it represents the INO80 that the authors show is present constitutively at the *MAT* locus, in which the HO site resides. This leaves open the very intriguing question of what the function of recruited INO80 will turn out to be.

Tsukuda *et al.*[1] then examined the fate of DNA at the break site and found that histone eviction was critical for Rad51 loading, directly linking Mre11 complex–dependent INO80 chromatin remodeling to DNA repair. As expected, replication protein A (RPA) localized to resected DNA at the break site. The authors made the observation—surprising in light of the slower kinetics of histone eviction—that the kinetics of RPA recruitment were unaffected in *arp8*Δ mutants, suggesting that end resection does not require histone eviction. After RPA recruitment, Rad51, with the help of its mediator protein Rad52, displaces RPA and forms a filament on the single-stranded DNA tail[19]. In contrast to RPA, slower histone eviction in *arp8*Δ mutants strongly inhibited Rad51 loading at the break site, and the reduced Rad51 loading kinetics precisely followed those of histone eviction.

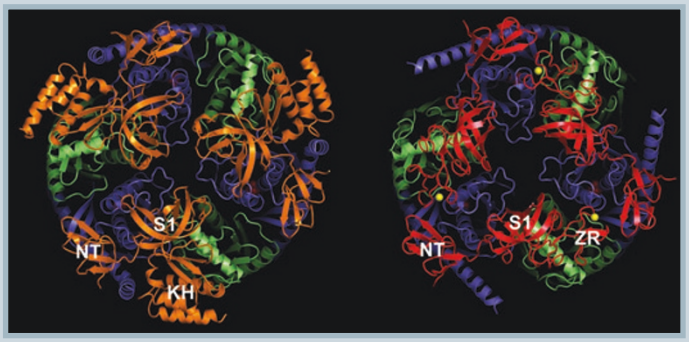
The implications of these results are summarized in a model proposed by Tsukuda *et al.*[1], in which the Mre11 complex influences nucleosome displacement via INO80 as well as via its effect on double strand–break end resection; this model is invoked to accommodate the observation that histone eviction is more severely impaired in *mre11*Δ than in *arp8*Δ. As their data clearly show that end resection and histone eviction are independent events, it seems equally likely that the Mre11 complex promotes the activity of additional remodeling components. In any case, the events described in this intriguing paper provide us with a much clearer view of the events required to achieve DNA repair in the complex architecture of chromatin.

1. Tsukuda, T., Fleming, A.B., Nickoloff, J.A. & Osley, M.A. *Nature* **438**, 479–483 (2005).
2. Redon, C. *et al. Curr. Opin. Genet. Dev.* **12**, 162–169 (2002).
3. Celeste, A. *et al. Nat. Cell Biol.* **5**, 675–679 (2003).
4. Paull, T.T. *et al. Curr. Biol.* **10**, 886–895 (2000).
5. Rogakou, E.P., Boon, C., Redon, C. & Bonner, W.M. *J. Cell Biol.* **146**, 905–915 (1999).
6. Shroff, R. *et al. Curr. Biol.* **14**, 1703–1711 (2004).
7. Huyen, Y. *et al. Nature* **432**, 406–411 (2004).
8. Shen, X., Mizuguchi, G., Hamiche, A. & Wu, C. *Nature* **406**, 541–544 (2000).
9. Bird, A.W. *et al. Nature* **419**, 411–415 (2002).
10. Downs, J.A. *et al. Mol. Cell* **16**, 979–990 (2004).
11. Morrison, A.J. *et al. Cell* **119**, 767–775 (2004).
12. Lee, S.E. *et al. Cell* **94**, 399–409 (1998).
13. Boeger, H. *et al. FEBS Lett.* **579**, 899–903 (2005).
14. Stracker, T.H., Theunissen, J.W., Morales, M. & Petrini, J.H. *DNA Repair (Amst.)* **3**, 845–854 (2004).
15. Usui, T., Ogawa, H. & Petrini, J.H. *Mol. Cell* **7**, 1255–1266 (2001).
16. D'Amours, D. & Jackson, S.P. *Genes Dev.* **15**, 2238–2249 (2001).
17. Grenon, M., Gilbert, C. & Lowndes, N.F. *Nat. Cell Biol.* **3**, 844–847 (2001).
18. Wiltzius, J.J., Hohl, M., Fleming, J.C. & Petrini, J.H. *Nat. Struct. Mol. Biol.* **12**, 403–407 (2005).
19. Krogh, B.O. & Symington, L.S. *Annu. Rev. Genet.* **38**, 233–271 (2004).

© 2005 Nature Publishing Group http://www.nature.com/nsmb

Threaded for degradation

RNAs are subject to degradation, whether for quality control, maturation or turnover. The primary bacterial exoribonuclease is PNPase. This protein contains two catalytic RNase pleckstrin-homology (PH) domains and two RNA-binding domains (S1 and KH); it assembles as a trimer. In eukaryotes and archaea, a major RNA-processing complex is the exosome, a multisubunit assembly that degrades messenger, ribosomal and noncoding RNAs from the 3′ end. Like PNPase, the exosome is composed of RNase PH-domain proteins (although in six separate subunits) and three additional S1-containing RNA-binding subunits. Exosome activity is regulated on several levels because it processes RNAs with different secondary structures, can degrade RNAs partially or completely and uses various stimulatory accessory factors.



Reprinted with permission from *Mol. Cell* **20**, 461–471 (2005).

Two recent studies have provided new insight into archaeal exosome structure and mechanism. Büttner *et al.* (*Mol. Cell* **20**, 461–471, 2005) solved the structure of two nine-subunit *Archaeoglobus fulgidus* exosome isoforms, and Lorentzen *et al.* (*Mol. Cell* **20**, 473–481, 2005) solved the structures of the hexameric *Sulfolobus solfataricus* exosome-processing domain bound to either RNA or ADP.

In the *A. fulgidus* exosome, the RNase PH–like subunits, Rrp41 and Rrp42, form a trimer of dimers (green and blue ribbons) and constitute the hexameric RNA-processing center. The other subunits, either Csl4 or Rrp4, constitute a homotrimeric cap (orange or red ribbons) that sits on one face of the hexameric ring. Both Csl4 and Rrp4 contain an S1 domain between their N- and C-terminal domains. In both isoforms, the S1 domains are positioned in the cap's interior and are involved in restricting access through a pore to the processing core of the hexamer. The caps have a positive surface charge, and the S1 domain is even more strongly positively charged, suggesting that the RNA is attracted to the cap and then directed toward the pore by S1-domain interactions. Each cap subunit interacts with both Rrp41 and Rrp42, although the specific interactions differ between Csl4 and Rrp4. Modeling with different stoichiometries of Csl4 and Rrp4 cap subunits, which are thought to occur in eukaryotic caps, shows that this might be possible structurally without steric clash.

The hexameric ring has a narrow pore where it contacts the cap, which leads to a wider channel that constricts again as an exit pore. Lorentzen *et al.* show that RNA binds in this cleft and that the four 3′-terminal nucleotides interact with arginines of Rrp41 and Rrp42 in an electrostatic, non–sequence-specific manner. The Rrp41 subunits contain the sites of phosphorolysis, in a pocket located between Rrp41 and Rrp42. Cleavage of the terminal nucleotide seems to cause little conformational change, and a short sliding movement may be sufficient to reposition the newly formed 3′ end at the active site.

The overall structure of the exosome suggests that RNA processing may have similarity to proteasome-mediated protein degradation. In this case, RNA enters through a lid-like structure having a pore that can accommodate only unstructured RNA; this pore regulates passage of the RNA into the cavity formed by the hexameric ring where processing occurs.

Angela K Eggleston