

EDITORIAL COMMENT

New Insight Into Cardioprotection From Anthracyclines



Still Converging on the Mitochondria*

Qun Chen, MD, PhD,^a Giselle C. Meléndez, MD,^{b,c} Edward J. Lesnefsky, MD^{a,d,e,f}

Anthracycline chemotherapy remains a cornerstone of multiple cancer treatment regimens, including for lymphoma and breast cancer, although concerns for anthracycline-mediated cardiac toxicity persist.¹ Although meticulous dose adjustment has largely alleviated acute cardiac toxicity, subacute and chronic anthracycline-induced cardiac dysfunction remains a substantial clinical challenge and has spurred extensive study into the mechanisms of anthracycline-mediated cardiac toxicity. Fortunately, the potential mechanisms of cardiac toxicity appear distinct from the mechanisms of anthracycline-mediated tumor cell killing. Previously studied mechanisms of anthracycline-mediated cardiac toxicity include the enhanced production of reactive oxygen species (ROS) from mitochondria,² with the oxidatively sensitive mitochondrial phospholipid cardiolipin a prominent target.³ Iron-catalyzed mechanisms enhance the

ROS-mediated injury⁴ and lead to iron-mediated cardiomyocyte death.^{5,6} Alternatively, anthracyclines inhibit topoisomerase 2 α , a key enzyme for DNA repair, leading to tumor toxicity. Unfortunately, inhibition of topoisomerase 2 β in the mitochondria leads to mitochondrial damage, increasing cardiac toxicity, potentially via greater mitochondrial production of ROS.^{7,8} Dexrazoxane was developed as a cell-permeable iron chelator to address potential iron-enhanced ROS-mediated cardiac toxicity. Intriguingly, this compound also exhibits partial inhibition of topoisomerase 2 β ,^{1,7,9} potentially consolidating mitochondria-based cardiac protection. However, clinical intervention with dexrazoxane has yielded only modest protection, mainly in the pediatric population.^{7,9} Thus, additional mechanistic insight into anthracycline-mediated cardiac toxicity is needed.

Cheng and his laboratory have shown that cyclin-dependent kinase 2 (CDK2) is induced by doxorubicin therapy, leading to cardiomyocyte cell death.^{10,11} In the study published in this issue of *JACC: CardioOncology*, they explored the downstream effector signaling of CDK2 activation.¹² They hypothesized that retinoblastoma-like 2 peptide (RBL2/p130), an endogenous inhibitor of CDK2, would mitigate CDK2-driven cardiac injury from anthracyclines. Using genetic murine models of retinoblastoma 2 (rbl2) knockout and overexpression, they found that knockout of rbl2 increased CDK2 expression and enhanced anthracycline toxicity both in vivo and in studies of cultured cardiomyocytes in vitro. In vivo, cardiac contractile dysfunction was increased, heart weight was decreased, and myocardial fibrosis was increased following 1 month of weekly doxorubicin therapy (5 mg/kg/wk). In vitro, down-regulation of rbl2 led to CDK2-dependent forkhead box O1

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From the ^aDivision of Cardiology, Department of Internal Medicine, Pauley Heart Center, Virginia Commonwealth University, Richmond, Virginia, USA; ^bSection on Cardiovascular Medicine, Wake Forest School of Medicine, Winston-Salem, North Carolina, USA; ^cSection on Comparative Medicine, Department of Pathology, Wake Forest School of Medicine, Winston-Salem, North Carolina, USA; ^dDepartment of Biochemistry and Molecular Biology, Virginia Commonwealth University, Richmond, Virginia, USA; ^eDepartment of Physiology and Biophysics, Virginia Commonwealth University, Richmond, Virginia, USA; and the ^fMedical Service of the McGuire Veterans Affairs Medical Center, Richmond, Virginia, USA.

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(FOXO1)-mediated increase in the mitochondria-localized proapoptotic protein bim, with evidence of increased cardiomyocyte programmed cell death and initial data to implicate dysfunctional mitochondria in the pathway. Anthracycline-induced CDK2-mediated activation of FOXO1 increased expression of *rbl2* mRNA with initial increases in *rbl2* content (net protective) but followed by decreased FOXO1 mediated *rbl2* protein stability (potential depletion of *rbl2* leading to additional cardiomyocyte injury). Overall, the investigators conclude that the net FOXO1-driven increase in *rbl2* gene expression represents an attempt at protective adaptation, though the potential complexity is apparent and provides possible insight into their human studies of *rbl2* polymorphisms. Appropriate models were used to establish the mechanistic pathway, with the minor limitations that the model of anthracycline toxicity was acute; molecular studies were performed in neonatal, not adult, cardiomyocytes; and the genetic manipulations were not cardiomyocyte specific. Also, the up- or down-regulation of *rbl2* content was present from birth and thus present during development, rather than conditionally induced only during adulthood. However, the alteration of *rbl2* during the entire life span would model the subsequent study of human *rbl2* polymorphisms.

Nonetheless, the investigators also supply intriguing initial human data that alteration in *rbl2* function likely affects clinical sensitivity to anthracycline cardiac toxicity. There are 6 missense variants in the human *RBL2* gene with allele frequencies >0.1%.¹² One, the rs17800727 G allele (A>G), is the most common, with a frequency >21%. This G allele has a lower expression of *rbl2* in the human left ventricle and is surprisingly associated with a decreased risk for anthracycline cardiomyopathy, lowest in homozygotes for the G allele in contrast to a 3-fold increased risk for anthracycline cardiomyopathy in AA homozygotes.¹² The traction to human disease is important, though the complexity of the association between *rbl2* and cardiomyopathy is complex, as initial interpretation would conclude that the human findings of reduced *rbl2* content in the left ventricle seen with the G allele should exacerbate, not reduce, cardiac risk. The investigators speculate that, consistent with the murine results, the G allele might lead to lower CDK2-FOXO1 activity than the presence of the A allele. Although these results certainly require further validation given the relatively small number of patients in each of the 2 clinical cohorts, the results merit further genetic study

given the potential to provide a prospective risk index for anthracycline-induced cardiac toxicity.

The study of Xia et al¹² is important in several aspects. First, CDK2 is identified as a mediator upstream of the mitochondria and topoisomerase 2 β ,^{7,8} as well as oxidative mitochondrial metabolism mechanisms.^{2,4} The possible regulation of topoisomerase 2 β and mitochondrial electron transport by the CDK2-*rbl2*-FOXO1 axis should be considered. As the investigators speculate, the potential to modulate CDK2 in order to increase *rbl2* (protective) expression in contrast to FOXO1 (deleterious) is a possible approach to cardiac protection¹² and certainly merits future investigation. Of equal importance, it becomes critical to evaluate whether potential known cardioprotective interventions against anthracycline cardiac toxicity, including remote preconditioning,¹³ moderate exercise,¹⁴ or pharmacologic therapy,^{15,16} affect the CDK2 signaling axis.

The present study of CDK2 signaling via FOXO1 and bim yet again highlights the importance of the mitochondria and places emphasis on the mitochondria as a major effector of anthracycline toxicity. Thus, potential approaches to chronically modulate mitochondrial metabolism to mitigate oxidant- and calcium-driven myocyte injury via the use of hydrogen sulfide,^{17,18} nitrite and nitrate production,² or even pharmacologic modulation of mitochondrial complex I^{19,20} deserve future consideration. Also, the potential to protect nonmyocyte cells in the myocardium, including fibroblasts, needs to be evaluated, as anthracyclines directly phenoconvert fibroblasts into myofibroblasts and promote the secretion of excess collagen, promoting interstitial myocardial fibrosis, independent of cardiomyocyte death and replacement fibrosis.^{21,22}

The CDK2-*rbl2*-FOXO1 pathway may provide a future opportunity to prospectively assess the potential for anthracycline-mediated cardiac toxicity,^{10,11} allowing the selection of chemotherapeutic agents or doses tailored to individual patient risk. It will be especially important to assess if clinically accessible tissues, including white blood cells,²³ or perhaps even skeletal muscle,²⁴ can serve as tissue surrogates for the heart to assess these key signaling pathways to use biochemical and molecular techniques to assess the patient-specific risk for chemotherapy-induced cardiac toxicity.

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ADDRESS FOR CORRESPONDENCE: Dr Edward J. Lesnefsky, Cardiology Section, Medical Service 111(J) McGuire VA Medical Center, 1201 Broad Rock Boulevard, Richmond, Virginia 23249, USA. E-mail: edward.lesnefsky@va.gov.

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