



ABSTRACT

“microRNA biogenesis and function in plants”

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MicroRNAs are small RNAs of ~21 nt that recognize partially complementary sites in target mRNAs and guide them to cleavage or translational arrest. The microRNAs are distinguished from other small RNAs by their unique biogenesis, which involves a precise excision from the stem of a fold-back precursor located in a long primary transcript. The type III ribonuclease DICER-LIKE1 (DCL1) with the aid of the accessory proteins cleaves the precursors to release the microRNAs. However, plant microRNA precursors come in variable sizes and shapes, and we are interested in understanding how these different precursors can be processed to generate the mature microRNAs.

We have found that many precursors are processed in a base-to-loop direction, while others are processed by a non-canonical loop-to-base mechanism. We use a combination of approaches to study microRNA processing, including the analysis of libraries of random mutant precursors and the identification of processing intermediates with the aid of next generation sequencing techniques.

In plants, many of the evolutionary conserved miRNAs regulate transcription factors, which in turn play key biological functions. Perturbation of these miRNA regulatory networks, by mutations in microRNA encoding genes or by interference with their activity usually causes severe developmental defects. We are interested in identifying the targets of plant microRNAs, as well as their biological functions. The lab specifically focuses in the control of cell proliferation and differentiation by two microRNAs, miR396 and miR319.

Related Publications:

Bologna, N.G., Mateos, J., Bresso, E.G., and Palatnik, J.F.. (2009) A loop-to-base processing mechanism underlies the biogenesis of plant microRNAs miR319 and miR159. *EMBO J*, 28:3646-56.

Mateos, J., Bologna, N.G., Chorostecki, U., and Palatnik, J.F. (2010) Identification of Structural Determinants for MicroRNA Processing in Plants by Random Mutagenesis of MIR172a Precursor. *Current Biology*, 20:49-54.

Rodriguez, R., Mecchia, M., Debernardi, J.M., Schommer, C., Weigel, D., and Palatnik, J.F. (2010) Control of cell proliferation by microRNA miR396. *Development*, 137:103-12.

Debernardi, J.M., Rodriguez, R.E., Mecchia, M., and Palatnik, J.F. (2012) Functional specialization of the plant miR396 regulatory network through distinct microRNA-target interactions, *PLoS Genetics*, 8: e1002419.

Chorostecki, U., Crosa, V.C., Lodeyro, A.F., Bologna, N.G., Martin, A.P., Carrillo, C., Schommer, C. and Palatnik, J.F. (2012) Identification of new microRNA-regulated genes by conserved targeting in plant species, *in press*.