EDITORIAL

A timely journal for the newly discovered RNA universe

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It is always difficult to justify the initiation of a new journal in these times of information excess in the sciences but particular new areas of investigation have such a profound impact on scientific research that the establishment of a new and dedicated journal is beneficial and warranted.

The discovery that cells contain a variety of small non-coding RNAs which impact genomic integrity, gene regulation, and patterns of development has profoundly changed the molecular view of the RNA world (Mattick and Makunin, 2005; Tomari and Zamore, 2005). Quelling in *Neurospora*, post-transcriptional gene silencing (PTGS) in plants, RNAi and microRNAs in *C. elegans* and *Arabidopsis*, the maintenance and organization of heterochromatin in *S. pombe*, centromeric integrity in mammalian cells and the methylation status of DNA in *Arabidopsis* are all united by a complex transcriptional/post-transcriptional RNA silencing pathway that depends upon the production of small double-stranded RNAs. A recent genome wide screen in *C. elegans* identified 90 genes required for RNAi that include, Piwi/PAZ proteins, DEAH helicases, RNA binding/processing factors, chromatin-associated factors, DNA recombination proteins, nuclear import/export factors, and 11 known components of the RNAi machinery, and the number of genes involved is likely to increase (Kim et al, 2005). Deciphering the protein interactions for the RNAi and gene silencing pathways will clearly be a daunting but important step in our understanding and exploitation of this ancient process. A single microRNA can impact the expression pattern of more than 100 genes in a tissue-specific and developmental manner and, with upwards of more than 250 known microRNAs, the regulatory potential is enormous (Lim et al, 2005). The staggering complexity of the RNAi-microRNA network, as well as its evolutionary conservation in both the plant and animal kingdoms, defines a new RNA "universe" in biological systems. The role of cellular RNA can no longer be viewed just in the context of protein production. In the cell these small RNAs are not only processed from both the introns and exons of normal transcripts but also arise from a significant amount of overlapping transcription of both annotated and unannotated sequences widely dispersed throughout the genome that are found in both polyA+ and polyA- forms within and out of the nuclear compartment. These overlapping transcripts may depend upon the elusive RNA-dependent RNA polymerase, essential for RNAi and gene silencing in lower eukaryotes, that is still unidentified in multicellular organisms more advanced than *C. elegans*. The reason for this overlapping transcriptional organization is unknown but it may impact all aspects of our current understanding of gene regulation and will likely redefine our concept of a gene (Cheng et al, 2005). The realization that the RNA silencing pathway involved in viral and genome defence can also be used to target the degradation of a specific mRNA through RNA interference (RNAi), first described in *C. elegans* gene silencing by Andy Fire and Craig Mello (Fire et al, 1998), opened a powerful new approach to study gene function in most eukaryotes, especially in organisms not amenable to genetic analysis. So now we are on the threshold of a new era in molecular biology that has the potential to redefine gene regulation and the research approaches used in medical therapeutics and health research. The rapid increase in the number of publications in the RNA silencing field will be greatly served by a specialty journal dedicated to the field and we are please to announce the planned publication of just such a new journal dedicated to this purpose: The Journal of RNAi and Gene Silencing. It will serve as a new venue for the rapid publication of articles covering all aspects of the RNA universe and we welcome your contributions.

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