Pharmaceutical Executive

Adjusting for Tumor Mutations: Q&A with Dr. Brian Corgiat

Mike Hollan, Dr. Brian Corgiat | November 10, 2026

Ignite Proteomics' senior clinical research scientist discusses how flaws in testing tumors may lead to some patients not receiving the correct treatment.

Pharmaceutical Executive spoke with Dr. Brian Corgiat, senior clinical research scientist at Ignite Proteomics, about potential issues in the way that cancer treatments are prescribed. According to him, errors may be made in the way that tumors are tested, which can cause problems down the road for the patient.

According to Dr. Corgiat, treatment plans don't always take tumor mutation into consideration. This is especially true when cancers resurface after initial treatments have ended and new tumors may have formed.

The solution is to view cancer tests as snapshots of a specific moment and measuring which proteins are being activated at that moment. If not, patients may receive treatments that are targeting elements of the tumor that aren't activated and reduce the effectiveness of the overall treatment.

Pharmaceutical Executive: How do tumors change over time, and how does this impact treatment?

Dr. Brian Corgiat: Tumors are effectively cells, right? They're living, breathing cells, and so tumors can easily change over time. Whether it's just through the course of natural development and biology, but also (typically in the cancer space) if you're applying some sort of therapeutic or drug toward a cell, you're going to kill off some of the cells that are active in certain parts, then you're going to see some of those cells survive.

Or you're going to see some resistance mechanisms in some of the cells shift, and so the cells that may survive or are going to be slightly different than the initial ones, or if these resistance mechanisms start to click on, they're going to be different than that kind of original cell.

This is why when you'll see tumors early on, they might be very different than what you see in a recurrent or later tumor. That's partially why it’s important to look at snapshots of these things to hopefully help align the therapeutic with the current tumor.

PE: In what ways can testing tumors after recurrence be improved?

Corgiat: One of the ways is a test that looks specifically at what's driving a tumor per se more so than what's the stable phenotype of the tumor. That’s a lot of genetic testing and a lot of immunohistochemistry testing.

You're going to get a very a somewhat static response if you either have the mutation or you don't. There are some cases where you maybe will induce a mutation, but those are a little more static across time.

We really like to have a test that can actually look at what's driving your tumor as you take out that biopsy, and so you want that snapshot. What we like to think about a phospho proteome, or active switches. The question is: is this protein inside the cell on or off at this specific time?

You can start to then say that in this recurrent tumor or this biopsy we have right now in front of us, what really is driving that tumor? You still will have some of those mutations, and you still will have some of those IHC readouts. But whether those are what is driving the tumor at that specific time is really missing in a lot of tests. And so, adding that to the panel of tests would be really exciting.

PE: Do changes in a tumor have a significant impact on treatment options?

Corgiat: If you have a change (such as a resistance mechanism), your old treatment is likely not going to work. You're targeting something that is no longer driving the tumor growth or expansion. If you're targeting the wrong thing, there's a high probability that your tumor is just going to grow and you're going to progress, and so I would say it's a significant issue.

If it's a as a major shift or even a minor shift, you want to be aligning with what is driving the tumor at that time.

If you're not targeting what the tumor is shifted to, then your treatment is likely going to be ineffective. You want to have a test or a readout of a biopsy of what is going on at that specific point in time to align the therapy with what's actually driving a tumor at that moment.

Using bad information or old information to guide treatment decisions is not what anybody wants. You're not going to have a highly successful response if you're charging the wrong thing.

PE: What is an effective method of accurately measuring tumors?

Corgiat: What we do is we look at the phosphoproteome. So, we are looking at phosphorylation states within the cancer of a specific patient at a very specific time.

We'll get a biopsy, and we'll say, “this is actually the active switches and this is looking at what the actual drug targets.” By looking at the phosphorylation state of these proteins, and we can hone in on whether IHC can tell you if a protein is present.

But, it can't really tell you if it's on and or driving the patient's tumor. We know these proteins are there, and now we can assess whether it's really on or off. Then we can say if there’s a therapeutic designed to target this protein.

If we're not really seeing that it's turned on, but we do see over here that these things are actually turned on, we may want to consider some of these other therapeutics that target these things that are actually turned on at this specific time.

We can really look at a snapshot and say, "Hey, this is what's turned on inside your cell, and this is where we think you should maybe take a look at some of these therapeutics, and maybe use those as treatments."

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