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## The Molecular Circuitry Linking Cancer Stem Cells and Chemo-Resistance

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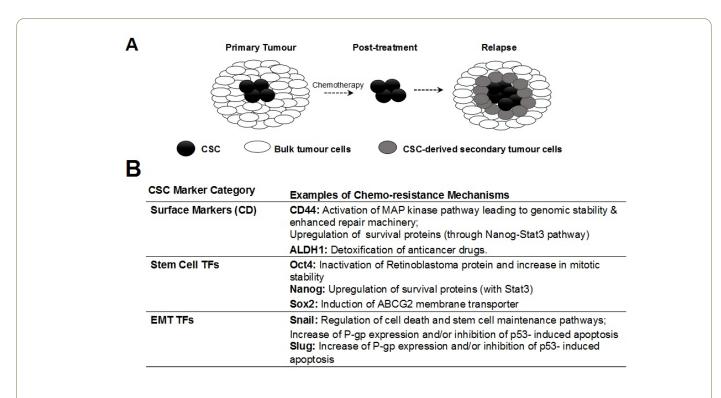
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## Commentary

The uncontrolled cellular growth known as cancer has been the evil companion of the human race throughout history with evidence of tumors dating back to fossilized bones and mummies in ancient Egypt. The deadly friend has ever since provoked immediate treatment measures, and hence research and development of novel therapies. Despite all advances however, the disease is far from "treatable" yet scoring the highest death rate in the modern world. Chemotherapy, the mainstream cancer treatment with various chemical reagents primarily targets actively proliferating cells, commonly through inhibition of the mitotic machinery or DNA replication, leading to downstream apoptotic events. The clinical application of chemotherapeutic agents is commonly perplexed by the fact that despite initial remission, most cancers show poor prognosis with metastatic and/or chemo-resistant relapse. Clinical and experimental evidence suggest a key role for the heterogeneous nature of tumours in this context [1,2]. We and others have defined multiple levels of heterogeneity for tumours, both at the levels of mutational landscape, and cellular phenotypes where independent of genetics, tumour cells cluster into functional subgroups displaying distinct molecular and cellular behavioural outcomes [3-7]. A key compartment of tumour heterogeneity, is a cluster of stem-like cells known as cancer stem cells (CSC), that have the capacity to self-renew and form the entirety of the tumour, once isolated [8-10]. Cancer stem cells are functionally implicated in chemotherapy resistance, where they often evade/resist the cytotoxic effects of chemotherapy, survive treatments and potentially seed secondary relapsed tumours [11] (Figure 1A). The molecular landscape of resistance to chemotherapy is yet to be fully delineated. Here, we would like to focus on specific markers of the cancer stem cell compartment, and ask whether they directly contribute to chemo-resistant outcomes (Figure 1B). Cancer stem cells have been isolated from a number of tumours, based on the expression of specific cell

surface antigens known as cluster of differentiation (CD). Experimental evidence supports a CD signature for CSCs that majorly involves expression of one or a combination of CD133, CD24 and CD44 antigens among others, though with little consensus between different tumours [12]. CD44 was shown to directly link to a chemo-resistant phenotype in T-cell acute lymphoblastic leukemia, by induction of a drug efflux activity [13]. Moreover, the ligand-activated CD44 pathway directly links to downstream survival mechanisms involving the MAP kinase pathway, leading to increased genomic stability, and enhanced repair machinery [14]. Apart from the surface antigen signatures, CSCs are as well marked by specialized classes of transcription factors linking to downstream stem cell-associated characters. Cancer stem cells express basic stem cell transcription factors including Oct4, Nanog and Sox2 in common with embryonic and some adult stem cells [15]. Oct4 inactivates the key cell cycle regulator protein, retinoblastoma (Rb) and enhances the mitotic stability in ovarian carcinoma cells, thus impairing the apoptotic response pathway during chemotherapy [16].

The other stem cell transcription factor Nanog, is activated downstream of CD44-mediated signalling, and together with Stat3, reduces the PDCD4 tumour suppressor protein, leading to upregulation of survival proteins, and chemo-resistance in head and neck squamous carcinoma [17]. Unlike Oct4 and Nanog that are mostly implicated in genomic stability, Sox2 regulates the key membrane transporter ABCG2, which is often implicated as a major factor in drug efflux and chemoresistance [18]. Adult and cancer stem cells as well as express members of the aldehyde dehydrogenase 1 (ALDH1) enzyme family including ALDH1A1, ALDH1A2 and ALDH1A3. These enzymes are known to detoxify a variety of endogenous and exogenous aldehydes involving some commonly used anticancer drugs like oxazaphosphorines [19,20]. Indeed, transcriptional activation of ALDH1 has been linked to poor cancer prognosis and acquired drug resistance [21].



**Figure 1** CSC pathways directly affect chemo-resistance; **A)** The CSC model of chemotherapy resistance. Note the difference between cellular compartments in primary and secondary/relapsed tumours. **B)** Summary of CSC-related chemo-resistance pathways.

Apart from the above-mentioned CSC-specific cell surface markers and transcription factors, cancer stem cells often demonstrate a state of reversible cell cycle dormancy known as cell cycle quiescence. This state per se can potentially resist/ evade a broad range of anticancer drugs, as they are often targeted against the proliferating compartments in the tumours [22,23].

Cancer stem cells are as well enriched with the molecular signature that is involved in a developmentally-conserved process known as epithelial to mesenchymal transition (EMT) [24]. Major EMT transcription factors include Snail, Slug, Twist and Zeb and their related subtypes [25]. Most EMT TFs are shown to associate with poor tumour prognosis and chemotherapy resistance [26-29]. In breast cancer cells, Snail-induced EMT contributes to drug resistance through regulating genes involved in cell death and stem cell maintenance [30]. Moreover, Snail and Slug contribute to the resistance of breast and ovarian tumour cells to multiple chemotherapy drugs by increasing the expression of the drug efflux transporter P-glycoprotein (P-gp) and/or inhibiting p53-induced apoptosis [31,32].

The direct role of CSC-related factors at various levels of chemotherapy response strongly suggests a key function for this compartment and its associated molecular machinery in the therapy evasion/resistance. The CSC characters are assigned through an orchestrated regulatory network involving the pathways mentioned above, and signaling cues from other cells within the tumour stroma and additional systemic factors [33]. The molecular machinery is, on the other hand, permanently fine-tuned in dialogue with the dynamic tumour micro-environment. A thorough understanding of the spatial and temporal tumour dynamics is therefore, absolutely essential for the design and development of more directed therapeutics.

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