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## article info

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### Article history:

Received 23 May 2014

Received in revised form

29 October 2014

Accepted 30 October 2014

Available online 4 December 2014

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### Keywords:

Redox

Stem cell

Progenitor cell

Oligodendrocyte/type-2 astrocyte

progenitor cell

c-Cbl

Redox/Fyn/c-Cbl pathway

Glioblastoma

Basal-like breast cancer

Tumor initiating cell

Tamoxifen

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## abstract

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This review discusses a unique discovery path starting with novel findings on redox regulation of precursor cell and signaling pathway function and identification of a new mechanism by which relatively small changes in redox status can control entire signaling networks that regulate self-renewal, differentiation, and survival. The pathway central to this work, the redox/Fyn/c-Cbl (RFC) pathway, converts small increases in oxidative status to pan-activation of the c-Cbl ubiquitin ligase, which controls multiple receptors and other proteins of central importance in precursor cell and cancer cell function. Integration of work on the RFC pathway with attempts to understand how treatment with systemic chemotherapy causes neurological problems led to the discovery that

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that progenitors from the cortex, which myelinates late and over a long time period, undergo extensive self-renewal in vitro under basal division conditions and are relatively resistant to inducers of oligodendrocyte generation



ubiquitinated by c-Cbl, it also appears that activation of c-Cbl is modulated by Fyn rather than by an activated RTK.

multiforme (GBM), multiple myeloma, and lymphoma) and which also can be used as part of a preparatory (conditioning) regimen prior to bone marrow transplantation. BCNU treatment has been associated with significant changes in mental status and with white matter degeneration [108,109]. Cisplatin is a DNA cross-linking agent used in treatment of various kinds of cancers, including sarcomas, some carcinomas, lymphomas, and germ cell tumors. At high doses, it has been associated with leukoencephalopathy and destruction of CNS white matter [110]. The antimetabolite cytarabine is a nucleoside analog used mainly in treatment of white blood cell tumors, such as acute myeloid leukemia, acute lymphocytic leukemia, and lymphomas. Application of cytarabine has also been associated with acute encephalopathy, confusion, memory loss, and white matter changes [110,111]. 5-Fluorouracil (5-FU) is a pyrimidine analog that inhibits thymidylate synthase and is used alone or as an important component of adjuvant

cells) in which vulnerability was comparable to that observed for primary neural progenitor cells, with most such cell lines being more resistant to these agents than the normal cells. This outcome was seen despite the fact that the cancer cell lines we studied often were chosen because of their previous use in studies on the response to the drugs studied.

In vitro analyses of purified cell populations were highly predictive of effects seen following systemic treatment with any of the chemotherapeutic agents in vivo, in terms of both the cellular targets and the ability of exposure to these agents to cause cell death and also to suppress precursor cell division. In particular, in vitro studies showed that doses of BCNU, cisplatin, and cytarabine that did not kill normal precursor cells were nonetheless sufficient to suppress their division.



BCNU and TMX are prooxidants—and TMX is potentially a very useful prooxidant for treatment of a wide range of cancers

Multiple standard anticancer agents appear to make cells more oxidized. It was thus a natural question for us to ask whether the effects of these agents on O-2A/OPCs might be mediated through activation of the RFC pathway.

The agents we chose for our first studies were BCNU and TMX.

We found that Cool-1/ $\beta$ pix—but not Cdc42—is a critical inhibitor of c-Cbl function in GBM cells (summarized in [Fig. 6](#)). In GBM



reactivation. Knockdown of Cool-1/

studies on BLBC cells, we found identical results on 7 independent BLBC cell lines representing Basal B triple-negative cells, Basal A cells, and Basal A cells with Her2 amplification [241]. In our studies on GBMs, five independent GBM cell lines all yielded identical results, as did examination of biopsies from five different patients [227]. In addition, analysis of five c-Cbl targets in GBM samples (via the Cancer Genome Atlas) showed increased levels of at least two c-Cbl target proteins in 73% of cases and of at least three c-Cbl targets in 43% of cases. A more focused examination of tumors with increased EGFR protein expression showed increased expression of Cool-1/ $\beta$  mRNA in 65% of samples, and in 52% of all GBM samples in the database. With the caveat that these databases provide no information on isoform changes and alterations in Cool-1/ $\beta$



knockdown cells to TMX caused a further decrease in EGFR levels [241]. In addition, it also was recently reported that transglutaminase-2 also can inhibit c-Cbl function in some GBM cell lines [361].

There also is a growing list of proteins known to regulate the activity of Cool-1/ $\beta$ pix and Cdc42, and each of these is of potential interest as a means of controlling c-Cbl activity. For example, inhibition of a particularly central activator of Cool-1/ $\beta$ pix might produce outcomes that were similar to knockdown of Cool-1/ $\beta$ pix itself. In addition, it has been reported that MEK inhibition also decreases Cool-1/ $\beta$ -pix phosphorylation [365], providing another possible means of regulating this inhibitor of c-Cbl.

The ways in which proteins that might regulate c-Cbl interact

of cancer cells is a puzzling one, and understanding how this can be accomplished is likely to provide insights important for developing better anticancer therapies. How a MEK1/2 inhibitor might have such different effects on normal cells and transformed cells is not yet known. It is curious, however, that there are previous observations indicating that MEK inhibition can also decrease Cool-1/ $\beta$ -pix phosphorylation [365]. It will be of great interest to determine if the MEK inhibitors we discovered through investigations on protective strategies have the unexpected property of also being able—at least in some cancers—of restoring normal c-Cbl function. If so, their value in cancer treatment may be considerable, but also would bene



analyses of the role of redox state in cell signaling do not argue against the importance of more standard approaches to analysis of signaling pathway function. Instead, it is the integration of all of these various approaches together that is likely to offer the greatest power going forward. Indeed, we suspect that one of the greatest opportunities going forward will be to combine our work with studies on genetic networks that also are shared by multiple cancers and that arise in specific response to the action of cooperating oncogenes. The network of cooperation response genes (CRGs) was first identified in studies by Hartmut Land and colleagues on cooperation between dominant-negative p53 and constitutively active Ras<sup>V12</sup> (Ras) mutants in a model of colon cell transformation [382]. Systematic functional analysis demonstrated that CRGs are highly enriched for regulators of malignancy, and resetting expression of individual CRGs to normal cell levels suppressed growth of both experimental tumors and naturally occurring human tumors [382,383]. Restoring normal expression of even a single CRG was, in most cases, sufficient to reduce tumor growth, and similar effectiveness was seen in both experimentally induced cancers and xenograft tumor formation by human cancer cells [382–384].

Regulation of cell transformation by CRGs appears to be a general principle, as CRGs that regulate transformation of colon cells play a role in multiple epithelial tumor types, and particularly in cancers (such as BLBCs) in which p53 and Ras pathway mutations are often found. Although there are distinct CRG sets





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