

them and will start preparing to do business as per the new policy reforms when Kharif crops will be harvested.

How it will Benefit the Farmers?

The main focus and goal of the three policy reforms were to help farmers get higher remunerative prices by creating new sale avenues and higher competition. The reduced marketing cost and market margin due to large intermediaries will led to increase the producer's share and lower the consumer's price. The high competitiveness levels in the sale of commodities will benefits producers and traders. Therefore, improved efficiency in the new marketing will benefit farmers having large marketable surplus. Small and marginal farmers here need to connect directly with consumers and also required to participate on sales platforms like e-NAM, etc. The small farmers can join hands with one another and form producer's group or Farmer Producer Organization. FPO is considered group/ organization/ institution for empowerment and protection of all type of farmers.

Significance of Move

1. It will help in unlocking rules of regulated agricultural markets which are wide spread across the nation.
2. It will create opportunities for the farmers

outside APMC market yards due to creation of additional competition.

3. This will supplement the existing MSP procurement system and help in doubling farmer income.
4. It further helps in integration of different inter and intra state markets.
5. The marketing cost would reduce to significant level.
6. The separate dispute resolution system/ mechanism will be set up for farmers which will resolve the matter within 30 days.

Way Forward

The major problem in agriculture marketing is not farmer's mindset but the restrictive as well as regulatory environment and missing opportunities for the small and marginal farmers. Better logistics, assurance about prices, sharing of market risk, farm-friendly infrastructure and incentive for diversification towards more paying quality produce and high-value produce will motivate farmers to go for transformation in farming and marketing of produce. We need to create enabling environment with favourable terms for the farmers to achieve the real goal of "**One Nation One Agricultural Market**" and for the success of "**Atam Nirbhar Bharat**".

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2. Long Non-coding RNAs (lncRNA): Governors in the Empire of Gene Regulation

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Introduction

Ribonucleic acids (RNAs) are one of the three important categories of biomolecules in the central dogma of molecular biology of living cells and virus particles (together called biological entities). Not that all the RNAs end-up with proteins that play structural and/or functional roles in the biology of an organism (or biological entity). RNAs that do not get translated into proteins are called non-coding RNAs. Among them, some (e.g., tRNA and rRNA) play assistive role in the process of translation of coding RNAs (e.g., mRNAs) into protein. Other non-coding RNAs, such as miRNAs and siRNAs, play regulatory role in deciding whether mRNAs should translate into protein or not. Yet another class of non-coding RNAs called long non-coding RNAs (lncRNAs) function as

master regulator of gene expression. They regulate gene expression by interacting with all the three molecules namely DNA, RNA and proteins as well as interfering at all levels of gene expressions namely chromatin organization, epigenetic modification, DNA replication, transcription, mRNA slicing and processing, translational and post-translational modification of structural and/or functional proteins, intra-cellular and inter-cellular signal transduction, and long-distance cell communication.

Long non-coding RNAs (lncRNAs) may be defined as RNAs longer than 200 nucleotides that remain untranslated and are distinct from other non-coding RNAs (ncRNAs) in terms of their genomic origin, biogenesis, subcellular localizations, and functions (Statello *et al*, 2021).

Genomic origin

Long non-coding RNAs are coded by RNA polymerase II and other RNA polymerases as well. Unlike mRNA, lncRNAs are transcribed from intergenic regions (e.g., long intergenic non-coding RNAs, lincRNAs), that overlap with other genes in sense or antisense orientation. They are capped at their 5' ends with 7-methyl guanosine (m⁷G) and polyadenylated at their 3' ends. In respect of splicing, they resemble mRNA. In some cases, enhancer regions are transcribed into enhancer RNAs (eRNAs) and promoter regions to promoter upstream transcripts that are sometimes parts of lncRNAs.

Biogenesis and subcellular localization

Biogenesis of lncRNAs can be discussed at two levels: first, their accumulation in the chromatin region of the nucleus, and, secondly, their transportation to cytoplasm followed by further distribution among organelles and cytoplasmic regions. Nuclear-localized and cytoplasm-localized lncRNAs are the two distinct categories and their molecular roles are also distinct, though their biological roles overlap in certain cases.

Nuclear localization (Chromatin-tethering)

Compared to mRNAs, lncRNAs have fewer and longer exons. Although they undergo splicing, lncRNAs are less efficiently spliced than mRNAs. Here comes an interesting question: what makes RNA Pol-II to switch-over to transcribe lncRNAs from its usual role of transcribing mRNAs? In order to entice RNA Pol-II to favour the transcription of lncRNAs and accumulation of lncRNAs in the nuclear region, these three molecular events must occur: (1) Phosphorylation of RNA Pol-II; (2) Impairing the recruitment of the transcription termination aggregator complex to chromatin complex; and, (3) Abolition of elongation factor SPT6 from its association with RNA Pol-II. Among them second and third events occur in a concomitant manner. The nuclear-accumulated lncRNAs remain tethered on to the chromatin in the form of DNA damage-associated R-loops (Nojima et al, 2018).

Besides these molecular events, certain intrinsic features of lncRNAs also help their nuclear localization: (1) weaker internal splicing signals; (2) Differentially expressed splicing regulators; (3) Intra-molecular polyadenylation signals; (4) longer distance between the 3'- splice site and the branch point; and, (5) Embedded motif sequences in *cis* (e.g., C-rich sequence derived from *Alu*-repeats) and factors in *trans* (e.g., repeating RNA domains (RRDs) of lncRNA functional intergenic repeating RNA elements, *FIRRE*) of lncRNAs.

Overall, nuclear-localized lncRNAs are restricted mainly to two nuclear regions: membraneless nuclear domains and chromatin.

Exportation to the cytosol and further distribution

Primarily, exportation from nucleus to the cytosol involves crossing of the nuclear membrane barrier. This happens with the help of RNA-exporter-pathway. RNA export factor 1 (NXF 1) is one such pathway widely deployed by the cell for exportation of lncRNAs from nucleus to the cytosol. The main reason for such preference is presence of fewer exons in lncRNAs compared to those of mRNAs.

After exportation of the lncRNAs to the cytosol, specific sorting processes operate to sort and distribute them among specific organelles. Till sorting as well as unsorted lncRNAs remain in the cytoplasm in the form of being associated with diverse RNA-binding proteins (RBPs) and they are called cytoplasmic lncRNAs. Majority of them (70%) are found in the polysomic region.

Certain intrinsic *cis* elements of lncRNAs also help them remain attached to ribosomes. For example, a long *pseudo-5'*-untranslated region (the name is given because this region lies upstream to the pseudo-open reading frame, ORF, in the lncRNAs; Carlevaro-Fita et al, 2016). The translation process, involving erstwhile lncRNA-bound ribosome, concomitantly triggers the degradation of ribosome-lncRNA association. The detailed mechanism remains to be investigated.

In the recent past, research evidences have shown that lncRNAs found in exosomes as well as in extra-nuclear genomes (i.e., genomes of chloroplasts and mitochondria) are also coded by nuclear genomes. After their transcription in the nucleus, lncRNAs enter these compartments through mechanisms of organelle-specific sorting process. Long non-coding RNAs are also found in the exosomes, extracellular membrane-bound compartments (vesicles) thrown into blood streams, for instance, in animals with circulatory system. Exosomes are also reported in plants (*Arabidopsis*). Exosomes play a particularly important role in long-distance cell-to-cell communication.

Potential Applications in Agriculture

They regulate gene expression pattern in specific manner in relation to tissue and physiopathological condition. Therefore, they can be used as targetable biomarkers and therefore lncRNA can be clinically modulated to regulate biological and physiopathological conditions in plants as well as in animals of agricultural importance.

Conclusions and prospects

Recent advances in transcriptomics have enabled detailed study of long non-coding RNAs (lncRNAs). The molecular and biological functions of the lncRNAs in plant system is yet to be studied in detail. Understanding role of the lncRNAs in plants in future may open new vistas in our understanding of plant growth and development and provide new

insights into understanding and manipulation of growth traits and disease manifestation.

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3. God of Ugly Things: A Tale of “WETAs”

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Insects are small animals but their stunning diversity is recognized since ages. About one million species are extant and certainly many more await discovery and description, especially in tropics. With more than 26,000 extant species, the orthopterans are the most diverse group among the polyneopteran insect lineages (Grimaldi and Engel, 2005). Researchers use these insects as model systems for studying anatomy, bioacoustics, chemical ecology, evolutionary ecology, life-history traits, neurobiology, physiology and speciation (Pener and Simpson, 2009).

New Zealand taxa from the Orthopteran family Anostomatidae consists of three broad groups, *Hemiandrus* (ground weta), *Anisoura/Motuweta* (tusked weta) and *Hemideina-Deinacrida* (tree-giant weta). These groups of insects are nocturnal, predominantly flightless and both herbivory and predatory in nature. Weta was classified as ‘Nationally Critical’ (Hitchmough, 2002) by the New Zealand Department of Conservation (DOC), which is the highest level of threat of extinction.



Tusked weta



Mountain stone weta



Cave weta