

Important questions about SepF remain. For example, does SepF play a role in septation in divergent species such as cyanobacteria? Can purified SepF from other species also spontaneously self-assemble into rings and orient FtsZ protofilaments into tubules? SepF may be essential for cell division of cyanobacteria because they lack FtsA and/or EzrA homologs [13,16]. Other Gram-negative bacteria, which lack SepF, must also maintain Z-ring integrity to coordinate constriction, septum formation, and outer membrane invagination. For the  $\gamma$ -proteobacteria, evidence suggests that ZipA and the well-conserved FtsA mediate this coordination [1] and it is likely that other bacteria have as yet unidentified, functionally related factors. Although the basic theme of cell division is becoming clear, unraveling the plethora of variations in the most diverse group of organisms on Earth remains a challenge.

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DOI: 10.1016/j.cub.2011.02.006

## Chromatin: Bind at Your Own RSC

Recent work has identified a novel RSC–nucleosome complex that both strongly phases flanking nucleosomes and presents regulatory sites for ready access. These results challenge several widely held views.

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Genome-wide experiments in yeast, fly and mammalian cells have identified the existence of nucleosome-depleted regions in promoters and enhancers [1–4]. Transcription factors are thought to bind to their cognate sites located in these nucleosome-depleted regions, subsequently recruit nucleosome-remodeling and modifying complexes, and evict or reposition flanking nucleosomes that block RNA polymerase assembly at the promoter. By using a novel, quantitative assay, recent work from the Ptashne lab has uncovered several striking insights into

nucleosome occupancy at the *GAL1/10* promoter of budding yeast [5–7]. These results challenge current ideas of whether nucleosome-depleted regions are completely nucleosome-free, whether strongly positioned nucleosomes are always incompatible with the binding of regulatory proteins, and whether the occupancy of a DNA fragment by a nucleosome is mostly determined by its sequence.

Nucleosome occupancy at a particular genomic location is measured by assessing nucleosome-mediated ‘protection’ (often assumed to be the canonical, mono-nucleosome size of 147 bp) of

that sequence from digestion by micrococcal nuclease (MNase). Typical nucleosome occupancy assays fix chromatin in cells, lightly digest chromatin at a single concentration of MNase, and quantify protected DNA fragments by quantitative PCR (qPCR), tiling microarrays, or next-generation sequencing. Unfortunately, DNA sequence itself influences digestion efficiency of MNase, a bias that can create a false apparent protection of ‘naked’ genomic DNA. Strikingly, recent papers show that MNase digestion of naked genomic DNA infers similar nucleosome occupancies to that obtained by MNase digestion of chromatin DNA [8,9].

Bryant *et al.* [5] developed a quantitative MNase protection assay that normalizes against such variability. The assay digests naked genomic DNA and fixed chromatin DNA over a wide range of MNase concentrations,



strongly positioned 'super-binder' nucleosomes decreased (presumably by *Swi/Snf*), although eviction was less complete and induction occurred more slowly as nucleosome affinity increased. These data suggest that the wild-type *GAL1/10* promoter has likely evolved a promoter sequence with low nucleosome occupancy to allow for rapid eviction upon galactose induction (Figure 1B,C).

These studies raise important questions that will keep the chromatin field busy: how accurate are nucleosome occupancies derived from a single MNase digestion with no naked genomic DNA control? Do such artifacts change our current understanding of genome-wide nucleosome-depleted regions and whether nucleosome position is encoded in the DNA? How many other regulatory nucleosomes remain undiscovered because of our presumption that all nucleosomes protect ~150 bp of DNA? How does partial nucleosome occupancy keep wild-type *GAL1/10* transcription low? Is there a correlation in positioning and occupancy between adjacent nucleosomes at positions -1, -2, and -3? If this nucleosome depletion is a result of histone turnover, what is the on/off rate? Lastly, how does cell-to-cell variability in nucleosome configuration affect the noise in gene expression levels and dynamics? If we take our cue from Ptashne and co-workers,

population-level and genome-wide assays may not be the best approach. Rather, biological insight will come from low-throughput approaches that measure nucleosome occupancy and gene expression of model genes in single cells [13,14].

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DOI: 10.1016/j.cub.2011.01.060

## Animal Navigation: Longitude at Last

Newly hatched sea turtles exposed to artificially generated magnetic fields with parameters characteristic of two sites 3700 km apart, differing only in longitude, can distinguish the two apparent locations and orient appropriately.

James L. Gould

Humans establish their global position by separately determining latitude and longitude. The east–west parameter (longitude) is notoriously difficult to measure accurately, depending as it does on knowing the time with nearly impossible exactitude. While the global position systems (GPSs) of animals manage to ignore time [1], longitude looks at first glance to be nearly as impossible for them too [2]. As reported in this issue of *Current Biology* [3],

however, new tests with sea turtles demonstrate that these creatures act as if they know their longitude, and infer this parameter on the basis of magnetic intensity and inclination.

A map sense is not necessary for many traveling creatures. For instance, some migrating animals simply fly a fixed compass vector (or a dogleg series of vectors); this is typical of many birds during their first autumn trip south. Some migrants and homing species depend instead on piloting, using their memory of landmarks

observed during a previous journey to place themselves; many group-flying diurnal migrants such as geese use this approach. Other homing animals — most famously homing pigeons younger than 12 weeks — rely on inertial navigation, using cues monitored on the outward trip to judge the return bearing and distance back to the loft [4].

Most interesting of all, however, are the creatures capable of true navigation, who act as though they know their current position based on real-time cues. For example, members of at least some nocturnally migrating species can be captured *en route* to their breeding or wintering grounds and then displaced hundreds or thousands of kilometers to novel locations in apparent sensory isolation. When