TO THE EDITOR: Because of irregularities in the randomization procedures, we wish to retract the following article: Primary Prevention of Cardiovascular Disease with a Mediterranean Diet. N Engl J Med 2013;368:1279-90. DOI: 10.1056/NEJMoa1200303.1 We have reanalyzed the data and have published a new report: Primary Prevention of Cardiovascular Disease with a Mediterranean Diet Supplemented with Extra-Virgin Olive Oil or Nuts. N Engl J Med. DOI: 10.1056/NEJMoa1800389.2
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Molecular Minimal Residual Disease in Acute Myeloid Leukemia

High-Flow Oxygen Therapy in Infants with Bronchiolitis

Are We Prepared for Nuclear Terrorism?
Molecular Minimal Residual Disease in Acute Myeloid Leukemia

TO THE EDITOR: Jongen-Lavrencic and colleagues (March 29 issue)1 highlight the clinical usefulness of a next-generation sequencing panel to identify minimal residual disease in patients with acute myeloid leukemia (AML) during complete remission. The authors found that the detection of nonclonal hematopoiesis–associated mutations (non-DTA mutations, or those not involving DNMT3A, TET2, or ASXL1) during complete remission predicted a poor prognosis; however, these findings are called into question by the considerable rate of false negative results of next-generation sequencing.

In Figure 3 of the article, available at NEJM.org, the rate of false negative results with next-generation sequencing (i.e., a negative result on next-generation sequencing and a positive result on multiparameter flow cytometry) was 12.1% (among 41 of 340 patients). Thus, next-generation sequencing had a disconcertingly high false negative rate of detection of non-DTA mutations during complete remission. Given that patients with negative results on next-generation sequencing and positive results on multiparameter flow cytometry have a worse prognosis than those with negative results on both tests, the data shown in Figure 2 of the article are called into question by the false negative results with next-generation sequencing. In that figure, next-generation sequencing was used to stratify patients according to detection or no detection of non-DTA mutations during complete remission.

Thus, it is likely that a considerable number of patients in the “no detection of non-DTA mutation” category were mistakenly classified because of a false negative result on next-generation sequencing. Do the authors have a sense of how many patients in this group had minimal residual disease that was detected by means of multiparameter flow cytometry?

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