Transcript Details
This is a transcript of an educational program. Details about the program and additional media formats for the program are accessible by visiting: https://reachmd.com/programs/project-oncology/risk-stratification-models-for-precursor-diseases-in-multiple-myeloma/26581/

ReachMD
www.reachmd.com
info@reachmd.com
(866) 423-7849

Risk Stratification Models for Precursor Diseases in Multiple Myeloma

Announcer Intro

This is *Project Oncology* on ReachMD, and on this episode, we'll hear from Dr. Elizabeth O'Donnell, who's the Director of Early Detection and Prevention at Dana-Farber and an Assistant Professor of Medicine at Harvard Medical School. She'll be discussing risk stratification models for precursor diseases in multiple myeloma. Here's Dr. O'Donnell now.

Dr. O'Donnell:

So the risk stratification models that we use currently, particularly for smoldering myeloma, are put forth by the International Myeloma Working Group, which is a consortium of myeloma physicians across the world, and they really rely upon the amount of protein or the burden of disease that's measurable, so looking at the amount of monoclonal protein, the free light chain ratios, percent of plasma cells in the bone marrow, and the cytogenetics that we find in the bone marrow biopsy. And those are a great starting place, and those are the tools that we use, and those risk models have continued to improve over time.

Dr. Ghobrial recently published the PANGEA model, which uses other metrics, such as change in hemoglobin and kidney function, and I think that that's a great starting point; but what we appreciate—anybody who's taking care of plasma cell dyscrasias—is that not everybody follows the rules. And so there are patients who have high-risk cytogenetics that don't progress and standard-risk that do, and when you see exclusively precursor disease—which is what I focus on now—when you start to see it in volume, what you realize is there really are people who are just indolent. Their levels stay flat, there are some that then trend up very gradually, and then there are others who have a much greater rate of change. And while the numbers may be low, I think that rate of change is very significant. So how do we incorporate something like that into our prognostication models?

And then beyond that, what are other factors, biological factors? Are there specific genes and gene expression profiles that really identify those high-risk people? So can we take a population, apply some of our known criteria, which are usually extremely helpful, but then go beyond and really think about next-generation sequencing and some of other techniques that we now have to look for other factors that might better help us identify who is at greatest risk of progressing versus those who are not? And if we can start to confidently say this person has these additional factors that put him at greater risk, then I think we can start to make a case for how we can identify people who might be the right people to treat in a precursor disease state.

Anybody who does precursor disease knows that there are those who progress and those who don't, and we all know that we're not great at—even when we use these risk models—being right all the time, and it creates an actual hesitancy to want to introduce treatments, particularly toxic treatments into people that may or may not progress. There are definitely people who want therapy, who need therapy, and who are clearly on a path to progression, but there are a lot in between, and I think we need to get better. We need to define better variables and create better tools to address that large portion of people who are unanswered questions about their risk of progression.

Announcer Close

That was Dr. Elizabeth O'Donnell discussing risk stratification models for precursor diseases in multiple myeloma. To access this and other episodes in our series, visit *Project Oncology* on ReachMD dot com, where you can Be Part of the Knowledge. Thanks for listening!