A Review of on the Spikelet Number in Rice

**Ali Sattari[1], ZA-Jahantigh Haghighi[2], HO-Nohtani[3], MO-Noorozi[4], Ab-Nokhbeh Zaeim[5],
K-Moradi[6] , Na-Mirzaie amirabad[7]**

[1]Phd. student of Dept. of Agronomy and Plant Breeding, Faculty of Agriculture, Zabol University
[2]M.Sc. Dept. of Agronomy and Plant Breeding, Faculty of Agriculture, Zabol University,Iran
[3]M.Sc. Dept. of Agronomy and Plant Breeding, Faculty of Agriculture, Zabol University,Iran
[4]Tanin Keshtzar Sabz Agricultural Research, Service and Production Cooperative Company, Iran
[5]M.Sc. Dept. of Agronomy and Agroecology, Faculty of Agriculture, Ferdowsi University of Mashhad,Iran
[6]Phd. student of Dept. of Agronomy and Plant Physiology, Faculty of Agriculture, Zabol University, Iran
[7]M.Sc. Dept. of Agronomy and Horticultural Plant Breeding, Faculty of Agriculture, Zabol University, Iran

ABSTRACT

Grain yield of rice (*Oryza sativa* L.) has four components: panicle number, total spikelet number per panicle (TSN), grain weight and spikelet fertility. There is wide variation in TSN among cultivated rice varieties and it is one of the targets of breeding programs to improve rice yield. Many hypotheses have been proposed to explain ecophysiological process that determines spikelet number per unit area. Nitrogen is one of the most yield-limiting nutrients in crop production, and its proper management is essential for improving grain yield. Grain number is linearly correlated with total plant N content. Nitrogen fertilizer might affect CKs levels to increase rice flower numbers. To identify the loci controlling panicle architecture, QTLs for panicle traits such as number of primary or secondary branches and spikelet number per primary or secondary branch have been mapped and studied. QTLs for TSN have been identified using various segregating populations, including F_2 populations, recombinant inbred lines (RILs), and doubled haploid (DH) lines.

Keywords: *Oryza sativa* L., total spikelet number (TSN), QTLs, recombinant inbred lines (RILs)

I. INTRODUCTION

Rice (Oryza sativa L.) is one of the most important crops in the world, especially in Asia. To meet the increasing demands of the booming population and urbanization of Asia, it is estimated that a 50% ncrease in rice yield is needed (Murchie et al., 2009). Therefore, finding traits that substantially increase rice yield is an urgent issue. Rice inflorescence architecture is a key agronomic factor that determines grain yield, and thus has been a major target for crop improvement. Rice inflorescence, called the panicle, consists of a rachis, primary branches, secondary branches, and spikelets. The primary branches are arranged in a spiral phyllotaxy, and spikelets are produced on both the primary and secondary branches. Understanding the genetic basis of inflorescence architecture will contribute to improving crop grain yield (Akter et al., 2014).Grain yield of rice (*Oryza sativa* L.) has four components: panicle number, total spikelet number per panicle (TSN), grain weight and spikelet fertility. There is wide variation in TSN among cultivated rice varieties and it is one of the targets of breeding programs to improve rice yield. However, genetic analysis of TSN is difficult because it is a complex trait controlled by multiple genes and influenced by environmental conditions. Quantitative trait locus (QTL) analysis using DNA markers has recently made it possible to understand the genetic basis of TSN and other complex traits. QTLs for TSN have been identified using various segregating populations, including F_2 populations, recombinant inbred lines (RILs), and doubled haploid (DH) lines (Hittalmani et al., 2003; Kobayashi et al., 2004; Mei et al., 2005; Xing et al., 2002; Yagi et al., 2001; Zhuang et al., 1997; Zou et al., 2005). Many hypotheses have been proposed to explain ecophysiological process that determines spikelet number per unit area. Those hypotheses may be classified into the following three types. The first is that

the spikelet number is proportional to nitrogen (N) content of plant (product of percentage N and crop biomass per unit area) at around spikelet formation stage (Murayama, 1969; Hasegawa et al., 1994; Kobayashi and Horie, 1994; Horie et al., 1997). The second is that the spikelet number is proportional to biomass production during the period from panicle initiation to heading (Kropff et al., 1994). The third is that the final spikelet number is represented as the difference between the numbers of spikelets differentiated and degenerated; the former is proportional to the crop-N content at the late spikelet differentiation stage and the latter to crop growth rate (CGR) during the period from the late stage of spikelet differentiation to heading (Wada, 1969).

II. METHODS AND MATERIAL

A. The Effect of Low Planting Density on the Spikelet Number

Whole rice plants, including panicles, leaves and stems, are harvested at the yellow ripening stage and made into whole-crop silage to feed to cattle. A salient problem with whole-crop rice silage is that some of the grain eaten by the animals is excreted in feces without being digested, causing a loss of nutrients (Koga et al., 2003; Matsuyama et al., 2005; Yamamoto et al., 2005; Shinoda et al., 2007; Shinde et al., 2008; Katoet al., 2009; Feng et al., 2011). To solve this problem, 'Tachisuzuka' was developed and released as the first rice cultivar with improved feed value and sugar content due to a radical decrease in grain yield (Kouno, 2011; Matsushita et al., 2011, 2012). This promising characteristic results from defective elongation of the primary branches at the basal part of the panicle axis, owing to ashort panicle 1 (sp1) mutant gene (Li et al., 2009). Tachisuzuka' has been developed for silage use with improved feeding value due to a radical decrease in spikelets. We investigated the effect of planting density on the spikelet number in 'Tachisuzuka' to find out how seed yields of this cultivar can be increased by means of cultivation methods. Moreover, the spikelet number increased by 67% under the low planting density. This result implies that the efficiency of seed production of 'Tachisuzuka' could be improved by low planting density through an increase in spikelet number per unit area(Kei et al., 2013).

B. The Effect of Nitrogen Fertilizer to Increase Spikelet Number Per Panicle

Nitrogen is one of the most yield-limiting nutrients in crop production, and its proper management is essential for improving grain yield. Grain number is linearly correlated with total plant N content (Makino, 2011). Nitrogen fertilizer might affect CKs levels to increase rice flower numbers. CKs regulate rice branch and flower numbers (Barazesh and McSteen, 2008). CKs oxidase/dehydrogenase (OsCKX) is an enzyme that degrades CKs and, in many plant species, is responsible for the majority of metabolic CKs inactivation (Werner et al., 2003). Reduced expression ofOsCKX2 causes CKs accumulation in inflorescence meristems and increases the number of reproductive organs and yield (Ashikari et al., 2005). The effects of nitrogen fertilizer on panicle branching may be mediated by CKs, in which accumulation in the inflorescence meristem can regulate panicle development, resulting in increased numbers of flowers and branches. Adenosine phosphate-isopentenyltransferase (IPT) catalyzes the rate-limiting step of CKs biosynthesis.The results showed that OsIPTs were markedly increased, and CKs accumulated in panicle when nitrogen fertilizer was applied. CKs biosynthesis in the roots and leaves was not up-regulated by nitrogen. These results suggest that nitrogen fertilizer enhances local CKs synthesis to increase flower numbers in the panicles of rice (Chengqiang et al., 2014).

C. OsSPS1, a Gene Increases Spikelet Number Per Panicle

Analysis of an NIL carrying a chromosome segment containing QTLph1 of Kasalath revealed that OsSPS1, a gene encoding sucrose phosphate synthase (SPS), is the target gene underlying QTLph1 (Ishimaru et al., 2004). SPS catalyzes the conversion of fructose 6-phosphate and UDPglucose into sucrose 6-phosphate, and it is generally considered to be the rate-limiting enzyme in sucrose synthesis (Huber, 1983). OsSPS1 is one of the 5 isogenes encoding SPS in the rice genome. Expression analysis revealed that OsSPS1 is preferentially expressed in the source tissue, particularly in leaf blades, and it plays a dominant role in sucrose synthesis in the source leaf blades among the 5 isogenes for SPS (Okamura et al., 2011). Analysis of the distribution of dry matter revealed that a higher source-leaf SPS

activity in NIL-SPS1 at the panicle formation stage might promote the distribution of dry matter to panicles and increase the number of secondary rachis branches. (Hashida et al., 2013).

D. QTL for Spikelet Number

To identify the loci controlling panicle architecture, QTLs for panicle traits such as number of primary or secondary branches and spikelet number per primary or secondary branch have been mapped and studied (Ando et al., 2008; Yamagishi et al., 2002). Several QTLs for TSN in rice have also been identified from wild relatives *O*. rufipogon, O. nivara and O. glumaepatula (Brondani et al., 2002; Li et al., 2006; Moncada et al., 2001; Onishi et al., 2007; Septiningsih et al., 2003; Thomson et al., 2003; Xiao et al., 1998; Xiong et al., 1999). The QTLs detected in these studies, which were located throughout all 12 rice chromosomes, have provided useful information with which to survey the genes that govern TSN within different populations. Additionally, five QTLs for TSN—*QSpp8* on chromosome 8, *qSPP1* on chromosome 1, *qSSP2* on chromosome 2, *qSPP3* on chromosome 3 and *qSPP7*on chromosome 7 have been mapped as single Mendelian factors (Zhang et al., 2006, 2009). Fine maps of three QTLs for grain number per panicle and TSN—*SPP1* on chromosome 1 (Liu et al., 2009) and two QTLs (*gpa7* and *qSPP7*) on chromosome 7 (Tian et al., 2006; Xing et al., 2008)—have been constructed. Furthermore, three QTLs for increasing grain number (*Gn1a* on chromosome 1, *Ghd7* on chromosome 7 and*WFP* on chromosome 8) have been cloned (Ashikari et al., 2005; Miura et al., 2010; Xue et al., 2008).

E. Importance Of IR64 Variety

Since the 1960s, IRRI-bred rice varieties have been distributed worldwide and used by both plant breeders and farmers. IR64, which was released in 1985, had been widely accepted as a high-quality rice variety in many countries (Khush, 1987). Because of the wide adaptability of IR64, breeding materials with an IR64 genetic background, such as DH lines, RILs and thousands of mutant lines, have been developed for research and improvement of rice varieties (Guiderdoni et al., 1992; Wu et al., 2005). In the late

1980s, a breeding program to develop a new plant type (NPT) of rice was launched at IRRI with the goal of increasing yield potential under tropical environments. Unlike IR64, the NPT varieties have several agronomic traits inherited from tropical *japonica*-type varieties: low tiller number, low number of unproductive tillers, large panicle, thick culm, lodging resistance and large, dark green flag leaves (Khush , 1995). Thus, the NPT varieties were chosen for experiments designed to improve the yield potential of IR64.

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