**Plant Breeding, Cultivation, and Grain Breeding techniques of Oats to improve the Nutritional Components**

**Abstract**

The purpose of this review is to provide an overview of advances in Oat (*Avena sativa* L.) breeding and agronomy, focusing on enhancing nutritional traits and discussing prospects for improving oat's nutritional value and climate resilience. Oat distinguishes itself among temperate cereals by its superior content of β-glucan, high-quality protein, unsaturated lipids and bioavailable micronutrients. Rising consumer demand for “functional” foods, together with the climate resilience of oats, has reinvigorated breeding programmes aimed at boosting grain nutrition without sacrificing yield or agronomic robustness. This review synthesises progress made in the last decade towards (i) conventional and molecular breeding to raise levels of β-glucan, protein, oil, antioxidants and key minerals; (ii) genomic and gene-editing tools that accelerate trait introgression; and (iii) cultivation and agronomic bio-fortification practices that complement genetic gain. The remaining bottlenecks—polygenic inheritance, limited trait phenotyping, and genotype × environment interactions—are discussed alongside a future outlook for integrative “omics” and climate-smart breeding strategies. Significant progress has been made in enriching oat grain with health-promoting compounds through integrated breeding and agronomic approaches. Future success depends on standardized phenotyping, supportive regulations for precision breeding, and climate-resilient cultivation practices.

Keywords:Avena sativa; β-glucan; biofortification; genomic selection; CRISPR; micronutrients; agronomy

**Introduction**

Oat (*Avena sativa* L.) is a multipurpose crop belonging to the family Poaceae and known for its grain and fodder nutritional qualities (Rana et al., 2023). Oat is regaining strategic importance in global cereal production, driven by its climatic resilience and its reputation as a “functional grain” rich in soluble fibre, high-quality protein, unsaturated lipids and a distinctive suite of phenolic antioxidants (FAOSTAT, 2024), (Wang and Ellis, 2014) (Alemayehu, et al., 2023) (Heusala et al., 2020). Although current output trails that of wheat or maize, oat acreage has expanded in Canada, northern Europe and parts of China as farmers seek crops suited to shorter growing seasons, lower nitrogen inputs and reduced pesticide dependence (FAO, 2025) (Huang, et al., 2024) (FAOSTAT, 2024). Simultaneously, the oat-based food and beverage sector is projected to grow rapidly, fuelled by regulatory health claims for β-glucan, consumer demand for plant-forward diets, and sustainability messaging that positions oats as a lower-carbon alternative to dairy, almonds and soy (Kebede, et al., 2023), (Li, et al., 2024), (Mathews & Chu, 2024) (Loskutov & Khlestkina 2021). Oat as a livestock feed has a unique nutritional value and consists of relatively high-quality protein. (Ranjan et al., 2024). Protein, fat, vitamin B, and minerals like iron and phosphorus are all abundant in it. Oats have the benefit of providing a large quantity of extremely nutritious fodder for rations for sheep, cattle, chickens, and other animals. Oats may be given in any form, such as hay, silage, or fresh forage, which helps to cover certain times of the year when there are shortages (Kour et al., 2024; Mary et al., 2022).

Despite this commercial momentum, modern cultivars are primarily the result of breeding for yield, lodging resistance and disease tolerance, with nutritional traits introduced only opportunistically (Hu, et al., 2021), (Trevaskis, et al., 2022), (Alemayehu, et al., 2023). Substantial genetic variation nevertheless exists: β-glucan ranges from ~2 % in some feed varieties to >8 % in select landraces, while grain protein spans 9–20 % and oil 4–12. Exploiting that diversity is complicated by oat’s hexaploid genome, extensive linkage drags, and the quantitative inheritance of most nutritional traits, all of which slow conventional selection. Moreover, genotype × environment (G × E) interactions can shift β-glucan or micronutrient levels by up to two percentage points across locations, challenging breeders to achieve stability alongside gain (Huang, et al., 2024) (Varma, et al., 2016) (Alemayehu, et al., 2023).

New technologies are redefining what is possible. High-density SNP arrays and the 2022 chromosome-level reference genome have accelerated quantitative-trait-locus (QTL) discovery for β-glucan, protein quality and lipid composition. CRISPR/Cas platforms offer the prospect of directly editing key loci such as *CslF6* (β-glucan synthesis) or *FAD2* (oleic-acid desaturation) without unwanted linkage drag. Parallel agronomic advances—precision nitrogen management, foliar iron-zinc bio-fortification and climate-smart sowing windows—provide further levers to express genetic potential under farmer conditions (Singh & Belkheir, 2013) (Huang, et al., 2024) (Li, et al., 2024) (Kim, et al., 2021).

Yet integrating these molecular, physiological and agroecological tools into coherent breeding pipelines remains a major challenge. Public programmes grapple with limited phenotyping bandwidth and intellectual property constraints on elite alleles, while private companies must balance niche nutrition targets with mainstream market acceptance. In addition, regulatory ambivalence toward gene-edited crops in some jurisdictions slows the deployment of CRISPR-enabled varieties, potentially widening the innovation gap between regions (Li, et al., 2024) (Kim, et al., 2021) (Huang, et al., 2024).

This review surveys the state of the art in oat improvement for enhanced grain nutrition. We (i) map conventional and molecular breeding strategies aimed at boosting β-glucan, protein, oil and micronutrient density; (ii) summarise cultivation and bio-fortification practices that complement genetic gain; and (iii) identify bottlenecks—G × E instability, polygenic trait architecture, regulatory hurdles—and emerging solutions such as speed breeding, pangenomics and participatory selection. By integrating insights across genetics, agronomy and supply-chain economics, we outline a pathway for delivering nutritionally superior, climate-resilient oat cultivars that can meet the rising demands of health-conscious consumers and sustainable food systems.

**2. Phytochemical Profile and Therapeutic Benefits of Oats**

**2.1 Macronutrient Matrix**

Oat groats typically contain 3–7 % β-glucan, responsible for viscosity-mediated metabolic effects. Protein (11–18 %) boasts a favourable lysine-to-arginine ratio, while lipid (5–10 %) comprises ~40 % oleic and 35 % linoleic acids, providing anti-atherogenic potential (Trevaskis, et al., 2022) (Kebede, et al., 2023).

**2.2 Micronutrients and Bioactives**

Compared with wheat and barley, oats retain higher concentrations of zinc, iron, and selenium because the hull is mechanically, not abrasively, removed. Avenanthramides—unique phenolic alkaloids—exhibit 10- to 30-fold stronger radical-scavenging capacity than other cereal phenolics. Additional constituents include tocopherols, phytosterols, and saponins, all of which synergise with fibre to confer multifaceted health outcomes (Gorash, et al., 2017) (Singh & Belkheir, 2013) (Kim, et al., 2021).

**2.3 Cholesterol and Lipid Modulation**

A recent meta-analysis showed that ≥3 g day⁻¹ oat β-glucan reduced LDL-cholesterol by 0.26 mmol L⁻¹ (95 % CI 0.19–0.32) relative to control. Viscosity and molecular weight (>1 000 kDa) correlated positively with lipid-lowering efficacy, supporting structure-function relationships (Mathews & Chu, 2024) (Varma, et al., 2016).

**2.4 Glycaemic Control**

In adults with type 2 diabetes, replacing breakfast cereals with 60 g rolled oats for eight weeks lowered HbA1c by 0.3 % and post-prandial glucose AUC by 19 %. Oat starch exhibits lower gelatinisation temperature and delayed amylolysis, contributing to a mean glycaemic index of 55 (Varma, et al., 2016) (Llanaj, et al., 2022) (Mathews & Chu, 2024).

**2.5 Blood Pressure and Vascular Function**

Daily consumption of an oat-based ready-to-eat cereal providing 5.5 g β-glucan for six weeks reduced systolic blood pressure by 4 mmHg in mildly hypertensive adults. Avenanthramide-rich extracts improved flow-mediated dilation by 3 % versus placebo in a crossover trial, linked to increased endothelial nitric-oxide synthase phosphorylation (Llanaj, et al., 2022) (Kim, et al., 2021).

**2.6 Fibre Fermentation and Prebiotic Action**

Human faecal fermentations reveal that oat β-glucan selectively enriches *Bifidobacterium* and *Lactobacillus*, elevating short-chain fatty acids—particularly propionate—by 35. In a 12-week RCT, 8 g day⁻¹ β-glucan increased faecal butyrate and improved stool consistency in constipated adults (Daou & Zhang, 2012) (Huang, et al., 2024) (Trevaskis, et al., 2022).

**2.7 Gut Barrier and Inflammation**

Mouse models of dextran-sulfate-induced colitis fed an avenanthramide concentrate exhibited 42 % lower myeloperoxidase activity and preserved tight-junction protein expression compared with casein controls. These findings support potential adjunctive roles in inflammatory bowel disease, pending human verification (Kim, et al., 2021) (Kebede, et al., 2023).

**3. Conventional Breeding Strategies**

Conventional oat breeding still underpins most progress in grain nutrition because it delivers multi-trait gain at the farm scale and is readily adopted by public programmes and private seed companies alike. Recent efforts have refined each step of the classical pipeline—from germplasm mining to multi-environment evaluation—while integrating “low-tech” innovations such as speed-breeding glasshouses and participatory‐on-farm selection (Wang and Ellis, 2014), (Varma, et al., 2016) (Kim, et al., 2021).

**3.1 Expanded Germplasm Exploration and Pre-breeding**

Global gene banks now hold numerous *Avena* accessions, yet a very small percentage have been phenotyped for soluble fibre or bioactive phenolics. Targeted “mini-core” panels from Ethiopia, Morocco and the Caucasus revealed landraces with β-glucan >8 % and avenanthramide content threefold higher than modern cultivars. Pre-breeding crosses between these landraces and elite Canadian lines are under way, with doubled-haploid technology accelerating the fixation of recombinants (Alemayehu, et al., 2023) (Huang, et al., 2024) (Mathews & Chu, 2024).

**3.2 Early-Generation Selection Tools**

Near-infrared reflectance spectroscopy (NIRS) calibrated with high-performance liquid chromatography now predicts β-glucan, protein and oil in single F₂ kernels, enabling low-cost fast selection of seedlings. Portable NIRS units deployed in winter nurseries in Mexico and New Zealand allow breeders to discard low-fibre families before shipping seed north, shaving a year off the breeding cycle (Gorash, et al., 2017) (Singh & Belkheir, 2013) (Kim, et al., 2021).

**3.3 Multi-Environment Testing and G × E Modelling**

For quantitative traits such as yield, a strong genotype-by-environment (G×E) interaction can reduce the reliability of general inferences and significantly hinder the selection of superior genotypes. G×E interaction refers to the variation in genotype performance across different environments—for instance, a genotype that performs well under well-watered conditions but poorly under drought stress. The primary objective of plant breeders in crop improvement programs is to develop genotypes with broad adaptability across diverse environmental conditions. Nutritional traits display stronger genotype × environment interactions than yield; β-glucan can vary ±1 % unit across locations. Factor-analytic mixed models now dissect stability parameters, allowing breeders to target “mega-environments” where high-nutrient lines perform consistently (Köse, 2022) (Wodebo et al., 2023).

**4 Molecular Breeding and Genomic Tools**

**4.1 QTL Mapping and GWAS**

Molecular markers are essential tools in modern plant breeding, enabling the accurate identification of genetic loci linked to key agronomic traits. Current research increasingly emphasizes the use of advanced techniques such as Quantitative Trait Locus (QTL) mapping and Genome-Wide Association Studies (GWAS) to unravel complex traits like stress tolerance, yield enhancement, and nutrient use efficiency. QTL mapping helps identify major genomic regions associated with target traits, while GWAS offers higher resolution by analyzing genetic variation across larger and more diverse populations. High-density consensus maps anchored to the hexaploid oat reference genome identify QTL for β-glucan on chromosomes 7D and 4C, explaining up to 38 % of phenotypic variance. GWAS across 635 accessions detected SNPs near *AsACCaseB* linked to oleic-acid concentration (Altaf, et al., 2024) (Gazal et al., 2014).

**4.2 Marker-Assisted and Genomic Selection**

The integration of multi-omics data has enhanced the prediction accuracy of oat agronomic and seed nutritional traits across multi-environment trials and genetically diverse populations, outperforming predictions based on single-environment data alone. Recent advances in oat DNA markers present an opportunity to investigate new selection methods for polygenic traits such as β-glucan concentration. Marker-assisted back-crossing has introgressed high-β-glucan alleles into elite lines within three cycles. Multi-trait genomic-selection models that couple grain-size morphometrics with β-glucan deliver 25 % higher prediction accuracy than univariate models (Asoro, et al., 2013) (Dhakal, et al., 2024).

**4.3 Transcriptomics and Epigenetics**

RNA-seq of developing grains reveals co-expression modules linking β-glucan biosynthesis to starch branching genes, providing candidate regulators for simultaneous improvement of dietary fibre and energy density. Methylome profiling suggests DNA demethylation in promoter regions of *Avenanthramide Synthase* under drought, hinting at epigenetic leverage points for antioxidant enrichment (Jie Qi, et al., 2024) (Zhu et al., 2024) (Gao, et al., 2018).

**4.4 CRISPR/Cas and Base Editing**

The recent decoding of the 12.5 Gb hexaploid oat genome has highlighted key breeding challenges arising from ancestral chromosomal translocations and inversions. These structural variations contribute to recombination suppression and pseudo-linkage, complicating conventional trait introgression. Despite the widespread application of the CRISPR-Cas9 system for crop improvement and functional genomics in other cereals over the past decade, its use in oats remains limited. This is largely due to the oat genome’s large size, high repetitiveness, presence of three sub-genomes, inefficient transformation protocols, and the recalcitrant nature of the species. Additionally, gene redundancy complicates molecular screening, posing further hurdles to successful gene editing in oats. The first CRISPR/Cas9 protocol for oat achieved 41 % editing efficiency in *AsTLP8* and *AsVRN3*, shortening the heading by ten days. Targeted mutagenesis of fatty-acid desaturase (*FAD2*) boosted oleic acid from 38 % to 52 % in T₁ kernels. Efforts are underway to knock out *CslF6* inhibitors to elevate β-glucan beyond 10 % (Kaye et al., 2025) (Donoso, 2021)

**5 Cultivation and Agronomic Practices**

**5.1 Soil Fertility and Nitrogen Management**

The response of four oat varieties to elevated nitrogen levels was evaluated across multiple locations and years, focusing on yield, grain quality, and metabolite profiles. The integrated phenotyping approach showed that nitrogen supplementation increased amino acid concentrations, total protein, and nitrogen-containing lipids while reducing levels of health-promoting avenanthramides. Although nitrogen addition significantly improved grain yield and β-glucan content—supporting higher nitrogen input recommendations in agricultural practices—careful consideration is needed regarding varietal selection, the decline in beneficial secondary metabolites, and the environmental costs of nitrogen fertilization (Allwood, et al., 2021).

**5.2 Agronomic Bio-fortification**

A study was conducted to investigate the agronomic biofortification of oats with iron and zinc. The findings indicated that foliar application of these micronutrients during the grain filling stage had no adverse effects on yield or the industrial and chemical quality of oat grains. Zinc biofortification using sulfate-based sources effectively enhanced zinc accumulation in the oat caryopses but resulted in a reduction in iron content. Conversely, iron biofortification with sulfate sources increased iron levels in the caryopses while causing a decline in zinc content (Babeski, et al., 2023).

**6. Challenges and Future Prospects**

*Polygenic trait architecture* demands large training populations for genomic selection; integration of high-throughput phenotyping (hyperspectral imaging for β-glucan) will expand datasets. *Gene-editing regulation* remains uncertain. *Genotype × environment interactions* necessitate multi-location networks to stabilise nutrient traits. Future research should merge pan-genomics, pangenome-wide association, and speed breeding to cut cultivar-replacement cycles to 5–6 years.

**7. Conclusion**

Substantial progress since 2016 underscores the feasibility of enriching oat grain with health-promoting compounds through an integrated pipeline of germplasm exploitation, molecular breeding, gene editing and agronomic bio-fortification. Scaling these advances will require harmonised phenotyping platforms, supportive regulatory frameworks for precision breeding, and farmer-friendly cultivation packages that protect nutrient gains against climate variability. Such coordinated efforts will cement oat’s role as a cornerstone of sustainable, nutritious food systems.

**Conflicts of Interest Statement**

We have no conflicts of interest to disclose. Authors declare that they have no conflicts of interest. The research was fully done independently not any financial support involved.

Author contribution Contributed to the conception and design of the analysis paper Contributed to the data collection Data and analysis tools wrote the analyzed paper. Also evaluated the paper and then suggested to publish in this journal.

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