

Cohesin jigsaw begins to fit

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The essential chromosomal protein complex cohesin has crucial roles in sister chromatid cohesion, DNA repair and transcriptional regulation. Despite its conserved function, cohesin's disparate association patterns in different organisms did not quite add up. New research published in the open access journal *Genome Biology* works towards completing the cohesin puzzle, reconciling some of these differences.

Christine Schmidt, Neil Brookes and Frank Uhlmann working together at the Cancer Research UK London Research Institute, performed high-resolution analysis of cohesin binding patterns along fission yeast chromosomes.

The authors' findings suggest that features thought to differentiate cohesin between organisms actually collectively define the overall behaviour of fission yeast cohesin. In fact cohesin's mechanisms of action might be much more similar between organisms than previously thought.

Earlier studies investigated cohesin's chromosomal binding sites in different model organisms, including *Drosophila* and budding yeast. Despite its conserved function in DNA repair and mitosis, no common rule had emerged that defined these sites.

"Our findings suggest that features that were thought to differentiate cohesin behaviour between organisms collectively define the overall behaviour of fission yeast cohesin", writes Uhlmann. "Apparent differences between organisms could reflect an emphasis on different

aspects, rather than different principles, of cohesin behaviour."

Cohesin complexes have a central role in cell division, mediating the association between sister chromosomes. Cohesin forms large proteinaceous rings, and is thought to bind to and holds sister chromatids together in a topological embrace.

More information: Conserved features of cohesin binding along fission yeast chromosomes, Christine K Schmidt, Neil Brookes and Frank Uhlmann, *Genome Biology* (in press), genomebiology.com/

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