

## QTL Mapping for Cold Tolerance at the Seedling Stage in Rice

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### Abstract

Rice (*Oryza sativa* L.) is a nationally and internationally important staple food. It is a cold sensitive crop. Abiotic stress factors are the major constraints not only in rice but also in present agriculture. Cold stress reduces crop yield, their quality and post-harvest life. Rice is injured or killed by non-freezing low temperature, and exhibit various symptoms of chilling injury such as chlorosis, necrosis, or growth retardation. In contrast, chilling tolerant species are able to grow at such cold temperatures. Sometimes the plant badly suffers from cold stress during seedling stage when they are grown in winter environment. Consequently, mining cold-tolerant germplasm and mapping cognate genes would provide an opportunity to ameliorate rice yield through marker-assisted selection (MAS). Many quantitative trait loci (QTL) for cold tolerance at seedling stage in rice have been identified and mapped. This information is necessary for understanding of the complex network of molecular changes that are important for chilling and freezing tolerance in crop plants. The development of cold tolerant plants by the introduction of molecular breeding seems to be a viable option to hasten the breeding of 'improved' plants. Intuitively, molecular breeding would be a faster way to mapping of beneficial QTL than through conventional breeding. Although much progress has been accomplished, joint achievement from breeders and plant biotechnologist could expedite the engenderment of cold-tolerant rice plants, and some possible approaches are suggested.

### 1. Introduction

Rice (*Oryza sativa* L.) is a nutritionally important food crop in the World. Around two billion Asians obtain more than 60% of their required energy from rice (Marathi et al., 2012). It remains today as leading and the most preferred cereal crop in Asia (Maclean et al., 2013). It is also an excellent model plant in biology due to its small genome size (430 Mb), availability of complete genome sequence as well as established gene transfer knowhow and also vast genetic resources. Rice is globally grown on about 165 mha annually with total production of 750 mt (FAO Rice Market Monitor, July, 2015). It ranks second in terms of Worldwide production among cereal crops (FAO Stat, 2014) with cultivation in more than hundred countries. Rice is mainly (90%) grown in Asian countries (Singh et al., 2013) with China and India being the large scale producers having almost 50% of the World rice production (EU Rice Economic Fact Sheet, Feb. 2015). India stands second with 155 mt as China occupies the first place in rice with 205 mt in the World's production table of 479.3 mt (USDA, 2013).

In India, with a population of over a billion people, rice is the staple food for almost 65% (Barah, 2005) of the total population accounting for about 21% of total global consumption and ranks second among rice consumers of the World (USDA, 2014). The country also accounts for about 21.38% of global rice production (NITI Aayog, 2015).

World population is increasing at an alarming rate and is expected to reach about 9.7 billion by the end of year 2050 (United Nations, 2015). On the other hand, productivity is diminishing due to the effect of various biotic and abiotic stresses. Biotic and abiotic stresses reduce the average plant productivity by 65% to 87% (Bayram et al., 2011). Cold is considered as one of the most important factors limiting the productivity of plants (Levitt, 1980; Larcher, 1995). Plant growth is often negatively influenced by cold stress (Sanghera et al., 2011). More than 15 mha of rice throughout the World suffer from cold damage at one or more growth stages (Zhang et al., 2014). Therefore, minimizing these losses is a major area of responsibility for all nations to cope with the incrementing



foodstuff requisites.

The development of rice varieties is thus important with increased tolerance to cold stresses, by both molecular breeding and conventional methods; as the molecular breeding in modern agriculture plays a vital role to harness the conventional breeding. Due to the complex polygenic nature of abiotic stresses, attempts have been made by the conventional breeders to improve this trait which has met with little success. Marker assisted breeding in this respect can play an immense role. Quantitative trait loci (QTL) identification followed by its mapping is worthwhile as this creates the enormous scope to transfer it in several mega varieties of rice. Screening of rice genotypes for development of cold tolerant varieties is now possible through the use of molecular markers linked with QTL for cold tolerance and can be eventually used as breeding materials for further improvement programme.

## 2. Cold Stress in Rice

Stress is an influence that is beyond the normal range of homeostatic control (Lerner, 1999) and stresses are classified in two groups viz. biotic and abiotic stress. Biotic stress means damage of plants by living organisms present in the environment e.g., bacteria, viruses, fungi, nematodes etc. Abiotic stress factors or stressors are environmental fluctuations e.g., excess/deficit of water, presence of excessive salt, high wind, temperature, drought, nutrient or heavy metal toxicity, etc. Low temperature is the most important abiotic stress for cereal crops. Rice is more sensitive to cold stress than other cereal crops (Ray et al., 2016). Therefore, in temperate areas, rice productivity is severely affected by cold stress (Xie et al., 2012). The optimum temperature for seed germination and early seedling growth is from 27 to 32 °C. This stage in rice is very important for the seedling growth and establishment, but the rice plants are mostly affected during seedling stage when the temperature falls below 10–13 °C (Yoshida, 1981). At this stage effects on seedlings can be manifested as poor germination, poor seedling establishment, slow growth, yellowing and drying of leaves, reduced tillering leading to seedling death (Nakagahra et al., 1997; Kaneda et al., 1974; Mackill et al., 1997). Cold stress also affects chlorophyll content and thus interferes photolysis (Kanneganti and Gupta, 2008; Kim et al., 2009). Seedlings are badly affected by cold stress when they are grown in winter environments. Yield loss due to prevailing of low temperature during growing season is a common and unavoidable phenomenon in rice production (Han et al., 2006). Therefore, improvement of seedling's cold tolerance has been one of the most important targets in rice breeding. In Northern and North-eastern parts of India cold stress prevails in winter season usually during December to February and the minimum temperature remains often below

12–15 °C. Sometimes minimum temperatures go below 20 °C during March and April in some parts of the northern states of India

## 3. QTL for Cold Tolerance

Studies on QTL mapping and linkage disequilibrium (LD) mapping have provided needed information on how gene combinations work under specific environments against particular genetic backgrounds. Progress is being made in developing cold tolerant rice germplasm through conventional breeding (physiological dissection) and the use of molecular tools. Identification of QTL conferring improved cold tolerance may facilitate breeding progress. The availability of saturated molecular maps enables scientists to work for betterment of the complex traits like cold tolerance using QTL (Price et al., 2002). The molecular linkage map for cold tolerance of rice at seedling stage has been reported (Park et al., 2013; Verma et al., 2014; Zhang et al., 2014). Breeders aim to develop rice germplasm that can produce high and stable yields in regions where low temperatures are found. Rice is cultivated virtually all country in the World, from the sea level up to 3000 m of altitude (Juliano, 1993), making cold tolerance an compulsory trait in many of these regions. Specific objectives include integrating qualities of other varieties into leading varieties. Traits include short-cycle maturity, medium stature, multiple resistances to pests and diseases and good grain quality. In order to develop cold tolerance in rice change of genetic makeup is the most effective approach that has been applied. Screening for cold tolerance in rice is highly complex (Singh et al., 2005), because responses to low temperatures differ between varieties, growth stages and actual temperatures used. For effective selection, the standard screening methodologies (Table 1) described by several scientist to screen rice genotypes for cold response under controlled temperature conditions at germination (seedling) stage are given below.

The *Oryza sativa* (L.) have two cultivated subspecies: *indica* and *japonica*. The *indica* subspecies includes cultivars better acclimatize to tropical environments likes India, China, and Indonesia, while *japonica* cultivars are more adapted to temperate climates likes Japan and Korea (Takahashi, 1984). Thus development of cold tolerance in *indica* rice through breeding with *japonica* rice has a tremendous scope (Jeong et al., 2000; Mackill and Lei, 1997). Some *japonica* cultivars viz. Silewah, Lambayque 1, and Padi Labou Alumbis are reported to be cold tolerant (Glaszmann et al., 1990; Saito et al., 2001).

Till recently, the main advancements in the development of cold tolerant rice varieties has been obtained mostly within the *japonica* cultivars. Therefore, enormous scope is there for improvement of *indica* type cultivars. This could be done simply by crossing *indica* genotypes with *japonica* ones,



Table 1: Methods and traits evaluated in the germination stage for cold tolerance selection in rice

Methodology of screening	Evaluated trait	Reference
10, 15, 20, and 25 °C for 5 to 30 days (on the basis of temperature)	Germination rate (radicle protrusion)	Bertin et al. (1996)
13 °C for 28 days and 28 °C for 7 days	Germination index and scoring for cold tolerance 1–9	Priyanka et al. (2015)
17 °C for 7 days	Germination (%) and its speed	Sthapit and Witcombe (1998)
13 °C to 15 °C for 7 days	Percentage of germination	Lee et al. (2001)
15 °C for 12–16 days	Low temperature germinability (LTG)	Sheng et al. (2001)
15 °C for 10 days	Coleoptile length	Hou et al. (2003)
15 °C for 6 days	Germination rate	Chen et al. (2006)
13/20 °C day/night and control condition 25/20 °C day/night 15 days	Leaf discoloration, SPAD value chlorophyll content	Park et al. (2013)
12-h light (15000 LX) 12-h dark. The seedlings were initially exposed to 14 °C for 2 h followed by 12 °C for 4 h and 10 °C for 4 h.	Seedling sensitive	Yang et al. (2013)
10 °C for 10 days, 10 °C for 13 days	Seedling survival percentage	Zhang et al. (2005)
12 °C for 10 days	Seedling vigor	Han et al. (2007)
4 °C for 48 h	Cold induced injury	Xiao et al. (2014)
25 °C for 4 days	Dormancy	Xie et al. (2014)
18–19 °C cold-water irrigation (field) 17–18 °C cold-air (glasshouse)	Cold sensitive	Jena et al. (2010)
4 °C for 9 days, 4 °C for 11 days and 4 °C for 14 days	Cold stress tolerance index and withering index	Juan et al. (2010)
14 °C for 7 d, 11 d, 14 d, and 17 d	Low temperature vigor of germination (LVG)	Han et al. (2006)
50 °C for 48 h to break dormancy, 32 °C for 36 h, 5 °C for 10 days, 20 °C for 10 days to recover	Seedling survival	Pan et al. (2015)
13 °C for 28 days, 28 °C for 7 days	Coleoptile and radicle length under	Bosetti et al. (2012)
13 °C for 28 days, 28 °C for 7 days	Radicle and coleoptile length and germination index	Dashtnian et al. (2013)

in order to transfer genes for cold tolerance from *japonica*. However, the combination of desirable characteristics between these two rice groups is difficult to manipulate for consumer acceptance. Molecular markers technology has great potential in molecular breeding of rice harnessing the breeding cycles required for advancing generations.

Although scientists have tried to explore the mechanism of cold tolerance in rice for a long time, its genetic mechanism is still not well understood. Both additive and non-additive gene interaction (da Cruz et al., 2006; Chen et al., 2006) are known to be present for controlling the character. Nagamine (1991) reported that cold tolerance in rice at seedling stages is controlled by a single dominant gene. Still at present rice scientists do not believe that one dominant gene regulates cold tolerance in rice rather this is a complex trait, with many genes interacting and each one having minor effects on the

overall cold tolerance phenotypes. Until now, more than 80 QTL (Table 2 and 3) for cold tolerance at seedling stage in rice have been identified (Qian et al., 2000; Andaya and Mackill, 2003; Han et al., 2007; Lou et al., 2007; Jianga et al., 2008; Koseki et al., 2010; Suh et al., 2012).

It is noticeable that most QTL are present in different rice chromosomal regions. The diversity of identified QTL varies for cold tolerance at seedling stage which may be due to the detection of QTL with such different screening procedure of cold tolerance at seedling stage in rice. A major QTL, *qCTS-2* (LOD=15.09) was on chromosome 2 flanked by RM561 and RM3 which explained 27.42% of the total phenotypic variation (Lou et al., 2007) and this region also identified by others with different parental materials.

Side by side different other common QTL ( Figure 1) has also



Table 2: QTL for cold tolerance at different growth stages in rice identified on 12 chromosomes

Trait	Parents	Mapping population	No. of QTL identified	Salient features	References
Low temperature germinability	JX17 (T) & ZYQ8 (S)	127 DH	2	QTL identified on chromosome 4 and 9 account for 11.1 and 12.6% phenotypic variation with a LOD score of 2.85 and 2.93, respectively.	Sheng et al. (2001)
	Italica Livorno (T) & Hayamasari (S)	122 RILs	3	QTL identified on chromosome 3 and 4. A major QTL, <i>qLTG3-1</i> identified on chromosome 3, accounts for 35.0% phenotypic variation with a LOD score of 15.7.	Fujino et al. (2004)
Survival percentage of seedling	M-202 (T) & IR50 (S)	191 RILs	15	QTL identified on chromosome 1, 3, 4, 6, 8, 10, 11, 12. The major QTL, <i>qCTS12a</i> identified on chromosome 12, accounts for 40.6% phenotypic variation with a LOD score of 20.34.	Andaya and Mackill (2003a)
	AAV002863 (T) & Zhen-shan97B (S)	193 DH Lines	5	QTL identified on chromosome 1, 2 and 8. A major QTL, <i>qCTS-2</i> , identified on chromosome 2 accounts for 27.42% phenotypic variation with a LOD score of 15.09.	Lou et al. (2007)
Survival percentage of seedling	JX17 (T) & ZYQ8 (S)	128 DH lines	4	QTL identified on chromosome 1, 2, 3 and 4 contributing 10.3 to 12.1% phenotypic variation with a LOD score ranging from 2.41 to 2.87.	pujasharma03@gmail.com
	Asominori (T) & IR24 (S)	71 RILs	3	QTL identified on chromosome 1, 5 and 6. A major QTL, <i>qSCT-1</i> , identified on chromosome 1 accounts for 24.51% phenotypic variation with a LOD score of 4.1.	Jiang et al. (2011)
Stable seedling establishment	Italica Livorno (T) & Arroz Da Terra (S)	3 mapping population of BILs	9	QTL identified on chromosome 1, 2, 5, 6, 7, 10 and 11 contributing 10.9% to 25.6% phenotypic variation with a LOD score ranging from 2.9 to 6.2.	Iwata et al. (2010)
Spikelet sterility	M-202 (T) & IR50 (S)	191 RILs	8	QTL identified on chromosome 1, 2, 3, 5, 6, 7, 9 and 12 contributing 11 to 17% phenotypic variation with a LOD score ranging from 3.6 to 6.0.	Andaya and Mackill (2003b)
Seed fertility	Hokkai-PL9(T) & Hokkai287(S)	F2 with 288 individuals	1	A major QTL, <i>qCTB 8</i> , identified on chromosome 8, accounts for 26.6% phenotypic variation with a LOD score of 10.6.	Kuroki et al. (2007)
Spikelet fertility	ZL1929-4 (T) & Towada (S)	F2 with 2,810 plants	1	A major QTL, <i>qCTB7</i> , identified on chromosome 7 accounts for 9 and 21% phenotypic variation with a LOD score of 7.74 and 11.2 in F2 and F3 generations, respectively.	Zhou et al. (2010)
Per cent seed set	IR66160-121-4-4-2 (T) & Geumobyeyo (S)	153 F8 RILs	3	QTL identified on chromosome 3, 7, and 9 contributing 7.4 to 9.4% phenotypic variation with a LOD score ranging from 2.5 to 4.9.	Suh et al. (2010)
Leaf discoloration, SPAD value chlorophyll content	Milyang 23 and Hapcheonaeng-mi3	80 RILs	4	QTL identified on chromosome 2, 4 and 1, 5. A major QTL, <i>qSPA-4</i> identified on chromosome 4 accounts for 16.0% phenotypic variation.	Park et al. (2013)



Trait	Parents	Mapping population	No. of QTL identified	Salient features	References
Seedling sensitive	Nipponbare ( <i>japonica</i> rice) and LPBG ( <i>Indica</i> rice)	F3	6	QTL were mapped on chromosomes 1, 2, 2a, 5, 8 and 10. The three most significant QTL on chromosomes 1, 2 and 8 were validated by comparison with previous studies	Yang et al. (2013)
Low temperature germinability (LTG) cold tolerance at the seedling stage (CTS)	Daguandao ( <i>japonica</i> ) and IR28 ( <i>Indica</i> )	227 RILs	7	QTL identified on chromosome 3, 8, 11,11,11,11 and 12 contributing 5.5 to 22.4% phenotypic variation with a LOD score ranging from 3.0 to 16.1.	Wang et al. (1999)
Seedling survival percentage	Lemont ( <i>japonica</i> ) and Teqing ( <i>indica</i> )	269 RILs	5	QTL identified on chromosome 3, 3, 7, 11 and 11 contributing 5.5 to 29.8% phenotypic variation with a LOD score ranging from 3.25 to 19.19.	Hong et al. (2005)
Per cent Ratooning Germinability (PRG) and Overwintering Germinability (POG)	89-1(Gr 89-1) and Shuhui 527	312 RILs in F9	5	QTL identified on chromosome 3, 3, 7, 11 and 11 contributing 6.7 to 17.8% phenotypic variation with a LOD score ranging from 2.7 to 5.8.	Zheng et al. (2012)
Leaf yellowing and leaf rolling	Lijiangxintuanheigu ( <i>japonica</i> ) and Sanhuangzhan-2 ( <i>indica</i> )	204 RILs	9	Four QTL on chromosomes 1, 6, 9 and 12 were detected using leaf Yellowing. And 4 QTL on chromosomes 7, 8, 9, 11 and 12 were detected using leaf rolling and per cent seedling survival, two major qCTS-9 and qCTS-12 contributing 15.8% and 14.7% phenotypic variation with a LOD score 8.0 and 7.7.	Zhang et al. (2014)
Novel cold tolerant cultivars using molecular breeding	Danteshwari and Dagad deshi	122 RILs in F13	5	QTL identified on chromosome 1, 3, 6, 9 and 12. One major QTL present on chromosome 9 had major effect with LOD value of 9.53.	Verma et al. (2014)
Root conductivity (RC)	DX as a cold-tolerant donor and Nanjing 11 (NJ) recurrent parent	151 BC 2F1	2	QTL identified on chromosome 10. QTL, named qRC10-1 and qRC10-2 contributing 9.4% to 32.1% phenotypic variation with a LOD score ranging from 3.1 to 6.1.	Xiao et al. (2014)
Seedling vigor	Cross of <i>indica</i> and <i>japonica</i> "Milyang 23/Jileng 1	200 F3	12	QTL were mapped on chromosomes 1, 1, 1, 1, 2, 2, 7, 8, 8, 8, 12, and 12. Contributing 5.2 to 17.9% phenotypic variation with a LOD score ranging from 2.01 to 5.02.	Han et al. (2007)
Seed vigor in germination and seedling establishment	Rice ( <i>Oryza sativa</i> L. ssp. <i>indica</i> ) cultivars ZS97 and MH63	120 RILs	8	QTL were mapped on chromosomes 1, 5, 5, 5, 6, 6, 8 and 11. Contributing 12.6 to 30.5% phenotypic variation with a LOD score ranging from 5.27 to 14.8.	Xie et al. (2014)
Cold stress tolerance index and withering index	TN1( <i>indica</i> ) variety and Chunjiang 06 ( <i>japonica</i> )	120 DH Lines	5	QTL were mapped on chromosomes 1, 2, 4, 10 and 11. Contributing 10.94 to 16.43 F-value.	Juan et al. (2010)



Trait	Parents	Mapping population	No. of QTL identified	Salient features	References
Low-temperature vigor of germination	Milyang 23 ( <i>indica</i> ) and Jileng 1 ( <i>japonica</i> ) rice	200 F2:3	20	QTL were mapped on chromosomes 1, 2, 3, 5, 6, 7, 8 and 11. Contributing 5.3 to 22.9% phenotypic variation with a LOD score ranging from 2.12 to 4.26.	Han et al. (2006)
Combining microarray with QTL-mapping	Guichao2 ( <i>indica</i> ) and IL112 ( <i>japonica</i> )	F2:3	7	QTL were mapped on chromosomes 1, 2, 5, 6, 7 and 10. Contributing 8.0 to 20% phenotypic variation with a LOD score ranging from 2.0 to 4.1.	Liu et al. (2013)
Cold tolerance at the plumule and seedling stages	A58 and W107	RILS	5	QTL were mapped on chromosomes 1, 5, 11, 11 and 112. Contributing 13.1 to 27.0% phenotypic variation with a LOD score ranging from 2.7 to 6.8.	Baruah et al. (2009)
Seedling survival and seed setting	Core collection	174	51	QTL for cold tolerance were dispersed across all 12 chromosomes; 22 detected at the germination stage and 33 at the booting stage. Eight QTL were identified. About 46% of the QTL represented new loci. The only QTL shared between <i>Indica</i> and <i>Japonica</i> for the same measure was qLTSSvR6-2 for SSVr. 18 positive and 21 negative genotypes in <i>Indica</i> and 19 positive and 24 negative genotypes in <i>Japonica</i> identify for cold tolerance	Pan et al. (2015)
Agricultural performances in cold airs	Milyang23 ( <i>O. sativa</i> ssp. <i>indica</i> ) & Hapcheonaengmi3	80 RILs	14	QTL were mapped on chromosomes 1, 5, 11, 11 and 112. Contributing 5.8 to 32.8% phenotypic variation with a LOD score ranging from 2.6 to 4.5.	Oh et al. (2004)
Main effects of QTL with regard to their interactions with environments	Dasanbyeo ( <i>indica</i> ) and TR22183 ( <i>japonica</i> )	RILs	57	QTL were mapped on all 12 chromosomes. Contributing 13.2 to 29.1% phenotypic variation with a LOD score ranging from 2.2 to 8.8.	Jiang et al. (2011)

been found by several scientists for cold tolerance at seedling stage in rice, viz. qSPA-1 and qCTS-1 on chromosome 1 (Park et al., 2013; Liu et al., 2013; Juan et al., 2010); qCTS-2 on chromosome 2 (Lou et al., 2007; Liu et al., 2013); qCTS-12 on chromosome 12 (Zhang et al., 2014; Suh et al., 2013; Anandya et al., 2006). Likewise, Suh et al. (2013); Verma et al. (2014) also found approximately the same region of Chromosome 3 with LOD score greater than 3. So the flanking marker of this region can be used for screening of the rice Germplasm for cold tolerance at seedling stage. It is evident that a remarkable work has been done in the understanding of cold tolerance in rice plants. Among the abiotic stresses cold stress is a major constrain to stability in production and yield under cold rice ecosystem.

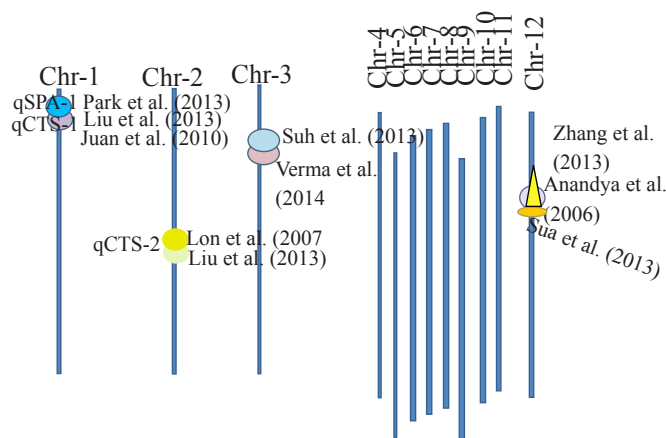


Figure 1: Common QTL for cold tolerance at seedling stage of rice observed by different scientists in different population

Table 3: Major QTL for cold tolerance at seedling stage mapped on 12 chromosomes of rice

Sl. No.	QTL name	Marker name	Chr. no.	Cm	LOD	Source
1.	qspa4	RM6333-RM6368	1	147.2	-	Park et al. (2013)
2.	qspa4	RM6333-RM6368	1	-	-	Andaya and Tai (2007)
3.	Qspa-1	RM323-RM428	1	1.0-19.3	-	Park et al. (2013)
4.	qcts-1a	RM84-RM522	1	26.2-40.6	6.33	Lou et al. (2007)
5.	qcts-1-b	RM493-RM9	1	79.7-92.4	6.65	Lou et al.(2007)
6.	qcts-1-c	RM315-RM472	1	-	8.03	Lou et al. (2007)
7.	-	RM265-RM104	1	155.9-186.6	4.33	Zhi et al. (2004)
8.	-	RM3475	1	-	-	Suh et al. (2013)
9.	qSPA-1	RM428-RM323	1	19.3-	-	Park et al. (2013)
10.	-	RM449-RM5	1	78.4-94.9	3.24	Verma et al, (2014)
11.	Qcts1-1	RM1282-RM3426	1	4.2-19.9	19.2	Liu et al. (2013)
12.	qwI-1	RM1282-RM428	1	4.2-19.9	-	Juan et al. (2010)
13.	qcts-1	RG811-RM562	1	-	3.9	Zhang et al. (2013)
14.	qcts-1	RM297-RM319	1	-	-	Andaya (2003)
15.	Qcts-2	RM561-RM341	2	74.1-82.7	15.09	Lou et al. (2007)
16.	Qcst-2	RM341-RM6318	2	82.7-96.6	4.1	Liu et al. (2013)
17.	-	RM-5764	2	7.9	-	Suh et al. (2013)
18.	Qspa-2	RM423-RM555	2	28.7-34.7	-	Park et al. (2013)
19.	Q11d-2	RM5607-RM208	2	142.5-186.4	-	Juan et al. (2010)
20.	Qcivg-1	RM29-RM118	2	-	-	Long et al. (2006)
21.	Qsct-3	RM156-RM16	3	-	4.25	Zhang et al. (2013)
22.	Qlvg 3	RM251-RM282	3	-	4.26	Zhi et al. (2006)
23.	Qspa-4	RM335-RM518	4	21.5-25.5	-	Park et al. (2013)
24.	Q9d-4	RM3735-RM252	4	81.7-99.0	-	Juan et al. (2010)
25.	Qspa-5	RM161	5	78.7	-	Park et al. (2013)
26.	Qcst-5	RM305-RM3620	5	96.9-104	-	Liu et al. (2013)
27.	Qcst-6	RM161-RM340	6	-	2.0	Liu et al. (2013)
28.	Qcts-6	RM30-RM400	6	-	3.1	Zhang et al. (2013)
29.	Qcst-7	RM6081-RM3826	7	-	2.4	Zhang et al. (2005)
30.	Qsct-7	RM336-RM10	7	-	3.33	Zhang et al. (2005)
31.	Qlvg 7-1	RM51-RM298	7	-	4.12	Zhi et al. (2006)
32.	Qlvg 7-2	RM336-RM118	7	-	2.63	Zhi et al. (2006)
33.	Qcts-8	RM506-RM152	8	-	5.59	Lou et al. (2007)
34.	Qcts-8	RM310-CG11	8	-	3.9	Zhang et al. (2014)
35.	Qcts-8	RM282-RM230	8	-	-	Andaya et al. (2003)
36.	-	RM256	8	-	-	Suh et al. (2013)
37.	Qcts-9	RM6854-RM566	9	-	6.8	Zhang et al. (2014)
38.	-	HvSSR9-7- HvSSR9-19	9	4.35-10.50	-	Verma et al. (2014)
39.	Qcts-9	RM328-RM245	9	82.4-112.3	-	Zhi et al. (2004)
40.	QRC10-1	RM1108-RM171	10	55.3-73.0	-	Xiao et al. (2014)
41.	QCR 10-2	RM25570-RM304	10	72.3-73.0	-	Xiao et al. (2014)

Continue...



Sl. No.	QTL name	Marker name	Chr. no.	Cm	LOD	Source
42.	-	RM590	10	117.2	-	Suh et al. (2013)
43.	QCST-10	RM33	10	-	2.4	Liu et al. (2014)
44.	Qcst-10	RM271-RM258	10	59.4-70.8	-	Juan et al. (2010)
45.	qRC10-1	RM171-RM1108	10	-	3.1	Xiao et al. (2014)
46.	qRC10-2	RM25570-RM304	10	-	6.1	Xiao et al. (2014)
47.	Q14d-11	RM286-RM1812	11	0.0-11.0	-	Juan et al. (2010)
48.	Qsct-11	RM202-RM209	11	54.0-73.9	19.19	Zhang et al. (2005)
49.	Qcts-11	RM224-RM2136	11	117.9-120.1	3.0	Zhang et al. (2013)
50.	-	RM512	12	43.2	-	Suh et al. (2013)
51.	Qcts12-a	RM101-RM292	12	-	-	Andaya et al. (2002)
52.	Qcts-12	RM27628-RM397	12	23.5-47.06	5.3	Zhang et al. (2013)
53.	Qcsh-12	RM270-RM17	12	91.3-109.1	-	Han et al. (2007)
54.	-	HvSSR12-35- HvSSR12-40	12	19.9-22.6	-	Verma et al. (2014)

#### 4. Conclusion

The improvement of rice cultivars with low temperature tolerance is an important task in increasing productivity. The complex nature of cold tolerance, lack of understanding of its inheritance and difficulty of effective cold tolerance screening complicate the development of cold tolerance varieties. The development of cold tolerant plants by the introduction of molecular breeding seems to be a meaningful approach to hasten the breeding of improved plants. Intuitively, molecular breeding would be a faster way to mapping of beneficial QTL than through conventional breeding.

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