



Assay Development and Inhibitor Characterization of Protein Kinases Using a Lab Chip 3000

Jeff Hirsch, Matt Saabye, John Schindler, Molly Hall and Joe Monahan
Pfizer Global Research & Development, St. Louis Laboratories, Pfizer Inc, St. Louis, MO 63017

Materials and Methods

All data shown were collected using the Caliper LabChip 3000 instrument and analyzed using a software package, HTS Well Analyzer, designed by Caliper for use with the LabChip3000. All assays performed were introduced onto the Slipper Chip via capillaries (i.e. Off-Chip Mobility Shift assays) as described in Figure 1. See figure legends for specific experimental conditions.

Steady State Characterization Data for determining steady state kinetic parameters were fit to Equation 1, where v is velocity, V_{max} is the maximum velocity, S is the substrate concentration, and K_m is the Michaelis constant:

$$\text{Equation 1 } v = V_{max} \cdot S / (K_m + S)$$

Mechanism of Action Data for determining the mechanism of inhibition were fit to Equations 2 and 3 (describing noncompetitive inhibition, respectively) where v is velocity, V_{max} is the maximum velocity, S is the substrate concentration, K_m is the Michaelis constant, I is the inhibitor concentration, and K_i is the inhibition constant:

$$\text{Equation 2 } v = V_{max} \cdot S / (K_m \cdot (1 + I/K_i) + S)$$

$$\text{Equation 3 } v = V_{max} \cdot S / (S + K_m) / (1 + I/K_i)$$

Inhibitor Kinetics The off-rate progress curves were fit to Equation 4, where p is product, v_0 is the initial velocity, v_{∞} is the final velocity, t is time, and k_{off} is the apparent first order rate constant (see Fig. 1). The progress curves for irreversible inhibition were fit using Equation 5. Second order regions (slope vs. inhibitor) were fit to Equation 6.

$$\text{Equation 4 } p = v_0 \cdot t + v_{\infty} (1 - e^{-k_{off} t})$$

$$\text{Equation 5 } p = v_0 \cdot t + v_{\infty} (1 - e^{-k_{off} t})$$

$$\text{Equation 6 } \text{slope} = k_{off} \cdot t / (K_i + I)$$

Introduction

Protein kinases represent potential drug targets across several therapeutic areas at Pfizer, an assay technology that can provide both medicinal chemistry support and mechanism of inhibition studies would be beneficial to a project team to help develop potential new drugs. Furthermore, the technology should be one that can be used for several projects and be low in cost. We demonstrate that the Caliper LC3000 instrument provides this type of technology for several current projects within St. Louis Discovery and appears to be applicable for a number of future projects within St. Louis Discovery. Traditional kinase assays are end point assays which are difficult, time consuming and low throughput when used to produce progress curves. The LC3000 provides a format which can generate progress curves in a quick and timely manner as well as provide a higher throughput than the traditional assay.

The current capabilities of Caliper technology allow reactions to be performed in a 384-well plate at an average cost of approximately \$0.001. The assay format described here is referred to as a "Off-Chip Mobility Shift Assay" and uses capillary electrophoresis on a microfluidic chip to measure the conversion of fluorescently-labeled substrate to product. The measurement can either be done in a real time mode ("kinetic mode") from a plate of quenched reactions. In the real time analysis, samples are spotted from a plate at specified intervals over a period of time through the capillaries and onto the chip where substrate and product are separated by electrophoresis. The same analysis is performed with the quenched reaction. However, in this case, each well is only sampled once. Caliper-based kinase and protease assays have been used in St. Louis Discovery for medicinal chemistry and hit follow-up library support, subset library screening, detailed inhibitor characterization, and as orthogonal assays to complement the HTS primary screen.

Off-chip Mobility Shift Assay

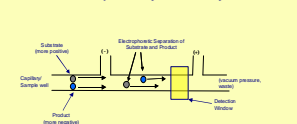


Figure 1. Diagram of Microfluidic "Slipper Chip". Samples are drawn into the inlet channels of the Slipper Chip through the capillaries using vacuum pressure. Voltage is applied to the upstream and downstream electrodes with alternating polarity for the separation of species with different electrophoretic mobilities. Fluorescently-labeled species are detected as they pass through the detection window of the Slipper Chip.

Off-chip Mobility Shift Data Trace

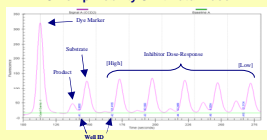


Figure 2. Analysis of data collected using the LabChip 3000. Caliper's HTS Well Analyzer software determines the height of the corresponding product and substrate peaks. Data output files, including the production rate of peak heights, were reformatted using Excel macros.

Early Assay Development for a Lipid Kinase

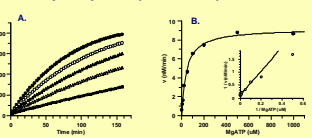


Figure 3. Assay Development for a lipid kinase. A) Lipid kinase activity in the presence of 1 μM PDC15 (2.5 nM enzyme, and 500 μM (closed circles), 100 μM (open circles), 10 μM (closed triangles), 2 μM (open triangles), or 1 μM (closed squares) of MgATP. Data were sampled by the capillaries every 5 minutes. Note: additional concentrations of MgATP were removed for clarity. B) Initial rates taken from A_{0-5} were fit to Equation 1 to yield $K_{m,app}$ values.

Steady-State Characterization of a Ser/Thr Kinase

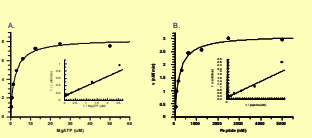


Figure 4. Characterization of steady-state kinetic parameters for a Ser/Thr kinase. A) Initial velocities were collected at several concentrations of MgATP and a fixed concentration of peptide (1 μM). The data were fit to Equation 1 to determine the apparent $K_{m,app}$. B) Initial velocities were collected at several concentrations of peptide and a fixed concentration of MgATP (2 μM). The data were fit to Equation 1 to determine the apparent $K_{m,app}$.

Small Library Screen against a Lipid Kinase

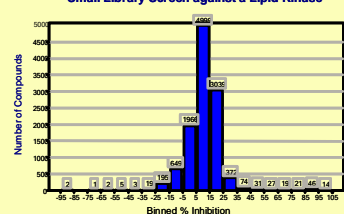


Figure 5. Compounds screened at a 100 nM concentration (single-point) against a lipid kinase. The screening assay was performed at the K_m level of MgATP and at less than K_m levels of PDC15.

Mechanism of Action Studies for the Inhibition of a Ser/Thr Kinase by PDC15

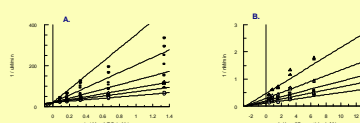


Figure 6. Characterization of the inhibition of a Ser/Thr Kinase by PDC15. A) PDC15 was varied at fixed concentrations of MgATP in the presence of 0.5 μM PDC15. The data fit best to a competitive pattern of inhibition (Equation 2) with a $K_i = 0.34 \pm 0.032 \mu M$. B) PDC15 was varied at fixed concentrations of PDC15 in the presence of 1.5 μM ATP. The data fit best to a noncompetitive pattern of inhibition (Equation 3) with a $K_i = 6.45 \mu M$.

Irreversible Inhibition of Ser/Thr Kinase by PHA-XXX83E

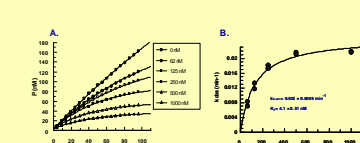


Figure 7. Kinetics of inhibition of a Ser/Thr kinase by PHA-XXX83E. A) Enzyme was diluted into MgATP (45 μM, 450 μM), peptide and inhibitor at the indicated concentrations. The data were fit to progress curve describing irreversible inhibition (Equation 5). B) Second order plots of PHA-XXX83E k_{off} derived from Figure 7A were fit to Equation 6.

$T_{1/2}$ value determination of compounds against a Ser/Thr kinase

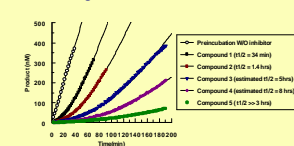


Figure 8. Inhibitor and enzyme were pre-incubated (50 nM enzyme and 50 nM inhibitor) for 1 hour at room temperature. The pre-incubation mixture was diluted into saturating amounts of MgATP (450 μM) to provide a final concentration of 0.1 nM enzyme and 0.1 nM inhibitor, respectively. The dissociation rates (k_{off}) were determined using Equation 4.

Limitations to Consider

- Fluorescent substrate availability for an assay
- Only one phosphorylation site can be analyzed, current data package can not analyze two phospho sites
- Limited fluorescent substrate concentration range (50 nM-20 μM) must instrument "heating"
- Charge and Mass of fluorescent substrate must be amenable to separation (generally, <20 AA and a charge of -5 to +5)
- Product conversion higher than desired for typical enzymology studies (~10%)
- Limited run time due to plate preparation and buffer disposal (max run is typically 6-8 hours)

Summary

- High quality of data generated by the LC3000 due to the measurement of both substrate and product
- A single assay format may be used for assay development, small library screening, and detailed inhibitor characterization
- Assay development is done in a quick manner because of the LC3000 ability to generate real time readout
- The LC3000 supports screening of small libraries and allows for easy identification of any compounds interfering with fluorescence
- The LC3000 allows for steady-state inhibitor characterization as both ATP and peptide substrate may be varied
- Evaluation of inhibitor kinetics (i.e. on- and off- rates) may be moved higher a project's testing scheme due to the ability to assay several compounds per run using the LC3000 in a "kinetic mode"
- Several Ser/Thr, tyrosine and lipid kinase projects are supported using the LC3000 technology at Pfizer-St. Louis