Target acquisition and acute promyelocytic leukemia

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Acute promyelocytic leukemia (APL) is characterized by a variety of chromosomal translocations into the retinoic acid receptor-α (RARα) gene. The first of these cloned was t(15;17), a translocation that results in fusion of the PML gene with RARα. This translocation is also the most prevalent, found in 95% of APL cases. Other translocations associated with fusion proteins in variant APLs were subsequently discovered: t(11;17) PLZF-RARα (found in less than 5% of cases), another t(11;17) translocation, NuMA-RARα (less than 1%), and t(5;17) NPM-RARα (less than 1%). All of these, with the exception of the PLZF-RARα translocation, are associated with a disease that responds to high doses of retinoids (1). The realization that all of these translocations involved RARα led to the proposal that the disease is caused by dysfunctional regulation of retinoid-inducible genes critical to myeloid differentiation. Recent work supporting this idea has shown that PML-RARα has a reduced ability to release transcriptional corepressors such as SMRT and NCoR in response to retinoids and that the PLZF portion of the PLZF-RARα fusion constitutively binds these repressors (2, 3). This would suggest that in APL cells, RARα target genes may be transcriptionally super-repressed, and may also explain why PML-RARα APL responds to high doses of retinoids, whereas PLZF-RARα APL is retinoid resistant. The ultimate proof of the hypothesis, however, has awaited the […]

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Previous studies have shown that C/EBPε transcription is induced by retinoids during granulocytic, but not monocytic, differentiation (5). Mice in which the gene is deleted exhibit impaired granulopoiesis (6). Therefore C/EBPε has many of the predicted characteristics of a critical target gene in APL. It remained to be demonstrated that its promoter contained a functional retinoic acid response element (RARE) and that overexpression of C/EBPε alone was sufficient to induce granulocytic differentiation. These key experiments are presented in this issue.

The authors identified a RARE in the C/EBPε promoter and showed it to be functional in transfection assays. They demonstrated that C/EBPε expression could be induced in a ligand-dependent manner by PML-RARα (a fusion product found in a retinoid-sensitive APL) but not by PLZF-RARα (a fusion product found in a retinoid-resistant APL). Overexpression of C/EBPε in U937 cells was then shown to be sufficient for the induction of granulopoiesis, as evidenced by morphological changes and the expression in the expression of granulocytic markers such as CD11b, CD66b, lactoferrin, and collagenase. The expected decrease in proliferation and increase in apoptosis were also observed. Therefore, the authors are justified in proposing that C/EBPε may be an important downstream target of RARα in myeloid differentiation.

What makes C/EBPε especially intriguing in this role are the findings, outlined in an earlier paper from the Koeffler laboratory, that suggest that C/EBPε expression may be a node at which cross-talk between regulatory pathways occurs. The differentiation agents DMSO and HMBA were shown to induce C/EBPε mRNA in the NB4 APL cell line, but only after the cells were primed by a transient 30-minute incubation with retinoic acid (7). The characterization of the pathways that cooperate with retinoids in the induction of C/EBPε, and indeed independent pathways that regulate C/EBPε expression or function, will now be a priority. Knowledge of such pathways may lead to the development of therapeutic strategies whereby C/EBPε transcription can be induced in the absence of retinoids. These strategies might be especially useful for the treatment of retinoid-resistant APLs, such those resulting from the t(11;17) PLZF-RARα translocation, or APLs in which retinoid resistance is mediated by mutations in the PML-RARα ligand-binding domain. It will be a challenging task, however, to unravel the complexities of the gene’s regulation. It is already known, for example, that the C/EBPε gene can be transcribed from alternate promoters (8).

Identification of the genes regulated by C/EBPε will give a more complete understanding of its role in myeloid differentiation; the application of recently developed DNA array technologies may accelerate this process. C/EBPε is a member of a growing family of transcription factors; in addition to C/EBPε, at least 3 of these factors (C/EBPα, β, and δ) are expressed during hematopoiesis (9). The various C/EBP family members are known to be capable of both homo- and heterodimerization, and because the

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in U937 cells in the absence of retinoids did not repress C/EBPε expression, whereas the overexpression of PML-RARα did. This would suggest that PLZF-RARα and PML-RARα might act through different pathways, with different target specificity.

Now that we are beginning to identify downstream targets of the retinoid receptors, we can look forward to a great increase in our understanding of the molecular basis of myeloid differentiation. This, allied with recent studies that have shed light on the function of PML in cell growth, apoptosis, and transcriptional regulation (1), should pave the way for a deeper understanding of the molecular events that are involved in the development of APL.