Abstract

Cohesin is a multisubunit protein complex that plays an integral role in sister chromatid cohesion, DNA repair, and meiosis. Of significance, both over- and underexpression of cohesin are associated with cancer. It is generally believed that cohesin dysregulation contributes to cancer by leading to aneuploidy or chromosome instability. For cancers with loss of cohesin function, this idea seems plausible. However, overexpression of cohesin in cancer appears to be more significant for prognosis than its loss. Increased levels of cohesin subunits correlate with poor prognosis and resistance to drug, hormone, and radiation therapies. However, if there is sufficient cohesin for sister chromatid cohesion, overexpression of cohesin subunits should not obligatorily lead to aneuploidy. This raises the possibility that excess cohesin promotes cancer by alternative mechanisms. Over the last decade, it has emerged that cohesin regulates gene transcription. Recent studies have shown that gene regulation by cohesin contributes to stem cell pluripotency and cell differentiation. Of importance, cohesin positively regulates the transcription of genes known to be dysregulated in cancer, such as Runx1, Runx3, and Myc. Furthermore, cohesin binds with estrogen receptor α throughout the genome in breast cancer cells, suggesting that it may be involved in the transcription of estrogen-responsive genes. Here, we will review evidence supporting the idea that the gene regulation function of cohesin represents a previously unrecognized mechanism for the development of cancer. Mol Cancer Res; 9(12); 1587–607. ©2011 AACR.

Introduction

Cohesin is a multisubunit complex that serves essential functions in chromosome biology, including mediating sister chromatid cohesion in meiosis and mitosis, and DNA double-strand break repair. Its importance in these roles indicates that disruption of normal cohesin function could contribute to aneuploidy and genome instability, features that are frequently associated with cancer (1, 2). Indeed, mutations in cohesin subunits, as well as cohesin over- and underexpression, have been associated with tumorigenesis (reviewed in refs. 3 and 4). However, in addition to its roles in the cell cycle and DNA repair, cohesin has a crucial function in transcriptional regulation. Control of transcription by cohesin is independent of the cell cycle and is thought to be key to the pathology of developmental syndromes (i.e., cohesinopathies) that result from insufficiency of proteins in the chromosome cohesion pathway. Over the past year, it has emerged that cohesin regulates genes that are crucial for cell proliferation and maintenance of pluripotency. This raises the possibility that the gene regulation function of cohesin could be just as central to neoplasia as are its cell-cycle and DNA repair roles. In this review, we highlight the potential for cohesin to contribute to cancer via its transcriptional role. In particular, we discuss cohesin’s ability to positively regulate oncogenes and genes that maintain pluripotency, as well as its participation in hormone-dependent pathways underlying cancer.

Cohesin: A Protein Complex That Is Crucial for Cell Division and DNA Repair

Cohesin is best known for its essential role in holding together sister chromatids from DNA replication in S-phase until chromosome separation occurs in anaphase (5, 6). The cohesin complex consists of 4 main protein subunits: structural maintenance of chromosomes (SMC) subunits Smc1 and Smc3, and 2 non-SMC subunits, Mcd1/Sccl/Rad21 and Scc3/Stromalin (SA; see Table 1 for cohesin subunit nomenclature). These proteins form a large ring-like structure, large enough to encircle DNA (5). In the leading model for sister chromatid cohesion, cohesin topologically entraps sister chromatids (7); however, alternative models have been proposed to explain how cohesin physically holds 2 molecules of DNA together (8, 9).

Several other proteins regulate the loading and unloading of cohesin onto DNA, its DNA binding stability, and its turnover and recycling (Table 1; reviewed in ref. 10).
Loading of cohesin onto chromosomes takes place in telophase in most organisms and is facilitated by a protein complex containing Scc2 (Nipped-B in *Drosophila* and NIPBL in human) and Scc4/MAU-2. Once loaded, cohesin exhibits highly variable residence times on chromosomes, indicating that it binds DNA with different modes of stability (11, 12). It is thought that the more stably bound fraction of cohesin has functions in addition to chromosome cohesion, including regulation of gene expression (11). During S-phase, stably bound cohesin becomes cohesive by interaction with the DNA replication machinery (13–15), in association with the acetyltransferase Ctf7/Eco1 (yeast), or Esco1/2 (vertebrates; refs. 15–17). Esco1/2 acetylates cohesin subunit Smc3 to generate the cohesive form of cohesin that is necessary to hold together the sister chromatids through G2–M-phase (18–20). However, in humans, it appears thatESCO2 is primarily required for cohesion in heterochromatic regions, and patients with Roberts syndrome who lackESCO2 exhibit heterochromatin repulsion without chromosome segregation defects (21). In human cells (but not yeast), the sororin protein is additionally required to establish and maintain cohesion (22, 23).

After DNA replication is complete and before mitosis occurs, most cohesin is removed from chromosome arms by the prophase pathway. This process involves phosphorylation of cohesin subunit SA2 by Polo-like kinase (Plk) and Aurora B (24, 25) and interaction of a cohesion disestablishment complex containing Pds5 and Wapl with SA to unlock the cohesin ring (26–28). In the competing establishment activity, sororin and Esco2 function to antagonize the activity of the Pds5/Wapl complex (29–32), and the phosphatase Ssu72 appears to promote cohesion by countering the phosphorylation of SA2 (24, 33). During chromosome condensation, the prophase pathway prevails, and by metaphase, most cohesin has been removed from chromosome arms. The remaining, primarily centromeric cohesin, protected from removal by Shugoshin (34), is all that remains to hold the sisters together. Shugoshin binds to protein phosphatase 2A (PP2A), and this interaction is necessary for location of Shugoshin to centromeres in yeast and human cells (35, 36). Because depletion of Plk restores localization of Shugoshin to centromeres in PP2A-depleted cells (35), it is likely that the Shugoshin–PP2A complex protects sister chromatid cohesin by countering phosphorylation of cohesin by Plk.

At anaphase, APC-mediated degradation of a protein called securin (37) releases the protease separase, which becomes available to cleave the Rad21 subunit of cohesin (38–40). The remaining cohesin rings are opened, allowing chromosomes to separate (41). At the next cell cycle, the Smc3 subunit of cohesin can be recycled onto chromosomes, but deacetylation of Smc3 by class I histone deacetylase (HDAC) Hos1 (yeast) is required before this can happen (42–44). Figure 1 provides a simplified overview of cohesin function in the cell cycle.

Sister chromatid cohesion is necessary for homologous recombination-mediated DNA double-strand break repair in yeast and vertebrate cells (reviewed in ref. 45). For double-strand breaks to be effectively repaired, the cohesive form of cohesin must be established at the location of the break (46). Stabilization of cohesin at double-strand breaks depends on acetylation of the Rad21 subunit by Esco2, plus antagonism of the disassociation complex containing Wapl (47). Cohesin is recruited de novo at double-strand breaks in G2–M phase.

### Table 1. Nomenclature and function of cohesin subunits

<table>
<thead>
<tr>
<th>Generic name</th>
<th>Saccharomyces cerevisiae</th>
<th>Schizosaccharomyces pombe</th>
<th>Drosophila melanogaster</th>
<th>Homo sapiens</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>Smc1</td>
<td>SMC1</td>
<td>psm1</td>
<td>SMC1</td>
<td>SMC1A</td>
<td>Core cohesin subunit</td>
</tr>
<tr>
<td>Smc1β</td>
<td>SMC1B</td>
<td></td>
<td></td>
<td>SMC1B</td>
<td>Cohesin subunit (meiosis)</td>
</tr>
<tr>
<td>Smc3</td>
<td>SMC3</td>
<td>psm3</td>
<td>Cap</td>
<td>SMC3/CSGP6/ Bamacan</td>
<td>Core cohesin subunit</td>
</tr>
<tr>
<td>Rad21</td>
<td>rad21</td>
<td></td>
<td>Rad21</td>
<td>Rad21</td>
<td>Core cohesin subunit</td>
</tr>
<tr>
<td>Rec8</td>
<td>rec8</td>
<td></td>
<td>c(2)M</td>
<td>Rec8</td>
<td>Cohesin subunit (meiosis)</td>
</tr>
<tr>
<td>SA-1</td>
<td>psc3</td>
<td></td>
<td>SA</td>
<td>STAG1</td>
<td>Cohesin subunit</td>
</tr>
<tr>
<td>SA-2</td>
<td>psc3</td>
<td></td>
<td>SA2/Stromalin</td>
<td>STAG2/Stromalin</td>
<td>Cohesin subunit</td>
</tr>
<tr>
<td>SA-3</td>
<td>rec11</td>
<td></td>
<td>—</td>
<td>STAG3</td>
<td>Cohesin subunit (meiosis)</td>
</tr>
<tr>
<td>Nipbl</td>
<td>mis4</td>
<td></td>
<td>Nipped-B</td>
<td>NIPBL</td>
<td>Cohesin loading</td>
</tr>
<tr>
<td>Scc4 (or MAU-2, <em>Caenorhabditis elegans</em>)</td>
<td>ssc3</td>
<td></td>
<td>SCC4</td>
<td>SCC4</td>
<td>Cohesin loading</td>
</tr>
<tr>
<td>Esco1/2</td>
<td>eco1</td>
<td></td>
<td>deco</td>
<td>ESCO1/2</td>
<td>Acetyltransferases, establishment of cohesion</td>
</tr>
<tr>
<td>Pds5A</td>
<td>pds5</td>
<td></td>
<td>pds5</td>
<td>PDS5a</td>
<td>Cohesin dissociation</td>
</tr>
<tr>
<td>Pds5B</td>
<td>wap1</td>
<td></td>
<td>wap1</td>
<td>WAPAL</td>
<td>Cohesin dissociation</td>
</tr>
<tr>
<td>Wapl</td>
<td>RAD61/WPL1</td>
<td></td>
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</tbody>
</table>
(48), and in vertebrates, this association also involves another SMC complex, Smc5/6 (49, 50). Other molecular events contribute to cohesin function in double-strand break repair. In budding yeast, it was shown that the phosphorylation of Mcd1 (Rad21) through the ATR and Chk1 pathway is important for cohesion and double-strand break repair (51). In human cells, cohesive cohesin at double-strand breaks also depends on the pro-establishment activity of Sororin (23).

Mutations in sister chromatid cohesion proteins lead to chromosome segregation defects and impaired repair of DNA double-strand breaks. Chromosome instability (CIN) can result from the mis-segregation of chromosomes or defective repair of DNA double-strand breaks. The consequences of CIN are chromosomal rearrangements and aneuploidy, which can lead to loss of heterozygosity at tumor suppressor genes, causing neoplasia. Although many tumors are aneuploid, debate remains as to whether CIN drives the formation of tumors or is a consequence of their rapid proliferation (reviewed in ref. 1). Mathematical models have shown that it is theoretically possible for CIN to arise before other cancer-causing mutations and to form the initial driving cancer mutation (2, 52). In support of a driver hypothesis, more than 20% of colorectal cancers have mutations in the chromosome cohesion pathway (53). Somatic mutations in SMC1, SMC3, STAG3, and NIPBL were found in colorectal tumors at a statistically higher rate than in normal cells (53). However, for cells carrying chromosome cohesion defects to be viable, the spindle assembly checkpoint (SAC) would somehow need to be bypassed. The function of the SAC is to sense correct bipolar attachment of spindle fibers to kinetochores, together with the presence of tension across the kinetochores (54). Normally, sister chromatid cohesion defects lead to SAC activation and subsequent apoptosis; thus, additional mutations compromising SAC function are likely to be necessary if such cells are to survive and proliferate. Arguing against the idea that aneuploidy is an initial driver of tumorigenesis, studies in several organisms have shown that aneuploidy on its own has multiple harmful effects on growth and development (reviewed in ref. 55). In yeast (56) and mammalian cells (57), artificial generation of aneuploidy for single chromosomes was detrimental to cell proliferation and placed additional metabolic stress on cells. The disadvantages of aneuploidy are manifest in human tumor cells and may provide an opportunity for tumor therapy (58). In particular types of cancer, cohesin proteins are overexpressed rather than underexpressed or mutated (Table 2), making it more difficult to explain mechanistically how CIN and aneuploidy could result. It is possible that overexpression of a particular cohesin subunit could lead to sequestration of other subunits and decrease the amount of cohesin available for sister chromatid cohesion. However, because only a small proportion of cohesin actually represents the cohesive pool (12), stoichiometry would have to be severely disrupted before effects on sister chromatid cohesion become apparent.

**Cohesin Regulates Tissue-Specific Gene Transcription**

Over the last decade, a new role for cohesin in the regulation of gene expression has emerged. The first evidence for this role came from a forward genetic screen in *Drosophila* that identified the Scc2 ortholog Nipped-B as a modulator of enhancer–promoter interactions at the cut and Ubx genes (59). Depletion of cohesin subunits also affected expression of the cut gene but in the opposite direction from Nipped-B (60, 61). The best explanation so far for these divergent effects are that small changes in the dose of cohesin and Nipped-B can have variable or biphasic effects on gene expression, leading to opposite effects on transcription...
Table 2. Evidence for cohesin’s involvement in cancer

<table>
<thead>
<tr>
<th>Cancer</th>
<th>Cohesin subunit involved (context of study)</th>
<th>Description of study</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Breast cancer</td>
<td>† RAD21 mRNA expression (cell lines)</td>
<td>Quantitative gene expression analysis revealed that RAD21 mRNA expression is lower in normal and immortalized breast cancer cell lines compared with 9/11 tumorigenic breast cancer lines. siRNA knockdown of RAD21 effectively inhibited proliferation of MCF-7 and T-47D cell lines. RAD21 knockdown in MCF-7 cell line renders cells more sensitive to the DNA-damaging chemotherapeutic agents etoposide and bleomycin.</td>
<td>149</td>
</tr>
<tr>
<td>Breast cancer</td>
<td>† RAD21 mRNA expression (primary tumors)</td>
<td>cDNA microarray analysis of primary breast tumors from patients without tumor cells in local lymph nodes at diagnosis (lymph node–negative) identified a gene expression signature strongly predictive of a short interval to distant metastases (poor-prognosis signature). RAD21 was found to be significantly upregulated in the poor-prognosis signature.</td>
<td>95</td>
</tr>
<tr>
<td>Breast cancer</td>
<td>† RAD21 mRNA expression (primary tumors)</td>
<td>cDNA microarrays were profiled to identify functional pathways that determine the outcome of breast cancer patients with supraclavicular lymph node metastases. Thirty-one breast cancer patients with supraclavicular lymph node metastasis without distant metastases were divided into poor, intermediate, or good-prognosis groups. Wnt signaling and mitochondrial apoptosis pathways emerged, with 6 genes (DVL1, VDAC2, BIRC5, Stathmin1, PARP1, and RAD21) found to be overexpressed in the poor-prognosis group compared with the good-prognosis group.</td>
<td>96</td>
</tr>
<tr>
<td>Breast cancer</td>
<td>† RAD21 mRNA expression in response to BRCA1 overexpression (cell lines)</td>
<td>Suppression subtractive hybridization was used to compare the expression profiles of control MCF7 cells with MCF7 cells ectopically expressing BRCA1, to identify genes whose expression is regulated by BRCA1. RAD21 is upregulated following overexpression of BRCA1.</td>
<td>153</td>
</tr>
<tr>
<td>Breast cancer</td>
<td>† RAD21 protein and mRNA expression and RAD21 gene amplification (primary tumors)</td>
<td>Immunohistochemistry was used to evaluate RAD21 expression in a cohort of in situ and invasive breast cancers. RAD21 levels were significantly lower in invasive cancers compared with in situ cancers. Levels of RAD21 correlated with larger tumor size and lymph node involvement but not with tumor grade, HER2 status, or ER status. Positive RAD21 protein expression was seen in 37% luminal, 24% basal, 22% HER2, and 18% null cancers, and significantly correlated with shorter relapse-free survival. RAD21 expression correlated with relapse in grade 3 but not in grade 1 or 2 tumors. Further analysis of grade 3 tumors according to subtype showed a significant correlation between RAD21 expression and shorter relapse-free survival in the luminal, basal, and HER2 cancers but not the null-type cancers.</td>
<td>97</td>
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<table>
<thead>
<tr>
<th>Cancer</th>
<th>Cohesin subunit involved (context of study)</th>
<th>Description of study</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>In patients not treated with chemotherapy, there was no correlation between RAD21 expression and overall survival, whereas in patients treated with chemotherapy, there was a significantly shorter overall survival in patients whose tumors were RAD21-positive. Array comparative genomic hybridization and transcription data from 48 grade 3 invasive ductal carcinomas of luminal, basal-like, and HER2 subtypes were integrated to examine the association of RAD21 mRNA expression with RAD21 copy number. RAD21 mRNA expression correlated with gene copy number in luminal, basal, and HER2 tumors, suggesting that the positive RAD21 expression observed in a subset of grade 3 tumors may be due to gene amplification. shRNA-mediated gene silencing of RAD21 in the MDA-MB-231 basal-like breast cancer cell line rendered the cells more sensitive to the chemotherapy drugs cyclophosphamide and 5-fluorouracil in a manner that directly correlated with the level of RAD21 expression.</td>
<td>154</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Prostate cancer</td>
<td>t RAD21 mRNA expression and RAD21 gene amplification (cell lines and primary tumors)</td>
<td>Sought to identify genes that are overexpressed, especially from gene amplification, in prostate cancer. Quantitative RT-PCR revealed that RAD21 expression was increased in the PC-3 prostate cancer cell line. In tumors, RAD21 was 1 of 7 genes that were overexpressed, mainly in samples found to contain amplification in the chromosomal regions harboring the genes. Expression of these 7 genes was examined by quantitative RT-PCR in cases of benign prostate hyperplasia, untreated prostate carcinoma, and hormone-refractory prostate carcinoma. RAD21 expression was significantly higher in carcinomas than in benign prostate hyperplasia. FISH results showed that RAD21 was amplified in PC-3 cells. Furthermore, in a screen of 10 xenografts and 12 hormone-refractory prostate carcinomas, RAD21 showed high-level amplification in 32% of samples.</td>
<td></td>
</tr>
<tr>
<td>Oral squamous cell carcinoma</td>
<td>( \downarrow ) RAD21 expression in invasive growth pattern vs expansive growth pattern (primary tumors)</td>
<td>Investigated the relevance of RAD21 in invasion and metastases of squamous cell carcinoma. Laser microdissection and quantitative PCR revealed that RAD21 expression was significantly decreased in areas of INF-( \gamma ) invasion (associated with poorer prognosis) compared with areas that showed INF-( \alpha ) invasion.</td>
<td>98</td>
</tr>
</tbody>
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(Continued on the following page)
according to the severity of consequences for dose reduction (the consequences of halving the gene dose is more severe for Nipped-B than for cohesin subunits; refs. 62 and 63). Evidence that cohesin also has a gene regulatory role in vertebrates initially came from work showing that expression of the runx1 and runx3 genes was abolished in a tissue-specific manner in early zebrafish embryos mutant for cohesin subunit rad21 (64).

Shortly after the findings in Drosophila emerged, mutations in genes encoding the NIPBL (human Scc2 ortholog),

<table>
<thead>
<tr>
<th>Cancer</th>
<th>Cohesin subunit involved (context of study)</th>
<th>Description of study</th>
<th>Reference</th>
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</thead>
<tbody>
<tr>
<td>Colorectal cancer</td>
<td>Mutations in several subunits (primary tumors)</td>
<td>Systematically identified somatic mutations in potential CIN genes in colorectal cancers by determining the sequence of 102 human homologs of 96 yeast CIN genes known to function in various aspects of chromosome transmission fidelity. In a panel of 132 colorectal cancers, 11 somatic mutations, distributed among 5 genes, were identified. Ten of these mutations were found in the genes encoding the cohesin subunits SMC1L1, NIPBL, CSPG6, and STAG3. RNAi was used to reduce SMC1L1 and CSPG6 protein levels, and resulted in CIN and chromatid cohesion defects in human cells.</td>
<td>53</td>
</tr>
<tr>
<td>Colon carcinoma</td>
<td>↑ SMC3 mRNA (cell lines and primary tumors)</td>
<td>SMC3 expression was increased in mouse colorectal carcinoma cells compared with a primary colon cell line. Similarly, SMC3 expression was increased in colon carcinoma tissue compared with normal colon tissue, and 5 independent human colon carcinoma cell lines displayed the same degree of SMC3 overexpression as the colon carcinoma sample. 70% of human colon carcinoma tissue samples (n = 19) displayed a significant increase in SMC3 mRNA levels compared with matched normal colon tissue samples.</td>
<td>155</td>
</tr>
<tr>
<td>Myeloid leukemia</td>
<td>RAD21 and STAG2 gene deletions (leukemia cells)</td>
<td>To identify potential new genes involved in myeloid diseases, array comparative genomic hybridization was performed on 167 samples, including myelodysplastic syndrome, chronic myelomonocytic leukemia, and acute myeloid leukemia. In a case of chronic myelomonocytic leukemia diagnosed in 2007, a small heterozygous deletion at 8q24 was revealed. This region includes the RAD21 gene. This chronic myelomonocytic leukemia transformed to M5 FAB acute myeloid leukemia in 2008, and array comparative genomic hybridization again revealed the RAD21 loss but no other additional alteration. The patient died 6 months after transformation. In a case of M6 FAB acute myeloid leukemia diagnosed in 2005, a small deletion centered on the STAG2 gene was identified. The patient died in 2007, 5 months after relapse. In both cases, the karyotype did not show any abnormality, and no other array comparative genomic hybridization alterations were noticed.</td>
<td>156</td>
</tr>
</tbody>
</table>
SMC1A, and SMC3 cohesin proteins were found to cause Cornelia de Lange syndrome (CdLS), a developmental disorder characterized by mental retardation, upper-limb abnormalities, growth delay, and facial dysmorphisms (65–68). Of interest, affected individuals were shown to have altered gene expression and developmental effects without overt defects in chromosome segregation, suggesting that the pathology of CdLS is independent of cohesin’s role in sister chromatid cohesion (69). Animal models of CdLS also support the idea that the pathology is due to altered expression of numerous developmental genes (70, 71). An emergent, diverse spectrum of human developmental disorders resulting from mutations in various proteins responsible for sister chromatid cohesion led to coining of the term “cohesinopathies” to refer to such disorders (72).

The strongest support for a cell-cycle–independent role for cohesin in gene regulation arose from studies that examined cohesin expression and function in postmitotic tissues, where cells no longer require cohesin for proliferation. Cohesin can be expressed in postmitotic cells in a tissue-specific manner; for example, cohesin genes are expressed in nonproliferating cells in the developing zebrafish brain (73). In Drosophila, a function for cohesin was identified in the pruning of postmitotic neurons. An insertional mutagenesis screen identified the cohesin subunit Smc1 as being essential for pruning γ neurons in mushroom bodies (74). In an elegant strategy for cohesin ablation, the placement of a TEV-cleavage site into cohesin subunit Rad21 enabled artificial cleavage of cohesin to remove its function in postmitotic neurons of the Drosophila mushroom body. TEV-mediated cohesin cleavage abolished the developmentally controlled pruning of both axons and dendrites of γ neurons (75). Ablation of cohesin function in Drosophila salivary glands by the same technique confirmed that cohesin directly regulates the expression of a distinct set of genes, including the edysone receptor (Ecr) and other genes that mediate the edysone response (76). The responsiveness of gene expression to cohesin depletion was sufficiently rapid to suggest that cohesin acts directly on genes to control their transcription.

Mechanisms of Gene Regulation by Cohesin

The notion that cohesin is a regulator of gene expression in metazoans is supported by evidence that cohesin and NIPBL bind to transcriptionally active regions of the genome in Drosophila (77) and mammals (78, 79). Genome-wide analyses of cohesin binding were among the first to shed light on potential mechanisms for cohesin-dependent transcription. In 2008, several studies revealed that much of cohesin colocalizes genome-wide with the CCCTC-binding factor (CTCF) insulator protein (78–81). CTCF has been well studied, and a recent comprehensive analysis of its role in three-dimensional chromatin organization showed that it is an integral organizer of chromosome conformation in the nucleus (82). A whole-genome investigation of CTCF-mediated interactions in the nucleus of mouse embryonic stem cells identified chromatin loops anchored by CTCF that demarcate distinct chromatin domains (82). The ability of CTCF to mediate the formation of chromatin loops may in some cases depend on cohesin action. For example, chromosome conformation capture revealed that cohesin is necessary for CTCF-dependent chromatin conformation at the imprinted H19-IGF2 locus (83). Consistent with cohesin-dependent chromatin conformation having a regulatory role, depletion of the Rad21 subunit of cohesin caused increased levels of IGF2 mRNA (83). Potentially in association with CTCF, cohesin has also been found to mediate chromatin looping at a number of other genes, including the interferon γ locus (84), the locus control region of the β-globin gene (85, 86), and the HoxA locus (87) in mice. At the β-globin locus, cohesin or Nipbl depletion interfered with transcriptional activation of globin genes and abrogated the formation of chromatin loops (88). These findings lend support to the increasingly popular theory that cohesin regulates gene expression by mediating long-range chromosome interactions.

Several recent studies suggest that cohesin need not always cooperate with CTCF to regulate chromatin interactions. It appears that cohesin localizes on chromosomes with a variety of transcriptional regulators in a tissue-specific manner. In MCF7 breast cancer cells, cohesin binding coincides with estrogen receptor α (ER), whereas in liver cells, binding of cohesin coincides with that of HNF4A (88). Furthermore, several genomic sites bound by both cohesin and ER in MCF7 cells were associated with ER-anchored chromatin loops (88, 89). Therefore, it is possible that cohesin is functionally involved in the formation of ER-anchored loops in a tissue-specific manner. Stage-specific recruitment of cohesin to immunoglobulin and β-globin loci in mice adds credence to the idea that cohesin is involved in forming tissue- and developmental-stage–specific chromatin structures (86, 90). Of significance, in mouse embryonic stem cells, cohesin and the Mediator complex have been shown to mediate long-range interactions between distal enhancers and the pluripotency genes Oct4 and Nanog (91). In all of these cases, there is evidence that the contribution of cohesin to chromatin structure has diverse functional consequences ranging from the concatenation of immunoglobulin loci (90) to gene transcription (91).

Regulation of local chromatin structure is another potential mechanism by which cohesin might contribute to transcriptional control. Polycromb group (PcG) and trithorax group (TrxG) protein complexes maintain chromatin in silent and activated states, respectively, through modification of histone tails. Cohesin function has been implicated in both PcG and TrxG activity. A Drosophila rad21 mutant called wrthbndi behaves like a TrxG mutation in that it can suppress PcG mutations in some tissues (92). Cohesin binding to Drosophila chromosomes is predominantly excluded from regions enriched in trimethylated lysine 27 on histone H3 (H3K27Me3), a signature of PcG repression (93). Of interest, some genes that respond the most to changes in cohesin or Nippled-B dose are enriched in both H3K27Me3 and cohesin (62), raising the possibility that PcG proteins sometimes cooperate with cohesin to regulate
transcription. In support of this idea, an inducible biotinylation-tagging approach used to purify PcG-associated factors from Drosophila embryos identified an association of PcG protein complexes with cohesin (94). Furthermore, Polycomb-dependent silencing of a transgenic reporter was shown to depend on cohesin function (94).

Thus, it is possible that cohesin contributes to gene regulation by modifying chromatin at both local and global levels.

**Altered Cohesin Expression Is Associated with Distinct Cancer Phenotypes**

Of significance, both over- and underexpression of cohesin are associated with cancer. The expression of cohesin is dysregulated in a number of cancers, including breast, prostate, and oral squamous cell carcinoma, and alterations in genes encoding cohesin proteins are found in colorectal cancer and myeloid malignancies (Table 2).

The level of the RAD21 subunit of cohesin is frequently elevated in cancer (Table 2). **RAD21** overexpression in breast cancer is associated with more aggressive cancers and results in a poorer prognosis for the patient (95–97). For example, **RAD21** was identified as part of a gene expression signature that conferred a short interval to distant metastases in breast cancer patients, with **RAD21** found to be significantly upregulated in the poorer prognosis group (95). Similarly, **RAD21** overexpression was associated with a poor prognosis in breast cancer patients with supraclavicular lymph node metastases (96).

There is some evidence to indicate that raised levels of cohesin may be associated with tumor proliferation, at the expense of tumor metastasis (97, 98). In breast cancer, **RAD21** expression was shown to be significantly lower in invasive tumors compared with their in situ counterparts (97). Although **RAD21** overexpression did correlate with larger tumor size, perhaps indicative of increased proliferation, there was no correlation with tumor grade. However, raised **RAD21** expression significantly correlated with shorter relapse-free survival in grade 3 tumors compared with grade 1 and 2 tumors (97). Grade 3 tumors are characterized by a high proliferative index, and it is possible that **RAD21** contributes to the proliferative potential of the cancer. Conversely, Yamamoto and colleagues (98) showed that in oral squamous cell carcinoma, **RAD21** expression was downregulated in tumors that displayed an invasive growth pattern compared with tumors that grew more expansively, consistent with a proliferative role for cohesin in tumor progression. Of interest, the authors speculated that hypoxic conditions, which are known to downregulate **RAD21** in many human tumor cells, may lead to an invasive potential (98). These observations raise the possibility that changes in **RAD21** expression are associated with switching between tumor invasiveness and tumor proliferation.

A variety of studies have provided strong evidence that cohesin has an important role in cancer (Table 2). Cohesin dysregulation can lead to aneuploidy, which is usually assumed to be the pathological driver in cancers with cohesin mutations. However, the potential effects on transcription resulting from altered cohesin function should also be considered. It is interesting to note that the cancers in which cohesin involvement is associated with a worse prognosis are those in which cohesin is overexpressed. There is likely to be ample cohesin available for intact mitosis in such cancers, and therefore, alternative cause-and-effect relationships between cohesin and cancer could be in play.

Individuals with CdLS have reduced cohesin function and thus may be informative regarding a role for cohesin in cancer. There is little conclusive evidence that CdLS patients have overt defects in sister chromatid cohesion, even though these individuals are compromised for cohesin loading or function (99). Anecdotally, cancer is, if anything, under-represented in CdLS cohorts. A higher than normal incidence of Barrett’s esophagus leading to carcinoma is likely to be linked to the prevalent gastrointestinal reflux found in individuals with CdLS (100). It is interesting to speculate that the prominent cohesin insufficiency in CdLS patients could actually protect against cancer, perhaps because cancer genes that are positively regulated by cohesin are downregulated. For example, expression of the **c-MYC** oncogene is downregulated in cells from CdLS patients (ref. 101 and see below).

The overexpression of cohesin in many cancers raises the possibility that cohesin contributes to cancer via transcriptional regulation. Below, we describe 2 means by which cohesin-mediated gene transcription could contribute to cancer, namely, regulation of oncogenes and genes that maintain pluripotency, and cohesin’s participation in hormone-dependent pathways underlying cancer.

**Links between the Expression of Pluripotency Factors and Cancer**

Embryonic development relies on pluripotent stem cells that derive from the inner cell mass of the early stage blastocyst and have the unique ability to self-renew and differentiate into all of the cell lineages present in the embryo and adult. This cellular paradigm of embryonic development is the basis of the cancer stem-cell model of carcinogenesis that is currently at the forefront of the ongoing debate surrounding the initiation and progression of cancer (102). The cancer stem-cell model suggests that cancer propagation is usually driven by subpopulations of cancer cells with stem-cell properties, including self-renewal and multilineage differentiation (103). Cancer stem cells are predicted to give rise to a heterogeneous population of tumor cells comprising more cancer stem cells, progenitor cells with limited proliferative potential, and aberrantly differentiated cells with no proliferative potential (103). If this model is correct, understanding normal stem-cell self-renewal and differentiation is fundamental to understanding cancer.

The cancer stem-cell model of carcinogenesis posits that tumor cells hijack properties of normal stem cells, including the capacity for self-renewal. Therefore, it is not surprising that the expression of pluripotency transcription factors is
dysregulated in many cancers, including breast, prostate, and colorectal cancers (Table 3). For example, OCT4, NANOG, MYC, and SOX2 are important transcription factors that are critical for the establishment and maintenance of pluripo-
tency and that show altered expression in cancer. Of interest, expression of pluripotency transcription factors is frequently upregulated in cancers that also have elevated cohesin levels. Furthermore, overexpression of pluripotency transcription

<table>
<thead>
<tr>
<th>Cancer</th>
<th>Pluripotency factor involved (context of study)</th>
<th>Description of study</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Breast cancer</td>
<td>↑ OCT4 and NANOG mRNA expression (primary tumors and cell lines)</td>
<td>Quantitative RT-PCR on a stage 3 breast carcinoma sample showed increased NANOG and OCT4 expression compared with nondetectable levels in normal breast tissue. Immunohistochemistry revealed NANOG protein in breast carcinoma sample but not in normal breast tissue. The MCF7 breast carcinoma cell line was found to express OCT4 and NANOG.</td>
<td>157</td>
</tr>
<tr>
<td>Breast cancer</td>
<td>↑ SOX2 protein levels (primary tumors)</td>
<td>Immunohistochemistry was used to analyze SOX2 protein levels in a cohort of 95 patients with sporadic, postmenopausal, early breast cancer. Four expression scores were defined to distinguish SOX2-negative and -positive samples (score 0 = no SOX2-positive cells; score 1 = &gt;0 and &lt;10% SOX2-positive cells; score 2 = &gt;10 and &lt;50% SOX2-positive cells; score 3 = ≥50% SOX2-positive cells). SOX2 was expressed in 24/86 invasive breast carcinoma samples and 4/9 DCIS samples. Tumors expressing ≥50% SOX2-positive cells were significantly larger and significantly associated with lymph-node metastases. FISH of selected samples revealed that increased SOX2 protein levels were not due to SOX2 gene amplification, suggesting that the aberrant gene expression is driven by other mechanisms.</td>
<td>104</td>
</tr>
<tr>
<td>Breast cancer</td>
<td>↑ NANO, OCT4, SOX2 mRNA expression (mammospheres)</td>
<td>Investigated the effects of estrogen on the stem/progenitor cell population in normal breast and breast cancer tissues. NANO, OCT4, and SOX2 expression was used to monitor the differentiation status of breast stem cells in the presence of either estrogen or tamoxifen. Expression levels of NANO, OCT4, and SOX2 were determined in freshly isolated organoids from reduction mammaplasties, breast epithelial cells derived from the organoids and grown as adherent cells in the presence of serum, and mammospheres originating from single breast epithelial cells. Compared with freshly isolated organoids, NANO, OCT4, and SOX2 mRNA expression was lower in differentiated (adherent) cells and significantly higher in the mammospheres. Estrogen treatment significantly reduced NANO, OCT4, and SOX2 expression in mammospheres. Furthermore, estrogen treatment reduced the percentage of stem/progenitor cells in mammospheres, whereas tamoxifen increased the percentage. NANO and SOX2 mRNA expression levels were determined in breast tumor samples and compared with levels in normal adjacent tissue. Increased expression of NANO and SOX2 was seen in the breast tumor samples.</td>
<td>158</td>
</tr>
</tbody>
</table>

(Continued on the following page)
### Table 3. Evidence for pluripotency factor involvement in cancer (Cont’d)

<table>
<thead>
<tr>
<th>Cancer</th>
<th>Pluripotency factor involved (context of study)</th>
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<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Breast cancer</td>
<td>Possession of embryonic stem cell expression signature correlates with aggressive tumor behavior</td>
<td>Gene set expression analysis methods were used to assess whether the expression signatures and regulatory networks that define human embryonic stem-cell identity are also active in human tumors. Thirteen partially overlapping gene sets were compiled that represent the core expression signature of embryonic stem cells and reflect the activity of the regulatory pathways associated with their identity. These gene sets fall into 1 of 4 groups: embryonic stem-expressed genes; Nanog, Oct4, and Sox2 (NOS) targets; Polycomb targets; and Myc targets. Expression profiles from 6 published breast cancer studies, comprising a total of 1,211 tumors, were collected and analyzed. Grade 3 tumors showed an enrichment pattern resembling that observed in embryonic stem cells, including underexpression of Polycomb target gene sets and overexpression of embryonic stem-cell-expressed sets, Myc-target gene sets, and some of the NOS-target gene sets. ER-positive tumors showed an embryonic stem-cell-like enrichment pattern compared with ER-negative tumors. Tumors of larger size at the time of diagnosis were more likely to possess the embryonic stem-cell signature compared with smaller tumors, even within a given grade.</td>
<td>105</td>
</tr>
<tr>
<td>Colorectal cancer</td>
<td>† NANOG protein levels (primary tumors)</td>
<td>Western blot was used to analyze NANOG levels in 175 fresh colorectal cancer samples. NANOG protein levels were higher in most of the colorectal cancer samples compared with paired normal mucosal tissue. Immunohistochemistry was used to analyze NANOG localization in paraffin-embedded colorectal cancer tissue. NANOG was mainly localized to the cytoplasm of cancer cells. Nuclear accumulation of NANOG was only observed in a small fraction of cancer cells. NANOG expression positively correlated with lymph node status and Dukes classification of patients. High NANOG expression correlated with a shorter survival or recurrence free survival. Colorectal cancer cells were studied for the effects of NANOG overexpression on proliferation, invasion, and motility. Overexpression resulted in increased proliferation, colony formation, and invasive ability.</td>
<td>106</td>
</tr>
<tr>
<td>Rectal cancer</td>
<td>† CD133, OCT4, SOX2 mRNA expression associated with distant recurrences (primary tumors)</td>
<td>CD133, OCT4, and SOX2 levels were analyzed before and after chemoradiotherapy to clarify the association between expression of stem-cell markers and chemoradiotherapy resistance in rectal cancer. Thirty-three patients. Quantitative RT-PCR on pre-chemoradiotherapy endoscopic tumor samples revealed a positive correlation between OCT4 and SOX2 but not between CD133 and OCT4 or SOX2.</td>
<td>108</td>
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</table>
Table 3. Evidence for pluripotency factor involvement in cancer (Cont’d)

<table>
<thead>
<tr>
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<th>Pluripotency factor involved (context of study)</th>
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</tr>
</thead>
<tbody>
<tr>
<td>Prostate cancer</td>
<td>↑ OCT4 and SOX2 protein expression (primary tumors)</td>
<td>Analysis of formalin-fixed, paraffin-embedded, post-chemoradiotherapy residual cancer samples showed significant positive correlations among CD133, OCT4, and SOX2. Patients who developed distant recurrences had significantly higher post-chemoradiotherapy levels of CD133, OCT4, and SOX2 compared with patients without recurrences. Of the 33 patients, 28 received a low dose of radiation and 5 received a high dose of radiation. Post-chemoradiotherapy OCT4 levels were significantly higher in the high-dose radiation group compared with the low-dose radiation group. CD133 and SOX2 levels were also higher, but this difference did not reach statistical significance. Immunohistochemistry was used to confirm protein expression in residual cancer cells after chemoradiotherapy. CD133 was observed diffusely in the cytoplasm of residual cancer cells and at the apical/endoluminal surface of residual cancer cells with the formation of lumina and ducts. OCT4 and SOX2 were observed diffusely in the cytoplasm of residual cancer cells.</td>
<td>107</td>
</tr>
<tr>
<td>Bladder cancer</td>
<td>↑ OCT4 mRNA expression (primary tumors)</td>
<td>Investigated OCT4 expression in bladder cancer. Semiquantitative RT-PCR showed OCT4 expression in almost all (96%) of the examined bladder cancer samples. Expression was also detected in 23% of nontumor marginal tissues from the same patients and 33% of nontumor bladder tissues obtained from patients with no obvious signs of bladder cancer. Densitometric evaluation of the semiquantitative RT-PCR results revealed that the intensity of OCT4 expression was significantly higher in neoplastic tissues compared with nonneoplastic samples. Protein levels were also examined by immunohistochemistry. OCT4 was primarily localized to the nuclei of tumor cells, with no immunoreactivity in normal cells adjacent to the tumors.</td>
<td>159</td>
</tr>
</tbody>
</table>
factors in cancer leads to similar outcomes as cohesin over-
expression, namely, poorer prognosis (104–107) and resis-
tance to therapy (108). In breast cancer, tumors expressing
>50% SOX2-positive cells were shown to be larger and associ-
ated with lymph node metastases (104). A meta-
analysis of gene expression profiles from grade 3 breast
tumors showed enrichment resembling that observed in
embryonic stem cells, including underexpression of PcG
target genes and overexpression of embryonic stem-cell–
expressed genes, MYC target genes, and some NANOG/
OCT4/SOX2 target genes (105). In colorectal cancer,
NANOG protein levels were increased compared with
normal adjacent mucosal tissue, and higher levels correlated
with a shorter overall survival (106). A significantly greater
number of OCT4/SOX2-expressing cells were observed in
prostate tumors compared with normal and benign prostate
hyperplasia (107). Furthermore, increased numbers of
OCT4- and SOX2-expressing cells were associated with
more-aggressive tumors that have a worse prognosis
(107). Increased expression of pluripotency genes in rectal
cancer contributes to chemo/radiotherapy resistance, and
patients who relapsed had significantly higher postthera-
pic levels of OCT4 and SOX2 compared with patients
without relapse (108).

Cohesin-Mediated Transcription of Pluripotency
and Proliferation Genes

Maintenance of the pluripotency of embryonic stem cells
depends on the correct regulation of a network of transcrip-
tion factors, PcG repressor complexes, and microRNAs that
are responsible for the transcriptional and epigenetic regu-
lation of key stem-cell genes (102). Genome-wide binding
analyses suggest that OCT4, SOX2, and NANOG contrib-
ute to pluripotency and self-renewal by activating their own
transcription and that of other genes that are important
during early development. OCT4, SOX2, and NANOG
activate genes encoding components of the TGF-β and
WNT signaling pathways, and they repress genes involved
in differentiation processes (109). Although the function of
these early pluripotency factors is relatively well understood,
the upstream pathways that regulate their transcription
remain enigmatic. Evidence that cohesin binds and pos-
tively regulates the expression of Oct4, Nanog, and Sox2 in
embryonic stem cells from human and mouse (91, 110) and
Myc in fish, flies, and mammals (111) suggests that cohesin
is an upstream regulator of pluripotency factors.

A short hairpin RNA (shRNA) screen for pluripotency
factors identified subunits of the Mediator and cohesin
complexes as proteins required to maintain the mouse
embryonic stem-cell state (91). The Mediator complex is
thought to bridge interactions between transcription factors
at enhancers and the transcription initiation apparatus at
core promoters (112). Reducing the levels of Mediator,
cohesin, and Nipbl had the same effect on the embryonic
stem-cell state as did loss of Oct4 itself, suggesting that they
are important for maintaining expression of the key plur-
ipotency transcription factors. ChIP followed by high-
throughput sequencing identified a CTCF-independent
subset of cohesin-binding sites that occupied the enhancer
and core promoter sites bound by Mediator. Although these
sites were associated with RNA polymerase II (RNAPII,
indicating transcription), the cohesin-CTCF–bound sites
were not.

The co-occupancy of Mediator, cohesin, and Nipbl at the
promoter regions of Oct4 and other active embryonic stem-
cell genes indicates that these proteins may all contribute to
the control of their transcription. Approximately one quarter
of the genes co-occupied by Mediator, cohesin, Nipbl, and
RNAPII showed significant gene expression changes when
Mediator, cohesin, and Nipbl were each knocked down,
suggesting that these actively transcribed genes depend on
each of those factors for normal expression (91). This normal
expression is likely to occur through looping between
enhancers and the core promoters of the active genes, given
that chromosome conformation capture identified physical
contact between enhancers and the promoters of Nanog,
Peh1, Oct4, and Lefty1 in embryonic stem cells (91). These
interactions were not detected in differentiated fibroblasts
in which these genes are silent. Depletion of cohesin or Nipbl
abolished enhancer–promoter interactions and decreased
Oct4 and Nanog expression (91).

A further recent study in human embryonic stem cells
identified CTCF-independent RAD21-binding sites that
coincided with binding of the transcription factors OCT4,
NANOG, SOX2, KLF4, and ESRRB (110). Analysis of
global gene expression changes following the knockdown
of RAD21 in embryonic stem cells revealed the downregula-
tion of stem-cell maintenance genes, including Oct4,
Nanog, Tbx3, Esrrb, and Klf4, and the upregulation of a large
number of developmental genes. Changes in gene expression
were similar to those reported following depletion of pluripotency
transcription factors, in particular NANOG-depleted cells.
Of interest, many CTCF-independent RAD21-binding sites
were not present in differentiated embryoid bodies, indicat-
ing that the colocalization of RAD21 with pluripotency
transcription factors is specific for embryonic stem cells.

Studies in zebrafish were among the first to reveal a role
in cohesin in the transcriptional regulation of Myc. Depletion
of Rad21 and Smc3 in zebrafish resulted in a reduction in
myca (zebrafish Myc) transcription in early embryos (111).
This regulation is likely direct, because cohesin (Rad21)
binds at the transcriptional start site and the Myc insulator
element (MINE) just upstream of myca. Positive regulation
of Myc by cohesin is also apparent in Drosophila, mouse (71),
and human (101), suggesting this regulation is conserved
through evolution. While the exact mechanism by which
cohesin regulates Myc remains elusive, studies in zebrafish
rule out involvement of the CTCF insulator protein (111).
Depletion of Ctcf in zebrafish embryos had no effect on myca
expression, and Rad21 was still able to bind the transcrip-
tional start site and Myc insulator element of myca in the
absence of Ctcf. In fact, there was a statistically significant
increase in Rad21 binding at the Myc insulator element in
Ctcf-depleted embryos (111). It is possible that cohesin
regulates myca expression by modulating local chromatin

Rhodes et al.
structure. In Rad21-depleted zebrafish embryos, elevated H3K27me3 and reduced H3K9Ac (histone H3 lysine 9 acetylation) were present at the msyca locus, with a predominant peak around the transcriptional start site. Reduction of the H3K9Ac modification indicates a less open chromatin status, as does an increase in H3K27Me3, reflecting repression of msyca gene expression. The latter modification is mediated by PcG activity, which could involve cohesin function (discussed above).

Stem-cell factors appear to modulate cohesin binding to feed back on their own regulation and to modulate transcriptional control of other developmental genes by cohesin. Some stem-cell transcription factors influence cohesin binding to gene targets. In embryonic stem cells, NANOG facilitates the placement of cohesin at CTCLF-independent transcription factor binding sites through an interaction with the core cohesin protein STAG1 and the cohesin-associated protein WAPL (110). At the mammalian HoxA locus, the Oct4 protein antagonizes cohesin binding to a CTCLF-bound chromatin barrier, which regulates chromatin looping of the HoxA gene (87).

Cancers that exhibit high levels of cohesin and/or pluripotency factors share similar genetic profiles and prognostic outcomes. Because cohesin modulates the transcription of key pluripotency factors, there is a strong possibility that cohesin-mediated gene transcription underlies certain types of cancer upstream of pluripotency factors. Cohesin could participate in reprogramming cells to have stem-cell-like characteristics, conferring a selective advantage, including self-renewal, to the tumor. Furthermore, because cohesin also regulates genes involved in cell fate determination (e.g., Runx1 and Runx3 (64)), it is tempting to view cohesin as a gatekeeper of cell fate, maintaining the balance between stem- and differentiated-cell populations through its gene regulation role (Fig. 2).

Role of Cohesin in Hormone-Mediated Gene Regulation

Hormones induce dramatic and dynamic alterations in gene transcription. A small proportion of the transcriptional response to hormones is direct, via hormone receptors (HR) binding to promoters to activate transcription (113). However, a more significant component of hormone-dependent transcriptional response is accounted for by chromatin rearrangements and epigenetic modifications. A growing body of evidence suggests that cohesin regulates the modulation of genes by nuclear HRs and that this role is conserved through evolution (Table 4).

The first example of cohesin’s role in hormone response was observed in Dro sophila, where cohesin was found to be necessary for EcR-dependent axon pruning (74, 75). Cohe sin’s role in the response to ecysyne involves regulating transcription of the EcR gene (74–76) and directly regulating ecysyne-responsive gene transcription (76, 77). Remarkably, in humans, cohesin also appears to play an important role in the transcriptional response to androgen and estrogen (88, 114–116).

PDS5 is a HEAT-repeat–containing protein that is required for sister chromatid cohesion and that regulates the removal of cohesin from chromatin. Vertebrates possess 2 homologs of PDS5: PDS5A and PDS5B (Table 1). PDS5A/B-deficient mice exhibit CdLS-like developmental defects, including genital defects, without alterations in sister chromatid cohesion (70, 117). Of interest, PDS5B has been identified as an androgen-proliferation shutoff gene in prostate cancer cells, because it is essential for androgen-dependent growth inhibition both in vitro (115) and in vivo (116). In cells of the prostate, androgens initially increase proliferation but then induce quiescence. Regulation of gene transcription by androgens occurs through several epigenetic mechanisms, including histone modification, nucleosome remodeling, and chromatin looping (reviewed in ref. 118). It has been suggested that PDS5B regulates the androgen response through a chromatin modification role (116). Growth-inhibitory levels of androgens induce transcription of PDS5B, and PDS5B is also induced by the active metabolite of vitamin D, 1,25(OH)2D3, another inhibitor of prostate cancer cell growth (114).

Estrogen-bound ER modulates genes that are required for reentry into the cell cycle, driving proliferation (119). In estrogen-dependent breast cancer cells, ligand-bound ER is recruited to thousands of specific sites throughout the genome (113, 120–122). Most ER-binding sites are cell-type specific and correlate with estrogen-regulated gene expression (120). Recently, a genome-wide binding study revealed tissue-specific, inducible cohesin binding in breast cancer cells in response to estrogen (88). This study showed that genes regulated by estrogen exhibit enriched binding of
cohesin together with ER. Although the functional significance of cohesin binding is not known, it has been shown that cohesin depletion prevents the estrogen-responsive G0/G1→S transition in breast cancer cells, indicating that cohesin influences the physiological estrogen response (88).

A cell’s transcriptional response to hormone signaling is complex. Entire cohorts of genes are turned on or off at different times poststimulation, both directly via canonical mechanisms of gene activation and less directly by altering the chromatin milieu. How does cohesin influence gene regulation by hormones? We suggest 3 possible ways in which cohesin could modulate hormone-mediated gene transcription:

- Altering the levels or binding of HRs.
- Stabilizing chromatin interactions required for gene activation/repression.
- Modulating histone modifications in response to hormones.

It is possible that any one of these 3 options, or a combination thereof, could be in play at any one time (Fig. 3). Below, we discuss each possibility.

### Does cohesin alter levels or binding of nuclear HRs?

Rather than modulating the transcriptional activity of HRs, cohesin could act farther upstream by influencing HR levels. In support of this idea, it was shown that cohesin directly regulates EcR transcription in *Drosophila* salivary glands (75, 76). However, ablation of cohesin function affects the transcription of some ecysysone-regulated genes hours before EcR levels are reduced, as shown by chromosome puffs associated with ecysysone-regulated genes (76). Therefore, although cohesin appears to directly regulate

<table>
<thead>
<tr>
<th>Organism</th>
<th>Steroid hormone</th>
<th>Evidence of role for cohesin</th>
<th>Reference</th>
</tr>
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<tbody>
<tr>
<td><em>Drosophila</em></td>
<td>Ecdysone</td>
<td>Cohesin is necessary for EcR-dependent axon pruning in the mushroom body. Ecdysone-responsive genes have high levels of cohesin binding. Cohesin regulates EcR at the transcriptional level. Cleavage of cohesin affects expression of ecysysone-dependent genes. Changes in ecysysone-responsive genes occur before EcR levels can be affected, indicating that cohesin’s role in ecysysone gene response is more than solely regulating EcR levels.</td>
<td>74, 76, 77, 75–77</td>
</tr>
<tr>
<td>Human</td>
<td>Estrogen</td>
<td>Cohesin is required for estrogen-mediated reentry into the cell cycle (G0/G1→S-phase transition). Global analysis of cohesin binding to chromatin shows that cohesin colocalizes with the ER at many sites throughout the genome. In ER-positive MCF7 breast cancer cells, cohesin binding is positively correlated with estrogen-regulated genes. Genome-wide analysis of chromatin interactions throughout the genome identified ER-anchored chromatin loops in estrogen-responsive genes. Cohesin binding is enriched at sites involved in ER-mediated chromatin interactions, suggesting that cohesin may stabilize these loops. An extensive shRNA screen revealed that downregulation of individual subunits of cohesin increased survival of MCF-7 breast cancer cells exposed to tamoxifen over an extended period. Clones of ER-positive ZR-751 breast cancer cells expressing ectopic RAD21 exhibit reduced sensitivity to the antiestrogen ICI 182780 or to tamoxifen in an agar growth assay. MCF7 cells with acquired resistance to tamoxifen have 1.6-fold higher expression of RAD21 and 3-fold lower expression of PDS5B than tamoxifen-sensitive cells.</td>
<td>88, 89, 136</td>
</tr>
<tr>
<td>Androgen</td>
<td>PDS5b is required for androgen-mediated proliferative arrest in G0/G1. AR mediates looping of androgen-regulated genes. PDS5b is induced by levels of androgens that inhibit cell growth. Rad21 levels are higher and PDS5b levels are lower in androgen-independent vs. androgen-dependent prostate cancer cell lines.</td>
<td>116, 114, 160, 123, 125</td>
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EcR transcription, this does not account for all of the ecdysone-regulated transcriptional response that also occurs downstream of cohesin.

In contrast to EcR in *Drosophila*, there is little evidence to suggest that cohesin regulates the levels of steroid HRs in vertebrates. In human breast cancer cells, depletion of RAD21 blocked estrogen-mediated reentry into the cell cycle without altering ER protein levels (88). Furthermore, microarray analysis of zebrafish depleted for Nipbl and a variety of cohesin subunits showed no alteration in the transcript levels of ERs (ref. 111; M. Mönnich and J. Horsfield, unpublished results). These results argue against the idea that cohesin contributes to steroid hormone response by modulating transcription of HRs, at least in vertebrates. It is not known whether receptor stability is influenced by cohesin.

Cohesin may affect the ability of HRs to bind to chromatin or affect where HRs bind by modulating histone marks or even direct interactions with the receptors; however, there is no experimental evidence for this as yet.

**Cohesin mediates chromatin interactions in response to nuclear HR binding**

HR-binding sites can be located at some distance from the promoter of hormone-regulated genes (113, 118). For example, loops that bridge a distal androgen receptor (AR) site to the proximal promoter have been identified by chromosome conformation capture in several androgen-responsive genes, including prostate-specific antigen (123), FKBP5 (124), and TMPRSS2 (125). Fullwood and colleagues (89) identified loops anchored by ER in human breast cancer cells using a genome-wide technique to analyze chromatin interactions (chromatin interaction analysis–paired end tag, ChIA-PET). These chromatin interactions are enriched in estrogen-responsive genes,
suggesting that the loops play a functional role in gene regulation.

The looping of regulatory elements to promoters of hormone-responsive genes suggests that cohesin, which has a function in the formation of chromatin loop structures, could contribute to a hormone response by this mechanism. In support of this idea, it was shown that cohesin colocalizes with ER at many sites in ER-positive breast cancer cells (88). Several of these sites have been shown to act as intrachromosomal loop anchors, suggesting that cohesin may play a role in stabilizing these loops (88, 89). It is possible that cohesin also stabilizes AR-mediated chromatin interactions; however, there is no evidence for this as yet.

Although cohesin may activate transcription of hormone-responsive genes by mediating enhancer–promoter communication, some cohesin-mediated interactions may also be repressive. Normal breast epithelial cells exhibit transient repressive DNA looping in response to estrogen. In breast cancer cells, the repressive loops are stabilized, resulting in long-range epigenetic silencing (126). RAD21 mRNA levels are elevated in breast cancers relative to normal breast tissue (Table 2), raising the possibility that cohesin may also stabilize repressive loops and/or interactions that activate genes in response to estrogens.

**Cohesin may modify chromatin in response to steroid hormones**

Estrogen-responsive gene transcription results in 3 cycles of transcription (1 unproductive cycle followed by 2 productive cycles of transcription within 180 minutes) characterized by waves of chromatin modification and transcription-factor binding (reviewed in ref. 127). In each cycle, binding of ligand-bound ER is immediately followed by recruitment of the SWI-SNF chromatin remodel remodeling complex and subsequently histone methyltransferase and histone acetyltransferases, leading to an open chromatin conformation that facilitates gene transcription (127). Of significance, ER functionally interacts with chromatin-modifying enzymes. For example, ER copurifies with the histone demethylase JMJD2B, the depletion of which inhibits estrogen-induced entry into the cell cycle (128). ER also interacts with the PHD-bromodomain chromatin reader TRIM24 to activate estrogen-responsive genes (129). AR also recruits histone acetyltransferases and HDAC to androgen-regulated genes, and these enzymes modify not only the chromatin conformation but also AR itself (reviewed in ref. 130). AR is coactivated by TIP60, a histone acetyltransferase, whereas HDAC1 directly interacts with and represses AR activity (131). In addition, AR interacts with several histone demethylases (132).

The cohesin subunit RAD21 was identified in an siRNA screen to identify epigenetic silencing factors in human cells, alongside known epigenetic factors such as DNMT3a, HDAC1, and TRIM24 (133). As described above, experiments in *Drosophila* have shown that cohesin influences the activity of chromatin modifiers; for example, the *Drosophila* varthandi (rad21) mutation genetically behaves like a TrxG member (92), and cohesin physically interacts with PcG proteins (94). TrxG and PcG proteins have a diverse range of roles in transcriptional activation and repression, including regulation of histone methylation and ATP-dependent nucleosome remodeling complexes (reviewed in ref. 134). In humans, cohesin was shown to be part of an ISWI-containing chromatin remodeling complex; indeed, the RAD21 subunit directly interacts with the ATPase subunit SNF2h of this complex (135). Thus, cohesin interacts with TrxG, PcG, and chromatin remodeling complexes, and it likely modulates their function. This raises the possibility that the chromatin remodeling complexes recruited by ER and AR also interact with cohesin, with functional consequences for hormone-dependent cancers.

Of significance, cohesin also appears to influence the function of selective ER modulators and estrogen antagonists. In a recent study, whole-genome shRNA screening was used to identify genes that confer resistance or sensitivity to the selective ER modulator tamoxifen in the invasive ductal breast cancer cell line MCF7 (136). Silencing of several individual components of cohesin (NIPBL, SMC3, and RAD21) led to reduced sensitivity to tamoxifen in MCF7 cells (136). This is in contrast to the observation by Van Aghoven and colleagues (137) that increased expression of the cohesin subunit Rad21 resulted in resistance to tamoxifen or the antiestrogen compound ICI 182780 in a semi-solid growth assay. The authors transduced ZR-75-1 ductal breast cancer cells with cDNA expression libraries from which they identified clones with increased resistance to various antiestrogens. The screen identified 15 genes, including RAD21, that when overexpressed led to antiestrogen resistance. A study that compared the gene expression profiles of MCF7 cells with acquired resistance to tamoxifen showed a significant increase in RAD21 expression (and a 3-fold decrease in PDSSB expression) in tamoxifen-resistant versus tamoxifen-sensitive cells (138). These studies are consistent with the idea that increased cohesin activity leads to resistance to selective ER modulators. How cohesin levels affect the response of ER-positive breast cancer cells to selective ER modulators is not yet clear. The evidence to date suggests that under- or overexpression of cohesin could result in a dysregulated transcriptional response to estrogen (88, 136, 137, 139). How cohesin levels affect ER binding, transactivation, and interaction with antiestrogens remains to be determined.

The MYC proto-oncogene is estrogen responsive (140) and regulates more than half of the genes in the estrogen proliferation pathway (141). Elevated levels of MYC can lead to endocrine resistance in breast tumors (142–144). ER-binding sites are found at the MYC promoter and at enhancers both upstream and downstream of the MYC locus (88, 89). Cohesin binds at the MYC gene and at several putative enhancers in an estrogen-dependent manner (88). Some enhancers are >300 kb away from the MYC gene, yet they interact long-range with the MYC promoters (145–147). Single-nucleotide polymorphisms associated with breast, colon, and prostate cancer reside within these
enhancers, and in at least one case, the single-nucleotide polymorphism genotype influenced MYC transcription (146). Binding of cohesin to distant enhancers for MYC raises the tantalizing possibility that cohesin participates in their long-range interaction with the MYC gene. However, evidence that cohesin is involved in these long-range interactions has not yet emerged.

Given the positive regulation of stem-cell and proliferation genes by cohesin, it may be possible that elevated cohesin levels can bypass the hormone dependency of tumors. Hormone-independent, ER-negative breast cancer cells are able to proliferate in the absence of a mitogenic estrogen signal. A recent meta-analysis and gene-set enrichment analysis revealed that the basal subgroup of ER-negative breast cancer mimics the ER-positive transcriptional response to estrogen, with increased levels of MYC (148). As discussed above, we have shown an evolutionarily conserved role for cohesin in the direct, positive regulation of MYC expression (111). Of significance, we found that cohesin is necessary for MYC expression in several human cancer cell lines, as well as for estrogen induction of MYC in ER-positive breast cancer cell lines (McEwan and Horsfield, unpublished data). It is tempting to speculate that elevated cohesin facilitates MYC transcription, which could lead to bypass of hormone dependency. It is not clear whether distant enhancers for MYC are involved in its cohesin-dependent regulation. However, because the location of Myc relative to its regulatory elements differs vastly between zebrafish and human (Rhodes and Horsfield, unpublished observations), we suspect that alternative, as yet unknown, mechanisms are also involved.

Cohesin: A New Therapeutic Target in Cancer?

Evidence suggests that a disruption of normal cohesin function could have positive outcomes for cancer. It is known that chemotherapy responses are compromised in patients whose tumors overexpress RAD21 (97). Knocking down RAD21 expression in MCF-7 breast cancer cells sensitized the cells to chemotherapeutic agents, including etoposide and bleomycin (149). Silencing of RAD21 in a basal-like breast cancer cell line, MDA-MB-231, rendered the cells more sensitive to the chemotherapy drugs cyclophosphamide and 5-fluorouracil in a manner that directly correlated with the level of RAD21 expression (97). In breast cancer patients not treated with chemotherapy, no correlation was found between RAD21 expression and overall survival, whereas in patients treated with chemotherapy, a significantly shorter overall survival was observed in patients whose tumors were RAD21-positive (97). Mice heterozygous for a null mutation in Rad21 are more sensitive to ionizing radiation (150), raising the possibility that chemicals targeting cohesin could be effectively used in combination with radiotherapy in patients. These studies suggest that elevated cohesin is associated with resistance to therapeutics and that targeting cohesin as part of a combination therapy may produce better patient outcomes.

How might cohesin be targeted? Like many other proteins, cohesin subunits are posttranslationally modified at different stages of the cell cycle, with a range of functional consequences. For example, forward/reverse phosphorylation and acetylation events regulate cell cycle stage-specific binding of cohesin to chromatin (Fig. 1). Designing drugs to interfere with enzymes that mediate cohesin modifications could pave the way to new combination therapies and overcome problems with tumors that are refractory to current therapies. For example, deacetylation of SMC3 by a class I HDAC is required for cohesin recycling onto chromosomes after cell division (42–44). Clinically available HDAC inhibitors slow the growth of breast tumors and reverse hormone therapy resistance in ER-positive breast cancers (151, 152). It is not yet known whether this class of compounds affects cohesin function.

In conclusion, genetic alterations that lead to an imbalance of cohesin levels may result in cancer through mechanisms other than aneuploidy and genome instability. Regulation of gene expression by cohesin, through mechanisms that affect chromatin structure and three-dimensional organization, may play a significant role in tumorigenesis. In support of this concept, multiple lines of evidence show that cohesin maintains the expression of pluripotency and cell proliferation factors and that it modulates hormone-dependent gene transcription in cancer cells.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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Gene Regulation by Cohesin in Cancer: Is the Ring an Unexpected Party to Proliferation?

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