Study of microRNA in Plants
Recent published work by LC Sciences’ Customers

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Basic Research / Discovery - Identification of novel miRNAs in various plant species / specific tissues and understanding their mechanism of action and regulatory roles.

- Soybean (Glycine max) – Shoot Apical Meristem – Identify miRNAs that may have regulatory roles in various developmental processes including in SAM during shoot development.
- Coconut (Cocos nucifera) – Endosperm – Identify miRNAs potentially involved in tissue development and compound abnormalities.
- Rapeseed (Brassica napus), Pumpkin (Cucurbita maxima) – Phloem, Phloem Sap – Determine if small RNAs involved in long-distance information transfer via the vasculature of the plant.
- Tomato (Solanum lycopersicum) – Fruit, Leaf – Identify miRNAs that may be associated with vegetative growth, generative growth and flower development.
- Rockcress (Boechera sp.) – Flower – Determine if miRNAs are involved in the switch from sexual to apomorphic reproduction, a potentially important agronomic trait.
- Crow Dipper (Pinellia ternata) – Leaf – Provide the first report on the miRNAs in the species, which will enable further investigation of their roles in plant with specific physiologic characteristics and important medicinal value.

Stress Response – Identification of specific miRNA based markers that play essential roles in plant growth, development, and stress response.

- Biotic Stress
  - Viral Infection
    - Tomato response to Cucumber mosaic virus infection
  - Squash response to Zucchini yellow mosaic virus infection
  - Fungal Infection - Soybean resistance to Phytophthora sojae
- Abiotic Stress
  - Salt – Maize
  - Cold – Rice
  - Submergence – Maize
  - Drought – Wheat, Rice
- Others Stresses
  - Chemical Exposure – Festuca arundinacea – follicle glycophosphate application
  - Pollution Exposure – Medicago truncatula – heavy metal exposure

Identification of conserved miRNAs and their targets from Solanum lycopersicum

By searching known miRNAs identified from plant species against tomato nucleotide sequences, 13 conserved miRNAs were predicted.

To confirm the prediction, a miRNA-detecting microarray was designed with probes complementary to all non-redundant mature plant miRNAs documented to date.

After hybridizing with small RNAs extracted from tomato leaf tissue, 78 highly expressed mature miRNAs were detected, including all the miRNAs predicted above.

Identification of miRNAs expressed during solid endosperm development in coconut

Studied miRNA expression profiles in endosperm of coconut (Cocos nucifera) at different developmental stages to identify miRNAs potentially involved in tissue development and compound abnormalities.

Measured a total of 179 miRNAs in mature (56 expressed miRNAs) and mature tissues (123 expressed miRNAs).

The comparative analysis on miRNA expression profiles between these two groups of tissues showed that 25 miRNAs were up-regulated and nine miRNAs were down-regulated in mature endosperm.

Abiotic Stress: Salt tolerance in maize roots

miRNA-microarray hybridization revealed that a total of 98 miRNAs, from 27 plant miRNA families, had significantly altered expression after salt treatment.

18 miRNAs were found which were only expressed in the salt-tolerant maize line, and 25 miRNAs that showed a delayed regulation pattern in the salt-sensitive line.

A gene model was proposed that showed how miRNAs could regulate the abiotic stress-associated process and the gene networks coping with the stress, heterosis.

Heterosis (Hybrid Vigor) Studies

Analyzed the expression of miRNAs in two rice subspecies (indica vs. japonica and indica vs. indica) and their reciprocal hybrids using microarrays.

Found that all of the 1156 small RNAs tested, 140 (122, 140, 127, and 127) were identified being significantly differentially expressed in two reciprocal hybrids, respectively.

21 miRNAs showed complete expression trends relative to end-parent in reciprocal hybrids.

These findings reveal that small RNAs play roles in heterosis and add a new layer in the understanding and exploitation of molecular mechanisms of heterosis.

Plant Breeding – Identification of miRNAs that regulate key traits such as hybrid vigor, reproduction, could be useful for plant breeding and environmental protection programs; Germplasm screening – identification of miRNA based signatures for cataloguing plant genotypes and accessions.

Sexual vs Apomorphic Reproduction Studies

Bioinformatic analysis used to identify potential miRNAs.

Validation with a custom synthesized miRNA containing all known plant miRNAs that were available in the miRbase Release 16 (total 1137 unique mature miRNAs) and the Plant miRNA Database, psRNATarget (total 5668 unique mature miRNAs)

This study constitutes the first extensive insight into miRNAs involved in the switch from sexual to apomorphic reproduction in Boechera species.