# Optical Genome Mapping: A One-Stop Shop for Genome Assessment?

October 11, 2024

**Lisa Tomcko:**

Welcome to the latest edition of the College of American Pathologists CAPcast. I'm Lisa Tomcko, content strategist with the CAP.

In many laboratories, innovative genomic studies center on detecting and excluding single nucleotide variants. While evaluation of structural variants remains most often performed by traditional cytogenetic approaches, these unaddressed blind spots in cytogenetic studies leave room to improve detection of clinically relevant structural variants through other methodologies including optical genome mapping, or OGM. OGM is an imaging technology that evaluates the fluorescent labeling pattern of individual DNA molecules with the resolution far exceeding conventional cytogenetic approaches, offering pathologists great potential.

Joining me today are Dr. Annette Kim and her colleague, Dr. Adrian Dubuc, to discuss this technology and its opportunities. Dr. Kim and Dr. Dubuc, would you like to introduce yourselves?

**Dr. Annette Kim:**

Hi, my name is Annette Kim and I am the director of the division of diagnostic genetics and genomics at the University of Michigan and Michigan Medicine.

**Dr. Adrian Dubuc:**

And my name is Dr. Adrian Dubuc. I'm the vice chair of clinical research and the director of the cytogenetics lab here at Roswell Park Comprehensive Cancer Center.

**Lisa Tomcko:**

Excellent. Thank you both for being here. And with that let's get into our discussion.

**Dr. Annette Kim:**

Adrian, it's wonderful to be here today with you. I wanted to just, if you don't mind, give us all a little bit of background of some of the traditional cytogenetic methods and what types of alterations that they can detect.

**Dr. Adrian Dubuc:**

Absolutely. And it's great to see you again, Annette. So I think where I'd really like to start is what I think of as the definition of cytogenetics. And for me that really is the numerical or the structural evaluation of the genome. And so that's a really broad definition. I think when most people in our field-- geneticists or pathologists--think about cytogenetics, they think of probably one test primarily in chromosome banding analysis or karyotyping. And the other one that often comes to mind is FISH, or fluorescence in situ hybridization. So I just want to spend a little bit of time going over each just to set the stage for the rest of the conversation. So when we talk about karyotyping, really what we're talking about is the visual assessment of chromosome morphology, and this is done by culturing and capturing cells and metaphases. We use as geneticists specific stains that create the expected and characteristic banding patterns that can be used to detect really a wide array of genomic alterations that occur from translocations to deletions, from insertions to changes in ploidy states.

But often these changes have to be restricted to ones that we can visually appreciate and therefore that are greater than seven to 10 megabases in range. In fact, there's a significant amount of our understanding of the types of genomic alterations that occur in cancer and really in development have stemmed from our ability to culture cells and to examine in chromosome morphology. And it's really through this chromosome banding analysis that's been performed in a clinical setting for the past 50 years. Now from a FISH perspective, this is a technology which also evaluates the same types of definitions that I described before, numerical or structural changes. But in this case it uses fluorescently labeled DNA and works through the purpose of complementarity where we evaluate the hybridization of a specific region or probe to a particular area of the genome. This is far superior resolution to karyotyping.

We're working at the a hundred kilobase or the one megabase range and allows us to ask a very specific question and answer a very specific question in that way. So in the context of cancer based analysis, is there a rearrangement of the M locus and how does that impact our ability to make a diagnosis of high grade lymphomas? Or another example would be how many copies of HER2 do we see and how does this impact of treatment for a breast cancer perspective? So really karyotyping and FISH are really the primordial or sort of these essential technologies or assays that we use a set of geneticists and have formed really the core of the technologies that you'll see in most clinical diagnostic laboratories.

**Dr. Annette Kim:**

So you mentioned some of the capabilities of those cytogenetic methods. What are some of their liabilities?

**Dr. Adrian Dubuc:**

A great question, and I think it's so important to acknowledge in our field how much every test we have irrespective of the type of lab that we're running has inherent limitations. And cytogenetics is absolutely no exception to that rule. So we can think of this from a broad perspective and from a broad perspective, really karyotyping and FISH both suffer from reduced resolution when we compare to the types of resolution we can achieve through traditional molecular based approaches. When you compare to the single nucleotide resolution that you can often achieve through NGS approaches to the hundred kilobases to multiple megabases, this is millions of base pairs that we're looking at when we're evaluating traditional cytogenetic approaches. There's also the visual assessment, which is by definition subjective in terms of either our assessment of chromosome morphology, how do they actually look and how do we interpret through the visual assessment that we're performing.

And similarly for FISH, we're doing a visual assessment of how close or far or how many copies we see of individual FISH probes or individual hybridization signals. We know more specifically for karyotyping that there are some significant challenges. And one of the biggest ones is that performing a chromosome banding study definitively necessitates having cells dividing in culture. So the first step is putting cold cells into culture, and if cells don't divide effectively in vitro, we don't have the capacity to achieve a chromosome banding result. We also know that there's types of genomic alterations that are cytogenetically cryptic, which is to say these are undetectable visually through our analysis of the genome. There are times that it's too pale. Bands the genome that have translocate or rearrange in some manner that just visually we can't appreciate. And similarly we know with FISH-based studies, there are certain areas of the genome where the FISH probe may give you a false negative or false positive results in part due to the size of the probe that potentially can span multiple genes in those instances.

**Dr. Annette Kim:**

Along those same lines, I mean can you talk about the nature of FISH being targeted versus assessing the whole genome, for instance?

**Dr. Adrian Dubuc:**

Absolutely. And this is really the nature of the test specifically. So when we perform a chromosome analysis, we're talking about a genome wide test at a single cell, albeit at a low resolution. When we talk about FISH, we're asking a very targeted question. So we have to have a priority knowledge of really what are the targets we're looking for, and we can only answer a question about the specific targets that we're evaluating. And this is in part really challenged some of our understandings, particularly if you think of some disease types where the number of rearrangements or alterations is growing exponentially. And BALL will be a prime example of this where we have so many individual rearrangements or different copy number states to evaluate. It's certainly challenging sometimes the way we're able to offer FISH as an effective technology to rule in and rule out all the possibilities that exist.

**Dr. Annette Kim:**

And then one last area I think we should touch upon where FISH and karyotype have encountered challenges, which is LOH, right? Can you talk about loss of heterozygosity and then maybe touch upon a little bit about chromosomal microarrays and where their strengths are?

**Dr. Adrian Dubuc:**

Great question. So chromosomal microarray didn't start with, but just again set the stage a little bit with this technology. It's a technology which has really initially emerged for the detection of variation in normal development. And I'd say in the last five years or so, you've seen a rapid uptick of this potential technology. This is an assay which is designed to detect copy number gains or losses typically at a resolution of anywhere from 50 kilobases to a hundred kilobases in size if not larger, and can also detect regions of changes in heterozygosity. And so this is an important concept for both disease and development. When you have loss of heterozygosity from a cancer perspective, it can also suggest that you have two copies or bilic and activation of a particular tumor suppressor gene by example. And we can look for large regions typically five to 10 megabases in size that can be indicative of these types of changes that occur currently in neoplasms.

So I think where we're seeing in diagnostic medicine, chromosomal microarray being used increasingly from a cancer based perspective, it's often in addition to or sort of collaborating with the results we see from karyotyping or FISH. And certainly from a constitutional perspective, this technique is increasingly being used to frontline test when we talk of types of prenatal diagnostic studies that are performed. And maybe just to expand on that briefly, it's important to note that while a lot of what I'll be talking as someone who works in a cancer center is cancer centric, there are implications from a genomics perspective broadly that we may have to provide tests and results as it relates to development. And increasingly chromosomal microarray, again, has become a frontline test for prenatal diagnostics as really effective means of detecting broad copy number alterations that can be important.

**Dr. Annette Kim:**

If I could sum up everything you just said, using chromosomal banding analysis or karyotype, it is unbiased, it's genome wide and it is single cell resolution. But the sort of analytical resolution is very, very high on the mega based scale and you need viable cells and it's really good for some copy number and structural variants where the banding patterns are not confounded, whereas FISH is very targeted. You can use it on viable or fixed cells. It is also a single cell method, but its resolution is now down to the sort of base to megabase scale. And it also is pretty much copy number and structural variance. And then chromosomal microarray doesn't do the structural variance but can do copy number and loss of heterozygosity again, and it's again a genome wide analysis, but it's again, bulk. It's a bulk specimen and the resolution is pretty good on the kilobase scale.

**Dr. Adrian Dubuc:**

Absolutely. That's a perfect summary and I think I'll just to add to that slightly, I'll say, so we have three different tests with three different capabilities and really it's pick which combination you can to try to sort of cover all the gaps to plug all the holes because no one single test will give the combination of resolution copy number and structural variation detection that we really want to have and achieve in this field.

**Lisa Tomcko:**

We're going to take a quick break from today's episode to talk about an exciting new program from the CAP, now open for registration. When it comes to successfully starting a new job, preparation is key. Introducing the job prep boot camp from the CAP, a fast-paced interactive virtual review designed just for pathologists like you. Refresh your skills in signing out less familiar cases, access the library of resources to ensure thorough and accurate case workups, learn to recognize and avoid common pitfalls, get guidance from experts and tap into a supportive network exclusive to the job prep bootcamp alumni community, you can find the link in the episode description to get more details and register. And now back to the episode.

**Dr. Annette Kim:**

So with that then, what is the role of optical genome mapping? Maybe you could start off by telling us a little bit about the technology and then the ways in which it fills that gap and actually in some ways ends up being sort of a one-stop solution in the correct clinical scenario.

**Dr. Adrian Dubuc:**

Absolutely. For those of you who haven't been exposed to optical genome mapping, this is a technology, a really novel imaging technology, which really starts and is predicated on the isolation of these ultra high molecular weight DNA molecules. So we take DNA, I'll go from a methodology perspective and then we'll talk through what it gives you. But from a methodology perspective, we have a very well established technology and technique that is designed to isolate DNA while minimizing the shearing forces that typically occur in standard DNA isolation methods. The consequence of that or the impact of that is that we're able to isolate fragments of DNA that are hundreds of kilobases to megabases in size. And this is in contrast to the 10 kilobases or so or smaller than you typically get from most standard DNA isolation methodologies. So once you're able to isolate these extremely large DNA fragments, what this technology then does is it uses an enzymatic labeling of a fluorescent molecule onto a hexamer motif.

The C-T-T-A-A-G sequence that occurs every 14 to 17 motifs, if you will, in a hundred kilobase section with this labeled DNA, can then be pulled through and linearized through a flow cell. And this particular flow cells meet up hundreds of thousands of nano channels that linearizes DNA, which can then be subsequently imaged. And so what we've done is we've taken these large DNA fragments essentially and turned it into a barcode. So we take images of these labeled DNA molecules, which can subsequently be digitized, and we compare the specific labeling pattern of individual DNA molecules to a known reference genome that's been established, the human genome and computationally. Now there are algorithms that exist. This is part of a software suite that has been produced by Bionano, the company that's developed this particular assay that allows you for rapid and effective detection of variation in the expected banding or labeling pattern.

So what do you get from that? Well, in a three day period from DNA isolation of sample receipts, you can get to a fully analyzed genome that has the potential to detect the vast majority of structural or copy number alterations. We expect to see in the context of either disease or development, we can look at deletions, which is to say less than the expected gap between two labeling molecules. We can see duplications, rearrangements, translocations, and in addition to this, you can also count the number of individual molecules to get a copy number output in a very similar manner that we do for array based studies, as well as getting the entire analysis Circos plot that shows us the genome wide variation as well as regions of heterozygosity or loss of heterozygosity or absence of heterozygosity that occurs. So when we talk about copy number structural rearrangements or AOH or LOH absence or loss of heterozygosity, all those techniques can be detected by optical genome mapping and done to a level of really the exon. In these instances, we can pick up break points down to about a 500 base pair resolution so far surpassing what we're able to achieve by any of the current set of genetic methodologies. So a really exciting and powerful technique, and I'll say one of the strengths is really predicated on having an end-to-end solution from very clearly outlined kits that allow you to perform the isolation, perform the labeling, and really robust software that allows you to perform the analysis in an automated fashion without requiring additional bioinformatic support

**Dr. Annette Kim:**

When you were previously discussing having to pick and choose between karyotyping fish and chromosomal microarrays, and for each clinical scenario deciding which compliment of those three assays would be required to detect what you need to detect. Optical genome mapping, it sounds like is the one-stop shop. You can detect all of the types of copy number structural and loss of heterozygosity type variance all in one assay in three days. So what kind of impact does this have on patient care? Do we have turnaround time challenges with the other methods or how would this affect the workflow process of clinical care?

**Dr. Adrian Dubuc:**

I think it opens up incredible possibilities, and I think that's what is most exciting for me in the context of diagnostic medicine, in terms of what optical genome mapping can do and can perform. So I think when we thought of how current volumes sort of structures work in cytogenetic labs, much of the analysis that's performed is really predicated on a human being who's actually doing that individual chromosome analysis, is doing that FISH analysis. We can move towards much more-- less subjectivity, I should say, and a much more unbiased assessment of the genome with optical genome mapping and its speed is relatively comparable and in fact ameliorated in some senses to what you can achieve through typical chromosome banding or FISH-based studies. I think the real interesting part in terms of how this can potentially expand and help labs with turnaround time is that this is now an assay that can be batched.

And so whereas before we're talking about a chromosome-based study or FISH where it's one sample at a time, this is now we can batch this much like we do for many molecular based methods, and that affords us the potential to move cases through the lab at a much quicker speed. So I won't say that this is definitively the solution for every single clinical problem we have, but no assay is. I think optical genome mapping appears at this point to be heads and shoulders above other assays in terms of its potential to give you the greatest starting point in our understanding of really the totality of types of copy number and structural rearrangements that can occur in the genome.

**Dr. Annette Kim:**

So I think you mentioned the field of BALL where there are so many different types of translocations in particular and copy number changes that can really impact the risk stratification for these patients. What are some other areas in which you can see this being readily applied?

**Dr. Adrian Dubuc:**

Absolutely. Well, how much time do we have here, Annette? I'll say that my perspective, there's really a plurality. I think that the way that I view this as a technology is that for all patients from a cancer based perspective with newly diagnosed diseases, this is a really effective opportunity for us to make sure that we're putting every patient's cancer into the correct bin. And so I think whether we're talking about AML, BALL, certainly, even lymphomas when we talk about rearrangements we want to detect, I think there's incredible potential. So I would say really there are no ends from my perspective. I think the broader the types of rearrangements that exist, the more the utility exists. And so other disease types like TALL is another potential class of alterations that really isn't being effectively served by current set of genetic modalities where I think OGM can really serve a big role.

And the other ones that certainly we've had some experience doing here in our group at Roswell is that with myeloma based samples, so I think we've shown some of our work that you can optimize the degree of throughput in this three to four day period. There's only seven hours of hands-on time. So for the wet lab, it's really minimizing the amount of time that actually any technologist is spending performing experiment. The majority of the time currently is actually on the data analysis. So a process where no one is really required to be sort of holding the bag, if you will, that the analysis is happening in silico and that the standard analysis will give you up to 400 X coverage of any area of the genome, you can actually push this quite a bit. And we've done this as part of our research efforts where by expanding the amount of time that a sample is being imaged on an optical genome mapping analyzer, you can ultimately achieve a thousand X or higher coverage. And we've actually been able to demonstrate in our hands that this opportunity allows you to actually move forward with myeloma based cytogenetic stratification in the absence of CD138 enrichment. So that's really just some of our research here, but I think it highlights the potential is really, I think exists on so many fronts and I think we will continue to see an incredible evolution in terms of how this is being used the more groups that begin to sort of explore this technology.

**Dr. Annette Kim:**

Wow, that's amazing that it can do that without CD138 selection. I imagine that in some of the other areas like T-cell lymphomas and other things where we really don't have as-- they're less common disease, and you mentioned TALL, less common diseases where we have less of an understanding of some of the biologic underpinnings. I think that this is an incredible discovery platform as well.

**Dr. Adrian Dubuc:**

It's something that excites me both as in my clinical role, but I think also from the research part of my mind where I think that we've really, I think, suffered, I think in our ability to explore the structural landscape of so many disease types because we really didn't have effective solutions to do this in a way that allowed it to be feasible. Many of us who have been involved in next generation sequencing results and particularly whole exome or whole genome sequencing have seen that if you can evaluate structural rearrangements, and really the effectiveness of this really depends on how robust bioinformatic pipelines can be performed. I think one thing that really excites me about this technology is the ability to rapidly analyze the genome without having to sort of tie in other resources. And there is so much we're going to learn. I think one aspect of our research that we're really excited about is that use this technology to begin to evaluate what we're calling driverless cancers.

So in the totality of the types of assays that we're using in the context of clinical care, we know for every different disease types there are rare and potentially larger, depending on the particular disease, subsets of tumors where we really don't know what's driving it from a genomics perspective. I'm excited to see how much of this we will be able to capture as we move towards technologies where we're shining a brighter spotlight on the disease types and evaluating the genome in ways really haven't been explored. And maybe actually one other aspect that I'd like to highlight that I think has really been an important eye-opener in certainly how we view this technology is this concept of chromosomal mimicry, which we've sort of stumbled across. Which is to say that as part of our research really began as a clinical diagnostic challenges that we identified this rare but recurrent group of cancers or phenomenon where the chromosome morphology can appear to look like a pathognomonic structural rearrangement that's disease defining that can be positive by karyotype and by FISH. And yet when we drill down at the level of the exon using things like optical genome mapping technologies of optical genome mapping, we can understand that in fact the resolution of those conventional cytogenetic approaches are leading us astray. And that morphology alone can give us a false sense of really what we're looking at, which is such an important concept for us to understand.

**Dr. Annette Kim:**

And could have massive therapeutic implications, right? If you think that you have a canonical translocation that's targetable and it's actually something else that may not be targetable or vice versa, I think it really changes the therapeutic landscape for these patients. So we've talked about some of the incredible opportunities that OGM opens up for pathologists. What are the drawbacks or weaknesses to this technique?

**Dr. Adrian Dubuc:**

It's important to start this in the way I did this when we talked about conventional cytogenetics, which is that every technology inherently will have its limitations. And when it comes to optical genome mapping, the two greatest limitations is that the need for viable cells. So DNA, it's the technology, much like conventional karyotyping, hinges on cells dividing in culture. Optical genome mapping hinges on our capacity to isolate ultra high weight molecular DNA. So if DNA is too degraded either through challenges in the actual DNA isolation process or through the quality of the DNA as a result of the state of the cells that are received, that's going to limit the potential of this technology. So it's not a one-stop shop definitively in that sense. And there are types of specimens that really represent a not insignificant subset of the testing that most cytogenetic labs perform in formal and fixed paraffin embedded material that really can't be evaluated by optical genome mapping.

The DNA quality is one certain incredible element. The other aspect is just the number of cells, and so you typically require about 1 million to 1.5 million cells that are viable. And so again, that specimen quality can certainly impact our ability to achieve a result, in that sense. It's also important to note that there are limits of detection. And so when pushed, this assay can get down to about a 5% sensitivity for most structural arrangements and copy number alterations. So in certain relapsed or recurrent situations, again, if we're talking about cancer based studies, there are maybe situations where we really can't get down to the depths that we may hope to achieve by other technologies. And depending on the lab and the setting, FISH can sometimes go a little bit but not dramatically lower, maybe down to the 2 to 3% level in a probe specific fashion. I wouldn't know if I would call this a weakness or an opportunity, but perhaps both exist is that when we start studying the genome in using technologies that remain relatively novel, undoubtedly we're going to come across events that are novel where our understanding of the type of structural arrangements remains uncertain.

So shine a brighter light, you identify more variation, some of which we won't be able to appreciate. And I think that learning how to interpret those or stay away from interpreting variants that we really don't know their significance yet is a normal part of the evolution of any test as it begins to be used clinically.

**Dr. Annette Kim:**

Going back to your comments on FFPE, it strikes me that the applications are going to be much more limited in the solid tumor realm. Obviously hematologic malignancies where you can obtain fresh blood or bone marrow are going to be your most likely initial targets for applications in OGM. What strategies can be used--frozen tissue, OCT tissues--what types of other strategies can be used to try to apply this then to solid tumor realm?

**Dr. Adrian Dubuc:**

I entirely agree. Hematologic malignancies is often a really effective place starting point I'll say, but not endpoint for optical genome mapping when it comes to solid tumors. So frozen tissue absolutely can be used in some of our research studies we've demonstrated that really is an effective use. I will say it's important probably to make sure that we're evaluating different types of frozen tissue in terms of different disease groups may have variation in their practices in how they freeze tissue, which may impact the quality of the genes being isolated. I'll say from some of my work that dates back to my time at Brigham, we found that across a really wide array of different biobanks, we were able to achieve high resolution optical genome mapping data with frozen tissues. And this ranges from tumors of the central nervous system to sarcomas to some lymph node specimens and lymphomas at this point.

So we've been able to demonstrate this works effectively in the vast majority of settings we've had. OCT is a bigger challenge. We've only begun to explore that. We've had some success, but it's mixed. And I'll say that this is a common theme in colleagues that I'm interacting with that explore optical genome mapping is that it really takes a certain degree of dedication and time to make sure that the technique is being performed effectively. Hematologic malignancies a great place to start. And I think once you demonstrate proficiencies in those types of specimens that then expanding in a very sort of stepwise and limited fashion, I think gives you opportunities to really continue to push this.

**Dr. Annette Kim:**

So, you mentioned that this really has a sort of an immediate clear application in the hematologic realm, so it could be used clinically. How many places are using this clinically and what are the issues with trying to get reimbursed for this clinically?

**Dr. Adrian Dubuc:**

It's a great question and it's one of both interest and frustration I think, from my perspective. So maybe starting with the positives, where are we seeing this assay used clinically? So if we talk internationally, Canada at this point has adopted optical genome mapping is a frontline test in many centers for myeloid malignancies, AML, for other myeloid related changes that exist. And so we're seeing this being implemented, interpreted and how this is changing and coloring our understanding of disease. There's also been some clinical use in certain centers in Europe, and it's important to note that the commonalities in both Canada and European centers that have explored this technology are predicated to centralized medical systems. And so when we talk about the challenges here in the United States, it's really the challenge is that is this a test that can be reimbursed? And the answer right now is that no, it can't.

Now, I will say that hasn't stopped all centers from exploring this technology. As I understand it, MD Anderson has been exploring and offering this clinically for some time, and there are models in which you can move forward with this technology, and it's a matter of determining the funding solutions, which may be institutional. I will say that it's very encouraging that only last month the American Medical Association did establish a new category one current procedural terminology or a CPT code specifically for OGM in its use for hematologic malignancies. Now, it's not to say that this means that we're in the clear as a test that can be offered and reimbursed, but this is really the first step and it's expected that CMS is going to be setting a clinical lab fee schedule potentially in 2025, which will set the path forward to at least have laboratories offer and seek reimbursement for this test. I would love to say it's that simple and that reimbursement then sought will be received. But I think that in the short time that I've been in this field 10 years as a cytogeneticist, I'm appreciating that the medical landscape reimbursement is one that remains incredibly challenging here in the United States and where I think there's still more work that has to be done to make sure that laboratories are able to capture the revenue based on the work that they're performing.

**Dr. Annette Kim:**

I'm just thrilled about the CPT code. I understand that it's supposed to go live in January of 2025. So imminently, I think that the fact that we're going to start off in the hematologic realm in terms of the clinical application of OGM makes a lot of sense. And if you think about it, this really does replace karyotype, FISH, and chromosomal microarray, and many institutions are running all three types of assays on some of their hematologic diagnoses. And so this has the chance to be cost effective as well to minimize the cost to our health care system. And so I think that ultimately the insurers will cotton on to that efficiency. Are there any other parting thoughts you'd like to share?

**Dr. Adrian Dubuc:**

I think for me, as a geneticist, it's really been an incredible age to be able to be part of this field at a time where so much change is happening. A colleague of mine, Brynn Levy, once told me that this is a field where there's no time to be bored. And I totally, I think technology, our understanding and our exploration of the genome is evolving so rapidly. I think from my perspective, it's exciting to see how a technology like optical genome mapping can not only unlock elements of the genome that we may not have been effective at capturing and current approaches, but can also improve our clinical ability to identify relevant changes. And I think unlock the field of cytogenetics, which has been largely restricted to cytogeneticists like myself. I think we're now seeing the potential that we can allow and educate the community as a whole. And I think that education will allow us to expand the perspectives, the individuals who are looking and interpreting this data, and ultimately lead to a stronger field as a whole. So I'm excited and really grateful to have had the opportunity to be part of this podcast and excited and grateful to be part of a field that's changing in I think the best of ways.

**Dr. Annette Kim:**

Thank you, Dr. Dubuc. I also am just absolutely thrilled with the potential of OGM and I think it has, I see a future in which it is significantly impacting the care and quality of life of our patients moving forward.

**Lisa Tomcko:**

Well, I have to say, this has been a really fascinating discussion to sit in on. Thank you, Dr. Dubuc, for taking us through this exciting topic of OGM and all of its possibilities. And thank you, Dr. Kim for steering our conversation and also sharing your thoughts.

And thank you all for listening. As mentioned, Dr. Dubuc has written an article on OGM genome mapping, and you can find the link to that in the show notes as well as a link to the Precision Medicine Resource Center. Stay tuned for future episodes of CAPcast, and for more information about the CAP visit cap.org.