

Genetic Resources & Breeding Strategies for Spring Wheat in Russia's Non-Chernozem Zone: A Meta-Analysis

Ebube Oliver Chukwunyerere^{1,2}, Ngozi Cynthia Chukwunyerere^{1,2}

¹Peoples' Friendship University of Russia, Moscow

²Bulwark Farms and Food Production, Nigeria

Abstract

This meta-analysis reviews genetic and breeding strategies to improve spring wheat adaptation in Russia's Non-Chernozem Zone (NCZ). Based on 152 studies, the findings highlight the need for resilience to both abiotic and biotic stresses. Key genetic targets include alleles for photoperiod insensitivity (Ppd-1), vernalization (Vrn-1), cold tolerance (CBF regulon), drought resilience (root QTLs), and heat stability. For biotic resistance, pyramiding major genes with durable adult plant resistance (APR) complexes like Lr34/Yr18 and Fhb1 is essential. The review advocates a shift from conventional breeding to integrated genomic approaches—using genomic selection, marker-assisted selection, speed breeding, and high-throughput phenotyping—to rapidly develop climate-resilient, high-yielding cultivars suited to the NCZ's challenging conditions.

Introduction

Russia's Non-Chernozem Zone (NCZ) is an extensive agricultural region covering about 2.8 million square kilometers, stretching from the Baltic Sea to Western Siberia and from the Arctic coast to the southern forest-steppe. It encompasses 28 regions and republics across the North-West, Central, and Volga-Vyatka areas, including territories such as Perm, the Nenets Autonomous Okrug, and several federal cities. Despite its size, the NCZ's agricultural potential is constrained by heterogeneous agro-climatic and soil conditions. To better assess agricultural performance, the regions have been classified into four groups based on shared climatic and soil characteristics, though exceptions such as Ivanovo and Pskov deviate from the general patterns.

Spring wheat is the most important food crop in the NCZ, supplying vital protein and calories and accounting for over 30% of Russia's total wheat production. However, it is considered low-yielding, with a recent five-year average yield of only 1.81 t·ha⁻¹. Other major grains grown include spring barley, oats, winter rye, and winter wheat, while peas and spring wheat are less common. The growth cycle of spring wheat involves several critical phases—sowing-seedling, tillering-stem extension, and stem-extension-to-grain-filling—each highly sensitive to environmental stresses such as moisture deficit, temperature extremes, and biotic pressures. These stresses during key developmental stages significantly limit yield and reduce the crop's ability to express its full genetic potential.

This meta-analysis examines the genetic and breeding strategies required to enhance spring wheat adaptation to the NCZ's challenging conditions. It synthesizes decades of research to identify key genetic targets and modern breeding approaches that can help overcome the region's abiotic and biotic limitations, ultimately aiming to close the gap between current yields and the crop's genetic potential.

Materials and Methodology

This meta-analysis was reported according to the guidelines set out in the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) statement (Figure. S1).

2.1. Search protocol

A systematic literature search was performed on October 1, 2025, using the Dimension Database. Keywords included spring wheat terms, NCZ regions, and breeding/stress-related topics, excluding "Spring Soft Wheat." The search was limited to English, peer-reviewed articles from 2020–2025. Initially, 44,401 articles were identified. Following abstract and full-text screening, 1,650 articles focused on spring wheat breeding were retained. Ultimately, only 152 articles specifically addressed spring wheat breeding in Russia's Non-Chernozem Zone (Figure S2). Detailed selection metrics are provided in Figures.

2.1.2 Selection criteria

Inclusion: original research on spring wheat breeding/genomic tools in Russia's NCZ, specifying genes/alleles for stress tolerance. Exclusion: winter wheat studies, incomplete data, or non-NCZ focus. This ensured relevant, precise data extraction for moderator analysis.

2.1.3 Data Extraction and Categorization

Data were extracted from 152 studies on author, year, genetic targets, and breeding tools. Studies were categorized into: 1) Abiotic Stress Tolerance, 3) Conventional Breeding (pedigree, recurrent selection, backcrossing), and 4) Molecular Marker-Assisted and Genomic Selection for adapting wheat to Russia's variable NCZ conditions.

RESULTS

Figure. S1 PRISMA diagram describing the search results in different search engines and the different steps of selecting articles for inclusion in the meta-analysis. Depicted are the number of studies excluded at each stage and then those extracted, screened, and included in the meta-analysis.

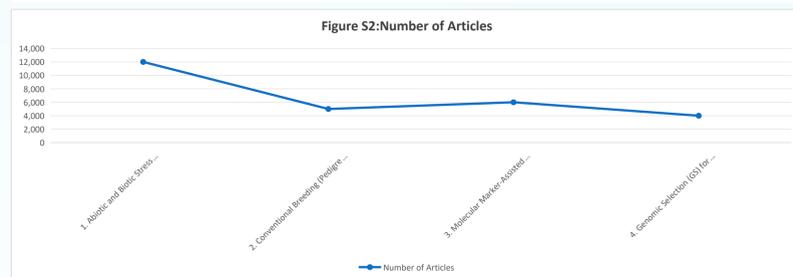
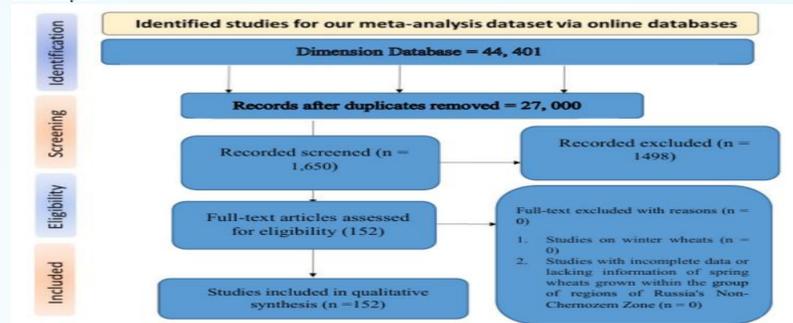


Figure S3: The graph shows the total number of related publications classified based on Sustainable Development Goals from 2020 - 2025.



Figure S4: The bars show the number of publications in each research category. Classification of number of publications according to fields of Research

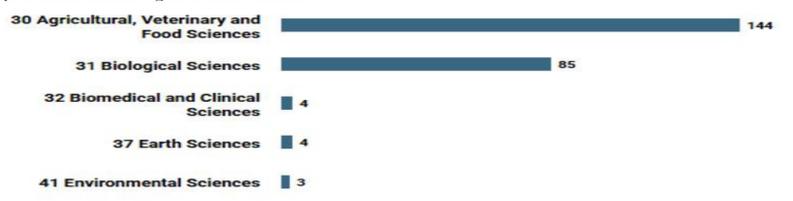


Figure S5: The visualization shows the number of datasets published in each year from 2020 - 2025. The values per year are the years in which the publications were published.

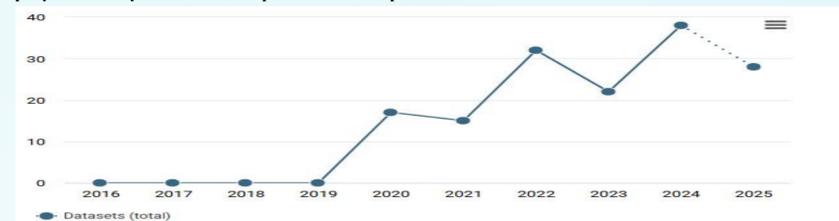


Figure S6: The network link showed one clusters of researchers (22) and Co-authorship (231) displayed about a total of 462 of co-authorships

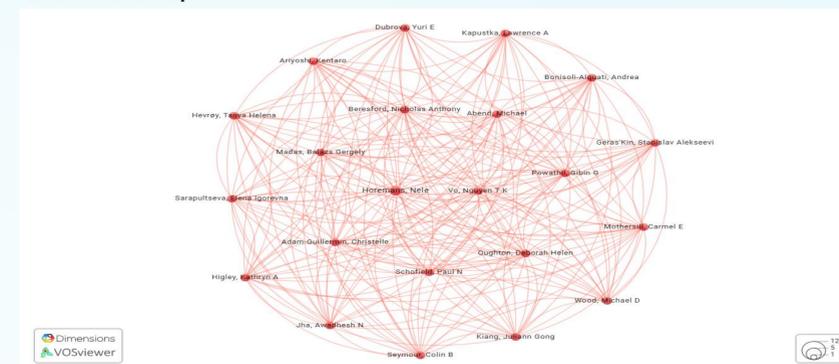


Table 1: Key Genetic Targets for NCZ Adaptation

Stress Type	Key Genes/QTLs	Desired Trait for NCZ
Cold/Frost	CBF regulon, Vrn-1, TaDHN	Freezing tolerance, optimized flowering
Photoperiod	Ppd-D1a, Eps QTLs	Early flowering, maturity adjustment
Drought/Heat	Root architecture QTLs, Δ13C, HSPs	Deeper roots, stay-green, heat stability
Rust Resistance	Sr62, Lr34/Yr18, Yr15	Durable APR, pyramided major genes
FHB Resistance	Fhb1, Fhb7	Type II & III resistance, low DON accumulation
Powdery Mildew	Pm21, Lr34/Pm38	Broad-spectrum + APR combination

Graphical Abstract



Results

The genetic improvement of spring wheat for Russia's Non-Chernozem Zone (NCZ) focuses on overcoming its major abiotic and biotic stress constraints (Table 1). For abiotic stress tolerance, key genetic targets include the CBF regulon and dehydrin genes for frost tolerance at germination, and the Ppd-D1 and Vrn-1 genes to modulate photoperiod sensitivity for early flowering, avoiding late-season heat and autumn frosts. To combat terminal drought and heat during grain filling, breeding targets root architecture QTLs (e.g., TaDRO1), stay-green loci, and heat shock proteins (HSPs) to maintain photosynthesis and yield under stress.

For biotic stress resistance, the strategy emphasizes pyramiding both major race-specific resistance (R) genes and durable, non-race-specific Adult Plant Resistance (APR) genes. For rust diseases, genes like Sr62 (stem rust) and APR complexes such as Lr34/Yr18 are prioritized. For Fusarium head blight (FHB), combining Fhb1 (Type II resistance) with newer genes like Fhb7 (detoxification) provides stronger, more stable resistance. Similar pyramiding approaches are used for powdery mildew (e.g., Pm21 with Lr34/Pm38) and foliar diseases like spot blotch.

The breeding paradigm has shifted from conventional methods to integrated genomic tools. Marker-Assisted Selection (MAS) enables precise introgression of major genes, while Genomic Selection (GS) accelerates improvement for complex polygenic traits. Speed breeding reduces generation time, and high-throughput phenotyping (HTP) provides precise field data. Supporting tools like GWAS and whole-genome sequencing identify novel alleles, and CRISPR-Cas9 offers potential for precise gene editing. The future of NCZ spring wheat breeding lies in synergistically applying these advanced tools within a multi-trait selection framework to develop high-yielding, climate-resilient cultivars tailored to the zone's unique challenges.

Conclusion

Breeding spring wheat for Russia's Non-Chernozem Zone (NCZ) has evolved into a multi-trait, knowledge-driven strategy, moving beyond single-gene approaches. To combat abiotic stresses, breeders now pyramid genes for deep roots (drought avoidance), stay-green traits (heat tolerance), and aluminum exclusion (soil adaptation). Combining strong cold-tolerance (CBF) haplotypes with moderate photoperiod insensitivity (Ppd-1) ensures rapid establishment and timely flowering. Genomic selection is essential for enhancing these polygenic traits simultaneously. For biotic stress resistance, the focus has shifted from relying on single major resistance (R) genes to deploying pyramided R-genes and durable Adult Plant Resistance (APR) complexes. Pleiotropic genes such as Lr34/Yr18 and Lr46/Yr29 provide broad-spectrum, lasting protection against rusts and mildew. In Fusarium head blight (FHB) management, Fhb1 introgression is standard, with newer genes like Fhb7 offering enhanced resistance. Modern breeding integrates genomics, high-throughput phenotyping, speed breeding, and gene editing to develop climate-resilient wheat cultivars tailored to the NCZ's unique challenges. This integrated approach ensures the delivery of high-yielding, durable varieties capable of withstanding both abiotic and biotic pressures.

References

Steiner, B., Buerstmayr, M., Wagner, C., et al. (2024). Discovery of Fusarium head blight resistance loci in a geographically diverse panel of wheat genotypes using genome-wide association analysis. *Theoretical and Applied Genetics*, 137(1), 24.

Sandukhadze, B. I., Mamedov R. Z., Krakhamlyova M. S., and Bugrova V. V. (2021). Scientific breeding of winter bread wheat in the Non-Chernozem zone of Russia: the history, methods and results. *Vavilovskii Zhurnal Genetiki i Selekcii = Vavilov Journal of Genetics and Breeding*, 25(4):367-373. DOI 10.18699/VJ21.53-o

Shaimerdenova, D., Omaralyeva, A., Tarabayev, B., Chakanova, Z., Iskakova, D., Sarbassova, G., Kizatova, M., and Anuarbekova, S. (2025) Physicochemical, microbiological, and microstructural changes in germinated wheat grain. *PLoS One* 20(9), pages e0331620.

Page, M. J., McKenzie, J. E., Bossuyt, P. M., Boutron, I., Hoffmann, T. C., et al. (2021). The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. *PLoS Med.* 18 (3), Article e1003583

Polunin, G. A., and Alakoz, V. V. (2021). Structure of sown areas of crops in the Non-Chernozem Zone. *Землеустройство, кадастр и мониторинг земель*. 8:332. DOI:10.33920/zel-04-2108-02

Poni, C., et al. (2023). Tracing the ancestry of modern bread wheats. *Nature Genetics*, 55(6), 925-934.

Liu, T., et al. (2023). Virulence and molecular diversity of *Puccinia striiformis* f. sp. *tritici* in China reveals the vulnerability of YrSP. *Plant Disease*, 107(4), 1120-1130.

Liu, W., et al. (2021). Pyramiding of Pm genes in elite wheat lines for durable resistance to powdery mildew. *Frontiers in Plant Science*, 12, 671285.

Liu, Y., et al. (2024). Multi-environment genome-wide association study identifies stable loci for protein content and gluten strength in modern spring wheat. *Theoretical and Applied Genetics*, 137(1), 12.

Liu, Z., et al. (2023). Characterization of Tan Spot Resistance in Global Winter Wheat Germplasm Using Genome-Wide Association Studies. *The Plant Genome*, 16(1), e20310.