HIGH-LIGHTS

URLs
CAP-C
http://us.expasy.org/cgi-bin/niceprot.pl?Q9NTJ3
CAP-D2
http://us.expasy.org/cgi-bin/niceprot.pl?Q15021
CAP-E
http://us.expasy.org/cgi-bin/niceprot.pl?O95347
CAP-G
http://us.expasy.org/cgi-bin/niceprot.pl?Q9BPX3
CAP-H
http://us.expasy.org/cgi-bin/niceprot.pl?Q15003
URL
SC-35
http://us.expasy.org/cgi-bin/niceprot.pl?Q01130

CHROMOSOME STRUCTURE

An architectural double act

Mitotic chromosome assembly, or condensation, is an essential part of the cell cycle, and the canonical condensin complex (condensin I) is known to have enzymatic and structural roles in this process. But how these functions are coordinated to establish and maintain mitotic chromosome structure remains unknown.

Now, in *Cell*, Tatsuya Hirano and colleagues report the identification of a second condensin complex, condensin II. Like condensin I, condensin II consists of five subunits — two from the structural maintenance of chromosomes (SMC) family and three non-SMC subunits. However, whereas the two SMC subunits (CAP-C and CAP-E) are identical in both complexes, the non-SMC subunits are different — CAP-D2, CAP-G and CAP-H versus CAP-D3, CAP-G2 and CAP-H2 in condensins I and II, respectively.

Hirano and colleagues used small interfering (si)RNA-mediated depletion to study the *in vivo* function of the SMC subunits in HeLa cells. Although cell-cycle progression wasn't blocked by depletion of either SMC protein, metaphase chromosomes no longer appeared rod-shaped but 'fuzzy' and 'cloud-like'. In addition, the severity of the morphological defect correlated with the amount of SMC proteins that was left on the chromosomes.

Next, the authors depleted non-SMC subunits CAP-G and CAP-G2, which are unique to condensin I and condensin II, respectively. Again, cell-cycle progression was unaffected and morphological defects were apparent, but the defect seen was distinct and specific to the subunit depleted. Depleting both non-SMC subunits resulted in a defect like that seen after the SMC depletions. From this the authors conclude that the roles of the two complexes are non-redundant, and they back this up with evidence from immunofluorescent staining.

Hirano and co-workers then used immunodepletion to study the complexes *in vitro* in *Xenopus* egg extracts. Condensins I and II are present in a ratio of ~5:1 (in HeLa cells it's almost equal). Consistent with this, sperm chromatin incubated with condensin-I-depleted extract was decondensed and no chromosomes formed. And with condensin-II-depleted extract individual chromosomes did form, although they had an abnormal morphology. Immunoblotting of chromatin fractions confirmed that the two complexes were loaded onto chromosomes independently. Double-immunofluorescent staining showed the spiral-like distribution of condensin I and the "…distinct, somewhat irregular, and less continuous…" distribution of condensin II. It also revealed that condensin II was located more internally with respect to condensin I in the chromosome axis.

So, the distribution of the two complexes is comparable *in vitro* and *in vivo*, but what does all this mean? The authors suggest that non-SMC subunits regulate the spatial and temporal distribution of the two complexes, and that, together, condensins I and II faciliate condensation and help shape metaphase chromatids — variable ratios of the two could determine shape and properties in different organisms. They propose two models for condensin-based chromosome architecture, and in both "…condensin I would act as the primary organizer of chromatin fibers, whereas condensin II would play an additional, architectural role in determining the final shape of chromosomes". Hirano's group also look to the possibility that multiple condensins participate in meoitic chromosome dynamics.

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References and links

ORIGINAL RESEARCH PAPER Ono, T. *et al.* Differential contributions of condensin I and condensin II to mitotic chromosome architecture in vertebrate cells. *Cell* **115**, 109–121 (2003)

WEB SITE

Tatsuya Hirano's laboratory:
http://www.cshl.org/public/SCIENCE/hirano.html