EuropaBio sat down with new Member Inscripta, to find out what gets them fired up with their ground breaking 'benchtop biofoundry' Onyx™

Interview with... Dr. Jim Lalonde, Head of Microbial Business Area at INSCRIPTA

About Jim Lalonde

With more than 25 years in research and development leadership, and having built world-class R&D teams, Jim most recently served as Senior Vice President of R&D at Codexis, Inc., where he oversaw the development of more than 50 enzymes for drug manufacture, nutrition, biotherapeutics, and molecular diagnostics.

Prior to his time at Codexis, Dr. Lalonde held a leadership role in chemical development at Altus Biologics. Originally a Senior Scientist at Vista Chemical Company, he holds a Bachelor's degree in Chemistry from Lakehead University and a PhD in Organic Chemistry from Texas A&M University.

1) What inspired the foundation of Inscripta?

Definitely the promise of CRISPR technology, as its ability to edit and re-engineer genomes became clear very quickly after its discovery. Scientists around the world recognized the tremendous potential to solve some of our greatest challenges ranging from curing of genetic disorders, to providing low-cost food production, to sustainable production of valuable materials, to probing the vast amount of DNA of unknown function.

But it was discoveries made by the founders of Inscripta that showed we could democratize CRISPR and enable broad adoption of genome-scale, massively parallel CRISPR genome engineering technology. The colocation of guide sequences, edits and barcodes on a single construct makes it possible to perform genome wide editing with 1000's of edits in a single experiment with unprecedented efficiency.

This, combined with a push-button instrument workflow and innovations in reagent chemistry, microfluidics and a novel CRISPR nuclease, delivered on the vision to provide researchers worldwide accessible genome-wide engineering. The platform is rounded out

with software; on the front end to automate experimental design and on the back end to help organize and interpret very large genotype and phenotype datasets.

2) What appetite have you seen for such a benchtop device?

We have seen tremendous interest in our platform. We have given several webinars on the Onyx™ platform and on applications to strain engineering and genome discovery. 100's of scientists routinely participate in these webinars and follow up with requests for more information and follow on discussions around their specific interests. During our development phase, we partnered with early access partners and key opinion leaders and we expect that the results from these collaborations will start to be published this year. As you can imagine, we are seeing broad interest from Academic, Government and Industrial lab with scientists in Basic Research, Healthcare, Industrial Biotech and related fields.

3) How is the role-out/testing going?

The product launch is going pretty well for such a next generation platform – it's completely new so we have to tell the whole story. Our recently completed Beta program went very smoothly so we are very happy with that. We are very proud of our Development, Operations and Applications teams and what they have achieved, it's been an amazing 12 months.

4) What are your plans for Europe?

We launched our Onyx™ platform simultaneously in Europe and North America and are now in the midst of taking orders and placing instruments in labs. We are supporting our efforts in Europe with a commercial team and the support of Field Service Engineers and Field Applications Specialists. We are getting involved with scientists before placing an instrument in discussions around potential applications, experimental design strategies and demoing our library design software.

5) How do you see Onyx being able to transform biotech R&D (in academia and industry)

The transformation is happening in two ways; dramatically lowering the amount of R&D to execute on a given Synthetic Biology program and enabling discoveries that were mostly unattainable until now. The amount of time and effort to design and implement a strain engineering program made it prohibitive for most labs. Now with automated strain library creation, the instrument frees up hundreds of hours of researcher time such that multiple programs can be done with a small team. The ability to go genome-wide with push button simplicity has allowed researchers to expand their approach from a narrow, hypothesis driven one to relatively unlimited genome interrogation; elucidating genotype-phenotype relationships in regions of heretofore unknown function.
