megazyme, Illinois, USA; https://www.megazyme.com/l-asparagine-l-glutamine-ammonia-rapid-assay-kit), which only needs a spectrophotometer (UV/VIS) to measure the absorbance of the sample solutions. This kit contains a coloured reagent required for spectrophotometric quantification at λ 340 nm (nicotinamide-adenine dinucleotide phosphate, NADPH), as well as three specific enzymes (glutaminase, glutamate dehydrogenase (GIDH) and asparaginase), and their appropriate buffers. This kit is suitable for the analysis of L-asparagine, L-glutamine and ammonia. The detection of these compounds takes place in a three-step reaction. Reaction 1: glutamine from the sample is converted to glutamate and ammonium ions. Reaction 2: both ammonium ions from the sample and from reaction 1 react with 2-oxoglutarate and NADP to form glutamate and $NADP^+$. Reaction 3: asparagine is hydrolysed to aspartate and ammonium ions and then the liberated ammonium ions enter into reaction 2, which leads to a fall in absorbance that is stoichiometric with the amount of asparagine (Figure 3).

This method has been adapted for wholemeal wheat flour, with quantification of free asparagine from the sample carried out after total deproteinization (Lecart et al., 2018). Xie et al. (2023) validated the enzymatic kit protocol on wholemeal flour through the comparison with the two well-established analytical methods, Ultra High-Performance Liquid Chromatography (UHPLC) and ^{1}H-NMR. A strong correlation between the enzymatic test and UHPLC was obtained. In particular, the authors stated that the enzymatic test had consistent accuracy, excellent precision of 1.0 or less (CV%), good sensitivity (0.0389 AU L mg^{-1}) of free asparagine signal detection, as well as the lowest cost. Recently, the comparison of this enzymatic assay *vs* UHPLC for free asparagine determination in pea and lentil seeds was carried out by Sá et al. (2025). The procedure set up by Lecart et al. (2018) has been used successfully in several studies on free asparagine accumulation in wheat grain (Lavoignat et al., 2024; Tafuri et al., 2023; Covino et al., 2024; Tafuri et al., 2025; Guarino et al., 2026). This method is simple and cheap, but the procedure (acid deproteinization and enzymatic assay) is more suitable for research activities than for use by seed or food companies.

More recently, Alhazzani et al. (2025) presented a novel and selective method for the determination of free asparagine on potato, based on carbon dots (CDs): nanoscale particles known for their excellent photoluminescent properties. Upon enzymatic hydrolysis of free asparagine by L-asparaginase, liberated ammonia induced a pH increase in the reaction medium. This pH shift enhanced the fluorescence of blue-emitting CDs (B-CDs) while simultaneously decreasing that of orange-emitting CDs (O-CDs), enabling sensitive and selective free asparagine quantification. This method displayed excellent sensitivity (LOD = 0.31 µM) with low relative standard deviation, confirming its accuracy and precision. Fluorescence emission spectra were recorded using a spectrofluorometer. The use of CDs offers several advantages, such as low toxicity, low environmental impact, and versatility, making this method suitable for a wide range of applications (Alhazzani et al., 2024).

Finally, the company Curtis Analytics has developed an innovative at-the-gate, rapid and easy-to-use test for asparagine in flour (with later applications in coffee and potato) called "ASNInsta Test" – Instant test for asparagine in food. The "ASNInsta" sensor is able to measure free asparagine in the

analysed product instantly (Curtis Analytics, Harpenden, UK; https://curtisanalytics.co.uk/research-asparagine-test/). The development of the commercial "ASNInsta Test" is still in progress; however, it will represent the first test of its type and could be a key tool to help European companies to solve the acrylamide problem in food and to comply with EU Regulations.

3. Strategies for the next 5 years research

3.1. Soil and crop management

Future research on the effect of crop management strategies on free asparagine accumulation should address several key aspects. A holistic approach is required to determine the optimal levels and ratios of N and S fertilization, as well as the influence of other agronomic practices, to develop effective and sustainable strategies for mitigating acrylamide formation in food. Integrated soil fertility management practices, such as the use of organic amendments and cover crops, can further improve N retention, enhance N use efficiency, and reduce leaching losses (Drinkwater & Snapp, 2007), thereby indirectly supporting the control of free asparagine accumulation. In addition, the use of precision agriculture could improve N-use efficiency through N application synchronized with crop demand.

A comprehensive and balanced approach to soil management and fertilization is essential to control free asparagine accumulation in cereal grains. Integrating precision nutrient management, regular soil testing, S supplementation, and micronutrient balancing can effectively reduce free asparagine levels while maintaining yield and grain quality. Looking ahead, coupling these agronomic practices with innovations in soil biology and digital agriculture offers a sustainable pathway to reduce acrylamide risk in cereal-based foods, improve crop N efficiency, and enhance resilience in future agricultural systems. Research should also address the effects of agronomic practices beyond fertilization, such as fungicide application, leaf area duration, and senescence control to evaluate their potential for reducing free asparagine and mitigating acrylamide formation. In addition, it is necessary to better understand the impact of abiotic stresses, particularly drought and salt stress, on free asparagine accumulation in cereals. Also, the use of AMF to counteract environmental stresses and simultaneously decrease free asparagine content needs to be further investigated.

3.2. Identification of genetic resources for breeding

Breeding low-asparagine wheat varieties without compromising product quality is a possible target, as shown in paragraph 2.3. To achieve this goal, diversity assessment through germplasm screening for the identification of genetic resources with low free asparagine content is essential. These sources should also perform well in other key traits including grain yield, disease resistance and baking quality if farmers and food businesses are to use them. The methodology to accomplish this objective includes: i) characterization of genotypes for free asparagine content, using, for instance, germplasm collections; ii) selection of varieties that exhibit the widest possible range of free asparagine content; iii) establishing field trials with the selected varieties at different locations to evaluate the stability of the trait across environments.

Most studies reported in the literature evaluated a limited number of varieties. A promising strategy to assess diversity for this trait is the investigation of asparagine level across a broad range of European elite varieties, as well as non-European varieties (global collections), landraces and representative sets of cereal species that have been less studied to date, including durum wheat, spelt, rye, emmer and

einkorn. The screening of this large diversity panel should be conducted across multiple environments and under different farming practices, with particular focus on mineral fertilization and fungicide treatments. This will allow the identification of genotypes with consistently stable asparagine content, which can then be prioritized for use in pre-breeding and breeding. For this kind of screening, it would be desirable to leverage varieties that are already included in national experimental trial networks in some European countries (*e.g.,* Italy, Germany and UK), as reported in the study by Tafuri et al. (2023). These networks annually evaluate varieties across multiple locations, representing an important tool for orienting breeders in the current varietal landscape. Coordination of this network is usually managed by a research organization with the support of several collaborators belonging to public and private institutions. Testing the grain from these varieties for free asparagine content by both official governmental bodies and private companies, giving multiple replicates across diverse environments, would provide an efficient starting point for identifying the best varieties currently available on the market.

Another important aspect is the coordination of this kind of experiment among different countries, which can further enhance the assessment of genotype stability under diverse environmental conditions. Information on which European varieties contain low concentrations of free asparagine would be useful as a recommendation for farmers regarding the appropriate varietal choice to produce purpose-built raw materials for the food industry. Furthermore, based on these data, authorized institutions could develop a database to set targets for the reduction of free asparagine levels in cereal grains. Including free asparagine levels in standard cultivar information, potentially as part of regulatory criteria, should be evaluated. From both agronomic and breeding perspectives, the ambition to assess the diversity of asparagine levels in cereal cultivars and the identification of genetic resources for breeding purposes should be specified within guidelines.

Another important aspect to be considered is the presence of important gaps in the transfer of knowledge and information along the cereal supply chain that may limit the practical implementation of breeding strategies aimed at reducing free asparagine in grain. This issue has been highlighted by a recent survey performed in the frame of a Virtual Mobility Grant granted by ACRYRED (Szafrańska et al., 2026). The survey was conducted on 31 breeders and 240 farmers in Poland. The survey among breeders indicated that free asparagine is not yet routinely considered in breeding programmes. The respondents recognised the potential of genetic markers and genomic approaches for selecting varieties with low asparagine content. Farmers showed limited awareness of the relationship between soil S status and asparagine formation, indicating that conscious management of S and N fertilisation is not yet sufficiently supported by knowledge or market requirements. These findings highlight the need for improved communication and education of farmers about the factors affecting free asparagine formation, as well as stronger cooperation between breeders, farmers, grain buyers and the food industry to facilitate the uptake of low-asparagine varieties and appropriate agronomic practices.

3.3. Integration of genetics and -omic technologies

The integration of genomics and quantitative genetics plays a pivotal role in dissecting the genetic architecture underlying free asparagine accumulation and, in turn, the selection of cereal varieties with low and stable levels across environments. We discussed in paragraph 2.4 how GWAS can help to identify genomic regions and candidate genes involved in this trait. To exploit their potential in dissecting a complex trait like free asparagine accumulation, these studies should be designed using

large, genetically diverse populations, incorporating environmental and agronomic data as covariates to increase statistical power and enable the detection of minor-effect QTL. Expanding genetic diversity through the exploration of wild relatives, landraces, and ancient subspecies is essential for identifying novel alleles associated with reduced free asparagine content. On the other hand, multi-parental populations such as Nested Association Mapping (NAM) and Multi-parent Advanced Generation Inter-Cross (MAGIC) provide valuable resources for dissecting complex traits due to their high recombination rates and broad genetic backgrounds (Samantara et al., 2021; Kitony, 2023).

The integrated use of –omic techniques represents a powerful strategy to dissect the genetic architecture underlying free asparagine metabolism. Genomics can identify chromosomic regions associated with the trait of interest, as well as putative candidate genes involved in free asparagine metabolism. Proteomics can provide insights into the protein interactions involved in asparagine metabolism, while combining genetic and proteomic data offers a more comprehensive understanding of the mechanisms controlling free asparagine accumulation. Metabolomics, in turn, provides a detailed profile of cereal grain composition, enabling the identification of molecules whose levels correlate with free asparagine accumulation.

The combination of these -omic datasets can uncover novel regulatory components of free asparagine metabolism in cereal grains. Exploiting this complex network will ultimately facilitate the identification of genes with a key role, thus taking advantage of the potential of genome editing on novel targets for lowering free asparagine accumulation. Finally, genomic selection represents a promising breeding strategy for reducing free asparagine levels in the grain, particularly when low acrylamide-forming potential is incorporated as a selection criterion within genomic prediction models. Such integrative approaches may accelerate genetic gain and facilitate the identification of lines that combine stable, low free asparagine content with strong agronomic performance across diverse environments.

4. Conclusions

Lowering free asparagine content in cereal grains implies the use of different and complementary actions that range from agronomic strategies to advanced breeding programs and the use of biotechnological approaches. Several studies have been reported in the last two decades about the environmental and agronomic factors that influence this trait, and the related information is increasing. Obtaining and sharing data is not just of value for farmers and food business operators, but also for authorized institutions. This brings together plant breeders, the farming sector, food processors, toxicologists, public regulators, and consumer advocacy groups to establish research standards for free asparagine accumulation in plants. Sharing data could bring strong improvements in the management of free asparagine accumulation in cereal grains:

i) gathered information may be of great importance for farmers, helping them to select appropriate cereal varieties and implement good agricultural practices to produce raw materials with low free asparagine content;

ii) enhancing farmers' awareness and adoption of best crop management practices through targeted education, training, and outreach initiatives remains crucial for minimising asparagine levels in cereal production systems;

iii) continuous improvements in agronomic practice are crucial to ensure regulatory compliance and food safety, and to reduce potential acrylamide-associated risks to consumers' health.

On the other hand, slower progress has been made in the creation of cereal varieties with low asparagine concentration in the grain. Although plant breeding is inherently a long-term process, more than two decades have now passed since the discovery of acrylamide in food, and progress towards low asparagine varieties remains slow. The metabolic interdependence of free asparagine with primary metabolism, nutrient balance and stress response presents a biological challenge, but also an opportunity for innovation at the interface of breeding, agronomy, and biotechnology:

i) the use of an advanced multi-disciplinary approach combining genetics, field phenotyping, metabolomics, and biotechnology could help to unravel the complex regulatory networks underlying free asparagine accumulation and identify novel candidate genes useful for advanced breeding programs;

ii) with the support of regulations governing the use of the technology, genome editing could substantially accelerate the development of crops with reduced acrylamide-forming potential.

In conclusion, the obtaining of high-performing, low free asparagine genotypes offers a promising path toward reducing acrylamide-forming potential in cereal products while maintaining agronomic performance and quality. This multidisciplinary strategy ensures compliance with food safety regulations, fosters industry innovation, and promotes good health by developing safer and healthier food products aligned with sustainability goals.

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