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JAK2-STAT5 signaling

A novel mechanism of resistance to targeted PI3K/mTOR inhibition

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A recent article published by Britschgi et al. in *Cancer Cell*, "JAK2/STAT5 Inhibition Circumvents Resistance to PI3K/mTOR Blockade: A Rationale for Cotargeting These Pathways in Metastatic Breast Cancer," describes a positive feedback loop of JAK2/STAT5 activation that drives resistance to PI3K/mTOR inhibition in breast cancer. The authors found that genetic or pharmacological inhibition of JAK2 circumvents resistance to PI3K/mTOR inhibition and go on to show the efficacy of combined PI3K/mTOR and JAK2 inhibition on reducing cancer cell number, tumor growth, and metastasis as well as increasing in vivo survival. These results provide strong support for combination therapy with JAK2/STAT5 and PI3K/mTOR inhibitors in breast cancer. Here we discuss how the article by Britschgi et al. proposes a novel mechanism to explain how breast cancer cells overcome inhibition of a key signaling pathway driving cell proliferation. We also discuss the interplay between activation of the transcription factors STAT5 and STAT3 in breast cancer.

The authors' findings pertain to triple-negative breast cancer (TNBC), a clinically aggressive subtype of breast cancer defined by lack of expression of estrogen receptor, progesterone receptor, and human epidermal growth factor-related 2 (HER2) amplification. Accounting for about 15% of all invasive breast cancers, TNBCs do not respond to hormonal therapy or targeted antibodies to HER2. Some TNBCs respond to conventional chemotherapy, and others harboring mutations in the breast cancer susceptibility gene 1 (BRCA1) have deficient homologous recombination repair, sensitizing them to poly ADP-ribose polymerase (PARP) inhibitors.[1] Still, TNBCs have limited treatment options and are characterized by high rates of metastases and poor prognosis.

One therapeutic strategy for TNBC is targeting the signaling pathways that regulate critical mediators of tumor formation and metastatic progression. Activation of mTOR signaling is commonly observed in TNBCs.[2] In addition, PI3K pathway aberrations have been reported to occur in approximately one third of breast cancers, pointing to a critical role for this signaling pathway in breast tumorigenesis.[3] While inhibiting mTOR alone has limited therapeutic efficacy due to activation of PI3K signaling that upregulates pro-survival genes,[4] dual PI3K/mTOR inhibitors represent an effective alternative for TNBC therapy. In animal models, the combination of the mTOR inhibitor rapamycin with the cytotoxic drug cyclophosphamide decreases the incidence of lung metastases compared with treatment with rapamycin alone.[5,6] It has been shown that PI3K pathway aberrations are more common in hormone receptor-positive tumors and less common in basal-like cancers like TNBC,[3] suggesting that PI3K mutations play different roles in the pathogenesis of different subtypes of breast cancer. Although Britschgi et al. describe a mechanism involving JAK2/STAT5 to circumvent PI3K/mTOR inhibition in TNBC, hormone receptor-positive tumors, which

more commonly harbor PI3K pathway aberrations, may rely on other mechanisms to circumvent PI3K/mTOR inhibition. More studies are needed to elucidate the mechanisms by which modulation of signaling pathways drives tumor resistance to anti-cancer therapies.

Since the neoplastic phenotype of a cell is largely driven by its pattern of gene expression, another treatment strategy for TNBC focuses on targeting the transcription factors that are inappropriately activated in these tumors. STAT5 and STAT3 are two closely related members of the STAT family of transcription factors that regulate the expression of genes involved in cell growth, survival, and angiogenesis.[7] In normal cells, STAT signaling is tightly regulated by inhibitory molecules including suppressor of cytokine signaling (SOCS) proteins, protein inhibitor of activated STAT (PIAS) proteins, and protein tyrosine phosphatases. Cancer cells frequently have persistent STAT activation, from hyperactivation of upstream tyrosine kinases or loss of function of negative regulators, which can then contribute to malignant transformation.[8] In cancer cells with inappropriate constitutive STAT3 activation, inhibition of this protein leads to a reversion of the malignant phenotype and cell death whereas normal cells lacking STAT3 activation are unharmed. Although STAT5 and STAT3 are structurally similar and recognize similar DNA response elements, these factors play contrasting roles in normal mammary function. STAT5 promotes terminal differentiation of mammary epithelial cells necessary for lactation while STAT3 promotes involution of the mammary gland following weaning. In addition, STAT5 and STAT3 have been shown to exert opposing effects on the expression of select target genes such as Bcl-6 in breast cancer cells.[9]

Thus far STAT5 activation has been associated with a more favorable prognosis in breast cancer patients. Studies performed in five different cohorts of breast cancer patients showed decreasing STAT5 activation with disease progression.[10] STAT5 mediates the effects of prolactin (PRL), a hormone that stimulates lactation during pregnancy.[11] PRL induces STAT5 activation via JAK2 and also functions in suppressing the invasive capacity of breast cancer cells.[12,13] Restoring PRL receptor expression in TNBC cell lines decreases their invasive capacity while blocking JAK2/STAT5 in luminal breast cancer cell lines increases their invasiveness, suggesting that PRL activation of STAT5 restricts the metastatic potential of breast tumors. Conversely, accumulating epidemiologic data strongly suggest that circulating PRL levels are associated with increased risk of developing estrogen receptor (ER) positive, but not ER negative tumors like TNBCs.[14,15] These divergent effects of PRL in breast cancer may reflect the hormone's dual physiological effects on promoting proliferation as well as differentiation in preparation for lactation. Taken together, these data implicate STAT5 as playing both a tumor-suppressive and neoplastic role in breast tumors.

In contrast to STAT5 activation, STAT3 activation has been associated with a worse prognosis in breast cancer patients in part due to its effect on evasion of apoptosis. This may contribute both to resistance to therapy and to subsequent recurrence. Whether a cell undergoes apoptosis is largely based on competition between pro- and anti-apoptotic proteins in the mitochondria. Anti-apoptotic proteins like Bcl-2 normally sequester pro-apoptotic proteins from binding to and activating Bak/Bax, which form pores in the mitochondrial outer membrane to trigger cell death.[16] STAT3 is known to upregulate the Bcl-2 family of anti-apoptotic proteins, and Bcl-2 and Bcl-xl expression levels decline with JAK2 inhibition. The PI3K/AKT pathway also controls expression of mitochondrial apoptotic regulatory proteins, and inhibiting PI3K/mTOR leads to decreased levels of the inactive form of the pro-apoptotic protein Bad. Since STAT3 and PI3K signaling both modulate mitochondrial apoptosis, inhibiting both pathways may further tip the balance of pro- and anti-apoptotic proteins in favor of cell death. Indeed, Britschgi et al. found that combined inhibition of PI3K/mTOR and JAK2/STAT5 leads to activation of the pro-apoptotic protein Bim and degradation of the anti-apoptotic protein Mcl-1.

Breast tumors with co-activation of STAT5 and STAT3 generally have less aggressive features (low histologic grade, lymph node negative status, sensitivity to chemotherapy) than tumors with activated STAT3 alone, suggesting that the tumor-suppressive effect of STAT5 activation may be dominant over the tumor-promoting effect of STAT3 activation. Interestingly, STAT5-mediated gene repression is dominant over STAT3-mediated gene induction for shared target genes.[9] Breast tumors with co-activation of STAT5 and STAT3 are also more likely to be estrogen- or progesterone-receptor positive, making them sensitive to hormonal therapy, and less likely to be triple-negative and thus more clinically aggressive. In a panel of primary breast tumors, 29% display dual activation of STAT3 and STAT5, 40% display STAT3 activation alone, and only 7% display activation of STAT5 alone.[9] The relatively small number of breast cancers with STAT5 activation alone suggests that STAT5 activation may limit the aggressiveness of tumor cells, most likely via its physiologic function of promoting breast epithelial cell differentiation.[8] In light of evidence that STAT5 activation is associated with differentiated breast tumors with more favorable prognoses while STAT3 is associated with more aggressive cancers, it is somewhat surprising that Britschgi et al. discover an apparently contradictory role for STAT5 activation in driving resistance to PI3K/mTOR inhibition. Given the dual functions of STAT5 in promoting proliferation as well as differentiation, the net effect of STAT5 activation on breast cancer pathogenesis may depend on other molecular events in the cell. The authors also report that TNBC lines have a higher baseline of phosphorylated STAT5 than luminal breast cancer cell lines. However, others have consistently observed constitutive activation of STAT3 instead of STAT5 in TNBC cell lines.[9,17]

In summary, Britschgi et al. show that activation of JAK2/STAT5 signaling in response to PI3K/mTOR inhibition enhances the invasiveness and metastatic behavior of TNBC cells. The authors demonstrate that JAK2/STAT5 hyperactivation drives resistance to PI3K/mTOR inhibitors by first restoring activation of AKT downstream of PI3K inhibition and then upregulating IL-8 secretion, a
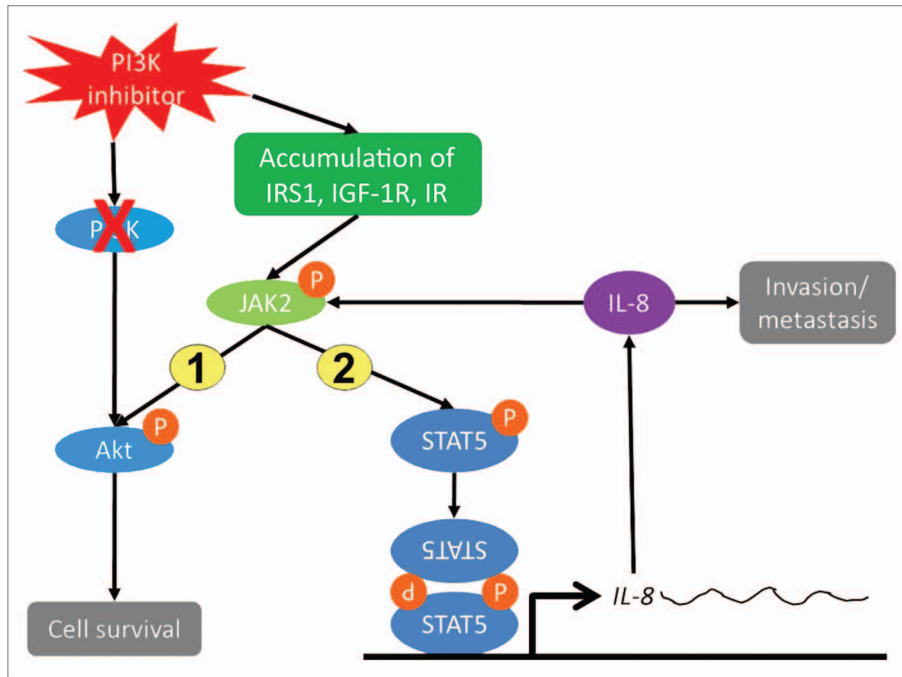
Figure 1. A bimodal JAK2/STAT5 resistance mechanism to PI3K/mTOR inhibition. PI3K/mTOR inhibition leads to (1) accumulation of insulin receptor (IR), insulin-like growth factor 1 receptor (IGF-1R), and insulin receptor substrate 1 (IRS1), which catalyzes JAK2/STAT5 phosphorylation and restoration of Akt phosphorylation and (2) STAT5 transcriptional upregulation of IL-8, which further activates JAK2/STAT5 via a positive feedback loop.

pro-metastatic chemokine that induces positive feedback on JAK2/STAT5 (**Fig. 1**). In the first wave of resistance, accumulation of insulin receptor (IR), insulin-like growth factor 1 receptor (IGF-1R), and insulin receptor substrate 1 (IRS1) lead to JAK2/STAT5 phosphorylation which in turn activates the PI3K/AKT pathway via interaction with the scaffold protein Gab2.[18] This step is independent of CXCR1. In the second wave of resistance, STAT5 upregulates expression of IL-8, which binds to its receptor CXCR1 to trigger increased invasiveness and metastatic behavior.[19] Britschgi et al. found that CXCR1 is differentially expressed among tumor cells, with only 3% of primary tumor cells expressing CXCR1 whereas almost all (96%) circulating tumor cells express CXCR1. The authors clearly demonstrate that inhibiting JAK2 preferentially leads to apoptosis of the CXCR1^{+} subpopulation which is thought to be responsible for tumor seeding and metastasis. Consequently, in addition to circumventing drug resistance, dual inhibition of PI3K/mTOR and JAK2/STAT5 may have the added benefit of reducing metastasis by specifically impacting the survival of tumor-initiating cells.

To our knowledge, this publication is the first description of a JAK2/STAT5 hyperactivation mechanism by which tumors escape from PI3K/mTOR inhibition. The clinical benefit from the combined treatment regimen proposed by Britschgi et al. is potentially of great importance for TNBCs, which are clinically aggressive and highly metastatic tumors. Therefore, this research highlights the importance of understanding the interactions among signaling pathways in cancer cells in order to improve the efficacy of cancer therapies.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

References

1. Foulkes WD, Smith IE, Reis-Filho JS. Triple-negative breast cancer. N Engl J Med 2010; 363:1938-48; PMID:21067385; http://dx.doi.org/10.1056/NEJMra1001389
2. Montero JC, Esparís-Ogando A, Re-Louhau MF, Seoane S, Abad M, Calero R, et al. Active kinase profiling, genetic and pharmacological data define mTOR as an important common target in triple-negative breast cancer. Oncogene 2012; In press; PMID:23246963; http://dx.doi.org/10.1038/onc.2012.572
3. Stemke-Hale K, Gonzalez-Angulo AM, Lluch A, Neve RM, Kuo WL, Davies M, et al. An integrative genomic and proteomic analysis of PIK3CA, PTEN, and AKT mutations in breast cancer. Cancer Res 2008; 68:6084-91; PMID:18676830; http://dx.doi.org/10.1158/0008-5472.CAN-07-6854
4. Wander SA, Hennessy BT, Slingerland JM. Next-generation mTOR inhibitors in clinical oncology: how pathway complexity informs therapeutic strategy. J Clin Invest 2011; 121:1231-41; PMID:21490404; http://dx.doi.org/10.1172/JCI44145
5. Zeng Q, Yang Z, Gao YJ, Yuan H, Cui K, Shi Y, et al. Treating triple-negative breast cancer by a combination of rapamycin and cyclophosphamide: an in vivo bioluminescence imaging study. Eur J Cancer 2010; 46:1132-43; PMID:20156674; http://dx.doi.org/10.1016/j.ejca.2010.01.014
6. O'Reilly KE, Rojo F, She QB, Solit D, Mills GB, Smith D, et al. mTOR inhibition induces upstream receptor tyrosine kinase signaling and activates Akt. Cancer Res 2006; 66:1500-8; PMID:16452206; http://dx.doi.org/10.1158/0008-5472.CAN-05-2925
7. Sansone P, Bromberg J. Targeting the interleukin-6/Jak/stat pathway in human malignancies. J Clin Oncol 2012; 30:1005-14; PMID:22355058; http://dx.doi.org/10.1200/JCO.2010.31.8907
8. Desrivières S, Kunz C, Barash I, Vafaizadeh V, Borghouts C, Groner B. The biological functions of the versatile transcription factors STAT3 and STAT5 and new strategies for their targeted inhibition. J Mammary Gland Biol Neoplasia 2006; 11:75-87; PMID:16947086; http://dx.doi.org/10.1007/s10911-006-9014-4
9. Walker SR, Nelson EA, Zou L, Chaudhury M, Signoretti S, Richardson A, et al. Reciprocal effects of STAT5 and STAT3 in breast cancer. Mol Cancer Res 2009; 7:966-76; PMID:19491198; http://dx.doi.org/10.1158/1541-7786.MCR-08-0238

10. Peck AR, Witkiewicz AK, Liu C, Stringer GA, Klimowicz AC, Pequignot E, et al. Loss of nuclear localized and tyrosine phosphorylated Stat5 in breast cancer predicts poor clinical outcome and increased risk of antiestrogen therapy failure. J Clin Oncol 2011; 29:2448-58; PMID:21576635; http://dx.doi.org/10.1200/JCO.2010.30.3552

11. Vafaizadeh V, Klemmt P, Brendel C, Weber K, Doebele C, Britt K, et al. Mammary epithelial reconstitution with gene-modified stem cells assigns roles to Stat5 in luminal alveolar cell fate decisions, differentiation, involution, and mammary tumor formation. Stem Cells 2010; 28:928-38; PMID:20235097.

12. Nouhi Z, Chughtai N, Hartley S, Cocolakis E, Lebrun JJ, Ali S. Defining the role of prolactin as an invasion suppressor hormone in breast cancer cells. Cancer Res 2006; 66:1824-32; PMID:16452244; http://dx.doi.org/10.1158/0008-5472.CAN-05-2292

13. Sultan AS, Xie J, LeBaron MJ, Ealley EL, Nevalainen MT, Rui H. Stat5 promotes homotypic adhesion and inhibits invasive characteristics of human breast cancer cells. Oncogene 2005; 24:746-60; PMID:15592524; http://dx.doi.org/10.1038/sj.onc.1208203

14. Tworoger SS, Hankinson SE. Prolactin and breast cancer risk. Cancer Lett 2006; 243:160-9; PMID:16530327; http://dx.doi.org/10.1016/j.canlet.2006.01.032

15. Tworoger SS, Hankinson SE. Prolactin and breast cancer etiology: an epidemiologic perspective. J Mammary Gland Biol Neoplasia 2008; 13:41-53; PMID:18246319; http://dx.doi.org/10.1007/s10911-008-9063-y

16. Letai A, Sorcinelli MD, Beard C, Korsmeyer SJ. Antiapoptotic BCL-2 is required for maintenance of a model leukemia. Cancer Cell 2004; 6:241-9; PMID:15380515; http://dx.doi.org/10.1016/j.ccr.2004.07.011

17. Marotta LL, Almendro V, Marusyk A, Shipitsin M, Schemme J, Walker SR, et al. The JAK2/STAT3 signaling pathway is required for growth of CD44$^+$CD24$^-$ stem cell-like breast cancer cells in human tumors. J Clin Invest 2011; 121:2723-35; PMID:21633165; http://dx.doi.org/10.1172/JCI44745

18. Vafaizadeh V, Klemmt PA, Groner B. Stat5 assumes distinct functions in mammary gland development and mammary tumor formation. Front Biosci 2012; 17:1232-50; PMID:22201800; http://dx.doi.org/10.2741/3983

19. Waugh DJ, Wilson C. The interleukin-8 pathway in cancer. Clin Cancer Res 2008; 14:6735-41; PMID:18980965; http://dx.doi.org/10.1158/1078-0432.CCR-07-4843