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COMMENTARY

In this commentary, Rob Kulathinal discusses two papers from the Perrimon lab that describe new online resources to assist geneticists in the design of their RNAi experiments. Hu *et al.*'s "UP-TORR: online tool for accurate and up-to-date annotation of RNAi reagents" and "FlyPrimerBank: An Online Database for *Drosophila melanogaster* Gene Expression Analysis and Knockdown Evaluation of RNAi Reagents", are published, respectively, in this month's issue of *GENETICS* and the upcoming issue of *G3*.

INVESTIGATIONS AND AUTHOR SUMMARIES

Lynch Syndrome, a leading cause of inherited cancer mortality in the United States, is a consequence of defects in mismatch repair. Cells lacking DNA mismatch repair accumulate mutations at a high rate, but how these mutations are distributed across the genome and how local sequence context affects the rate of mutation remains unknown. Theses authors used passaged yeast mismatch repair defective cell lines combined with whole-genome sequencing approaches to address questions surrounding mutation rates, mutation accumulation context, and mutation spectra. Their findings provide mechanistic insight into the mutagenic processes in mismatch repair deficient cells.

Variation among and within tuber-bearing potatoes for genes that contribute to accumulation and quality of steroidal glycoalkaloids (SGAs) in the plant may affect their defense against insects and the flavor and toxicity of the tubers. The authors examined sequence diversity in amplified regions of five genes—three in primary and two in secondary metabolism—along the biochemical pathway leading to SGA production in six wild and one cultivated potato species. Single nucleotide polymorphisms within the amplicons were analyzed for possible effect on SGAs measured in the leaves. The authors discovered that some common allelic differences were associated with SGA production. They found more variation within intronic vs. exonic regions and in the genes of secondary vs. primary metabolism.

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