Review of: "QTLs Detection for Low-Temperature Germination in Rapeseed by QTL-seq and Linkage Mapping Approach"

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Low temperature is a major factor limiting crop productivity and geographical distribution. Both oil (Rapeseed) and food (rice, barley) for major crop in the world are susceptible to low-temperature stress, which delays seed germination and increases seedling mortality, adversely afecting crop growth and production. This article reveals that the genetic mechanisms of seed germination under low temperatures in rapeseed based on a total of 574 $F_{2:3}$ families of derived from 3429×Huyou21 using the QTL-seq approach and linkage analysis of the populations: a total of 319,059,584 reads were generated for low tolerant bulk and 23,983,156 reads for tolerant parent (Huyou21), 335,343,844 reads for low sensitive bulk and 337,990,498 reads for susceptible parent (3429); 5,600,575 genome-wide SNPs and 1,215,792 InDels were obtained for low tolerant bulk and 5,604,534 SNPs and 1,217,972 InDels for low sensitive bulk by comparing with the reference genome; One *qLTGA9-1* was mapped to a 341.86 kb interval with 69 genes between the SSR markers Nys9A212 and Nys9A215 on rapeseed chromosome A09; Another *qLTGC1-1* was mapped to a 1.31 Mb interval with 133 genes between the SSR markers Nys1C96 and Nys1C117 on chromosome C01[1]. The Ningyou7 identifed that seven of the predicted genes encode proteins associated with plant growth or temperature stress response but three genes (one genes in qLTGA9-1 and two genes in qLTGC1-1) no annotation (See table 1). These results provide a basis for genetic breeding and genes cloning for cold tolerance in rapeseed, It also develops new ideas for the gene excavation of cold tolerance and its molecular breeding during crop germination period.

Table 1. The candidate genes with functional efect variants in *qLTGA9-1* and qLTGC1-1 Regions [1]

QTL	Gene ID	Start base–end base (bp)	Functional efect	Chain	Predicted function
qLTGA9-1	ChrA09g005501	44842926–44843909	Moderate	Forward	Formiminotransferase
	ChrA09g005502	44845212–44845795	Moderate	Reverse	–
	ChrA09g005507	44864501–44865259	Moderate	Forward	Protein phosphatase 2C
	ChrA09g005509	44869664–44570813	High	Forward	Aminotransferase class I and II
	ChrA09g005523	44950207–44952401	Moderate	Forward	DRG Family regulatory protein
	ChrA09g005524	44954947–44959392	Moderate	Forward	DRG Family regulatory protein
qLTGC1-1	ChrC01g004357	48588162–48594007	Moderate	Forward	SWEET sugar transporter
	ChrC01g004359	48596431–48597483	Moderate	Forward	PHD-fnger
	ChrC01g004400	49078002–49082772	Moderate	Forward	Plant invertase/pectin methylesterase inhibitor
	ChrC01g004405	49166002–49166734	Moderate	Reverse	–
	ChrC01g004406	49193433–49194020	Moderate	Forward	–

China is one of origin centers of rapeseed; Wild rape in Yunnan *Brassica* L. is divided from 600~2300 meters above sea level, while mustard-type wild rape is distributed from 1550~2150 meters. The complex ecological environment of Yunnan forms rich and colorful rapeseed germplasm resources, especially the late autumn to early winter sowing contains many cold-resistant germplasm resources during the germination period. Yunnan cabbage rapeseed and mustard rapeseed are mainly distributed in 49 and 43 counties and cities, respectively; Low temperature occurs in late-autumn or early-winter quickly afects rapeseed germination for rapeseed in China, especially the winter sowing rapeseed germination period of 1900-2300 meters in Yunnan Province is usually at low temperature (5-8°C)

However, two QTL (qLTGA9-1 and qLTGC1-1) were identifed from ‘Huyou21’ with cold tolerance of seed germination. At low temperature (8°C), Huyou21 exhibited excellent tolerance to cold stress, whether the cold tolerance gene at germination of this cultivar is cold domesticated or derived from the wild rape gene is an interesting scientific question. We believe that further research can refer to cold tolerance genes in rice, based on near-isogenic line of cold tolerance at booting stage in rice, such as standing variation of CTB2 and de novo mutation of CTB4a (encoding a conserved leucine-rich repeat receptor-like kinase) underwent stepwise selection to facilitate cold adaptation to expand rice cultivation from high-altitude to high-latitude regions[2];Upregulation of CTB4a correlates with increased ATP synthase activity, ATP content, enhanced seed setting and improved yield under cold stress conditions[3]. The bZIP73 and OsAPX1 differentiating inter-subspecies evolved directly from wild rice, whereas the novel mutations CTB4a and Ctb1 arose in Geng during adaptation to colder climates[3]. Therefore, improved cold tolerance and expanded cultivation to high-altitude or high-latitude regions would help meet growing rapeseed demand.

References

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