

flattened cereal of premium grade makes up 77.8–82.1 %.

The output of flattened cereals of premium and first grade from the cereal № 1 of emmer wheat of Holikovska cultivar can be described with multiple nonlinear models:

$$\text{АШКЫЕ} \quad \text{ПКФВУ} \quad = \quad 68\text{Ю}8231-0\text{Ю}9054\text{ч}-6\text{Ю}6213\text{н}+0\text{Ю}0037\text{ч}^2+0\text{Ю}0109\text{чн}+5\text{Ю}5778\text{н}^2\text{б}$$

Where  $x$  – duration of grain radiation in the microwave, s;

$y$  – hydrothermal treatment, %

Uniformity and intensity of microwave energy absorption depend on the layer thickness of a product, moisture content and its distribution within a product [4]. Dry grain had balanced distributed moisture which led to the homogeneous heating of caryopses.

Moistening of cereals by 0.5 % is insufficient to saturate the inner layers of endosperm with moisture. A considerable amount of water remained in the upper layers of caryopses forming a wet layer. During the radiation a significant amount of energy is absorbed by created layer, and the part of reflecting radiation energy increases. Low thermal conductivity of grain restrains the penetrating of heat from upper layers into the endosperm thickness. As a result, there is low heating of caryopsis thickness. Increase of moistening level of the whole cereal by 1 % led to the deeper penetration of moisture into the endosperm. It resulted in the balanced heating of caryopses throughout their thickness, which leads to the decrease of the endosperm crumbliness. It is worth mentioning that the increase of moistening level of the whole cereal requires the prolongation of moistening term. As the moisture increases, the greater amount of vapor is created during the radiation with EMF, which has its drawbacks.

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# ADVANCES IN MICRORNA RESEARCH OF WINTER WHEAT

**Qiaoyan Chen**

PhD student  
Sumy National Agrarian University, Ukraine

**Wenhui Wei**

Professor  
Henan Institute of Science and Technology  
Chinese People's Republic

**Kandyba Nataliya**

PhD, Associate Professor  
Sumy National Agrarian University, Ukraine

MicroRNA (miRNA) is a type of non-coding small RNA (sRNA) with important regulatory functions found in eukaryotes in recent years, and its length is between 20-25 bp. A large number of studies have found that miRNA is involved in post-transcriptional regulation of genes and plays an important regulatory role in plant growth, development, and response to adversity stress. Gene expression can be regulated by degradation of its target gene miRNA or translation inhibition [1-2]. The earliest discovered miRNA coding gene is lin - 4 of *Caenorhabditis elegans*. Its product is a 24 nt small RNA that can bind to the 3'non-coding region sequence of its target gene lin-14 miRNA in a non-fully complementary form and inhibit the protein translation process, there by regulating the transformation of the nematode early development period [3]. Subsequently, miRNAs have been discovered in fruit flies, humans and other species [4, 5]. Since the first miRNA was discovered, nearly 40,000 mi RNAs have been discovered and included in the mi RBase (Release 22) database [6]. The mechanism of miRNAs regulating gene expression is also very complicated. The classic miRNA maturation pathway is as follows: RNA polymerase II or III transcribes miRNA-related genes into primary miRNA (pri-mi RNA) in the nucleus. At this time, miRNAs are several thousand not long. Subsequently, the primary miRNA is cleaved into precursor miRNA (pre-mi RNA). At this time, the precursor miRNA has a hairpin structure, and the above process is carried out in the nucleus. Then, the precursor miRNA is transported out of the nucleus. It can be decomposed into mature length by RNase Dicer enzyme. At this time, the miRNA still has a double-stranded structure. Finally, the double-stranded miRNA is transferred into AGO2 to form RISC (RNA-induced silencing complex). One strand of the mi RNA double strand is stored in the RISC complex, and the other strand is removed from the complex and quickly degraded [7, 8].

Research progress of miRNA in winter wheat growth and development. The growth and development of winter wheat is a complex process, and the regulation of

miRNA also runs through the entire growth and development process of wheat. Li Qiang and others are inoculating wheat after caulimodans discovered that *A. caulimodans* can increase the relative expression of miRNAs in winter wheat roots in response to nitrogen, phosphorus and trace elements to varying degrees, enhance the absorption and utilization of nutrient elements by winter wheat seedlings, and promote the morphogenesis of winter wheat roots. Among them, the excessive accumulation of wheat-specific miR1138 may regulate the expression of EIF4b (eukaryotic initiation factor 4b), which plays a key role in regulating protein biosynthesis and maintaining the balance of cell function [9]. Li et al. used 7, 14, 21, and 28-day Chinese spring wheat grains as materials and obtained 186 conserved miRNA and 37 new miRNAs through sRNA and degradome sequencing. Further analysis revealed that the expression patterns of the 55 miRNAs in the four stages of grain development were different.

The expression levels of miR408 and miR5048 increased with the growth of grains; the expression levels of miR319 and miR827 gradually increased during the early stages of grain development. The expression level of miR169, miR165, and miR444 gradually decrease with the growth of the grain. Zhu Yanfeng et al. used virus-induced gene silencing to silence *tae-miR9663* and found that the shape of wheat leaves changed and it also had a certain impact on the development of seeds [10].

In terms of fertility, studies have shown that miR159 affects the development of rice anthers. Overexpression of miR159 in rice will result in malformed flower development and no pollen in the stamens. In addition, overexpression of wheat miR159 in rice, or *tae-miR159* can also cause male sterility in rice [11]. Recent studies have found that miR1227 and miR2275 may be related to male sterility in wheat. MiR1227 and miR2275 target CAF1 (CCR4-associated factor 1) and SMARCA3L3, respectively (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A, member 3-like 3), these two genes are related to meiosis. CAF1 and SMARCA3L3 participate in DNA repair and transcription to maintain the chromosome and genome in the integrity of the meiosis process allows the meiosis to proceed normally [12]. Wheat miR156 has a similar effect to rice miR156, which can promote tillering and inhibit the formation of spikelets [13]. MiR159 may affect seed filling by regulating the transduction of ABA signals by seeds. The expression of miR164 in developing wheat seeds has an upward trend [14]. During the grain filling stage of winter wheat, miR396 affects the development of grains by regulating the expression of GRF genes (GRF1, GRF6, GRF9). The miRNA related to the regulation of winter wheat grain development has been found to be closely related to the process of grain development [15].

**Research progress of miRNA in wheat biological stress.** In the process of growth and development, wheat will be subjected to various biological stresses. Powdery mildew, rust, head blight, sheath blight, and stem bases that have recently become popular in Huanghuai wheat areas have a greater impact on wheat. Rot and mosaic virus disease, in addition to aphids, midge and red spider, also belong to the category of biological stress. Xin et al. analyzed the changes in the abundance of

miRNA in wheat leaves before and after powdery mildew infection and heat stress. Among the 153 miRNAs identified, 24 and 12 miRNAs were identified. The expression levels of miRNA were obvious before and after powdery mildew infection. Among them, the expression of miR156 in resistant and non-resistant strains decreased significantly, and the expression of its target genes increased [16].

Feng Hao inoculated a wheat variety Xingzi 9104 that was susceptible at the seedling stage but resistant to the disease at the adult stage. He studied the expression changes of 15 miRNAs at different time points and found that they could all be invaded by the rust. Induction of staining and showing a variety of expression trends, which indicates that the stripe rust resistance/susceptibility traits of Xingzi 9104 are not determined by the regulation of one or a type of miRNA, but the result of the joint regulation of multiple miRNAs [17].

**Research progress of miRNA in wheat abiotic stress.** During the growth and development of wheat, while experiencing biological stresses, it may also experience abiotic stresses such as floods, droughts, extreme temperatures, nutritional imbalances, or salinity. More and more studies have found that miRNAs are effective in crop response to these adversities. Plays an important role in the process. In drought-stressed wheat, the expression levels of miR10 and miR9654 are up-regulated [18].

Kantar et al. also used miRNA chip technology to analyze the expression patterns of miRNA in wheat under drought stress. They found that after 4 h and 8 h drought treatments, different miRNA expressions were found in the roots and leaves of the crop, and compared to the blank control group, the expression of miRNA in crops treated with drought stress was significantly higher [19].

Ma Yanhong et al. analyzed the expression of miRNA related to *Agropyron mongolica* and target genes analysis, because the target genes of amo-miR21, amo-miR82 and amo-miR62 all have high homology with the predicted target genes in wheat (68.6 - 95.6%), it is speculated that these three target genes are genes involved in drought stress response [20]. Wheat miR171, miR393 and miR408 have corresponding responses to salt stress, but the mechanism is still not very clear [21].

In terms of high temperature stress, many miRNA families in wheat, such as miR156, miR159, miR160, miR167, miR319, miR395, and miR398, are involved in the expression and regulation of high temperature stress-related genes such as HSP17, HSP70, and superoxide dismutase. miR159 and miR398 showed up-regulated expression after high temperature stress; miR160 showed moderate down-regulated expression; the target genes of miR156 under high temperature stress were Ta GAMYB1 and Ta GAMYB2 [22].

When wheat is subjected to low temperature treatment, as the temperature decreases, the expression levels of miR165, miR166, and miR319 show a trend of first increasing and then decreasing. However, when wheat is subjected to both low temperature and exogenous ABA stress, miR165 The expression of miR166 and miR166 showed a downward and upward trend, and miR319 showed a downward and then upward trend, indicating that ABA changed the expression patterns of these three miRNAs [23].

In terms of cold stress, two candidate miRNAs related to cold stress, miR1132 and miR1121, have been identified in wheat. They may be involved in the expression and regulation of cold stress-responsive genes; however, the targets gene of miR1132 and miR1121 have not been found yet [24].

In terms of cadmium stress, Qiu Zongbo et al. analyzed wheat cadmium treatment and found that 9 miRNAs were involved in the regulation of wheat cadmium stress response. Among them, after cadmium stress, the expression of miR167, miR171, miR399 and miR44 in seedling roots or leaves showed a downward-regulated trend, while the expression of miR319, miR396 and miR397 in wheat seedling roots and leaves showed an up-regulated trend. It shows that mi RNAs are involved in the regulation of wheat cadmium stress response, the response to cadmium stress in different time periods shows a dynamic change process, and the expression of most mi RNAs is tissue-specific [25].

Research by Zhang Jianing et al. showed that Ta miR167 responds significantly to low-phosphorus stress. After low-phosphorus treatment, the transcript abundance of this member in the roots and leaves increases. After the phosphorus abundance is restored, its expression level continues to decrease. Ta miR167 responds to low-phosphorus stress. The response and further action of target genes have an important impact on the ability of plants to resist low-phosphorus adversity [26].

Xie Wenzhao et al. found that Ta miR1129 has a certain function in resisting low-nitrogen stress, and super-expressed Ta miR1129 has significantly enhanced the ability of plants to resist low-nitrogen stress [27].

Although the progress of wheat mi RNA research is late, in recent years, there have been more and more reports on wheat miRNA, and the design aspects have become more and more extensive. Whether it is wheat growth and development, disease resistance and stress resistance, miRNAs play an important role. However, most reports only briefly introduce the corresponding adversity or speculate on its function. There are few reports on the specific miRNA regulation mechanism and regulation mechanism. In addition, the regulation network of miRNA is relatively complicated. Sometimes many mi RNAs control the same trait, sometimes one miRNA. Regulating multiple traits, there are still very few miRNAs that actually report major effects. It is believed that with the completion of the entire wheat genome assembly and the development of new technologies such as bioinformatics, the research on wheat miRNA will be more comprehensive and in-depth.

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