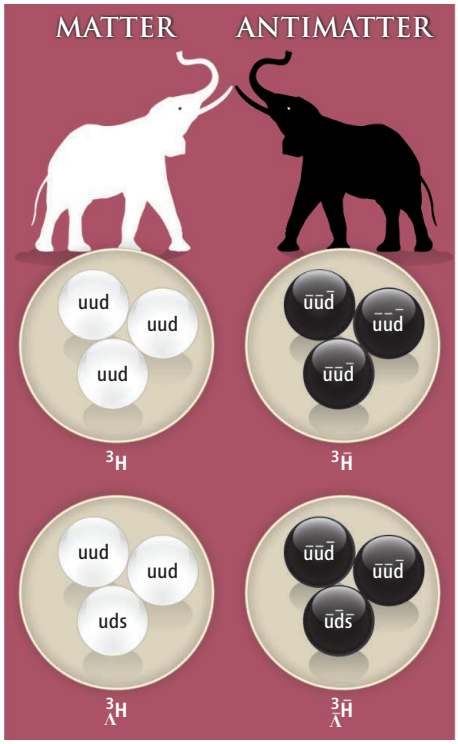

Strange quarks make nuclei hyper. In principle, all complex matter, even elephants (**top**), can exist in matter or antimatter forms. (**Middle**) Schematic representations of the tritium nucleus, or triton, depicts its up (u) and down (d) quark constituents (antimatter is indicated by a bar over a symbol). The white circles indicate the baryons (protons and neutrons) into which quarks are bound. (**Bottom**) The hypernuclear partner of the triton has one of the down quarks in a neutron replaced by a strange (s) quark to create a hyperon.

In the hypertriton, one of the ordinary down quarks in one of the neutrons is replaced with a strange quark. The particle that replaces the neutron is the hyperon.

This result is noteworthy because it is the first observation of any antinucleus with net strangeness (an antihypernucleus). Although not quite an antielephant, the antihypertriton is a complicated structure. To form it, nine antiquarks (four up, four down, and one strange), must come within a distance of a couple of femtometers (10^{-15} m) of each other without encountering ordinary quarks and annihilating.

The formation of antihypertritons requires extreme conditions that create numerous antiquarks in close proximity. Such conditions can be found in the ultrarelativistic heavy-ion collisions that are studied at RHIC. Two heavy nuclei, such as gold, are each accelerated to ultrarelativistic speeds—0.9995 times the speed of light. They then undergo a nearly head-on collision, and numerous collisions between the constituents of the nuclei occur on a very rapid time scale. These collisions create numerous interacting gluons, quarks, and antiquarks. Within a time of less than 10^{-23} s, the system is believed to achieve thermal equilibrium and forms a "fireball" at a temperature of a few times 10^{15} degrees Kelvin. Quarks and gluons are normally confined inside particles that feel the strong force, such as protons or pions, but at temperatures this high, they are thought to escape their confinement in a strongly interacting quark-gluon plasma (QGP) (*1*, *3*, *4*).

To a high level of accuracy, this QGP has an equal number of quarks and antiquarks; its temperature is high enough so that strange quarks, which are comparatively heavy and require much energy to produce, are abundant. This fireball expands and cools, ultimately to the point where quarks and gluons "hadronize" and are again confined into ordinary hadrons. The details of how this hot soup of quarks, antiquarks, and gluons form into ordinary hadrons is not completely understood. Most of the quarks and antiquarks combine to form mesons. A small fraction of the time, three quarks (or antiquarks) are sufficiently close together during hadronization to form baryons (protons, neutrons, or hyperons) or antibaryons.

The production rates of these various particles are used to infer both the properties of the QGP and the dynamics of how it expands, cools, and hadronizes (*1*, *3*). Statistically, it is much less likely that larger combinations of antiquarks form into antinuclei because this outcome requires correlations where numerous antiquarks are close enough to combine. However, the very large number of quarks in the QGP, and the large number of collisions produced at RHIC, means that even very unlikely final states, such as Λ antinuclei antihypernuclei, can form and be observed (*2*).

The discovery of the antihypertriton is significant for a number of reasons. First, it confirms our understanding that every physical system has an antimatter analog of the same mass in a new context, that of hypernuclei. The accuracy of the mass determination is far less precise than in many other antimatter systems, in part because of limited statistics and because antihypertriton is unstable and decays through weak interactions. Nevertheless, to within measurement uncertainties, hypertriton and antihypertriton have the same mass. Second, the result is noteworthy purely as a matter of technical virtuosity. In RHIC experiments, interesting physics must be pulled out of the extraordinarily complicated environments created in these collisions. The antihypertriton are a miniscule fraction of the total particles produced. The success in finding this needle in a haystack is remarkable. Finally, and perhaps most importantly, hypertriton and antihypertriton provide a new window for exploring the dynamics of ultrarelativistic heavy-ion collisions.

References

1. K. H. Ackermann *et al.*, *Nucl. Instrum. Methods A* **499**, 624 (2003).
2. The Star Collaboration, *Science* **328**, 58 (2010); published online 4 March 2010 (10.1126/science.1183980).
3. J. Adams *et al.*, *Nucl. Phys. A.* **757**, 102 (2005).
4. P. Braun-Munzinger, J. Stachel, *Nature* **448**, 302 (2007).

10.1126/science.1187769

MOLECULAR BIOLOGY

Mixing or Not Mixing

Dominique Ray-Gallet and Geneviève Almouzni

How are parental and newly synthesized histones distributed into nucleosomes during eukaryotic cell division?

Beyond DNA information, the organization of the proteins and DNA that constitute chromatin represents a means to regulate genome function (*1*). The inheritance and maintenance of the DNA sequence has been explained by a semiconservative mechanism of replication in which a complementary new strand of DNA is synthesized along each parental strand, resulting in an inherited double-stranded molecule that contains old and new DNA. But how is the inheritance of epigenetic traits—modifications of chromatin proteins (histones) and DNA that do not alter the sequence—affected by dynamic changes in chromatin organization during eukaryotic cell division? On page 94 of this issue, Xu *et al.* (*2*) explore how parental (old) and newly synthesized histones associate after replication.

The basic unit of chromatin, the nucleosome, has a core particle of eight histones—two pairs of histone H3-H4 as a tetramer flanked by two dimers of histone H2A-H2B. Histones can be present in distinct forms or variants, and they may harbor specific posttranslational modifications that can define a given epigenome (*1*, *3*). How do these particular markings sustain passage through

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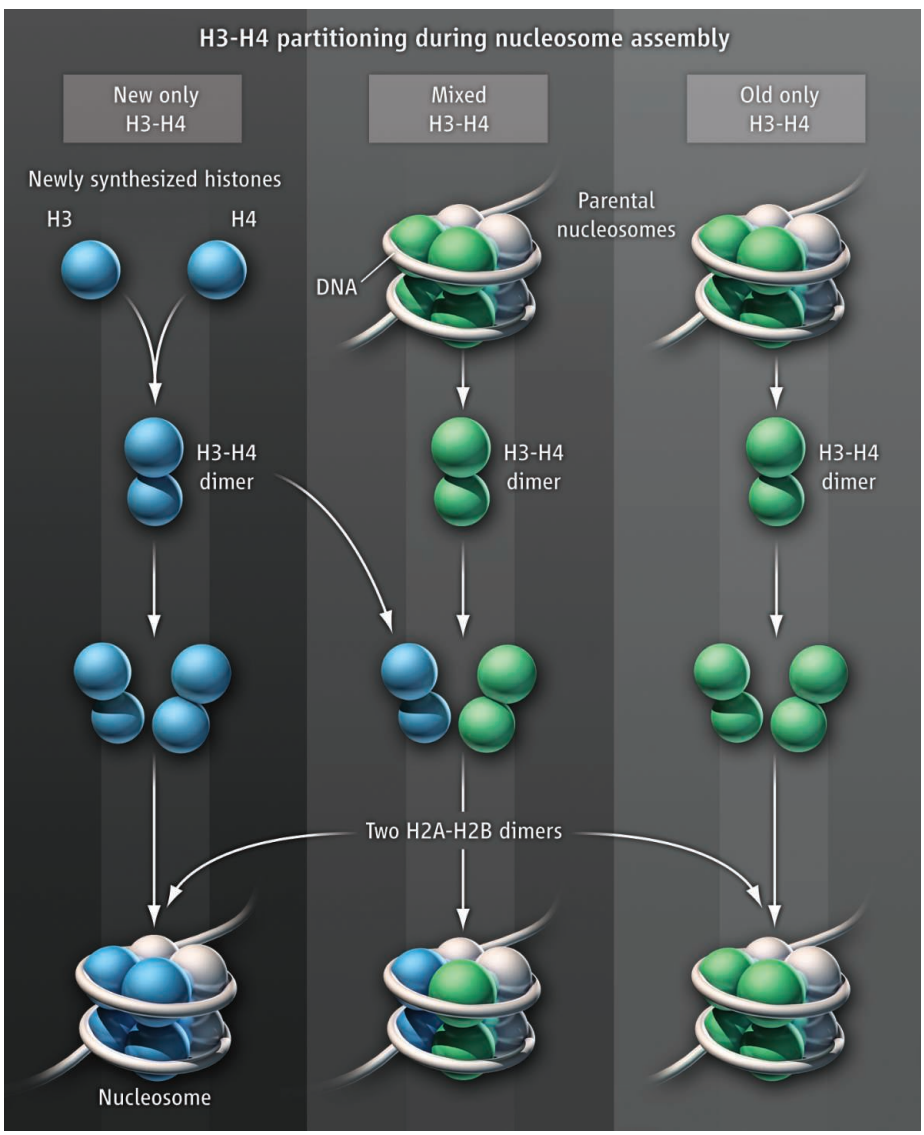
replication? An attractive hypothesis has been a semiconservative mechanism in which parental histones are combined with newly synthesized histones within the same core nucleosome. The presence of parental information as a template to reproduce the same marks on new histones provides a convenient means to ensure accurate reproduction of the initial marking at the same place. But can parental and new histones mix?

Histones H2A-H2B readily exchange as dimers, but H3-H4 tetramers are thought not to split (*4*). However, newly synthesized H3 and H4 can exist as dimers when associated with histone chaperones (*5*–*8*), spurring the debate.

Xu *et al*. use isotope labeling and mass spectrometry analysis of histone content to explore how new and old H3-H4 dimers associate after replication. Their model system is based on conditional expression in cultured human cells of tagged versions of distinct variants of histone H3: H3.1 and H3.3. H3.1 is a replicative histone variant, with a peak of expression in S phase of the cell division cycle, and is mostly incorporated into duplicated chromatin in a manner that is coupled to DNA replication (*3*). H3.3, known as a replacement variant, is expressed throughout all phases of the cell cycle and in quiescence, and can be incorporated into chromatin independently of DNA synthesis (*3*).



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Histone partitioning. New nucleosomes result from de novo assembly using newly synthesized H3 and H4 histones in the form of two H3-H4 dimers; after association with two H2A-H2B dimers, the result is a nucleosome containing only new H3-H4 dimers. Mixed particles will form using a newly synthesized H3-H4 dimer and an H3-H4 dimer recycled from a disrupted parental nucleosome. Old nucleosomes will form either by self-reassociation of two H3-H4 dimers recycled from a transiently disrupted parental nucleosome, or according to the generally accepted view, by inheritance of a stable H3-H4 tetramer from a parental nucleosome. [Adapted from (*10*) with permission from Cold Spring Harbor Laboratory Press]

Xu *et al*. did a genome-wide analysis of H3.1 incorporation into nucleosomes and observed no splitting of the H3.1-H4 tetramer, confirming earlier work on H3. Yet the H3.3-H4 tetramer did split. Both H3.1 and H3.3 variants were found in new and old nucleosomes and in mixed nucleosomes for H3.3. The authors considered the possibility that when selecting cells with H3.1 or H3.3 for analysis, they may have examined different populations of nucleosomes arising from distinct genomic regions. This is particularly critical for H3.3, which has been associated with actively transcribed regions. The question is whether splitting is region-specific or variant-specific. A previous analysis showed that in the vicinity of H3.3, H3.1 presented modifications similar to those found on H3.3 (*9*). In this case, what would the fate be of H3.1 nucleosomes that flank H3.3—would they split or not? It may be that H3.1 has a similar splitting feature when it is in the vicinity of H3.3.

Clearly, histone splitting is part of the histone inheritance picture during chromatin duplication, and three alternative modes for H3-H4 partitioning (*10*) can be considered as real (see the figure). The next challenge is to explore how these modes of distribution become articulated with the transmission of histone marks. The nonmixing options are compatible with proposed models in which histone marks are copied from neighboring histones, as observed with tightly packed heterochromatin regions (*1*, *10*–*12*). Yet, the possibility of an intranucleosome histone template for modifications may apply to particular genomic regions to ensure memory of critical active marks (*12*, *13*). Future work will investigate how the choice between histone splitting and nonsplitting is made within a cell and whether this is regulated during cellular life or during development.

References

1. C. D. Allis, T. Jenuwein, D. Reinberg, *Epigenetics* (Cold Spring Harbor Laboratory Press, New York, 2006).
2. M. Xu *et al*., *Science* **328**, 94 (2010).
3. K. Sarma, D. Reinberg, *Nat. Rev. Mol. Cell Biol.* **6**, 139 (2005).
4. A. T. Annunziato, *J. Biol. Chem.* **280**, 12065 (2005).
5. H. Tagami, D. Ray-Gallet, G. Almouzni, Y. Nakatani, *Cell* **116**, 51 (2004).
6. C. M. English, N. K. Maluf, B. Tripet, M. E. Churchill, J. S. Tyler, *Biochemistry* **44**, 13673 (2005).
7. L. J. Benson *et al*., *J. Biol. Chem.* **281**, 9287 (2006).
8. R. Natsume *et al*., *Nature* **446**, 338 (2007).
9. A. Loyola *et al*., G. Almouzni, *Mol. Cell* **24**, 309 (2006).
10. Y. Nakatani, D. Ray-Gallet, J. P. Quivy, H. Tagami, G. Almouzni, *Cold Spring Harb. Symp. Quant. Biol.* **69**, 273 (2004).
11. J. Nakayama *et al., Science* **292**, 110 (2001).
12. A. V. Probst, E. Dunleavy, G. Almouzni, *Nat. Rev. Mol. Cell Biol.* **10**, 192 (2009).
13. S. Henikoff, J. G. Henikoff, A. Sakai, G. B. Loeb, K. Ahmad, *Genome Res.* **19**, 460 (2008).

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