



The Nucleus Introduced

Thoru Pederson

Program in Cell and Developmental Dynamics, Department of Biochemistry and Molecular Pharmacology, University of Massachusetts Medical School, Worcester, Massachusetts 01605

Correspondence: thoru.pederson@umassmed.edu

Now is an opportune moment to address the confluence of cell biological form and function that is the nucleus. Its arrival is especially timely because the recognition that the nucleus is extremely dynamic has now been solidly established as a paradigm shift over the past two decades, and also because we now see on the horizon numerous ways in which organization itself, including gene location and possibly self-organizing bodies, underlies nuclear functions.

“We have entered the cell, the Mansion of our birth, and started the inventory of our acquired wealth.”

—Albert Claude

When I first read that morsel from Albert Claude’s 1974 Nobel Prize lecture it seemed Solomonian wisdom, as it indeed was. Though he was referring to cell biology *en toto*, the study of the nucleus was then at a tipping point and new advances were just at hand. Since then, the nucleus field has literally nucleated and we are now at a position to both admire the recent past and register excitement about the present and where the nucleus field may be headed.

THE NUCLEUS DISCOVERED

We cannot know who first saw the nucleus but we do know that the father of optical

microscopy, Antony van Leeuwenhoek, did so with amphibian and avian erythrocytes in 1710 and that in 1781 Felice Fontana did so as well in eel skin cells. More definitive accounts followed by Franz Bauer, who in 1802 sketched orchid cells and pointed out the nucleus (Bauer 1830–1838), as well as by Jan Purkyně, who described it as the *vesicula germanitiva* in chicken oocytes (Purkyně 1825), and Robert Brown who observed it in a variety of plant cells (Brown 1829–1832), earning additional fame for coining the term “nucleus” (for excellent accounts of these early descriptions of the nucleus see Gall 1996; Harris 1999). Of course, these early observations did not ascribe particular significance to this structure, the given name simply conveying its central location. Later, the nucleus was increasingly observed and became, with some prescience, a key tenet of the cell theory. The nucleus remained a rather lonely item in the eukaryotic cell’s parts list for many

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decades, until the discoveries of discrete cytoplasmic entities, e.g., mitochondria, the Golgi apparatus etc. (reviewed in Wilson 1925).

THE NUCLEUS INHERITED

We do not know how and when the genome of an ancestral cell first became encased in a primitive nucleus. We have no evidence that cells living in the RNA world ever had a membrane (or any other structure) around the genome, i.e., that they ever became nucleate. Once a ribozyme RNA replicase arose, anything would have been possible including the emergence of ribozymes with lipid biosynthetic activities.

Enthalpy-favored or free energy-driven events could then have led to stabilizing selection of RNA-lipid affinities and on from there. A cottage industry of experiments on the interactions of lipids with RNA has emerged in the chemical biology field in the past decade but the significance of these studies to prebiotic systems and the earliest cells remains speculative. As for the advent of the DNA world, and of eukaryotes, a major concept is that a prokaryote organism was invaded by another, non-nucleated cell, setting up an endosymbiotic relationship, with the entering organism's outer membrane seeding what would become the nuclear envelope. The major proponent of this plausible idea has also suggested that this hypothetical invader also brought in a centriole, the forerunner of what we know as the centriole/basal body in extant eukaryotes (Margulis et al. 2000). We can not play the videotape of life on Earth backwards and although we can reconstruct some things with a degree of empirical confidence, albeit amidst debate (reviewed by Misteli 2001a; Poole and Penny 2001; Rotte and Martin 2001), or speculation (e.g., Lake 2009), when it comes to how the nucleus arrived, we just do not know.

THE NUCLEUS ENVELOPED

Notwithstanding the uncertainty of its evolutionary origin, the nucleus is bounded by a double membrane, the nuclear envelope, which in many cells is contiguous with the endoplasmic

reticulum. The frequently observed intimacy of the nuclear envelope with the endoplasmic reticulum has been often under-appreciated, particularly as it bears on the isolation of nuclei and issues of resulting purity. There is also growing interest in how nuclear membrane proteins may be integrators of nuclear and cytoplasmic organization and dynamics (e.g., King et al. 2008; Roux et al. 2009; Starr 2009).

A seminal finding was that the nuclear envelope contains pores (reviewed by Gall 1964; 1967), which have now been defined in considerable compositional and structural detail (e.g., Alber et al. 2007; Fernandez-Martinez and Rout 2009). A somewhat less familiar but equally important area of investigation has revealed that the nuclear envelope harbors a signal transduction system of its own, featuring players in common with the plasma membrane, for example the lipid-linked inositol trisphosphate system (Martelli et al. 1991; for reviews see Divecha et al. 1993; Cocco et al. 2009; Barton et al. 2010).

THE NUCLEUS DIVERSIFIED

However the nucleus arose, it went on to display a variety of organizations. These range from the highly condensed nuclei of mature erythrocytes in nonmammalian vertebrates to the bimorphic nuclei in almost all ciliates. In the latter organisms a micronucleus perpetuates the genome whereas a macronucleus contains DNA fragments that represent only a fraction of the organism's genome complexity and which encode the RNAs and proteins needed for vegetative life. It was a particular feature of this genomic strategy, namely the macronuclear amplification of the ribosomal RNA genes (Gall 1974), that led to the discovery of the telomere DNA sequence (Blackburn and Gall 1978). It was also in these ciliates that self-splicing RNA was discovered and in which the era of chromatin epigenetic marks was launched (reviewed in Pederson 2010).

THE NUCLEUS VIEWED

Beyond early observations made by bright field microscopy, the staining method developed by



Robert Feulgen, which attaches a dye to acid-depurinated DNA, was a major tool in advancing the DNA = gene theory, based on studies of the DNA content of haploid versus diploid cells by a graduate student, Hewson Swift, in the laboratory of Arthur Pollister at Columbia University, and concurrent ones by Hans Ris in the laboratory of Alfred Mirsky at the Rockefeller Institute (reviewed by Pederson 2005). Although biochemical measurements of the DNA contents of germ versus somatic cells had revealed a twofold difference, these findings mostly remained in the biochemical community and did not have as much impact as might have been expected. It was the Feulgen cytophotometry results that helped catalyze the idea that DNA is genes. This was, to borrow part of Winston Churchill's famous phrase—"the end of the beginning" (Avery et al. 1944).

Meanwhile, phase contrast microscopy had beautifully revealed the interphase nucleus and mitotic chromosomes, the latter not "nuclear" in the strictest sense. Electron microscopy led to the visualization of the double nuclear membrane and nuclear pores (Gall 1964; 1967), the tripartite structure of the nucleolus (Bernhard et al. 1952), the nuclear lamina (Fawcett 1966), and subsequently the observation of chromatin ν -bodies (Olins and Olins 1974), later re-named nucleosomes (Oudet et al. 1975).

An intriguing nuclear structure first observed by the Spanish neuroanatomist Santiago Ramon y Cajal (Cajal 1903, 1910) underwent a renaissance of interest when one of its protein components was identified by Eng Tan and colleagues (Andrade et al. 1991; Raska et al. 1991). Initially termed the coiled body, a campaign in 1999 by Joseph Gall resulted in a consensus to rename this structure the Cajal body. Gall has made some of the most seminal advances in our understanding of this nuclear body (for reviews see Gall 2000; Handwerker et al. 2006; Gall 2009; Nizami et al. 2010). Similarly, in the 1990s the nucleolus, interchromatin granule clusters (a.k.a. nuclear speckles) and other nuclear bodies also underwent advances in molecular definition (reviewed by Spector 1993; Pederson 2002a; Spector 2001; 2006).

THE NUCLEUS ISOLATED

Using pus-soaked bandages from a local hospital, Friedrich Miescher discovered DNA in the late 1860s. As described in a richly detailed historical account (Portugal and Cohen 1977), Miescher wrote a manuscript and submitted it to a top journal but had to sit by and wait while the editor (and his former mentor), Felix Hoppe-Seyler, checked the findings in his own lab, resulting in the publication of two concurrent papers (Miescher 1871; Hoppe-Seyler 1871). Over the next 90 years, efforts to isolate nuclei did not go very far. In the 1960s Alfred Dounce at the University of Rochester, Van Potter and Conrad Elvehjem at the University of Wisconsin, and Philip Siekevitz and George Palade at the Rockefeller Institute pioneered the isolation of nuclei from animal tissue. (The Rochester and Wisconsin investigators had the homogenizers they developed named for them.) Important advances in isolating nuclei from plant tissue were made at approximately the same time by James Bonner's group at Caltech. Later, groups at Baylor College of Medicine (Harris Busch), Rockefeller University (Alfred Mirsky) and Albert Einstein College of Medicine (Sheldon Penman) published refined methods. As is the case for most cell fractionation methods, none of these proved to be perfect but they were major advances nonetheless.

The fact that the endoplasmic reticulum and the nuclear envelope are contiguous in many cells is but one example of this challenge, and the tendency of the cytoplasmic intermediate filament system to often collapse upon the nucleus during cell fractionation is yet another. The pioneer methods of nuclear isolation employed sucrose concentrations in which the tissue homogenate was exposed to hydrodynamic forces and/or sucrose density differences that caused cytoplasmic elements and adherent endoplasmic reticulum to separate from the nuclei. The most popular of the early methods (Chauveau et al. 1956) was subsequently refined in important ways to further minimize cytoplasmic contamination (Maggio et al. 1963; Blobel and Potter 1966), with these two latter advances constituting the gold standard of



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nuclear isolation for many years, and still today for many tissues.

As regards methods aimed at single-cell studies, an important method (Penman 1966) involved swelling cells in a hypotonic buffer so that the expanded cell volume would collide with the hydrostatic shear forces delivered by a 0.0015-inch clearance stainless steel device, patterned after ones introduced by Dounce. Detergent-based methods were also introduced (Traub et al. 1964). These typically employed Triton X-100 or Royal Dutch Shell's "nonionic P-40" (a.k.a. NP-40). These breach the plasma membrane and, depending on cell type, also strip away the endoplasmic reticulum. In some cases, NP-40 collapses some of the plasma membrane onto the nucleus, so that nuclei prepared by this method may not always be as pure as some investigators have assumed. For some cells, the main advantage of the NP-40 method is less the nuclear fraction, but the relatively high purity of the ribosomes that are released (Borun et al. 1967).

All methods of nuclear isolation must be monitored both for what remains attached from the cytoplasm (or is taken up from it), as well as what is lost from within. Various markers have been used to assess the depletion of cytoplasmic material in isolated nuclei, based on the presumption that the true intracellular locations of such markers are known to some degree of certainty. In one study, HeLa cell nuclei were isolated in a buffer consisting of a previous cytoplasmic fraction from ^3H -leucine-labeled cells (Bhorjee and Pederson 1972), thus allowing the level of cytoplasmic protein contamination of the nuclei to be readily estimated.

Issues of nuclear purity loomed large in early studies claiming that protein synthesis occurs in the isolated nuclei (and thus presumably within nuclei *in vivo*) but this work was challenged on several grounds (reviewed by Goldstein 1970; Pederson 1976). More recently this issue has resurfaced (e.g., Iborra et al. 2001, although this study also included intact cell experiments). Various controls for nuclear purity have been better but still not sufficient to quiet all doubts as to the source of apparent protein synthesis in isolated nuclei (for reviews

see Pederson 2001a; Dahlberg et al. 2003; Nathanson et al. 2003). Meanwhile, less attention has been devoted to analyzing not what is adsorbed to nuclei as opposed to what is lost from nuclei during various isolation methods.

There have been other instructive guideposts over the years for judging the purity of nuclear fractions. An instructive vignette is the saga of the biosynthesis of the U-rich spliceosomal small nuclear RNAs. We now know that they are exported to the cytoplasm as 3' extended precursors, there to be trimmed, 5'-cap hypermethylated and assembled with various proteins before re-entry into the nucleus as functional snRNPs. Although many studies had pointed to this pathway at varying degrees of cogency, it was the use of two particular nuclear isolation methods, each with exceptionally strong credentials, that led to acceptance of this pathway of snRNP biogenesis (Gurney and Eliceiri 1980; Zieve et al. 1988). This was further solidified by the demonstration that exogenous U2 snRNA precursor molecules introduced into the cytoplasm of mammalian cells enter this pathway and become 3' trimmed, cap hypermethylated, and assembled into snRNPs, followed by nuclear uptake (Kleinschmidt and Pederson 1990).

Another example of how the critical issue of nuclear purity was addressed arose in a study in which the total sequence complexity of nuclear versus cytoplasmic RNA was measured (Holland et al. 1980). Because the nuclear RNA was anticipated to have a higher sequence complexity than cytoplasmic RNA, contamination of the cytoplasmic fraction by leaked nuclear RNA loomed large. Accordingly, an experiment was undertaken in which the cells were labeled with an RNA tracer for a very short time (2 min), far too brief for any labeled transcripts to be exported to the cytoplasm *in vivo*, before cell fractionation. The label was followed throughout the isolation of the cytoplasmic fraction and polyribosome-associated mRNA, which revealed that no more than 0.03% of the nuclear RNA synthesized in the previous 2 min was present in the final mRNA preparation (Holland et al. 1980). Given that these

kinds of controls are conceptually obvious and experimentally quite facile, it is surprising how rarely they have been employed in studies in which knowing the purity of a nuclear or cytoplasmic fraction is essential to weighing the findings.

Beyond the isolation of nuclei in bulk, there is the gold standard of manual isolation of nuclei from material that affords this opportunity (e.g., Duryee 1954; later refined and reviewed by Lund and Paine 1990; Paine et al. 1992). In a recent application of this approach, frog oocyte nuclei were manually isolated under oil and the relative densities of the nucleolus versus surrounding nucleoplasmic bodies were determined by differential interference light microscopy, with results that defied most expectations (Handwerger et al. 2005). For most of the cells and tissues from which one wants to isolate nuclei, manual isolation is of course out of the question. But it is worth emphasizing that what has been learned from occasional studies employing manually isolated nuclei is likely to be a more reliable guide to understanding nuclear organization and function than has sometimes been realized by those members of the nucleus research community whose work is based on bulk nuclear isolation.

A general point to be made is that although isolated nuclei served many important experimental uses during the modern era of research on the nucleus, their role in advancing the biochemistry of gene expression was surprisingly short-lived and quite limited. Cell-free systems based on isolated nuclei played only transitory and rather minor roles in the areas of DNA replication, transcription, and mRNA processing—usually giving way to more efficient soluble systems in short order. An exception was the use of isolated nuclei to allow RNA polymerase II to continue transcription and thus, by hybridization analysis of the extended chains, determine the boundaries of a transcription unit (Weber et al. 1977). In contrast to these limited roles of isolated nuclei in the investigation of gene expression, a very different cell-free system derived from frog eggs (Newport and Forbes 1987) was of monumental importance in advancing our understanding of chromatin

and nuclear envelope assembly and the control of cell-cycle progression.

THE NUCLEUS COMPOSED

In 1976, the Federation of American Societies of Experimental Biology (FASEB) heroically collated all available information on the “properties of cells” and I was chosen to organize and edit the chapter on the nucleus. At the suggestion of the editors, and with FASEB’s permission, we are republishing here the tables of data on the nucleus from the original volume (Altman and Katz 1976) (see supplemental data online). These tables speak to painstaking analytical work carried out in a time gone by and rarely pursued today. But let there be no mistake, the concentrations of protein or RNA in various preparations of isolated nuclei, or extracts derived from them, can be a critical factor in the interpretation of certain kinds of studies. What is needed now to complement these important compositional data is additional biophysical information (reviewed in Pederson 2002a). One important step in this direction is that the fluid viscosity of the interchromatin space has now been estimated, based on diffusion coefficients of reporter molecules, to be approximately one-fifth that in water (Wachsmuth et al. 2000). The considerations of fluid viscosity and free versus anomalous diffusion are critical to the understanding of intranuclear transport and nuclear body dynamics (Wachsmuth et al. 2000). In terms of chemical kinetics one would also want to know the water concentration in the nucleus. Only then could one know, or at least estimate, the ionic strength of the solvent phase and the true concentrations of solutes. The importance of these biophysical parameters is conveyed by the fact that only a relatively small change in the intracellular ion concentration elicits a dramatic mitosis-like state, which is completely reversible (Robbins et al. 1970). Polyamines are abundant constituents of the nucleus in most cells and yet their possible functions are rarely considered. Iron is a surprisingly abundant component of the interphase nucleus and mitotic chromosomes and is essential for DNA

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replication (Robbins and Pederson, 1970). Many compositional issues such as these are rarely considered in current research on the nucleus and yet they can be extremely determinative. But, happily, there are steps in this direction, as biophysicists increasingly join the nucleus research community (for an “interdisciplinary” review see O’Brien et al. 2003).

THE NUCLEUS DECONSTRUCTED

Major advances in biology were made by teasing a cell or its parts out, as from the squid giant axon, leading to the discovery of kinesin, or by glycerinating rabbit muscle to discover the biochemistry of its contraction. The major conceptual discovery about the nucleus, that it contains the genome, did not involve its dissection. But a desire to know its parts naturally arose in due course. Early attempts to isolate chromatin were made by the laboratories of Alfred Mirsky (Rockefeller) and James Bonner (Caltech) but these fractions were of dubious enrichment and the major advances in the field of chromatin and chromosome structure came from *in situ* studies (reviewed by DuPraw 1970). One of the first, convincing isolations of a subnuclear component was that of the nucleolus from starfish oocytes (Vincent 1955). Later, three groups went further. Palade and Siekevitz at Rockefeller purified guinea pig liver nuclei, subjected them to sonication and isolated nucleolar and nucleoplasmic fractions (Maggio et al. 1963). The demonstrated degree of fractionation was impressive and this work constituted one of the most important advances in the nucleus field at the time. Meanwhile, the laboratory of Harris Busch at Baylor College of Medicine developed a similar, sonication-based method for isolating nucleoli from rat hepatoma cells (Muramatsu et al. 1963) and subsequently this group, notably Ramachandra Reddy, exploited this method to identify a number of small nucleolar and nucleoplasmic RNAs long before their functions became known (for a review see Reddy and Busch 1988). Shortly thereafter, Sheldon Penman developed a method to resolve a HeLa cell nuclear fraction into nucleoli and nucleoplasm (Penman 1966).

His method involved the use of DNase and high ionic strength and produced nucleolar and nucleoplasmic fractions that were less native than those obtained by the sonication method, although it led to spectacular advances in our understanding of RNA biosynthesis.

More recently, mammalian and plant cell nucleoli have been purified and subjected to extensive proteomic analyses (Andersen et al. 2002; Scherl et al. 2002; Pendle et al. 2005; Hinsby et al. 2006; for reviews see Dundr and Misteli 2002; Pederson 2002b; Couté et al. 2006; Leung et al. 2006). Nucleoplasmic bodies known as interchromatin granule clusters (a.k.a. “speckles”) were isolated by David Spector and colleagues (Mintz et al. 1999) and later subjected by this group to proteomics analysis (Saitoh et al. 2004; reviewed in Lamond and Spector 2003). Meanwhile, Cajal bodies (reviewed by Gall 2000, 2009; Nizami et al. 2010) were isolated by Angus Lamond’s laboratory (Lam et al. 2002). An exciting aspect of this recent period was that these nuclear bodies were being analyzed in such molecular detail at the very time the dynamics of their components were being observed in live cell studies, as will be discussed below.

Another nuclear structure appears in some cells, the perinucleolar compartment (Huang et al. 1997; 1998), and its presence has recently been found to have promising prognostic value in the staging of breast carcinoma (Kamath et al. 2005). It is a discoid, caplike structure intimately attached to the nucleolus and has thus resisted isolation so far. There presently are no clues to its function, beyond its accretion of certain small RNAs transcribed by RNA polymerase III (Matera et al. 1995; Weng et al. 2003).

THE NUCLEUS TERRITORIALIZED

A major development was the discovery that interphase chromosomes occupy specific locations (Zorn et al. 1979; Cremer et al. 1982), which to some extent had been anticipated from classical studies of the arrangement of chromosomes in the metaphase plate (Rabl 1885) and by the actual coining of the term “chromosome territory” (Boveri 1909). The

modern concept of chromosome territories was promptly adopted in certain sectors of the human genetics and radiation biology communities but took more than two decades to gain broader traction (reviewed by Cremer and Cremer 2001; 2006), now with appreciated relevance to chromosomal translocations (see Pederson 2003 for a review), genome evolution (Tanabe et al. 2002; Foster and Bridger 2005) and the entire issue of how chromosome location relates to gene density and/or expression. This latter area has been hyperactive in the past few years (reviewed by Spector 2003; Pederson 2004; Gilbert et al. 2005; Sprout et al. 2005; Cremer et al. 2006; Akhtar and Gasser 2007; Misteli et al. 2007; Sexton et al. 2007; Takizawa et al. 2008; Towbin et al. 2009; Deniaud and Bickmore 2009) but the results have been surprisingly variable and confounding (for a particularly lucid summary see the Introduction in Meaburn et al. 2008). A distinct possibility that has arisen recently is that gene positioning is self-organizing, based not on expression per se but on the potential for sets of genes to be coregulated (Rajapakse et al. 2009; reviewed by Misteli 2009).

A clinical feature of chromosome territoriality is the fact that the extreme cytological manifestation of gene repression, i.e., heterochromatin, has long served as a key landmark for pathologists, both in its extent and location. But an exciting new dimension of diagnostic potential lies in studies, mentioned earlier, of intranuclear gene locations in relation to not only reciprocal translocations (Roix et al. 2003; reviewed in Pederson 2003) but in more recent work on gene repositioning in solid tumors (e.g., Meaburn et al. 2009).

The nucleus is territorialized not only with respect to the locations of the chromosomes themselves but also to a considerable extent with respect to the layout of expressed versus silenced genomic regions. This aspect of the nuclear structure field has recently taken one particularly surprising turn, reminding us that we are still in the early days. In most cells, heterochromatin is located at the nuclear periphery or in close approximation to the nucleolus. Remarkably, it has recently been reported that

in the rod photoreceptor cell nuclei of nocturnal animals, the heterochromatin is coalesced into a large central domain in the nucleus with the euchromatin displaced to more peripheral locations, with plausible speculations as to the efficiency of light transmission and retinal harvesting (Solovei et al. 2009; reviewed by Ragozcy and Groudine 2009).

Another important recent development has been the introduction of methods to capture the interchromosome regions that lie in closest juxtaposition (Dekker et al. 2002; reviewed by Dostie and Dekker 2007). With this new methodology the field of genome organization is moving to a 4-D spatial-temporal registration, which is itself likely to be determinative of phenotype. The extraordinary packing density of interphase chromatin has been recently investigated with “Hi-C”, a powerful variation of the chromosome conformation capture methodology (Lieberman-Aiden et al. 2009; for a review see Langowski 2010).

THE NUCLEUS NOT LIKELY MATRIXED

Breaking up nuclei with sonication is one thing, extracting them with salt is another. The latter was a major effort of many labs in the 1950s and thereafter, most notably for isolating and characterizing histones. But others (e.g., Zbarsky and Georgiev 1959) employed graded salt extractions to fractionate total nuclear components. This yielded successive fractions of differing composition, not unexpected because the zwitterion concept of protein net charge had long been discovered by Arne Tiselius and advanced by John Edsall. There was therefore no reason to believe that cell components such as nuclei, mitochondria, or ribosomes would not release different sets of proteins as the ionic strength is elevated. Few cell biologists were comfortable with assigning a residue of the nucleus any relationship to the *in vivo* situation.

But in 1974 this nuclear residue got re-named a “nuclear matrix” (Berezney and Coffey 1974) and later work gave rise to the idea that chromatin and nascent RNA are attached to it.



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The notion took hold in some quarters and gained a degree of traction as all sorts of entities were observed to be present in this fraction. But there was never any proof of the *in vivo* existence of such a structure nor is there proof today (for detailed reviews see Pederson 1998; 2000) and many leaders in the field of nuclear structure and function question the nuclear matrix concept. The consensual skepticism as to a nucleus-wide, arborized network of filaments extending throughout the nucleoplasm certainly does not rule out the existence of short-range structural motifs.

THE NUCLEUS IN DIVISION

The current focus of the cell division field on chromosome capture by kinetochore–microtubule interactions, how anaphase works mechanistically and the operation of mitotic checkpoints is of course well justified. But it is also possible that this emphasis may be missing one of the most intriguing of all events—the formation of daughter nuclei. Precursors of the nucleolus, nuclear envelope, and nuclear lamina congress, mature, and assemble in “daughter to be” cells as early as anaphase and definitively in telophase. This presently subsidiary effort in the cell division field needs more momentum as it is no less intriguing than anaphase, and likely involves very different mechanisms such as the free energy of DNA–lipid affinities and other chemical phenomena that are unique to telophase and the assembly of daughter nuclei, seemingly via pathways whose memory had not been erased from the previous mitosis.

THE NUCLEUS IMAGED

In his detailed recipes, the histochemistry pioneer A.G. Everson Pearse described various ways to stain cells, including the nucleus (Pearse 1961). I tried many of these methods as a student including the aforementioned Feulgen reaction. The combination of methyl green and pyronin ended up as my favorite, with which I first saw nucleoli, to become a long-standing interest. At the end of the classical era, immunostaining and subsequently the

advent of GFP advanced the localization of nuclear proteins and bodies, and the discovery of *in situ* nucleic acid hybridization (Gall and Pardue 1969) made possible the localization of both genes and RNAs. These methods, especially when powerfully used in combination, have made it possible to even demarcate subregions of nuclear domains formerly thought to be relatively homogenous, such as the granular component of the nucleolus, which now appears to be a landscape of distinct molecular zones rather than a uniform lawn of nascent ribosomes (Politz et al. 2002; 2005). Of course, these light microscopy advances have left ample room for the continuing application of electron microscopy. Particular progress has been made in the past two decades with respect to the ultrastructural analysis of both nuclear pore complexes, as mentioned earlier, as well as a defined messenger RNP, sometimes the two caught together (Mehlin et al. 1992).

THE NUCLEUS IN MOTION, WITHIN

There was never much doubt that, around the less mobile chromosomes and nucleoli, molecules roam the nucleus. This emerged from numerous studies in which tagged molecules were microinjected into the nucleus and observed to display high mobility (e.g., Wang et al. 1990). Subsequently it became possible to express fluorescently tagged nuclear proteins and observe their dynamics. The first such study examined the dynamics of interchromatin granule clusters (Misteli et al. 1997) which revealed these nucleoplasmic bodies to be more dynamic than had been anticipated. Then, a new wave of studies appeared resulting from the application of the method of fluorescence recovery after photobleaching (FRAP). In the first of these, FRAP was employed to study the mobility of the DNA repair machinery tagged with GFP (Houtsmuller et al. 1999). This paper represented both a technical and conceptual milestone and soon thereafter FRAP was applied to several other nuclear proteins in a boomlet of important studies (Kruhlak et al. 2000; Lever et al. 2000; Misteli et al. 2000; Phair and Misteli 2000; Boisvert et al. 2001; Chen and

Huang 2001; reviewed in Pederson 2000b; Misteli 2001b; Pederson 2001b; Phair and Misteli 2001). These revealed much more rapid and/or more extensive dynamics than would have been anticipated from either earlier *in vitro* work, or from the apparent stasis of certain nuclear bodies, constituting a true paradigm shift in the nucleus field (reviewed by Misteli 2001b). Even the nuclear lamina, which had long been viewed as one of the most stable structures in the nucleus, was found to undergo dynamic exchange of subunits, leading to an appreciable nucleoplasmic concentration (Moir et al. 2000; reviewed by Dechat et al. 2008) and there is increasing evidence that the dynamic lamins have functions while in the nucleoplasm (Malhas et al. 2007; Lee et al. 2009; reviewed by Shimi et al. 2008; Shumaker et al. 2008), and it now appears that nucleoporins do as well (Capelson et al. 2010; Kalverda et al. 2010).

This wave of FRAP studies addressed the dynamics of protein constituents of nuclear bodies and was, of course, based on GFP. But GFP also enabled investigation of the movements of nuclear bodies and their constituents. Studies of the movements of chromosomes (Marshall et al. 1997; reviewed by Gasser 2002), promyelocytic leukemia (PML) bodies (Muratani et al. 2002) and Cajal bodies (Platani et al. 2002) were the first of these. The Marshall et al. study was ahead of its time and it was amusing to recall the incredulity expressed by some that interphase chromosomes, relatively giant structures, are moving, and with no dependence on metabolic energy. But others properly anticipated that there is of course no reason the chromosomes would not display this microscopic biophysical property, *viz.* the manifestation of the kinetic energy of any particle.

Although GFP enabled these studies (for reviews see Misteli et al. 1997; Eils et al. 2000; Pederson 2000b; Misteli 2001b; Pederson 2001b; Chubb and Bickmore 2003; Dundr et al. 2002; Gasser 2002), investigating the intranuclear movements of the other major nuclear species, RNA, required different innovation. The fact that microinjection of a pre-mRNAs

or small nucleolar RNAs into the nucleus of mammalian cells resulted in localization with sites known to contain splicing machinery or the nucleoli, respectively (Wang et al. 1990; Jacobson et al. 1995; Jacobson and Pederson 1998; reviewed in Pederson 2001c) showed that introduced RNA is mobile. Further innovations led to tagging of endogenous RNA and these studies confirmed that poly(A) RNA is highly diffusive in the nucleus (Politz et al. 1998; 1999; reviewed in Politz and Pederson 2000; Pederson 2001c), and subsequent studies revealed, importantly, that this was true of specific mRNAs (Singh et al. 1999; Shav-Tal et al. 2004) and also 28S ribosomal RNA (Politz et al. 2003). These approaches also made it possible to investigate the live cell dynamics of RNA in relation to specific intranuclear structures, e.g., interchromatin granules (Politz et al. 2006). An increasing number of single-molecule level studies of nuclear molecular dynamics have appeared recently (Dange et al. 2008; Grünwald et al. 2008; Siebrasse et al. 2009) and, together with revolutionary advances in the spatial resolution of diffraction-limited optical microscopy (for a brief review see Pederson 2006), one senses the dawning of a new era as systems biology enters the nucleus, or vice-versa (reviewed by Gorski and Misteli 2005). Another major advance was the introduction of a method to tag specific chromatin regions via the binding of GFP-tagged lac repressor to an integrated tandem array of the lac operator (Robinett et al. 1996), which in turn allowed the visualization in living cells of gene activation at discrete loci (Tsukamoto et al. 2000; Janicki et al. 2004) and the dynamics of transcription factors (Becker et al. 2002; Karpova et al. 2008; Sprouse et al. 2008). As mentioned earlier, the movements of interphase chromosomes have implications for the statistics of reciprocal exchanges between interphase chromosomes, with disease relevance (Roix et al. 2003; reviewed by Pederson 2003). Nucleoli also move to the extent that the chromosomes which contain the repeated rRNA genes are mobile. Diffusion, by definition, arises from the thermal energy inherent in the particle itself. However, the possibility that gene repositioning may be mediated by a process



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that uses metabolic energy has recently been the topic of initial studies (and debate). There is a growing body of evidence for actin and myosin in the nucleus, a field that has moved past its initial uncertainties and is now addressing functions (reviewed by Pederson and Aebi 2002; 2005; Pederson 2008). In particular, three recent studies have implicated actin-based processes in gene repositioning (Chuang et al. 2006; Dunder et al. 2007; Hu et al. 2008). This emerging concept is among the most deserving of vigilance in the nucleus field at this time.

THE NUCLEUS THAT AWAITS US

Speculation is always risky. One thing is clear—the question of how nuclear bodies arise in the first place (reviewed by Misteli 2001c) has taken on a new dimension because of the discovery that a Cajal body can assemble when key components are experimentally addressed to a specific nuclear site (Kaiser et al. 2008). Other recent studies raise the possibility that noncoding, nucleus-retained RNAs may play roles in nuclear architecture (Clemson et al. 2009; Sasaki et al. 2009; Sunwoo et al. 2009; reviewed by Wilusz et al. 2009). Also on the present horizon are stem cell issues that call for increasing input from experts on the nucleus. Stem cells have been hyped but it is early days and the nucleus cell biology community has much to offer, both by science and skepticism (for the latter perspective see Lander 2009). The essence of “stem-cellness” is an asymmetric descent of phenotypic potential vs. maintaining a continual seed of replenishment. So the two daughter cells have to be profoundly different but it is a difference we presently grasp very dimly. This is as deep a problem in cell biology as there is today, and there are already encouraging signs of progress (e.g., Parnell and Stillman 2008). Another field that is ripe for the intervention of nucleus experts is somatic nuclear transfer, in which it is the reaction of the introduced nucleus to the maternal environment, known to be dominant from classical studies, that sets in motion the reprogrammed developmental events. What are the molecules that underlie this powerful influence of the egg cytoplasm?

Finally, there can be no doubt that the increasing ability to study nuclear dynamics and function in living cells, now reaching single molecule level detection, constitutes one of the most powerful advances. The recent breaking of the classical diffraction limit of optical microscopy brings the nucleus into nanoscale range. The possible coaptation of these breakthrough approaches with instructive cell types and model systems stirs excitement for what lies ahead. The nucleus research community is living in very interesting times.

CODA

The assumption underlying this collection on nuclear structure and function is that the nucleus has reached a stage of enabling coherence as part of the epistemological structure of modern biological science. However, there are likely to be many things about the nucleus that we don't yet know and may not know anytime soon. We can only hope that what the geneticist J.B.S. Haldane posited on the cosmos will prove not to be true for the nucleus: “Now, my suspicion is that the universe is not only queerer than we suppose, but queerer than we *can* suppose.” If we appropriately bear in mind that the nucleus may be more complicated than we may have once thought, and yet just may be knowable, then this very belief may empower us and our students and successors to penetrate the subject's awaiting depths, the next of which now beckon. There is every reason to believe in this program. So let us be of good cheer.

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