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ORIGIN AND PHYLOGENETIC EVOLUTION OF WHEAT (TRITICUM L.) CYTOGENETIC AND EVOLUTIONARY ASPECTS

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Abstract

This article examines modern perspectives on the origin and evolutionary path of cultivated wheat. Particular attention is paid to the processes of natural hybridization and polyploidy, which led to the formation of modern genomes. The classification of species based on their ploidy and genomic composition is provided. The role of wild relatives in breeding adaptive varieties for the conditions of Uzbekistan is analyzed.

Keywords: Triticum, evolution, polyploidy, genome, breeding, Uzbekistan, drought resistance.

Introduction

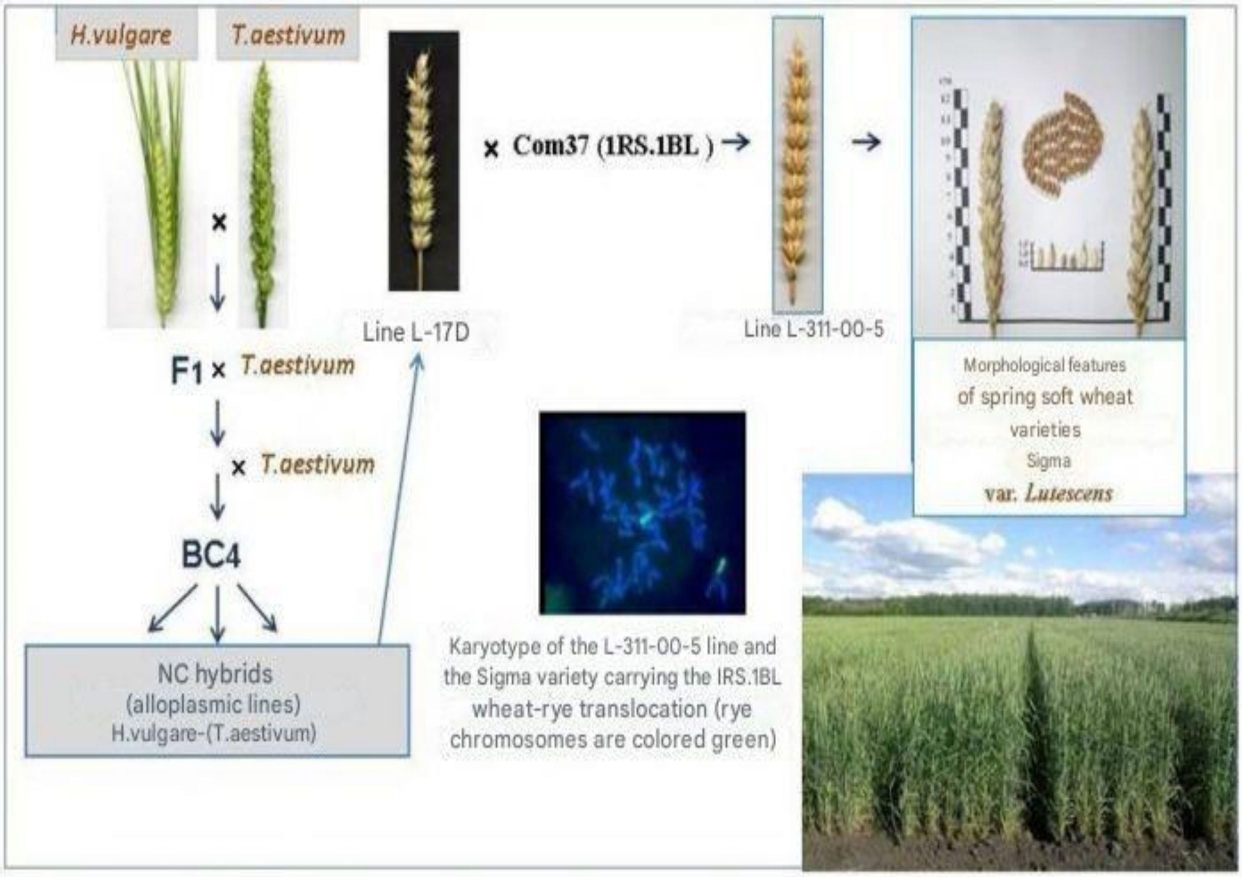
Аннотация. В данной статье рассматриваются современные представления о происхождении и эволюционном пути культурной пшеницы. Особое внимание уделено процессам естественной гибридизации и полиплоидии, которые привели к формированию современных геномов. Приводится классификация видов в зависимости от их плоидности и геномного состава. Анализируется роль диких сородичей в селекции адаптивных сортов для условий Узбекистана.

Ключевые слова: Triticum, эволюция, полиплоидия, геном, селекция, Узбекистан, засухоустойчивость.

Introduction

Wheat (Triticum L.) is a fundamental element of global food security and the most important strategic crop in the agriculture of Uzbekistan. In the context of global climate change and the aridization of Central Asian territories, understanding the phylogenetic roots of wheat becomes not only an academic task but also a practical necessity. Knowledge of cytogenetic history allows scientists at NUUz to effectively utilize the “dormant” genes of wild ancestors to combat modern challenges: soil salinity, irrigation water shortages, and new races of pathogens.

According to the fundamental works of N. I. Vavilov, the Near Eastern center is the primary center of origin for the genus Triticum. The evolution of wheat is unique in that it did not follow a path of simple divergent radiation, but rather developed through allopolyploidy—the unification of entire genomes from different cereal species (genera Triticum and Aegilops). This process, known as "reticulate evolution," allowed wheat to accumulate the genetic plasticity of several genera, making it one of the most adaptable crops on the planet.

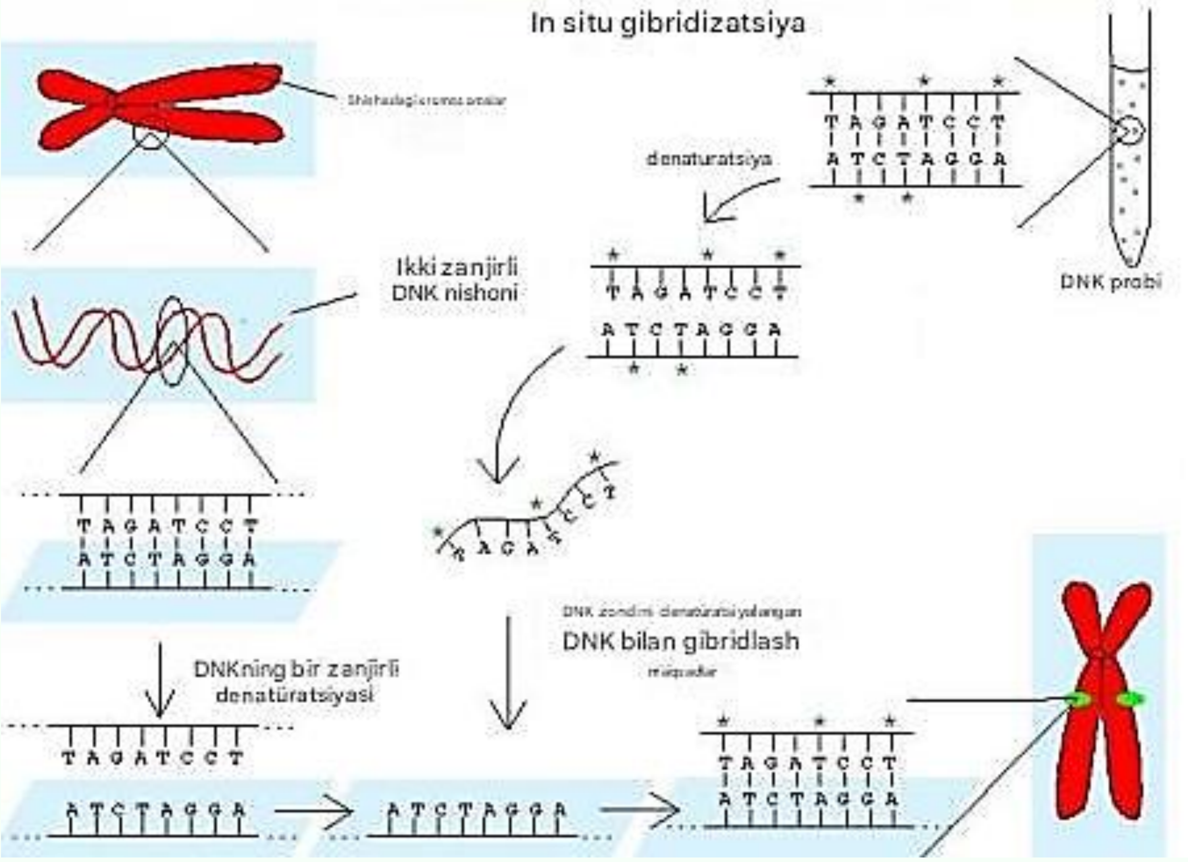


Main Stages of Polyploidization and Genome Formation.The phylogeny of wheat is traditionally divided into three hierarchical levels of ploidy:

Diploid level (2n=14): The starting point is considered to be wild einkorn (T. boeoticum), the carrier of the **AA** genome. This species is characterized by high viability but low productivity and a brittle rachis.

Tetraploid level (2n=28): Approximately 0.5–1 million years ago, diploid wheat hybridized with a wild relative closely related to the modern Aegilops speltoides (carrier of the **BB** genome). The result was wild emmer (T. dicoccoides), whose **AABB** genome became the foundation for all durum wheats (T. durum).

Hexaploid level (2n=42): The most recent stage (about 8–10 thousand years ago). Spontaneous hybridization occurred between cultivated emmer and the wild grass Aegilops tauschii (genome **DD**). This event led to the emergence of common wheat (T. aestivum).



For the scientific justification of breeding programs, a clear differentiation of species by their genetic composition is necessary.

Table 1. Genetic Classification and Origin of Species of the Genus Triticum

Ploidy Group	Species (Scientific Name)	Genome	Chromosomes (2n)	Status and Significance
Diploids	T. boeoticum	AA	14	Wild ancestor
	T. monococcum	AA	14	Cultivated einkorn
Tetraploids	T. dicoccoides	AABB	28	Wild emmer
	T. dicoccum	AABB	28	Emmer (Ancient hulled wheat)
	T. durum	AABB	28	Durum (Hard) wheat
	T. timopheevii	AAGG	28	Timopheev's wheat (Immune)
Hexaploids	T. aestivum	AABBDD	42	Common (Soft) wheat
	T. spelta	AABBDD	42	Spelt
	T. compactum	AABBDD	42	Club wheat

Wheat Evolution in the Context of Uzbekistan's Environment. Uzbekistan is characterized by extreme continentality. In this context, the cytogenetic nature of wheat plays a decisive role in the survival of varieties.

Durum Wheats (AABB Genome) tetraploid wheats (T. durum) possess natural resistance to high temperatures. NUUz is studying the heat resistance mechanisms of varieties such as “Zilol” and “Muruvvat”. The B genome provides these varieties with high grain density and a specific biochemical composition essential for the pasta industry.
Common Wheats (AABBDD Genome) and the Role of the D Subgenome: The D genome, inherited from Aegilops tauschii, has made an invaluable contribution to the adaptation of wheat to Central Asian conditions. It is responsible for salt tolerance the “Bunyodkor” variety is successfully cultivated on the saline lands of the Aral Sea region due to specific loci in the D genome.
Earliness varieties like “Andijon-2” and “Dustlik” manage to yield before the onset of extreme “garmsil” (hot dry winds).

Potential of Wild Relatives (Aegilops L.) endemic forms of Aegilops grow in the Tien Shan and Pamir-Alay territories. Research by NUUz staff confirms that using these wild species as donors allows for the introgression of resistance genes against rust (yellow and leaf rust), which is critical for the republic's food security.

Conclusion

The evolutionary path of wheat from wild diploids to high-yielding hexaploids is the result of complex genomic interactions. For Uzbekistan, the most promising direction is **“synthetic breeding”**-the recreation of hexaploids by crossing modern durum wheats with wild Aegilops. This will allow the reintroduction of resistance genes lost during domestication into the cultivated gene pool and the creation of varieties capable of providing stable yields in a changing climate.

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