In Conversation *With*

Magda Kordon-Kiszala

Damian Doherty, Executive Editor at *Inside Precision Medicine*, sat down with Magda Kordon-Kiszala, PhD, CEO and co-founder of intoDNA, to explore how a breakthrough in understanding DNA damage and repair could reshape the future of precision medicine.

Today, intoDNA is translating that science into tools for drug development and precision oncology, combining its functional DNA damage response (DDR) platform with artificial intelligence (AI)-driven single-cell analysis. Its ambition is bigger still: to move beyond what tumor genes say on paper and understand what the DNA repair machinery is actually doing. In this way, the company aims to bring the right therapies to the right patients at the right time.

Q: You founded intoDNA in 2017 alongside three fellow scientists from Jagiellonian University. What was the specific moment or frustration in the lab that made you decide to leave academia and build a company around the STRIDE® technology?

Kordon-Kiszala: While studying DDR processes as doctoral students and researchers at Jagiellonian University in Kraków, Poland, my co-founders and I discovered the need for a precise DNA damage detection tool. We recognized that this technology would not only serve our research, but could enable the development of safer, more effective, and more precise therapies. That recognition is what led us to co-found intoDNA. From there, the world's first method for the ultra-sensitive, precise detection of DNA damage and repair was born: the STRIDE platform.

We believed that by expanding access to functional biomarker technology and decentralizing precision diagnostics, there was potential to solve cost inefficiencies, expedite timelines, and maximize the likelihood of success, starting in preclinical development and as candidates progress into the clinic.

Q: As a scientist-turned-CEO, what has been the steepest learning curve for you—scaling the technology, raising capital, or translating bench science into a commercial product?

Kordon-Kiszala: As someone without prior experience building a company from the ground up, I've become a fast learner and frequently called on the skills of those around me. At intoDNA, I have the privilege of leading with and learning from a passionate and experienced team of scientists, engineers, and entrepreneurs. With their help, we've been able to translate the technology born out of a doctoral research project into a scalable product that's trusted by global pharma and biotech companies today.

Q: intoDNA's mission is "The right therapies for the right patients at the right time." Was there a patient story or clinical gap that personally galvanized this mission for you?

Kordon-Kiszala: In 2022, my father was diagnosed with an extremely aggressive brain tumor. The only options he was offered were standard high-dose chemo- and radiotherapy. It took months to access next-generation sequencing (NGS) and receive potential new treatment options, which were largely probability-based and offered no truly actionable direction. Unfortunately, it was also already too late. That was a harsh wake-up call, and a personal experience that reinforced my conviction that precision medicine needs better technologies. We have the ability to change what is possible for patients.

Sadly, our story is not unique. Every year, 20 million people are diagnosed with cancer globally, and 70–80% don't have access to precision oncology. Instead, they are treated with standard chemo and radiation, which damage healthy cells alongside tumor cells.

We thought, "What if we could see exactly how cancer therapies break DNA and measure it with x-ray-like precision?" This would enable the development of safer, more effective, and more precise therapies, bringing personalized treatments to patients faster [and] at a lower cost.

At intoDNA, we are guided by the belief that patients have a right to personalized, biomarker-driven treatment strategies. We know existing modalities can fall short and envision a future where the right therapies reach the right patients, at the right time.

Q: Existing methods like γH2AX have been the standard for DNA damage detection for years. What is the fundamental limitation of these indirect markers that STRIDE assays overcome by directly detecting individual DNA breaks *in situ*?

Kordon-Kiszala: γH2AX has been valuable to the field, but it's an indirect marker. It detects a chromatin modification that spreads out from a break site, not the break itself. That surrogate relationship creates several practical problems. It can't distinguish a single-strand break from a double-strand break [because] the same modification appears around both. It doesn't give you single-lesion resolution—what you see is a diffuse signal reflecting general damage burden in a cell, not a count of discrete, individually resolved breaks. Because it depends on antibody staining of a chromatin mark rather than the physical lesion, γH2AX is known to have real reproducibility challenges: signal-to-noise issues, variability across labs and protocols, and sensitivity to sample handling, including how quickly tissue is fixed after collection. In retrospective clinical samples, where fixation timing was never standardized at the point of care, that sensitivity becomes a real source of assay failure, not just noise.

STRIDE technology overcomes this by detecting the physical DNA break directly, *in situ*, at the level of individual lesions. Because we're not relying on a downstream chromatin proxy, we can resolve single-strand and double-strand breaks separately, quantify them at single-lesion resolution inside intact cells and tissue, and do it with a level of specificity and precision that an indirect marker structurally can't achieve. That difference is what makes STRIDE useful not just for detecting that damage occurred, but for revealing the actionable, mechanism-level insight into a drug candidate's pharmacodynamic effects, and for downstream assays like dSTRIDE™-HR, [which reveal] whether the cell is actually repairing that damage.

Q: Your platform combines direct DNA break detection with AI-driven single-cell analysis. How does the AI component enhance what a researcher or clinician can see that they couldn't before?

Kordon-Kiszala: Our platform quantifies DDR at single-cell resolution, then applies AI to extract decision-grade phenotypic insights. The STRIDE platform integrates with proprietary AI and machine learning algorithms, branded CABLES, for automated image segmentation, signal quantification, large-scale data correlation, and tissue scoring for clinical applications.

What this changes for a researcher or clinician are scale and consistency. A human reviewing single-cell images for damage and repair markers can do it accurately, but slowly, and with some inherent variability between reviewers. AI-driven quantification lets us consistently process that same signal across thousands of cells per sample and [find] surface patterns, like the distribution of repair activity across a tissue's cellular landscape, that would be impractical to detect by eye at that scale. That's what turns a single-cell measurement into a decision-grade, tissue-level insight.



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Beyond quantification, a core focus for us is building predictive models using deep learning techniques. The single-cell phenotypic data STRIDE technology generates—the spatial pattern, intensity, and distribution of damage-and-repair signal across a tissue—is exactly the kind of input deep learning architectures are built to learn from. Our aim is to move from measuring a DNA-repair phenotype to learning the relationships between that phenotype and the biological questions clinicians and researchers care about. So the platform doesn't just report a signal, but places it in a context that supports interpretation. This is where the combination of a direct molecular readout and modern deep learning becomes more than the sum of its parts.

Our models are trained with human oversight across a large and growing base of samples, and the platform is continuously validating and generating new data to refine them further.

Q: intoDNA works with leading global pharma companies and has processed a large and growing volume of sample images over the last two years. Would you describe intoDNA today as primarily a services and clinical research organization partner, or as a company building toward a clinical diagnostics product?

Kordon-Kiszala: intoDNA is currently at an exciting stage of growth. As we scale our revenue-generating preclinical and clinical trial drug development services, and look to expand our laboratory footprint to meet growing biopharma demand, we are also taking steps to support diagnostic readiness.

As interest increases in functional biomarkers that directly measure DDR biology, we are advancing U.S.-based translational programs and clinical utility studies designed to inform prospective clinical trials required for future diagnostic adoption. In short, [today] we're both an established partner to biopharma and a company deliberately building toward a clinical diagnostics future.

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Q: Precision medicine is crowded with genomics and transcriptomics companies. What makes DDR biology the "white space" that intoDNA is uniquely positioned to own?

Kordon-Kiszala: With STRIDE technology, intoDNA is revealing a functional intelligence layer that's been missing from precision cancer medicine: how proteins function, *in situ*, at single-cell resolution.

Unlike standard immunofluorescence (IF) or immunohistochemistry (IHC)-based methods, which detect the presence of a protein but not what it's doing, our assays measure the functional engagement of DNA repair proteins in genome maintenance. Genomics tells you what mutations are present. Transcriptomics tells you what genes are being expressed. Neither tells you whether the repair machinery those genes and mutations point to is actually working in that tumor, right now. That's the layer we directly measure, and it's the layer the rest of the field has had to infer rather than observe.

Q: Homologous recombination deficiency (HRD) has become a validated biomarker for poly (ADP-ribose) polymerase (PARP) inhibitor response, but current tests often miss patients or take too long. How could functional assays like dSTRIDE-HR decentralize and democratize HRD testing?

Kordon-Kiszala: As part of our platform, intoDNA is developing dSTRIDE-HR, a functional HRD test for real-time measurement of HR (homologous recombination) repair pathway activity in tumors. These insights help oncologists and clinical researchers understand the impact of DDR-targeting drugs, including Ataxia Telangiectasia and Rad3-related kinase (ATR) inhibitors and PARP inhibitors (PARPi).

Our path to broad access is deliberately phased. Our first milestone is bringing dSTRIDE-HR to market as a centralized laboratory-developed test, so any pathology lab can access it through the specimen workflows they already use, without needing specialized in-house capability. The wet lab assay is bundled with a proprietary automated image analysis platform built to fit into a standard histopathology workflow: no extra biopsy processing, and tissue structure is preserved throughout.

From there, once we've established a path to reimbursement, our goal is to take dSTRIDE-HR through the U.S. Food and Drug Administration (FDA) and toward decentralized deployment globally, so hospital and diagnostic labs can eventually run the assay locally on standard equipment. That's the full arc of democratization we're building toward: starting with centralized access through a workflow every lab already knows, and expanding over time to direct, local deployment as the regulatory and reimbursement path matures.

Q: You've published on mismatch repair, nucleotide excision repair, PARP1, and HR pathways. Beyond oncology, where else do you see DNA repair biomarkers playing a transformative role—neurodegeneration, longevity, radiation exposure, or something else?

Kordon-Kiszala: The power of STRIDE technology is being realized across markets including DDR therapeutics, radioligand-based therapies, immuno-oncology, antibody-drug conjugates (ADCs), aging and longevity, and neurodegenerative disease, among others. Additionally, our growing list of peer-reviewed publications and over 50 granted patents and pending patent applications have established intoDNA as a leading innovator not only in precision oncology, but in the broader precision medicine landscape.

For example, the gradual buildup of unrepaired DNA is now recognized as one of the hallmarks of aging. It drives cellular senescence, loss of tissue function, and age-related disease. That's why measuring DNA damage, and the efficiency of its repair, is becoming central to the field of longevity research. If we can monitor these processes in real time, we can better understand biological age, predict health span, and evaluate interventions that aim to slow aging.

Q: The field has struggled with "static" genomic biomarkers (mutations in *BRCA1/2*, etc.) versus "dynamic" functional readouts. Why is measuring the actual activity of a DNA repair pathway more clinically actionable than simply knowing if a gene is mutated?

Kordon-Kiszala: The actual status of DDR activity in cells is defining the response to multiple treatments. Static readouts do not measure biology in real-time. Current genetic biomarkers like BRCA or HRD status fail to capture the full complexity of patient response to therapies like PARPi. Therapy access is, presently, restricted to patients who test positive for BRCA deficiency or HRD status. These tests also have imperfect correlation with actual clinical benefit: trials have shown that some BRCA-negative patients respond, and that the magnitude of benefit varies widely among BRCA-positive patients. We lack a functional tool to predict sensitivity versus resistance across that spectrum, including when a patient's tumor has regained HR repair functionality over the course of treatment. The STRIDE platform enables real-time detection and quantification of DNA damage, repair, and replication stress, revealing critical insights into a drug's mechanism of action, efficacy, pharmacodynamics, and safety.

Our technology has already demonstrated a meaningful and measurable impact on drug development. STRIDE assays have been used across thousands of patient samples in hundreds of research studies and Phase I clinical trials. Sponsors use it to validate mechanism of action prior to investigational new drug (IND) filing, profile safety for off-target effects, monitor pharmacodynamics in both preclinical and clinical settings, and stratify patient responses. That range of application means sponsors can catch a failing biomarker hypothesis earlier, before it consumes a full clinical program, which translates directly into faster timelines, reduced development risk, and real cost savings compared to programs built on biomarkers that don't successfully transition from preclinical to clinical settings.

Q: In the next 12–18 months, what is the one scientific or commercial milestone you are focused on achieving to signal that intoDNA has truly "arrived" as a precision medicine platform?

Kordon-Kiszala: The first assay we're productizing as a therapy selection diagnostic is dSTRIDE-HR, designed to predict sensitivity to PARPi for patients with breast, ovarian, prostate, and pancreatic cancers. The test works by directly visualizing RAD51 loading at the site of DNA double-strand breaks with single-cell resolution within formalin-fixed paraffin-embedded (FFPE) tissue sections. RAD51 is the central recombinase in HR repair, so when we can see, cell by cell, whether it's being recruited to a break site, we get a real-time functional readout of whether that tumor's repair machinery is working. [We can see this] across the tissue microenvironment landscape, not just whether a gene is mutated on paper.

That distinction is the whole value proposition. Genomic tests tell you whether a *BRCA* or other HR repair gene carries a pathogenic variant. They don't tell you whether the repair pathway is functionally intact or broken in that patient's tumor right now, and a growing body of published data shows real discordance between genomic status and functional repair capacity. Patients can get missed by genomic-only testing, and patients with wild-type genomics but functionally deficient repair get missed too. A single-cell functional readout of the patient's tissue biopsy closes that gap.

We're intentionally building this across all four PARPi-approved tumor types because functional HR status is a biology-driven phenotype, not a tumor type-driven one. That gives dSTRIDE-HR a meaningfully larger [target] population than any single-indication companion diagnostic, as PARPi eligibility criteria vary by tumor type but the underlying biology we're measuring doesn't.

We're actively enrolling academic and biopharma collaborators to provide patient biopsy specimens for the analytical and clinical validation of our test, as well as [for] evidence generation.

Q: If you could look ahead 10 years, what would success look like for intoDNA—and what would it mean for a cancer patient walking into a clinic who might never have heard of your company?

Kordon-Kiszala: Success in 10 years looks like functional DDR testing being a standard part of the diagnostic workup across the full landscape of DDR-relevant cancers, the way genomic sequencing is today. Not a niche assay a handful of academic centers order, but something built into the treatment-selection pathway wherever DDR biology drives treatment response across small molecules, ADCs, radiotherapy, as well as immuno-oncology, spanning both the HR pathway that PARPi exploit and the replication stress pathway that WEE1, ATR, and checkpoint kinase 1 (CHK1) inhibitors depend on.

That second half matters as much as the first. PARPi selection has genomic proxies, however imperfect. WEE1, ATR, and CHK1 inhibitors don't have an equivalent genomic biomarker at all, because replication stress isn't something a DNA sequence can tell you. It's a dynamic, functional state of the cell, and right now the field has no direct way to see it. STRIDE is built to measure both sides of that biology in the same single-cell framework—RAD51 loading for HR status, and RPA, RAD9, and RAD17 recruitment for replication stress, which positions us to support patient selection for both drug classes as they mature clinically.

For the patient experiencing a new cancer diagnosis, they'll experience a shorter path to the right therapy, whether that therapy is PARPi or one of the next waves of replication stress-targeting agents. Instead of only a static mutation report that may or may not predict how their tumor behaves, the oncologist is armed with a functional readout of what that tumor's damage and repair machinery is actually doing.

The bigger shift, if we get this right, is in how the field thinks about biomarkers generally. Precision oncology today is built almost entirely on what the DNA sequence says. We think the next decade adds what the cell's protein machinery is actually doing, measured directly, at single-cell resolution, across the tissue. If the STRIDE platform helps make that functional data layer, across both repair and replication stress biology, a normal part of oncology decision-making, [then] that's what success looks like to us: not a company milestone, but a change in the standard of care. ■



The intoDNA team at headquarters in Kraków, Poland.