

Medical Research for Mankind Since 1933 Project by: Dr. Joe Taft Dr. Joe DeSautelle Dr. Chelsea Paresi Dr. Brent Iverson University of Texas at Austin

YESS-KI: Predicting Kinase Inhibitor Resistance

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YESS-KI: developing predictive biomarkers

- > YESS-KI is a technology that produces reliable predictive biomarkers for cancer therapy.
- While incredible progress has been made in treating cancer, there remains an unfortunate high level of treatment failure.
- Drug development efforts have been plagued with very low success rates, especially with regards to cancer therapeutics. The New York Times reported figures from a recent study showing that "only 3 percent of cancer drugs tested in clinical trials between 2000 and 2015 have been approved to treat patients."
- The use of patient selection biomarkers significantly increased success rates in drug development. For overall drug development efforts (all indications), success rates without biomarker usage were reported at 8.4% while with the use of biomarkers, this number increased to 25.9%.
- > But identifying a reliable and predictive biomarker is difficult
- > YESS-KI is an inexpensive, efficient and reliable platform to accompany drug development from early pre-clinical stages to patient stratification in clinical testing.

Kinase Inhibitors (KI).

- KIs are an extremely effective class of therapeutic drugs and due to their specificity are associated with low side effects.
- Cancer patients often require chronic KI treatment, and unfortunately many experience resistance and intolerance, necessitating a change to 2nd or 3rd line KI therapy.
- Prescribing the correct course of therapy is difficult, especially faced with an increasing choice of KIs. Question are raised such as:



- > Will the patient's disease respond to the new treatment?
- > Which therapy going forward will be most effective?
- > Will the new therapy also result in resistance or intolerance?

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Kinase Inhibitors (KI).

- With over 60 FDA approved KIs with hundreds in development, patients have many good options.
- > And with so many options, the hope is that an effective KI treatment will match each patient.
- However, we will need tools to predict which KI will work for a specific patient.
- Current methods for predicting resistance are slow, costly, and not comprehensive.
- Doctors and drug developers need better tools to select patients with a high likelihood of responding to treatment.
- KI pre-clinical candidates need better models to predict and translate their outcomes for patient use.

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Assay to predict drug resistance.

- Our solution: YESS-KI, a low-cost yeastbased assay to predict resistance mutations to KIs.
- Allows selection of KI therapy with fewer modes of resistance.
- By predicting the resistance of a kinase inhibitor, we can predict whether a drug will work for a given patient and thereby improve outcomes for patients.
- Also allows for creation of drug vs mutation matrix to help oncologists choose appropriate KI for given mutational landscape.

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Imatinib: A First-in-Class Cancer Therapy.

- First approved small molecule targeted cancer therapeutic
- Inhibits the BCR-ABL oncogene (a tyrosine kinase), and results in drastic increase in survival.
- However, acquired resistance in a large number of chronic-phase patients, leads to treatment failure.
- This has led to development of second- and thirdgeneration BCR-ABL inhibitors.
- Will these new 2nd and 3rd generation drugs overcome resistance mechanisms and provide better outcomes for patients on chronic therapy?



Data from Shah, NP. Hematology Am Soc Hematol Educ Program. 2005

Next-Generation BCR-ABL Inhibitors have been developed and implemented in the clinic.

- Second-generation:
 - Nilotinib
 - Dasatinib
 - Bosutinib
- Third-generation:
 - Ponatinib
- Fewer resistance mutations
- Increased affinity



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YESS-KI predicts acquired resistance in Bcr-Abl.

Does our YESS-KI assay accurately predict patient resistance to KI treatment? We compared dasatinib and ponatinib:

Dasatinib:

- All known dasatinib-resistant mutations were seen with our test.
- Of our top 5 most common dasatinib-resistant mutations, four have been previously reported.

Ponatinib:

- Top mutant, E255V, is the most resistant single mutation isolated from patients.
- Ponatinib-resistant clones were enriched for compound (2+) mutations, which have been observed in patients and validated in vitro.
- > IC50 of novel mutations measured by cell culture to validate results in YESS.

YESS-KI Resistance Assay - how does it work?

- From an initial population of random mutants, inhibitor-resistant mutations are enriched by cell sorting.
- Screened and initial libraries are sequenced.
- > Mutations are identified and compared to known data, if available.
- \succ Novel mutations are assayed first individually in the YESS-KI system, then validated by previously established in vitro methods.
- > Our libraries cover the entire single mutation space as well as most double mutations

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THE MECHANISM



YESS-KI correctly predicted acquired resistance.

We found EVERY ONE of the mutations seen in the clinic for both dasatinib and ponatinib (as well as some not yet seen). We showed that **ponatinib** activity required the much more rare situation of two mutations to see resistance. Resistance to **dasatinib** was seen with <u>single</u> mutations. $\cap \vdash$ • YESS-KI predicts that Ponatinib is a better drug with less resistance, even when used in longterm treatment. We could have predicted the futures of dasatinib vs. ponatinib in the clinic. Clayton Biotechnologies, Inc. www.clavtonbiotech.com

Ibrutinib and Alacalbrutinib are irreversible Kls.

> BTK inhibitors used to treat B-cell lymphomas and leukemias.

IBRUTINIB:

- In 2018 Ibrutinib earned \$3.6 billion in for AbbVie
- Projected sales for 2020 are \$5 billion/year
- Broad specificity (inhibits 8 other kinases)
- > 16-21% of patients acquire resistance

ACALABRUTINIB:

- Approved in October 2018 for mantel cell lymphoma.
- Less cross-reactivity than lbrutinib.

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C481S is most common resistance mutation for Ibrutinib and Acalabrutinib.



C481S mutations block KI binding irreversibly.

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YESS-KI predicts acquired resistance in BTK.

Does our YESS-KI assay accurately predict patient resistance to KI treatment?



We also identified previously unreported resistance mutations and validated in vitro.

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YESS-KI predicts acquired resistance and proposes alternative KIs

Screening multiple inhibitors in YESS-KI will allow us to create a rubric of inhibitors and their efficacy against resistance mutations as a prognostic tool for oncologists.

Profile for BTK inhibitors:

	WT	C4815	Mutant 2	Mutant 3	Mutant 4
Acalabrutinib	+	-	-	-	-
Ibrutinib	+	-	+	+	-
Vecabrutinib	+	+	+	-	+
Remibrutinib	+	-	+	+	-

YESS-KI is efficient, scalable, and broadly applicable.

- From screening to data analysis, YESS-KI can be completed in less than two weeks.
- YESS-KI can be applied to combination treatment or sequential treatment with kinase inhibitors to simulate treatment regimes.
- > YESS-KI can be performed in parallel for comparisons between inhibitors.
- Several kinases and multiple inhibitors have been shown compatible with YESS-KI system.
 - > Kinase Inhibitors tested: imatinib, dasatinib, ponatinib, gefitinib, and Osimertinib
 - > working on datasets for infigratinib, futibatinib, erdafitinib, pemigatinib.
 - generated libraries to several kinases (Src, Lyn, Abl, BTK, Bcr-Abl)
 - making and testing libraries for FGFR2, Her2 and Alk

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Summary: YESS-KI to predict resistance to KIs.

- > Diagnostic
 - > YESS-KI provides predictive biomarkers to determine the best KI treatment for a patient.
 - The rapidly expanding number of approved KI's have created the critical need for diagnostic tools capable of rapidly identifying which new drug is most appropriate for an individual patient
- Drug Development
 - > We offer a yeast-based assay to discover resistance mutations for approved and candidate kinase inhibitors (KIs).
 - > YESS-KI represents a tool for drug developers:
 - > To efficiently (under 2 weeks) select the best drug candidate in pre-clinical development
 - > For patient stratification in clinical trials

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Thank you for your attention

