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Use of Kinetic Isotope Effects to Delineate the Role of Phenylalanine 87 in $P450_{BM-3}$

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The substrate oxidation rates of $P450_{BM-3}$ are unparalleled in the cytochrome P450 (CYP) superfamily of enzymes. Furthermore, the bacterial enzyme, originating from *Bacillus megaterium*, has been used repeatedly as a model to study the metabolism of mammalian P450s. A specific example is presented where studying $P450_{BM-3}$ substrate dynamics can define important enzyme–substrate characteristics, which may be useful in modeling ω-hydroxylation seen in mammalian P450s. In addition, if the reactive species responsible for metabolism can be controlled to produce specific products this enzyme could be a useful biocatalyst. Based on crystal structures and the fact that the $P450_{BM-3}$ F87A mutant produces a large isotope in contrast to the native enzyme, we propose that phenylalanine 87 is responsible for hindering substrate access to the active oxygen species for nonnative substrates. Using kinetic isotopes and two aromatic substrates, *p*-xylene and 4,4′-dimethylbiphenyl, the role phenylalanine 87 plays in active-site dynamics is characterized. The intrinsic KIE is 7.3 ± 2 for *wt*$P450_{BM-3}$ metabolism of *p*-xylene. In addition, stoichiometry differences were measured with the native and mutant enzyme and 4,4′-dimethylbiphenyl. The results show a more highly coupled substrate/NADPH ratio in the mutant than in the *wt*$P450_{BM-3}$.

Key Words: P450BM-3; kinetic isotope effects (KIE); stoichiometry; ω-hydroxylation; biocatalyst.

INTRODUCTION

In general, cytochrome P450 enzymes can perform a variety of difficult chemistries. For example, they can oxidize unfunctionalized hydrocarbons (*1*). These chemistries have important roles in industrial processes and drug metabolism. Cytochrome $P450_{BM-3}$ originates from the soil bacterium, *Bacillus megaterium*. The bacterial $P450_{BM-3}$ possesses unique characteristics when compared to the superfamily of enzymes: (i) it can metabolize substrates much faster than other P450s, with oxidation rates as high as 4600 nmol/min/nmol P450 (*2*) and, (ii) the heme and FAD/FMN reductase of $P450_{BM-3}$ are fused together forming a large 119-kDa enzyme. The latter

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attribute is partly responsible for the increased rates, as the required collision event between the heme and the reductase prior to electron transfer is eliminated. Furthermore, the nature of the reductase classifies $P450_{BM-3}$ as a type II P450, grouping it with mammalian P450s. As such, the bacterial enzyme has often been used to model the metabolism of mammalian P450s. Such models are useful, especially when the P450 isoforms have similar metabolic profiles for a given set of substrates (*3*). For instance, the eukaryotic 4F family metabolizes long-chain fatty acids at the omega position (*4,5*) while $P450_{BM-3}$, also has a high degree of specificity for long-chain fatty acids, but produces only internal alcohols and no ω-hydroxylation in the wild-type enzyme (*4,6*)

The versatility of $P450_{BM-3}$ enables the study of this enzyme to overlap multiple disciplines: (i) to better understand the metabolism of endogenous chemicals in mammals by P450s and, (ii) to develop the catalytic powers of this enzyme for biocatalysis. (i) As stated, $P450_{BM-3}$ shows tendencies to metabolize similar substrates to the P450 4F family and shares the same sites of metabolic activity toward long-chain fatty acids. With a more complete understanding of $P450_{BM-3}$ dynamics, this system may be used to model the metabolic activity of the P450 4F family. (ii) Alternatively, defining the dynamics of substrate metabolism is important in the development of this enzyme as a biocatalyst and would allow the powerful oxidant and fast rates to be more fully utilized.

Several crystal structures of $P450_{BM-3}$ have been solved, with and without substrates bound (*7–9*). As a result, certain residues have been identified that directly participate in the binding of substrates once in the active site. Specifically, phenylalanine 87 has been shown to be in close contact with the heme on the distal side of the binding pocket, adjacent to the I-helix. This occupies a great deal of the active site as shown in Fig. 1A. To study the impact of phenylalanine 87 on substrate metabolism, residue 87 was mutated to alanine (*10*). $P450_{BM-3}$ F87A becomes an ω-hydroxylase, where the terminal carbon of the fatty acid becomes the principal metabolite much like that seen for the 4F family. This contrasts with *wt*$P450_{BM-3}$, where metabolism occurs only at the internal carbons of fatty acids. The measured difference in reactivity between these two positions indicates that without enzyme–substrate interactions, the omega-1 position would be favored over the omega position by a factor of 25 to 1 (*4,11*). The outcome shows that the mutant favors the least activated position for hydrogen atom abstraction, implying that in the F87A mutant the terminal methyl group can approach more closely to the active oxygen species when compared to the internal hydrogen atoms. By studying $P450_{BM-3}$ enzyme–substrate interactions, we hope to gain insight into why P450 4F metabolism occurs at the omega position.

The enzyme dynamics described above are also important in the development of enzymes for benign synthesis, biocatalysis, and bioremediation (*12*). The cytochrome P450 superfamily of enzymes is able to oxidize a range of structurally diverse organic compounds. In fact, substrate binding does not appear to reduce the transition-state energy for the hydrogen atom abstraction event in P450 enzymes (*12*). Therefore, substrate binding can result in multiple orientations producing numerous metabolites from a single substrate. The powerful oxidant responsible for hydrogen atom abstraction and subsequent oxidation in P450s is generally thought to be the iron–oxene species (*13, 14*). This highly reactive intermediate is capable of oxidizing most any

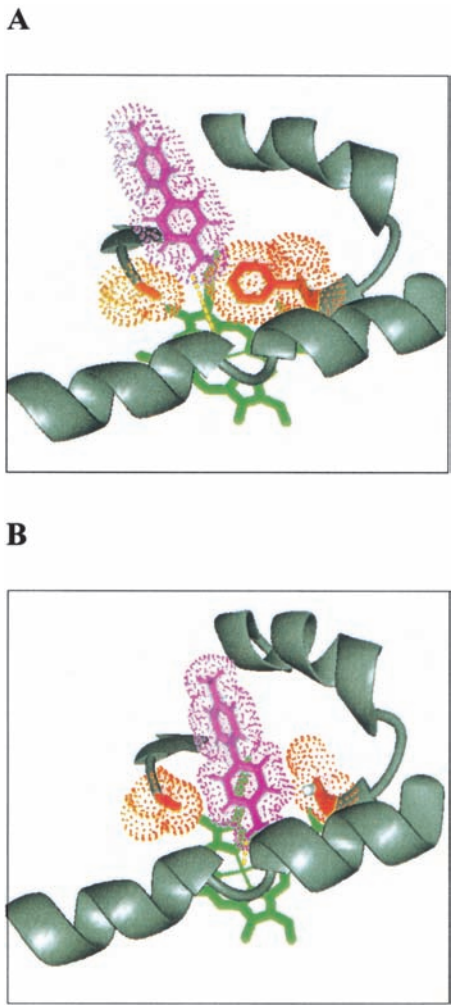


FIG. 1. The crystal structure of P450$_{BM-3}$ was taken from the Protein Data Bank. Subsequent docking of substrate, 4,4-dimethylbiphenyl was performed using Midas (San Francisco, CA). The substrate and enzyme were minimized using Amber 6 (UCSF, CA). van der Waal radii are highlighted. (**A**) From left to right, A328, 4,4-dimethylbiphenyl, and F87 are highlighted and show the high level of contact between F87 and 4,4-dimethlybiphenyl. (**B**) The F87A mutant increases substrate access to the heme.

hydrocarbon and is the reason why multiple products form. To develop P450s as biocatalysts, the enzyme dynamics must be more fully understood in order to limit binding orientations and to enhance a specific metabolic product.

The importance of understanding P450$_{BM-3}$ enzyme dynamics has been established, but methods used to identify enzyme–substrate interactions are limited and difficult. Several techniques in enzymology have been developed to study enzyme activity. The use of kinetic isotope effect experiments has been successful at determining complicated interactions associated with substrate motion in the active site of certain

enzymes (*3,15,16*). To measure the enzyme dynamics using KIE it is necessary to first estimate the intrinsic isotope effect. As described by Northrop (*17*), an intrinsic isotope effect will be observed in an intramolecular experiment if interchange between the enzyme–substrate complexes that lead to either hydrogen or deuterium abstraction is rapid. For the substrate shown in Fig. 2A this only requires rotation about a carbon–carbon single bond.

Since single bond rotation is fast, this type of experiment will almost always lead to an intrinsic isotope effect (*18,19*). A second intramolecular experiment can be used to measure the limit of dynamic motion associated with the substrate in the active site of an enzyme. Specifically, using a chemical that possesses a C_2 axis of symmetry such as the compounds shown in Fig. 2B, where one end of a molecule is deuterated and the other end possesses protons. In this case, reorientation of the entire molecule is required in order to produce the KIE_{intr} (Fig. 2B). If substrate reorientation is slow, the observed isotope effect will be smaller than the intrinsic isotope effects, but if reorientation is fast, the observed isotope effect will equal the intrinsic isotope effect.

To test the active-site dynamics of $P450_{BM-3}$ and the F87A mutant we choose to use kinetic isotope effect experiments with two intramolecular probes shown in Scheme 1, *p*-xylene **1** and 4,4′-dimethylbiphenyl **2** (*18*). Specifically, we hypothesize that the F87A mutant will allow the substrate to reorient faster in the active site. To test this hypothesis we will use the well-defined substrate probes to identify the capacity of substrate rotation and translation within the active site of $P450_{BM-3}$ and the F87A mutant enzyme.

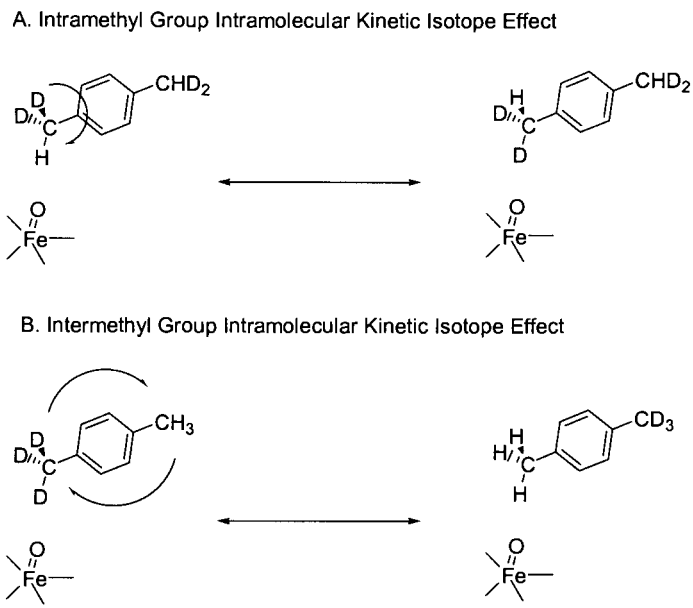
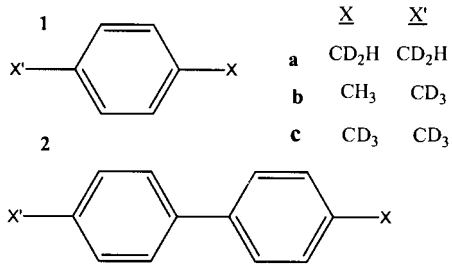


FIG. 2. The cartoon shows the difference between the (A) intramethyl KIE and the (B) inter-Methyl KIE.



SCHEME 1. Cytochrome P450 substrates used for the measurement of isotope effects.

METHODS AND MATERIALS

Materials and Reagents

p-Xylene and 4,4′-dimethylbiphenyl were purchased from Aldrich (Milwaukee, WI). G-6-P, G-6-P dehydrogenase, catalase, and NADPH were purchased from Sigma (St. Louis, MO). MTBSTFA was purchased from Regis Technologies, Inc. (Morton Grove, IL). DH5α competent cells were purchased from Gibco Life Technologies (Gaithersburg, MD). Site-directed mutagenesis was performed with the Quick Change site directed mutagenesis kit from Stratagene (La Jolla, CA). All solvents were purchased from J. T. Baker, Inc. (Phillipsburg, NJ). The remaining reagents were of the highest purity commercially available. Spectroscopic studies were performed on a SLM Aminco DW-2000 UV-VIS spectrophotometer. Oxygen consumption data were recorded with an iso-750 Clark-type oxygen probe from World Precision Instruments (Sarasota, FL). Proton NMR was obtained at 300 MHz on a Varian instrument. Site-directed mutagenesis was confirmed by sequencing in the molecular research facility LBB1 of Washington State University.

Expression

Recombinant P450$_{BM-3}$ from *B. megatarium* was expressed in DH5α *Escherichia coli* cells as described (*20*). Yields of pure protein after 2′, 5′-ADP column (*21*,*22*) were 200−300 nmol per liter of growth media. The protein was pure and homogenous as determined by SDS-PAGE. The concentration of protein was determined using the molar extinction coefficient 96 mM^{-1} cm^{-1} (*23*). Enzyme stocks were run through a PD-10 column (Sephadex G25 resin) equilibrated with 0.1 M potassium phosphate buffer (pH 7.4) to remove 2,3-AMP, concentrated and frozen at −80°C prior to use.

Synthesis of Substrates

(A) p-Xylene-α-$^2H_3$. *p*-Methyltoluate (5.2 g, 0.036 mol) in 20 mL of anhydrous diethyl ether was added drop wise to lithium aluminum detrude (1.6 g, 0.04 mol) suspended in 50 mL of anhydrous diethyl ether. The reaction was stirred at room temperature for 3 h under argon atmosphere and then quenched with 1 mL of ice, 2 mL of 15% sodium hydroxide, and with another 2 mL of water cautiously. The solution was filtered and the filtrate was rinsed with cold diethyl ether. The solution was then extracted 2 × 75 mL of pentane. The pentane was dried over magnesium

sulfate and concentrated under reduced pressure to yield *p*-methyl benzyl alcohol (3.8 g, 0.031, 90%). The resulting *p*-xylene was >99% pure by GC and by MS had a deuterium content of 98.20 at.% deuterium-d_3, 1.59 at.% deuterium-d_2, and negligible d_1 and d_0.

(B) Synthesis of p-Xylene-α-$^2H_2$-α'-$^2H_2$. Terephthalic acid (2.76 g, 0.015 mol) was added dropwise to lithium aluminum deuteride (1.2 g, 0.03 mol) suspended in 60 mL of ether. The reaction was stirred overnight and then terminated with 1 mL of ice while reaction was stirred in an ice bath. Followed by 1.2 mL of 3 M NaOH and 1.2 mL of water. The resulting mixture was filtered and the ether was then rinsed 2 × 50 mL of water. The remaining ether layer was dried over magnesium sulfate, filtered, and evaporated to yield 0.97 g (0.007 mol) of clear diol. The product was then stirred with 10 mL of 48% hydrobromic acid for 30 min. The resulting solid was recrystallized and filtered to yield 0.5 g (0.002 mol) of grayish-white solid. The dibromo product was suspended in minimal dimethyl sulfoxide and then added to a stirring solution of sodium borohydride (0.25 g, 0.006 mol) in 10 mL of dimethyl sulfoxide. After 12 h, 40 mL of pentane was added followed by the careful addition of 10 mL of water. The mixture was then carefully rinsed with 2 × 25 mL of water. The remaining pentane was dried over sodium sulfate and then evaporated. The resulting α-$^2H_2$-α'-$^2H_2$-*p*-xylene was applied to column chromatography over neutral silica and carefully evaporated and the corresponding fractions were stored in −80°C refrigerator until use, as these products are volatile. The resulting *p*-xylene was pure by GC and by MS had a deuterium content of 97.71 at.% deuterium-d_4, 1.64 at.% deuterium-d_3, and 0.65 at.% deuterium-d_2.

(C) 4′-Methylbiphenyl-4-carboxylic acid. 4,4′-Dimethylbiphenyl (2.3 g, 0.013 mol) was suspended in 100 mL of glacial acetic acid and 4.6 g (0.05 mol) of chromium trioxide was carefully added. The mixture was slowly heated and maintained at 90°C for 2 h. Then the reaction was allowed to cool before adding to 500 mL of ice-cold water. The green solution was filtered and washed with ice water until the precipitate was colorless. The precipitate was dissolved in 2 M ammonia in methanol, filtered, and then reprecipitated by acidifying with 75% hydrochloric acid solution. The precipitate was filtered and dried yielding (0.6 g, 0.003 mol) of 4′-methylbiphenyl-4-carboxylic acid.

(D) Synthesis of 4-$^2H_3$,4′-dimethylbiphenyl. To lithium aluminum deuteride (210 mg, 0.005 mol) suspended in 50 mL of dry tetrahydrofuran, 4′-methylbiphenyl-4-carboxylic acid (0.5 g, 0.0024 mol) was added slowly. The reaction was stirred for 16 h under argon. The reaction was terminated with 1 mL of ice, 1 mL of 15% sodium hydroxide, and 2 mL of water. The mixture was then filtered, dried over magnesium sulfate, and evaporated, yielding a crude oil. The product alcohol was purified by silica gel (12 g) column chromatography with chloroform:methanol (9:1) as eluant. The alcohol (310 mg, 0.0016 mol) was dissolved in dichloromethane and reacted with *p*-toluenesulfonyl chloride (380 mg, 0.0020 mol) and triethylamine (1 mL) for 48 h. The mixture was washed with 2 × 75 mL water and dried over sodium sulfate and evaporated to yield the tosylated product. The product was purified by silica gel (5 g) column chromatography with pentane as an eluant. The tosylate (65 mg, 0.2 mmol) was reduced with lithium aluminum deuteride (0.1 g, 0.003 mol) to yield 4-$^2H_3$,4′-dimethylbiphenyl. This compound was purified by silica gel (25 g)