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Editorial

The value of cell line validation

Cell line contamination and misidentification was first reported in HeLa cells in 1974 (1). However, the problem is still widespread: at least 15% of reported cell lines may be cross-contaminated or misidentified (2). As a result, numerous research findings have been invalidated, careers have been damaged, and millions of dollars have been wasted. Fortunately, the scientific community has been stepping up its efforts to address the problem. A statement about cell line validation is now a prerequisite for acceptance at all American Association for Cancer Research journals. Testing will also be considered in the review process for all National Institutes of Health grant proposals. Failure to address the issue is likely to lead to a rejection. In addition, many academic institutions require that their researchers validate their cell lines.

Some researchers are reluctant to validate their cell lines because testing costs time and money. However, access to more efficient technologies has made validation easier: short tandem repeat (STR) testing, the most commonly recommended method for cell line validation, can be outsourced; this makes it a viable option for small laboratories.

STR testing commonly involves 9 markers and a cut-off score of 0.8 (this score is a numerical code that can be compared with others in a database). In this issue of *Neuro-Oncology*, Bady et al (3) provide guidance for researchers who are validating their own cell lines. The authors performed a cell validation study of 39 commonly used glioma cell lines and found that a score of 0.8 was insufficient for reliably distinguishing cell line origins when using 9-marker profiles. The cell line scores were compared with those in the DSMZ database; 3 lines were found to be misidentified. However, a comparison of paired, randomly arranged profiles revealed a score of more than 0.8 for 1 pair and more than 0.7 for 8 pairs. When all markers were used, no pairs scored higher than 0.7. The authors concluded that a reference database with a limited number of duplicates and simulation procedures is useful for more accurately evaluating similarity values.

Hopefully, more precise testing standards, such as those suggested by Bady et al (3), will further minimize the effects of contaminated and misidentified cell lines on the body of scientific knowledge. In furtherance of this goal, *Neuro-Oncology* may soon require a statement about cell line validation for all submitted papers: where and when the cells were obtained, whether they were authenticated, the testing procedures used, and when they were last authenticated. We understand that requiring this information may be a burden for our authors, but we believe that it is crucial to ensuring the scientific integrity of our journal and the field at large.

W.K. Alfred Yung, Editor-in-Chief

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