ROLES OF LNCRNAS IN MAIZE

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ABSTRACT

Long non-coding RNAs (lncRNAs) are non-coding RNAs not coding for protein which are usually > 200 nucleotides in length and have various biological functions. Most recent advancements about role of lncRNAs in maize is compiled in this article. In maize lncRNAs function as abiotic stress tolerance including drought, boron, salt, help in growth regulation by influencing flowering time, help in seed development and play role in low phosphate tolerance, they are also responsive to mycorrhizal fungi. This review is intended to have overall view on maize lncRNAs and guide in further research on maize lncRNAs so that lncRNAs can be used in maize improvement.

KEY WORDS

Non-coding RNA, sequencing, stress tolerance, molecular genetics, genetic manipulation.

Development of sequencing technology and transcriptome analysis has given new prospective to the how non coding RNAs (ncRNAs) function (Nejat and Mantri, 2017) and has given newer prospective to central dogma. lncRNAs are among 98-99% of transcribed RNA that do not code protein (Fang et.al, 2018) which were considered as transcriptional noise for long time(Fok et. al,2017) and contain no more than one short(<100 amino acids) open reading frames. Open reading frames are part of reading frames that can be translated.

lncRNAs scans can be done by cDNA/ETS in silico mining, whole genome tilling array , RNA-seq approaches and epigenetic signature-based methods. Many similarities between lncRNAs and mRNAs (Derrien et.al, 2012; Goss et al, 2016) and their roles in regulation of complex mechanism has encouraged scientist to study more on lncRNAs. lncRNAs are expressed in tissue/ developmental stage specific manner, up and down regulated by transcription factor. A large proportion of lncRNAs are either derived from transposable elements or contain remnants of TEs.

lncRNAs are involved in transcriptional and post-transcriptional regulation through complex mechanism regulation and has come in highlight in recent years though study about plant lncRNAs are quite limited . In *Arabidopsis thaliana*, lncRNAs like COOLAIR and COLDAIR help in flowering time (Swiezewskiet al., 2009; Hoe et al., 2011) HID1 in photo morphogenesis (Wang et al., 2014), IPS1 in phosphate homeostasis (Franco et al., 2013), asHSFB2a play role in vegetative and gametophytic development (Wunderlich et al., 2014), APOLO in Auxin controlled development (Ariel et al., 2014), ASCO-lncRNAs in lateral root development (Bardou et al., 2014). In rice lncRNAs such as OSP11 in phosphate homeostasis (Wasaki et al., 2003). Similarly in Barley HvCesA₆lnc-NAT in cell wall synthesis (Held et al., 2008). In soya bean, GmeNOD40 in nodule formation (Yang et al., 1993) but study about lncRNAs in maize, their regulation, roles are long way to go. This review article summarize emerging functions of lncRNAs in maize as abiotic stress tolerance including drought, boron, salt, low Phosphorous tolerance, its role in growth regulation, response to mycorrhizal fungi.

Table 1 – lncRNAs in abiotic Stress tolerance

lncRNAs	Functions	Mechanism	Reference	Remarks
PILNCR1	low phosphate tolerance	lncRNAs by interacting with miRNA as PILNCR1-miR ₃₉₉ regulatory module	(Du et al., 2018)	PILNCR1 stands for Pi-deficiency-induced long non-coding RNA 1.
664 lncRNAs	drought responsive in maize seedlings		(Lv et al., 2016)	TCONS_00082174 and TCONS_00000649 show leaf specific expression in drought. TCONS_00037470 and TCONS_00012768 are down regulated in drought stressed root. GMRZM2G088590-TO4 shows temporal specific expression.
1724 lncRNAs	drought resistance		(Zhang et al., 2014)	GRMZM2G574383_TO1 exhibits roots specific expression. (Zhang et al., 2014) In comparison to protein coding genes drought responsive lncRNAs show higher tissue and development specificity. Reproductive stage is the most sensitive growth stage in drought. (Pang et al., 2019)
637 lncRNAs	nitrogen responsive		(Lv et al., 2016)	Nitrogen responsive lncRNAs are enriched in three co-expressed modules. Gene in enriched modules are mainly involved in NADH dehydrogenase activity, oxidative phosphorylation and nitrogen compounds metabolic process.
1710 lncRNAs	responsive to salt and boron stress		(Huanca-Mamani et al., 2018)	-

Table 2 – lncRNAs function in growth and development

lncRNAs	Functions	Mechanism	Reference	Remarks
HC-lncRNAs	paramutation in maize		(Lin et al., 2014)	Interaction between alleles that leads to mitotically and meiotically heritable change in gene expression is termed as paramutation
63 lncRNAs	Arbuscular Mycorrhizal (AM) fungi-responsive lncRNAs		(Han et al., 2019)	differentially expressed in fungal colonized root
GRMZm2G700665	influence flowering time in maize		(Salvi et al., 2007)	GRMZm2G700665 is located 70 kb upstream of ZmRap2 gene
TCONS-00089485	may play role in embryo seed and ovule tissue		(Lin et al., 2014)	TCONS-00089485 expressed in Vgt1 regulatory region (vegetative to generative transition 1)
7 novel lncRNAs	general development and metabolic processes in maize seed	as potential competing endogenous RNA (ceRNA)	(Zhu et al., 2017).	-

The inheritance of lncRNAs expression patterns shows apparent transgressive segregation. Maize lncRNAs are less affected by cis than by trans genetic factors. High confidence lncRNA having average length of 463 bp and coding for fewer exons than annotated genes are mostly expressed in tissue specific manner which is even supported by epigenetic marks (Lin et al., 2014).

Maize transposable elements contribute to long non-coding RNA that is regulatory hubs for abiotic stress response (Ly et al., 2019) in maize. Recent findings on lncRNAs functioning as abiotic stress tolerance are shown in the Table 1.

In silico bioinformatics pipeline used in maize on limited set of full-length cDNA sequence showed 1802 lncRNAs of which nearly 60% were precursors of small RNAs. Small

RNAs are non-coding RNA which helps to inhibit or increase expression of target genes (p2) and many other biological functions.

Conclusion. Though few studies have been done to study lncRNAs in maize there is still a lot to be done to explore other lncRNAs and their role in accurate detail and conformation by molecular and genetic approaches is yet to be done and their regulation in maize so as to use such lncRNAs in crop improvement programs such as stress tolerant varieties.

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