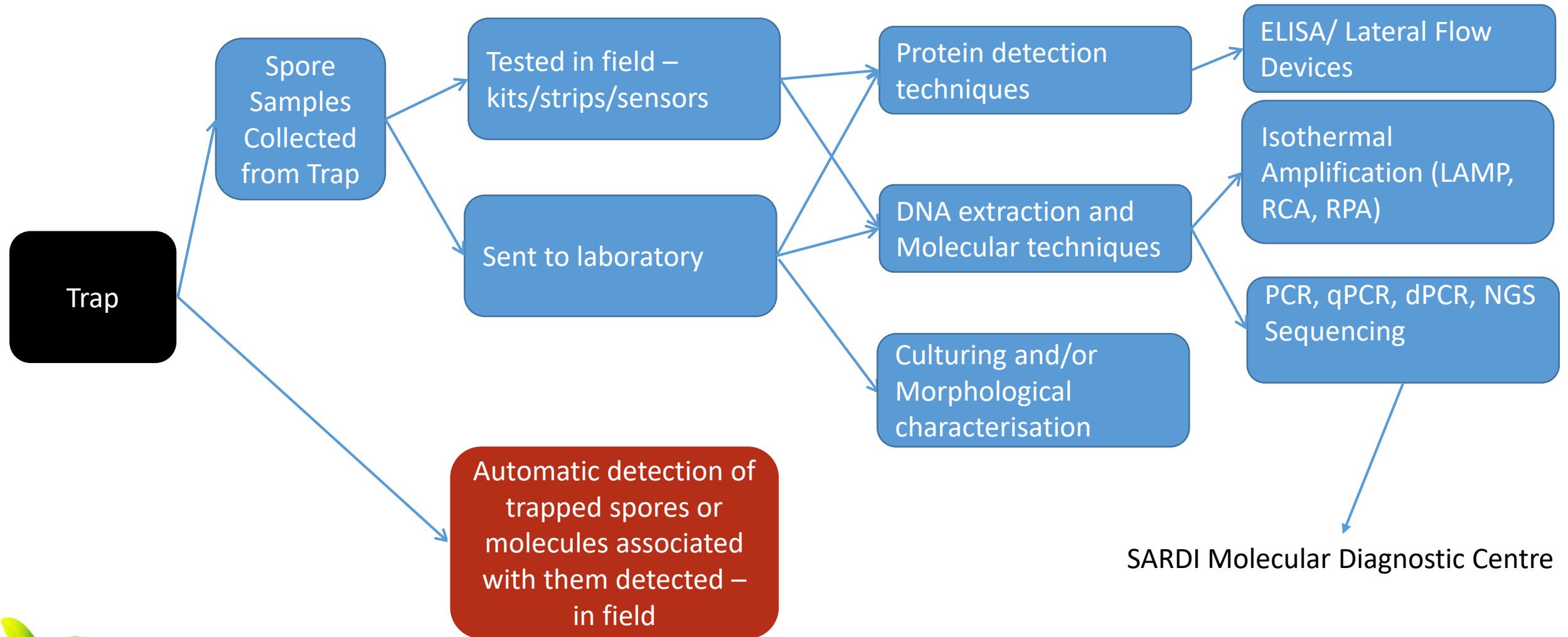


Development of probes and platforms for the detection and identification of captured fungal spores

Kelly Hill (SARDI)

Linh Nguyen (University of Adelaide)

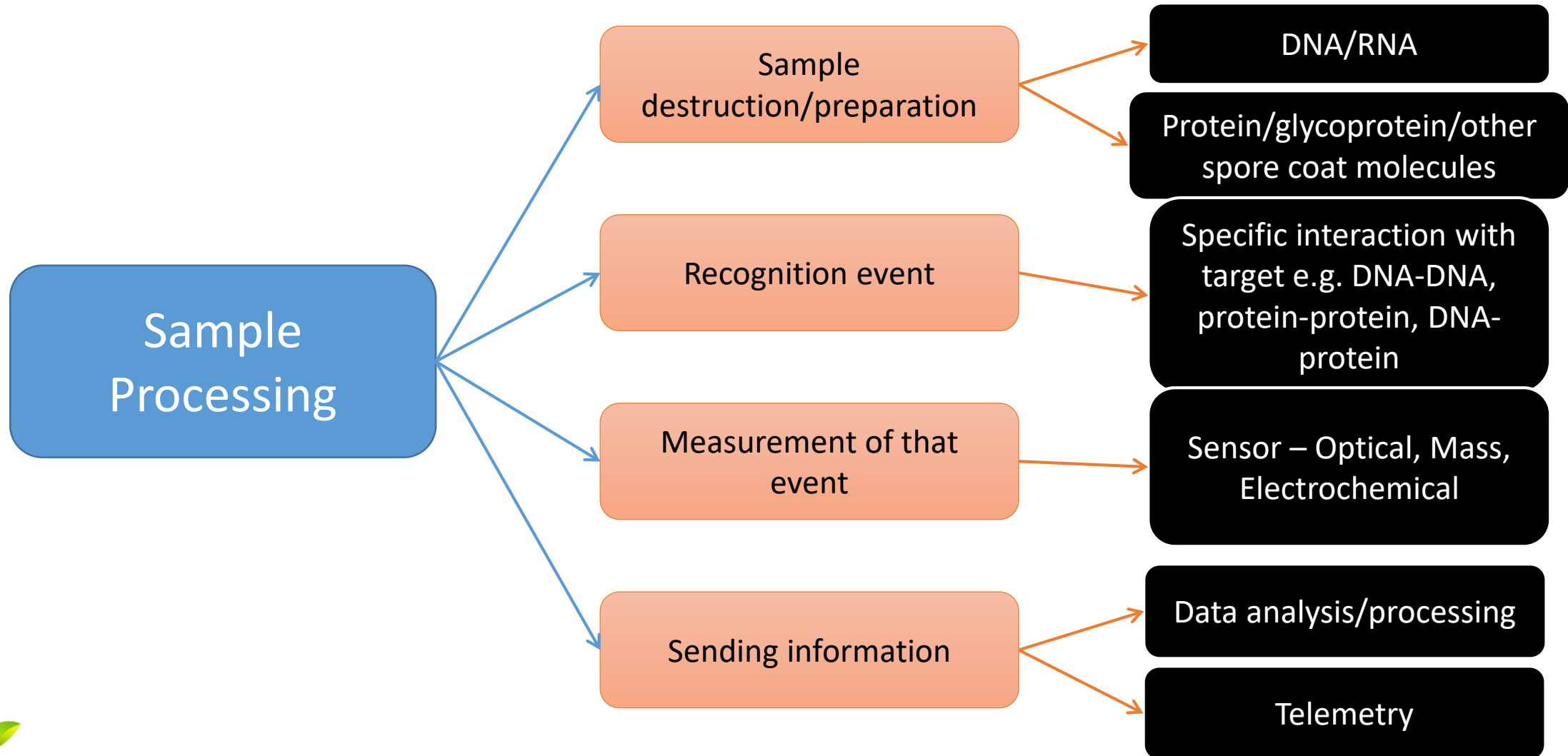
Processing of surveillance samples



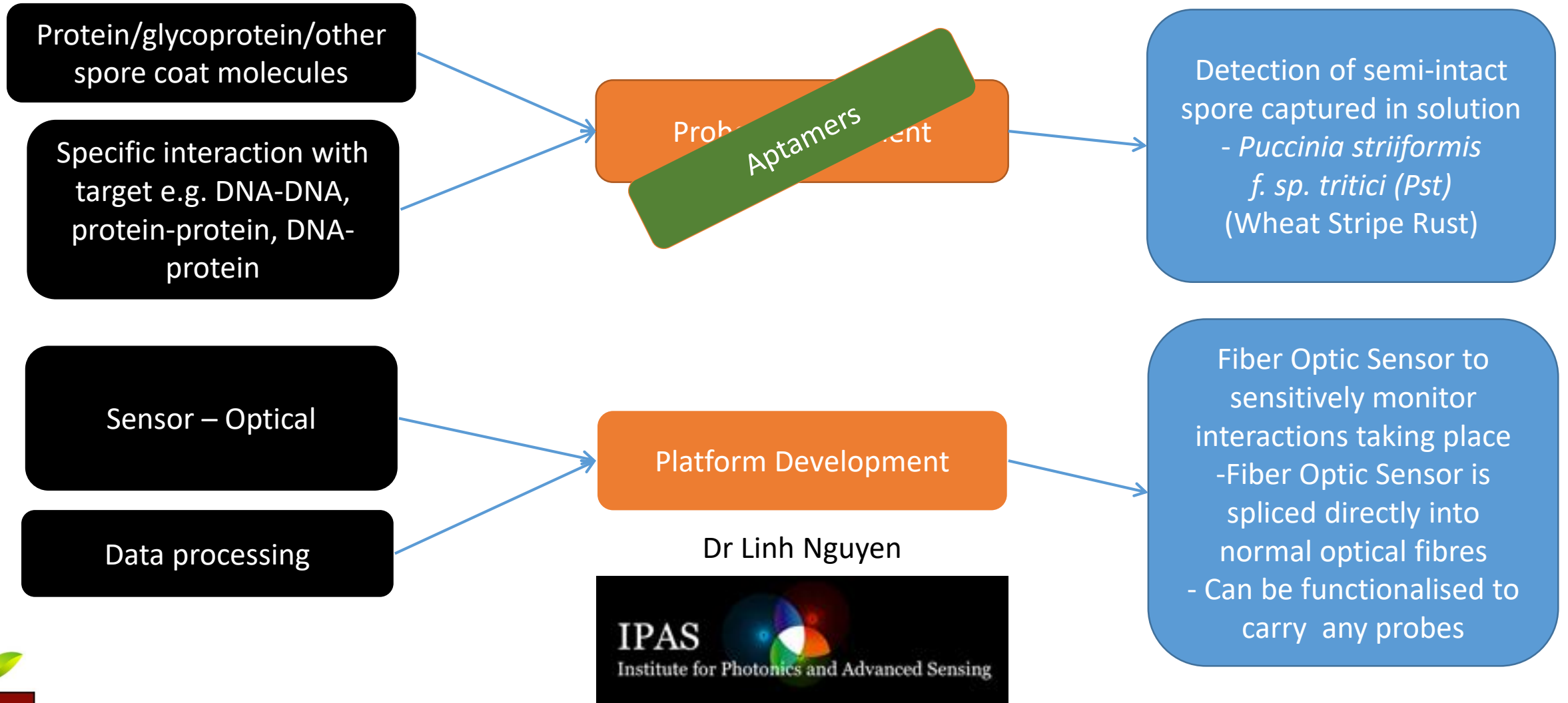
SARDI Molecular Diagnostic Centre

biosecurity built on science

Investigating how to make diagnostic tests for autonomous in-field use – components and considerations



Investigating how to make diagnostic tests for autonomous in-field use - key output

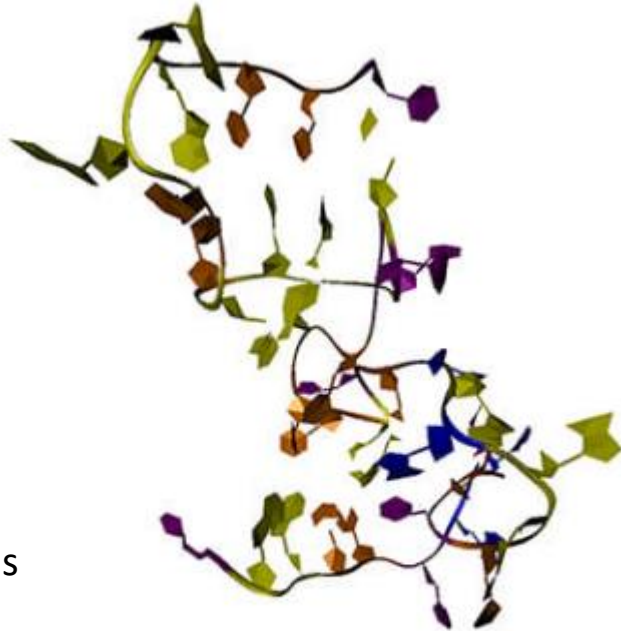


What are Aptamers?

Coined from the Greek word *aptus* “to fit”

ssDNA or RNA molecules – tertiary structure allows specific binding

Origins: a PhD study into the mRNA translational operator motif of the DNA polymerase of bacteriophage T4 – mutations produce hairpin with the same affinity to regulator protein



Structure of aptamer developed by Base Pair Biotechnologies to IL-7

Selected *in vitro* to chosen target

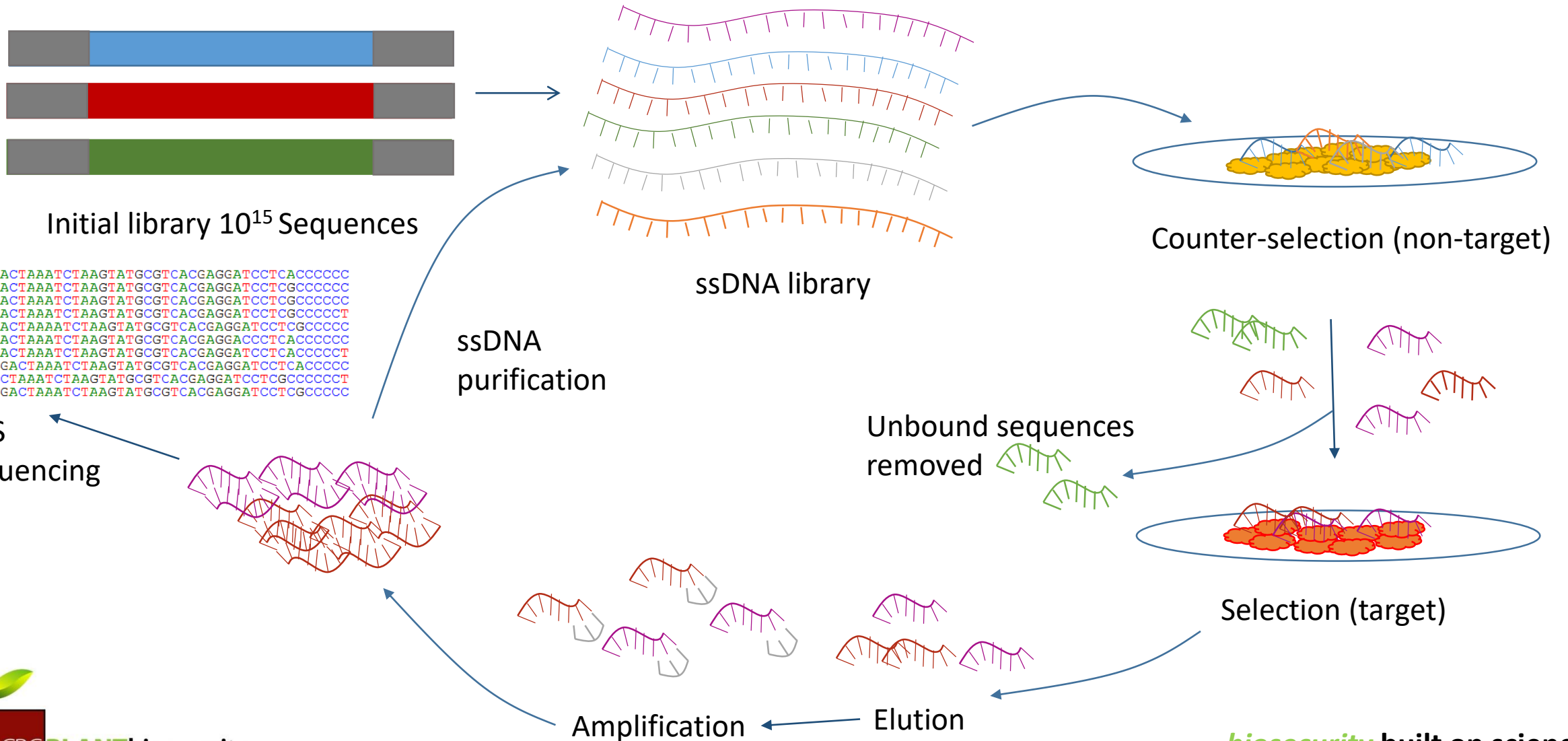
Chemically synthesised = lower cost for commercial production

Increased stability for transport, storage and field use

Aptamer Selection – SELEX

Cell SELEX (Sefeh *et al.* 2010)
Single Selection Protocol (Liu *et al.* 2012)

Systematic Evolution of Ligands by Exponential enrichment

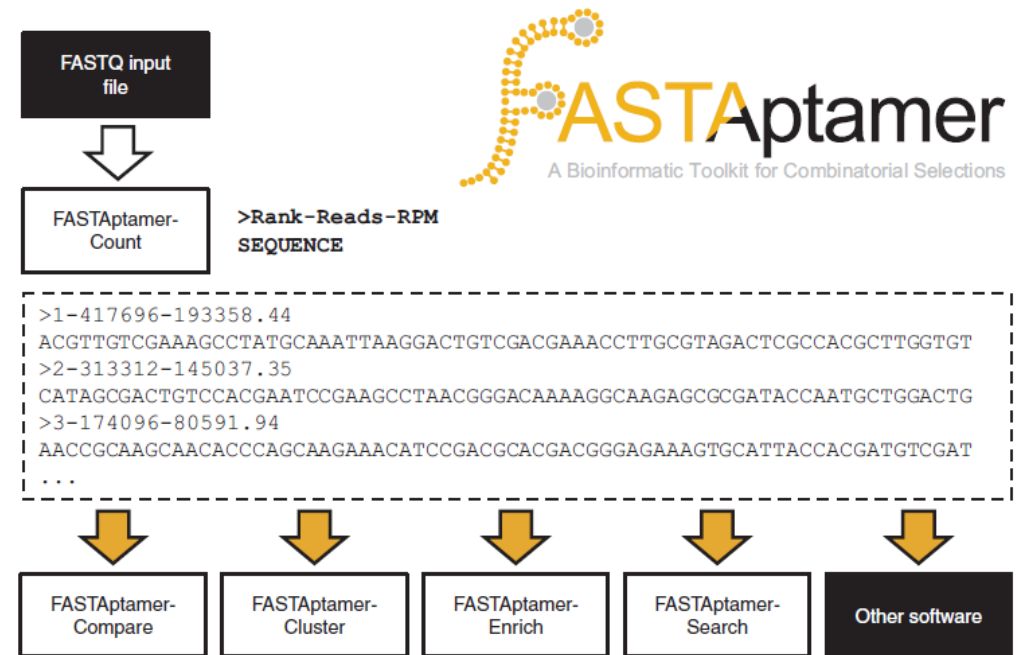


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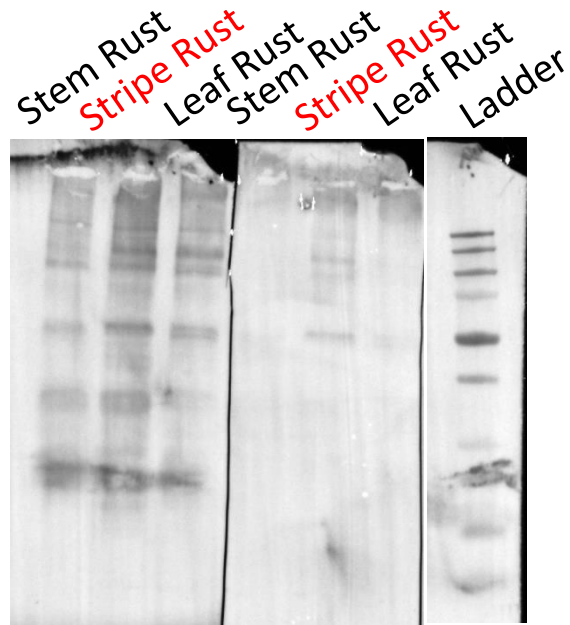
Aptamer Selection – NGS Analysis

Pipelines –

- FastAptamer (Alam *et al.* 2015) – based on sequence frequency and enrichment over cycles
- APTANI (Caroli *et al.* 2016) – based on a common structural motif within binding aptamers in a selected library
- APTATRACE (Dao 2016) – similar to APTANI but doesn't work on the assumption only a single motif is responsible for binding



Stripe Rust Aptamer Development

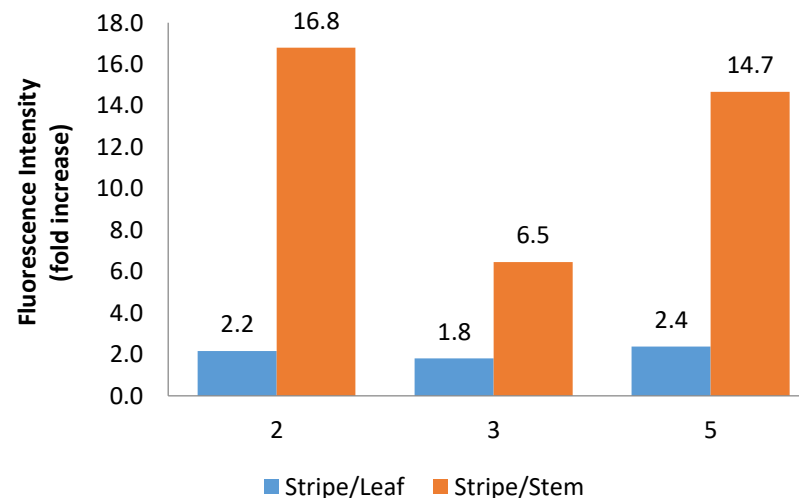


FAM Apt-
25-37-3&5

FAM Apt-
25-37-1&2

AP-conjugated anti-FITC Ab, developed
with NBT and BCIP

Name	Single-selection protocol		Multi-selection protocol		Enrichment (y/x)
	Reads (x)	RPM (x)	Reads (y)	RPM (y)	
25-37-2	1	3.81	900	20.24	5.31
25-37-3	1	3.81	802	18.04	4.73
25-37-4	1	3.81	750	16.87	4.43
25-37-5	1	3.81	614	13.81	3.62
25-37-6	1	3.81	530	11.92	3.13
25-37-7	1	3.81	280	6.3	1.65
25-37-8	1	3.81	268	6.03	1.58



More non-specific binding
with Leaf Rust (*Puccinia
tritcina*) than Stem Rust
(*Puccinia graminia* f. sp.
Tritici) which was used as
counter-selector

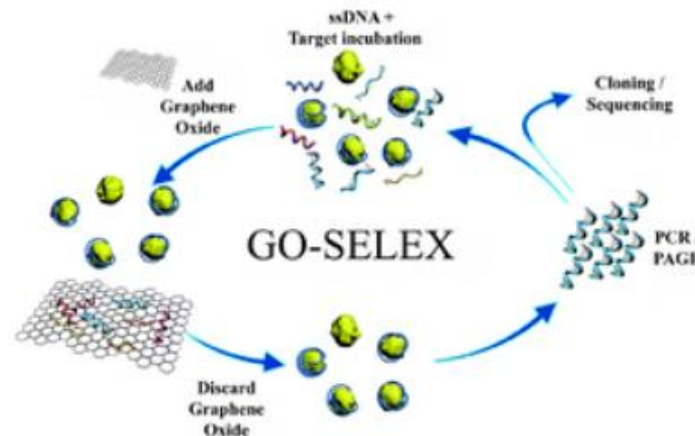
First Selection Results

- Non-specific Binding
- Low Sensitivity – as shown by SPR
- Developed against total protein extract

Aptamer Second Selection – Enriched Library



Surface Solubilised Targets



Park *et al.* 2012

Aptamer Development – Outcomes, Difficulties and Opportunities

- Feasibility of Approach – both probe and platform development – do they offer qualities that provide value over other techniques?
- Protocols to apply strategy to rust spores and potentially other targets
- Difficulties include:
 - Efficient purification of ssDNA – protocol change using asymmetric PCR (Zhang *et al.* 2015)
 - Analysis – HPC requirements especially for structural analysis of files containing millions of reads – Amazon Web Server
 - Immobilisation strategies can be problematic, we believe we may lose sensitivity as we move further from the fibre: solution interface
- Opportunities
 - Alternative targets – e.g. Viral and bacterial targets for aptamer development
 - Alternative platforms for aptamers (low tech) – lateral flow
 - Alternative uses for RI measurements for platform

- For more information, please email Kelly.Hill3@sa.gov.au

