



# Recognition of Aptitude in Regard to Wheat Mill Density

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## Abstract

The world's population growing rapidly today, ensuring an adequate wheat harvest for everyone is a constant challenge. Wheat yield can be increased by controlling 1000 mil weight, which is one of the key determinants. Quality control mil length, mil width, mil thickness and 1000 mil weight to determine mill density. To identify the qualities associated with mill density, 88 histis derived from a cross between JJ625LG, which has a high mill density, long spindle mills, and a low mill weight of 1000, and Namchan, which has a short, rounded mill stem and a heavy 1000 mil weight. In 2021 and 2022, we used 511 SNP markers to map plant density-related qualities on physical maps. Mill density-related qualities are evenly distributed across chromosomes 2, 3, 5, 10, and 11. QRLw5 on chromosome 5 was associated with the major previously cloned and detected genes, GS3 and qSW5, respectively, and was found to be related to mill density. Moreover, qGw10 and qGw10-1, which were further detected in this study, were found to be associated with Os10g0525200 (OsCPq10), a potential candidate gene involved in mill density regulation. This gene encodes a cytochrome P450 family of proteins and is thought to have beneficial effects on Mill density by interacting with proteins involved in the mechanisms that determine Mill density. Specifically, OsCPq10 was screened for two consecutive years in the same identified QTL region. This is expected to have a positive impact on mill density. These results help breed superior high-yielding wheat varieties by adding detailed mapping on mill density.

**Keywords:** Wheat; Mill density; Yield; Breeding; QTL

## INTRODUCTION

Globally, continued population growth, declining agricultural land, and unpredictable climate change threaten food security, creating a serious social problem. But the Green Revolution over the past half century has greatly improved wheat yields and has gradually solved the hunger problem. However, drastic climate change in recent years has reduced arable land and stagnated or destroyed yields of the world's major food crops such as wheat, corn and wheat, and the situation shows no signs of improvement. Feeding a growing world population requires steadily increasing yields of key food crops, including wheat (Mason N M et al., 2017).

Wheat is one of the typical food crops that are ground and sold to consumers. A mill's properties determine its

marketability through the complex influence of factors such as chalkiness, clarity, and weight of 1000 mils, in addition to mill geometry characteristics such as length, width, and thickness (Luo Y et al., 2017). Specifically, the shape of the mill is determined by the ratio of mill width to mill length. As it is closely related to the 1000 mil weight, it is recognized as a key factor in determining yield and is also an important property in determining appearance. Furthermore, mill geometry is strongly associated with yield, is one of the most commonly selected traits in the wheat breeding process, and can provide an excellent model for understanding wheat breeding lines (Wang H, 2017).

In general, mill density and shape are regulated by a complex interplay between major and minor grades and are critical factors in yield and mill quality. Numerous studies have therefore been performed to genetically map the

qualities associated with mill shape in wheat. As a result, thousands of Quality have been searched for in various mapping populations over the past decades. Moreover, the function of some of these qualities has been characterized at the genetic level. GS3 was the first gene reported to be associated with mil type and has been shown to increase mil length while regulating transmembrane proteins. It is also known that activation of DEP1 shortens mill length, and qGL3.1 regulates panicle phosphorylation to determine mill length and 1000-mil weight. In addition, GW2, identified on chromosome 2, is associated with mil width (**Baležentis T et al., 2021**). Loss of GW2 function has been reported to increase cell number and increase mil width and 1000 mil weight. Losses of function of qSW5/GW5 on chromosome 5 are associated with increased yield with increased plant width and sink density. qSW5/GW5 interacts with calmodulin proteins to regulate plasma membrane-associated proteins to a narrow mil width, and loss of its function increases the mil width and 1000 mil weight. Activation of GS5, located on chromosome 5, has been reported to be responsible for increased mil width and 1000 mil weight (**Balsalobre-Lorente D, 2019**). Additionally, in wheat, GW8/OsSPL16 has been studied at the genetic level and found to affect mill density and 1000 mill weight. Here, using a population derived from the cross of 'JJ625LG' and 'Nanchang', finally he reports the identification of the dominant QTL associated with the mill geometry controlling the weight of 1000 mils. The results of this study will be useful in the future for applying quality factors related to mill geometry. H. As cloning and breeding material (**Barbera AJ et al., 1990**).

## DISCUSSION

The rapid growth of world population and the unpredictability of climate change are important reasons for increasing wheat yields. To address this, trait qualities associated with yield were identified and mapped for use in practical crop production (**Adetutu MO et al., 2020**). Mill density is directly related to yield. As interest in mill quality grows with rapid population growth, many attempts have recently been made to search for genes that positively affect mill density and apply them to breeding programs. It's been done. Due to rapid climate change, the area under cultivation of wheat is decreasing. Therefore, there is a need to screen candidate genes that may produce high yields in limited areas and apply them to wheat breeding (**Z Meng J, 2017**).

High yields can be achieved by adjusting the number of tillers, panicle length and spikelet number, but mill density is also a key factor in achieving high yields (**Bhutta, Zulfiqar A, 2013**). Much work has been done to increase yield by controlling mill density, and most of the currently identified qualities are distributed in similar chromosomal regions. Most of the mill density-related grades identified in this study map to regions close to previously reported grades. Notably, GS3 and qSW5 were identified with quality

detected on chromosomes 3 and 5, respectively, validating the results of this study and demonstrating successful mapping of mill density quality using JNRIL. In 2015, GS2 was cloned on chromosome 2 and had a positive impact on mill density and yield (**Headey DD, 2013**).

## CONCLUSION

Mill density is directly related to yield and has a very strong impact. Quality related to mill density was mapped using JNRIL derived from a cross between JJ625LG and Namchan. A linkage map of 511 SNP markers was generated. QTL maps from two consecutive study years identified GS3 and qSW5, reported to be the major mill-density genes, on chromosomes 3 and 5, respectively. In addition, genotypic regions detected with different frequencies in the LLH and SSL groups were analyzed and the region C10\_21047555–C10\_21256365 was identified as important for mill density. OsCPq10 was found at C10\_21047555–C10\_21256365, which encodes a cytochrome P450 protein. OsCPq10 interacts with proteins that regulate mill density and was analyzed for homology to other proteins in crops by Gramene. OsCPq10 may be used to breed elite wheat cultivars that can produce high yields by positively influencing plant density.

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