sperm length is adaptive, these results, and others, show that physical selection by females influences sperm morphology — presumably because longer sperm preferentially occupy a favourable position in longer SRs.

The biological implications of both studies go well beyond flies. For example, given that the *takeout* gene was previously described for promoting starvation tolerance in flies, it would be interesting to find out any existing link between the appetite for food and for sex.

Tanita Casci

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WEB SITE

Scott Pitnick's lab: http://www-hl.syr.edu/depts/biograd/FACULTY/Pitnick.html

GENE REGULATION

Small but perfectly … regulating

One way for bacteria to modulate their gene expression is by attenuation — by which structural changes in the 5′ leader of a transcript bring about transcription termination of downstream genes in the same operon. In most cases, a ribosome, an RNA binding protein or an uncharged tRNA can alter RNA structure so that the so-called terminator loop doesn't form; instead, the alternative structure (referred to as the antiterminator) allows transcription to proceed. Now, Mironov and colleagues uncover a new mechanism of attenuation. They show that, in *Bacillus*, some small molecules can regulate their own transcription by interacting directly with specific sequences on RNAs that are transcribed from the operon to which they belong.

In *Bacillus*, genes that are involved in thiamin and riboflavin synthesis are organized in operons. Although much is known about these synthetic pathways, how the genes involved are regulated is unclear. Recent studies found that the 5′ leaders of RNAs from both operons contain evolutionarily conserved sequences, the structure of which indicated that they might fold into secondary structures — the *rfn* box (for the riboflavin (*rib*) operon) and the *thi* box (for the thiamin (*thi*) operon) — that could regulate the expression of genes in the two operons. To achieve this they would need to bind a cofactor. As no protein or tRNA — the usual suspects — could be found, it was suggested that riboflavin and thiamin or their derivatives, such as FMN and TPP, respectively, could have this role. Mironov *et al.* showed that this was indeed the case.

First, the sequence of both RNAs suggested that the binding of FMN or TPP could mask the antiterminator, allowing the formation of a termination loop and preventing downstream transcription. Conversely, in the absence of the ligand, the antiterminator loop would allow transcription to proceed.

To test whether this regulation involves antitermination, Mironov and colleagues made several RNA leader–*lacZ* fusions that included specific point mutations in the leader sequence of the *rib* operon. Monitoring the levels of β-gal expression, a marker of operon expression, in the different transgenic strains showed that FMN suppressed the *rib* operon through *rfn*-box-mediated termination. The same results were obtained when they monitored transcription directly *in vitro*.

The idea that FMN promotes the formation of an anti-antitermination loop was confirmed when the authors looked at the structure of the RNA leader in the presence or absence of FMN — by looking at which of the oligonucleotides that were homologous to different parts of the leader could base pair with the leader as transcription elongation proceeded. The results were clear — FMN triggers the formation of an anti-antitermination loop even before the elongation complex has reached the terminator.

So, Mironov *et al.* found a new way in which bacterial genes can be acutely and specifically responsive to changes in their environment. RNA sequences similar to *rfn* and *thi* boxes have been found in other bacteria, so this method of gene regulation might be widespread. Because some of these sequences overlap with the translation initiation sites and the start sites, the authors speculate that similar mechanisms might also operate at the level of translation.

Magdalena Skipper

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