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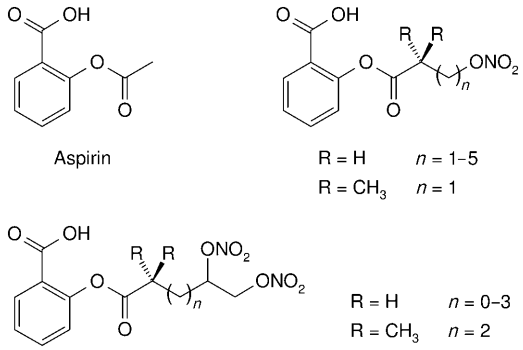
Mechanistic Insights into Cyclooxygenase Irreversible Inactivation by Aspirin

Paolo Tosco* and Loretta Lazzarato[a]

Aspirin (acetylsalicylic acid) belongs to the broad class of nonsteroidal anti-inflammatory drugs (NSAIDs), whose therapeutic effects are largely due to their inhibition of prostaglandin synthesis by cyclooxygenase (COX). Aspirin is unique among NSAIDs since it covalently modifies both isoforms of COX, thus inactivating them irreversibly. Its major drawback is a significant gastrotoxicity; symptoms may range from gastritis to peptic ulcer and severe gastrointestinal haemorrhage.[1,2] Our research group has recently realized a series of nitric oxide (NO)-releasing aspirin-like compounds aimed at reducing the gastrotoxicity of the parent drug.[3] These hybrid compounds, which combine the anti-inflammatory and antiaggregatory properties of the lead with NO-mediated gastroprotective effects, have proven to be irreversible inactivators of both COX isoforms; after in vitro incubation with the inhibitor, the enzymes do not recover their catalytic activity upon washing.[4] The molecular basis of irreversible COX inhibition by aspirin is the ability of the latter to selectively transfer the acetyl group to Ser 530. While this residue is not directly involved in the catalytic function of the enzyme, the increased bulk of the acylated side chain hinders proper binding of arachidonic acid in the cyclooxygenase channel.[5,6] Since our hybrids are nitrooxy-substituted higher homologues of aspirin, it seems reasonable to hypothesize that they might act as COX acylating agents in the same way. However, since other NSAIDs (e.g., indomethacin) behave as time-dependent, irreversible inhibitors of COX without forming any covalent bond within the active site,[7] we decided to undertake a theoretical investigation to clarify whether our compounds are actually covalent inactivators or tightly binding noncovalent inhibitors. While site-directed mutagenesis experiments and the X-ray structure of COX-2 inactivated by bromoacetylsalicylic acid[6] leave no doubt about how aspirin inhibits COX, they fail to elucidate the mechanism of acyl transfer at a molecular level. Therefore, before studying our hybrids, we needed a proof-of-concept on aspirin itself. Herein, we present our preliminary results and propose a putative mechanism of Ser 530 transesterification by acetylsalicylic acid.



Despite the low affinity of aspirin for COX ($K_i = 20$ mM), acetylation of Ser 530 takes place very efficiently once aspirin is bound in the active site, as indicated by the high values of k_{inact}.[8] Both the selectivity and the efficiency of aspirin are quite surprising, since no neighboring groups are present in the vicinity of Ser 530 to enhance nucleophilicity, such as histidine and glutamate in serine proteases.[9] Site-directed mutagenesis experiments have underlined the importance of Arg 120 and Tyr 385 for the biological activity of aspirin. Based on the reduced potency on Arg 120 Gln mutants and the loss of activity on Arg 120 Ala mutants, it has been suggested that acetylsalicylate initially forms a charge-enhanced H bond with Arg 120 through the carboxylate moiety, which puts the molecule in the correct orientation to subsequently acetylate Ser 530.[6,10] The loss of activity in Tyr 385 Phe mutants has suggested a crucial role of the Tyr 385 hydroxy group as a H bond donor in orienting and polarizing the acetyl group of aspirin, thus increasing its reactivity towards transesterification by Ser 530. Tyr 385 might then be able to stabilize the incipient negative charge of a putative tetrahedral intermediate, mimicking the oxyanion hole of serine proteases.[10]

This hypothesis is complemented by the finding that redox cycling of the peroxidase, which involves formation of a radical on Tyr 385, and consequent loss of H-bond-donating capabilities, prevents COX acetylation by aspirin.[11] The salicylate structure itself appears to selectively target Ser 530; in fact, unlike other acylating agents such as *N*-acetylimidazole, no other residues are acetylated.[12] The stability of the acetylated serine to hydrolysis has been ascribed to the low probability of interaction with bulk water due to the hydrophobic nature of the COX channel.[6] The carboxylate-binding region represented by Arg 120 and the target residue Ser 530 are often described as very close in space, and ideally located to promote inactivation of the enzyme by aspirin.[8,9] Actually, as Loll and co-workers pointed out,[6] acetylsalicylic acid, after its likely initial ion-pairing with Arg 120, needs to diffuse 5 Å upwards in the COX channel to reach a position from which Ser 530 acetylation can occur (Figure 1). Unfortunately, the precise sequence of events can only be inferred, since the X-ray structure shows the inhibitor–enzyme complex after acylation has already occurred.

[a] *Dr. P. Tosco, Dr. L. Lazzarato*
Dipartimento di Scienza e Tecnologia del Farmaco
Università degli Studi di Torino
Via Pietro Giuria 9, 10125 Torino (Italy)
Fax: (+39) 011-670-7687
E-mail: paolo.tosco@unito.it

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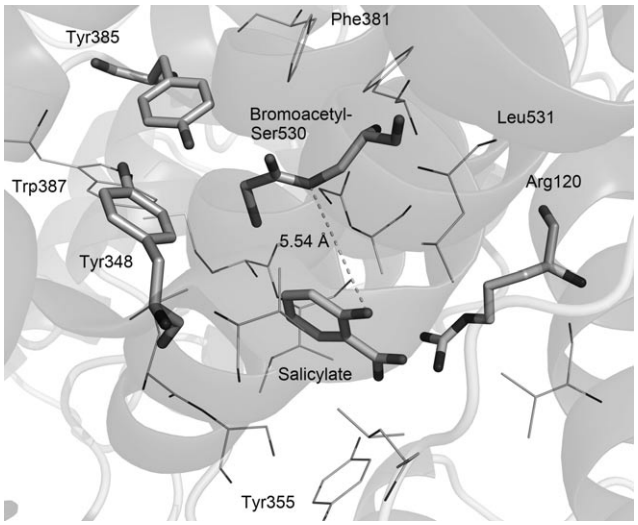

Figure 1. The crystal structure of the COX-2 active site after inactivation by bromoacetylsalicylic acid as obtained by Loll and co-workers.[6] All hydrogens were missing in the original coordinate file. The distance between the phenolic group of salicylate and the Ser 530 oxygen atom is represented as a dotted line.

With this observation in mind, we first attempted to dock aspirin in the active site of both COX-1 and COX-2 isozymes to see how intact acetylsalicylate would bind. Among those available in the Protein Data Bank,[13] the best resolved structures were chosen, namely 1Q4G for COX-1[14] and 1PXX for COX-2.[15] The co-crystallized ligands were removed and flexible docking of acetylsalicylate was accomplished with AutoDock 4.0,[16] keeping the protein structure rigid. On both isozymes a single cluster of binding poses, almost identical to each other, was obtained, largely reminiscent of the experimentally determined binding conformation of salicylate identified by Loll and co-workers. While this outcome was largely expected on the basis of mutagenesis data pinpointing the key role of Arg 120, in these poses the acetyl carbon lies 5 Å away from the Ser 530 OH group, and therefore acylation cannot be expected to occur. In order to find a reasonable starting conformation for a quantum mechanical/molecular mechanical (QM/MM) study, we needed to simulate the outcome of the upward diffusion following the initial binding as postulated by Loll and co-workers.[6] For this purpose, a biased conformational sampling was accomplished by molecular dynamics (MD) in CHARMM.[17] The two isozymes were solvated in a octahedral box of explicit water under periodic boundary conditions (PBC), then ten complexes were generated with aspirin assuming random orientations in the active site of each isoform, constraining the distance between the acetyl carbon and the Ser 530 OH group as less than 3.5 Å. After preliminary minimization and equilibration at 300 K, a simulated annealing (SA) procedure by MD was carried out using a dual heat bath thermostat, which allowed the ligand to be heated up to 1000 K and then slowly cooled to 300 K, while the enzyme and bulk water were maintained at 300 K. This procedure allowed thorough sampling of aspirin conformations inside the cavity, while preventing any distortion of the protein structure. Additionally, harmonic constraints of appropriate weight were set on backbone and side-chain atoms. The whole SA cycle was repeated five times, removing the 3.5 Å constraint on the acetyl carbon–Ser 530 OH distance after the first run. This precaution was taken since our goal was to set an initial bias in order to sample only relevant conformations, avoiding waste of CPU time on enzyme–inhibitor complexes that would never give rise to Ser 530 acylation. However, we did not want to force the protocol to find unreasonable, high-energy conformations just because of the presence of a tight constraint throughout all SA cycles. Performing four unconstrained SA runs prevents finding fake minima, due to an artificial biasing potential. The eight initial starting conformations gave only three different final enzyme–inhibitor complexes (a–c), very similar for both isoforms. Figure 2 shows those conformations obtained for COX-1. While complexes b and c appear compatible with the hypothesis of an initial ion pairing with Arg 120 through the carboxylate group, followed by upward diffusion towards Ser 530, complex a differs quite markedly from the X-ray structure pictured in Figure 1, since the carboxylate group is on the opposite side, facing Ile 523 instead of Arg 120.

Once we obtained the initial inhibitor–enzyme complexes, we switched from a pure MM potential to a hybrid QM/MM Hamiltonian, using the semiempirical SCC-DFTB level of theory as implemented in CHARMM[18] for the QM calculations. Since our interest was focused on the region were acylation should take place, all molecules that might potentially be involved in the acylation mechanism, namely aspirin, residues Tyr 348, Tyr 385, Ser 530, and nearby water molecules, were treated by QM, while the rest of the protein, as well as the bulk water, were treated by traditional molecular mechanics. The resulting Hamiltonian can be expressed as:

$$H = H_{QM} + H_{MM} + H_{QM/MM}$$

where H_{QM} is the Hamiltonian describing atoms treated by QM, H_{MM} the Hamiltonian of atoms treated by classic MM, and $H_{QM/MM}$ represents the interactions between the MM and the QM regions.[19] To further reduce the computational burden, we decided to switch from PBC to stochastic boundary conditions (SBC), cutting a 45 Å radius water droplet containing the whole enzyme–inhibitor complex out of the periodic system. A 16 Å radius sphere centered on the acetyl carbon of aspirin was defined as the region of interest, and left completely unconstrained. Instead, to remove possible distortions taking place at the periphery of the system under SBC, harmonic constraints derived from experimental B factors[20] were applied to the residues lying in a 4 Å-wide boundary region around the region of interest, while all atoms beyond this region were held fixed. The QM/MM approach, which takes into account the electronic structure of molecules enclosed in the QM region, allows bonds to be formed and broken in this region if the appropriate conditions are met, making it possible to study the feasibility of acetylation of Ser 530 by aspirin under the simulation conditions. As soon as a preliminary minimization of complex a was carried out on both COX-1 and COX-2 using the hybrid QM/MM potential, migration of the acetyl

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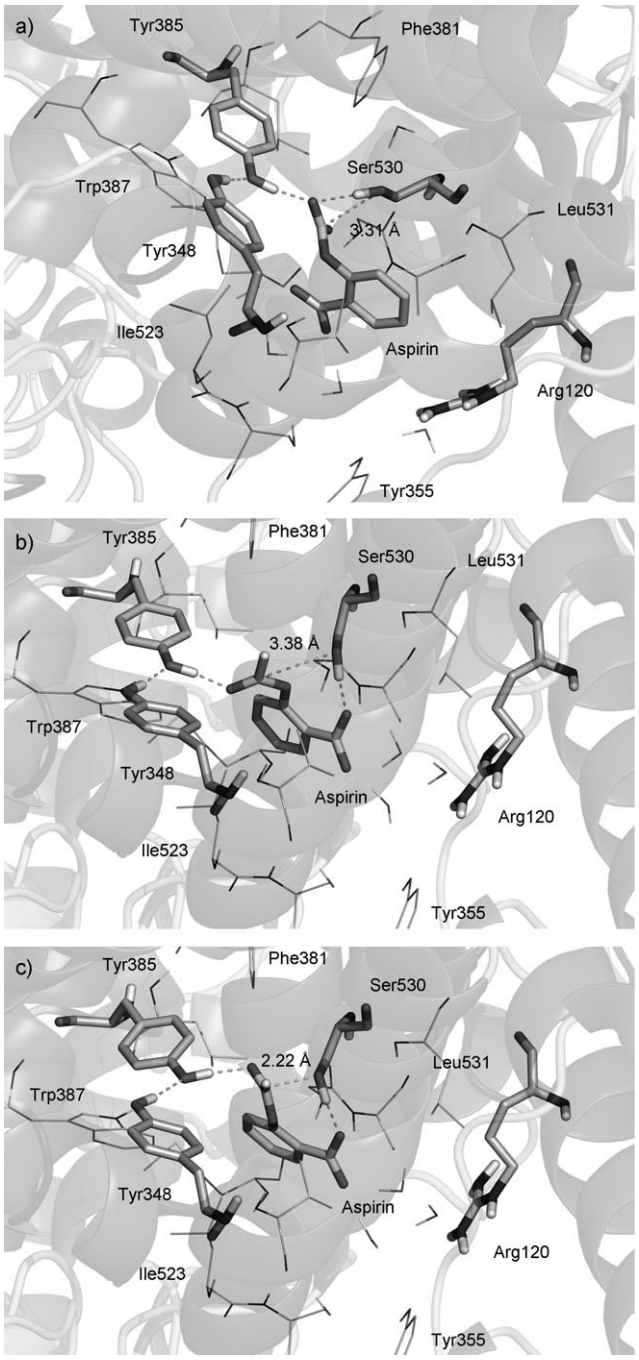


Figure 2. The three aspirin–COX-1 complexes a, b, c obtained by simulated annealing. Nonpolar hydrogens have been omitted for clarity.

moiety from the phenol to the carboxyl group was observed, giving rise to the corresponding anhydride (complex a′, Figure 3). We were quite surprised by this outcome; while the formation of an anhydride might be a reasonable explanation for the unusual reactivity of aspirin in the COX active site, if actually aspirin behaved as a mechanism-based inhibitor, this should result in peculiar inhibition kinetics,[21] which have never been reported. In the literature, there are some early reports about the "acid anhydride" character of aspirin,[22] confirmed by other authors who claimed the anhydride intermedi-

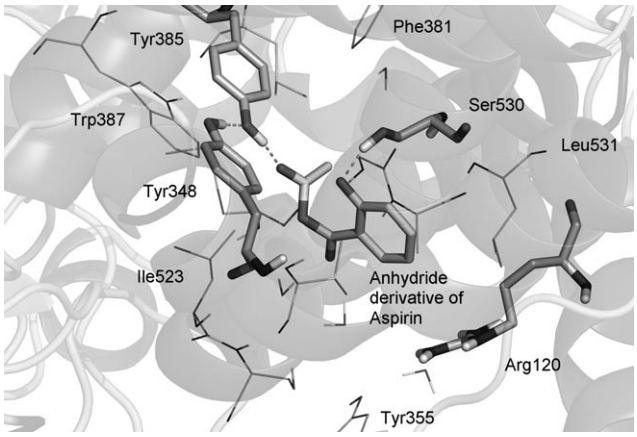
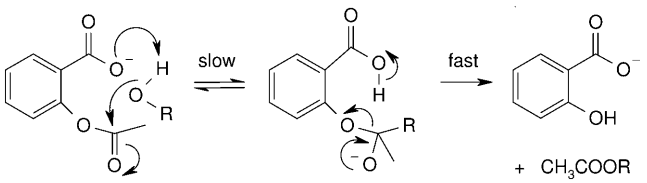


Figure 3. Complex a′, created by acetyl migration following a simple energy minimization using the hybrid QM/MM potential.

ate was involved in the mechanism of hydrolysis of aspirin to acetic acid and salicylate.[23] However, later independent works by Fersht,[24] Jencks[25] and Kemp[26] demonstrated through elegant experiments that, while aspirin can actually exist in the anhydride form, the latter is not involved in the mechanism of solvolysis (either by water or alcohols), which instead proceeds under intramolecular general base catalysis provided by the vicinal carboxylate moiety (Scheme 1). The anhydride intermediate is thought not to play a role in solvolysis of aspirin because



Scheme 1. Solvolysis of aspirin under general base catalysis conditions (R = H, alkyl).

the greater nucleophilicity of the phenoxide anion with respect to solvent favors the intramolecular reaction reforming aspirin.[24]

Indeed, taking a closer look at complex a′ (Figure 3), it is evident that the phenoxide anion is in a much more favorable position than the hydroxy group of Ser530 to react with the acetyl carbon to reform aspirin. To verify that this is actually the case, 1 ns QM/MM MD simulations on complex a′ were accomplished at constant *V* and *T*. No acetylation occurred on either isozyme; rather, the acetyl group was observed to migrate smoothly from the phenol to the carboxyl group and back, consistently with the experimental findings. Complex a has therefore to be regarded as a pose from which aspirin is not able to trigger acetylation of Ser530. Moreover, as previously noted, the collocation of the carboxy group on the opposite side with respect to Arg120 probably makes this binding mode rather unlikely. Complexes b and c, instead, appear to have the correct geometry to undergo the general base cat-

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alysis mechanism outlined in Scheme 1, since the hydroxy proton of Ser 530 faces the carboxylate moiety of aspirin, while the oxygen atom is within reach of the acetyl carbon. For both complexes, 1 ns QM/MM MD simulations were carried out. We were pleased to observe that after a few picoseconds these two starting conformations were able to trigger acetylation of Ser 530 both on COX-1 and on COX-2. In particular, complex b first evolves to complex c, which appears to be a very effective proacylating conformation; the first 250 ps of the MD trajectories of complex b on both isozymes are available in the Supporting Information. Careful examination of MD trajectories shows that acetylation needs the formation of a stable H bond between the hydroxy group of Tyr 385 (donor) and the oxygen atom of the acetyl moiety of aspirin (acceptor). Once this H bond has been established, as soon as the Ser 530 O–H bond and the C^{ar}–O(CO) bonds become parallel, a proton migrates from the Ser 530 OH group to the aspirin carboxylate, and immediately afterwards the acetyl moiety migrates from aspirin to Ser 530, passing through a tetrahedral intermediate.

Very interestingly, after the transesterification has occurred, the salicylate leaving group does not participate in a reverse reaction on the acetylated Ser 530, which is consistent with the experimental observation that COX inhibition is irreversible. The role of the carboxylate in providing intramolecular general base catalysis also gives a sound explanation to the stability of acetylated Ser 530 to hydrolysis. A longer MD simulation would probably be necessary to observe the salicylate leaving group moving away from the reaction site; regardless, it is evident from the experimental X-ray crystal structure[6] (Figure 1) that after aspirin has acetylated Ser 530, salicylate is involved in an electrostatic attraction with Arg 120. The only basic moiety has left the reaction site and, in the absence of a specialized proton relay system such as in esterases, water is not nucleophilic enough to regenerate the active enzyme.

Apart from the short simulation time, there is another reason why the 5 Å backward diffusion towards Arg 120 is not observed in the trajectory. In fact, after the acetyl group has been transferred from the aspirin phenol group to COX, the proton abstracted from the Ser 530 side chain would be expected to migrate from the carboxylate group to the phenoxide anion on the basis of the higher basicity of the latter. However, this transfer does not take place in the time span covered by the simulation. While this might well be considered an artefact of the semiempirical SCC-DFTB QM method, it is worth mentioning that the energy difference between the two tautomers was shown to be quite small, both experimentally and by ab initio QM.[27] Actually, after carrying out a QM minimization on the two isolated salicylate tautomers with a DFT RB3LYP/6-31G + (d) method, the phenoxide tautomer was 0.76 kcal mol^{-1} more stable than the carboxylate. When the same minimization was accomplished with the SCC-DFTB method, the carboxylate tautomer underwent spontaneous conversion to the phenoxide tautomer, probably due to underestimation of the interconversion energy barrier. During our MD simulations the negative charge remained on the phenoxide anion, which probably prevents salicylate from ion pairing with Arg 120 since a charge-enhanced H bond between the phenoxide anion and Tyr 385 OH group prevails. Nonetheless, even if salicylate does not move very far away from the reaction site, acetyl-Ser 530 appears absolutely stable.

Using the MD trajectories as a guide, an adiabatic potential energy surface (PES) describing the transesterification reaction was built. Starting from the 3D coordinates of complex c, two reaction coordinates *x* and *y* were defined as linear combinations of distances between atoms involved in the breaking and forming of covalent bonds (Figure 4). A series of sequential QM/MM energy minimizations were carried out, one for each

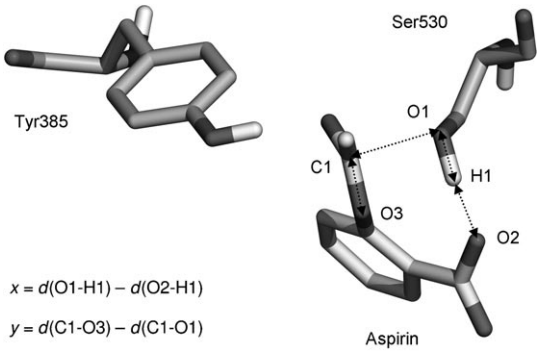

Figure 4. Definition of reaction coordinates *x* and *y*.

pair of (*x*,*y*) values, using the same conditions as for MD (SBC, harmonically-constrained boundary region, fixed outer region). The region of interest was left completely free to relax, except for the two reaction coordinates that were restrained with a high-force constant (1000 kcal mol^{-1} Å^{-2}), in order to drive the reaction from the initial to the final state along the path outlined by MD. The minimized geometries of the residues making up the QM region were isolated, and two single-point energy calculations were carried out, one with the semiempirical SCC-DFTB method, the other with a DFT method at the RB3LYP/6-31G(d) level. Diffuse sp functions were not included in the basis set since, when applied on a small test region of the PES, they proved not to significantly affect calculated energies, while inducing a 16-fold increase in CPU time. The DFT correction to the total QM/MM energy was accomplished as previously described,[28] subtracting the SCC-DFTB contribution for the QM region and adding the RB3LYP energy. The obtained RB3LYP/6-31G(d)//SCC-DFTB-CHARMM22 PESs for acetylation of COX-1 and COX-2 are shown in Figure 5 a and b, respectively, together with the plots of the potential energy and the structure of the relevant intermediates along the minimum energy reaction path (MERP).

A word of caution is needed when considering these data. Firstly, they represent simple potential energies, and not free energies. Secondly, they were obtained by sampling single snapshots along the MERP rather than an ensemble of conformations. For these reasons, it is probably safer to assume that they provide a rough, qualitative estimate of the energetic profile of the transesterification process in the COX active site. Analysis of the PESs obtained on the two isozymes explains

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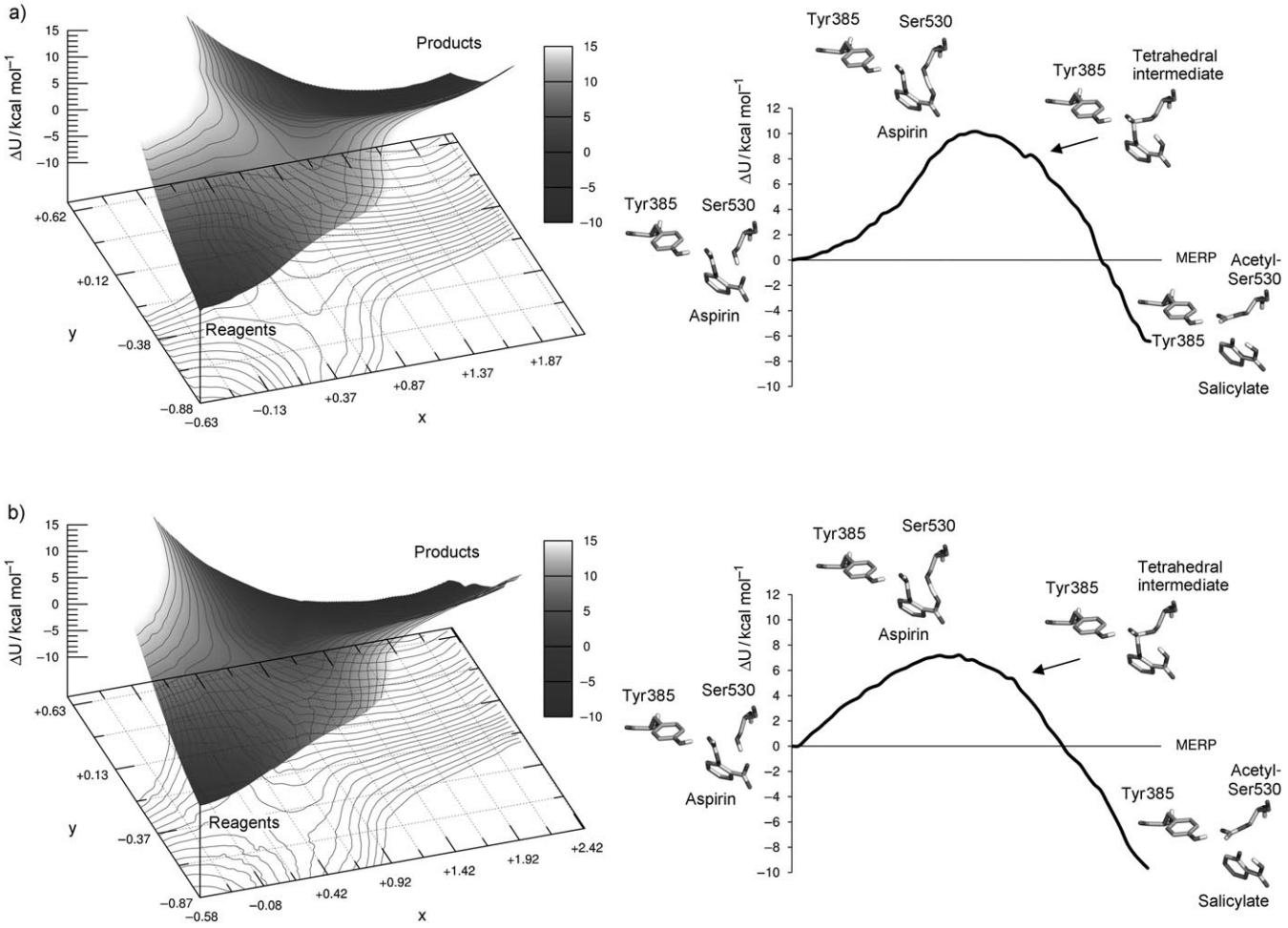

Figure 5. RB3LYP/6-31G(d)//SCC-DFTB-CHARMM22 Potential energy surfaces for the transesterification of Ser 530 by aspirin according to the proposed mechanism on a) COX-1 and b) COX-2. The potential energy of the system with respect to the initial state (ΔU) along the minimum energy reaction path (MERP) is also reported together with the 3D structures of relevant intermediates.

why the acetylation of Ser 530 takes place so smoothly during MD. In fact, the activation barrier to the transesterification is quite low, while the products are definitely more stable than the reagents, which explains why the backward reaction does not take place. Interestingly, the first, well-shaped saddle point corresponds to the structure of a complex where the tetrahedral intermediate has not yet formed, while a proton has migrated halfway between the Ser 530 OH and the carboxylate of aspirin. The involvement of such an intermediate in intramolecular general-base-catalyzed solvolysis of aspirin has been previously proposed by other investigators on the basis of experimental evidence.[29] The unusual stability of this transition state has been attributed to the formation of a particularly strong intramolecular H bond, termed a "one-proton solvation bridge".[29] The fact that our QM/MM simulation is able to reproduce this low-energy transition state gives robustness to our results. A second, more ill-defined saddle point is present corresponding to the tetrahedral intermediate, which forms after the proton transfer from Ser 530 to aspirin is complete. The structure of this tetrahedral intermediate is consistent with the role played by Tyr 385 in stabilizing the negative charge as proposed by Hochgesang and co-workers.[10] While the SCC-DFTB method appears to underestimate the energy of the transition states by ~5–7 kcal mol^{-1}, the overall shape of the PES is quite similar to the one obtained by applying the DFT correction; the pure SCC-DFTB-CHARMM22 PESs and MERPs are reported in the Supporting Information.

To further challenge our mechanistic hypothesis, we performed a Tyr 385 Phe in silico mutation on both COX isoforms in order to verify the true importance of this residue in the transesterification mechanism. It is immediately evident from the examination of the QM/MM MD trajectories (see Supporting Information) that, in the absence of the Tyr 385 OH group, aspirin is no longer univocally oriented as in the wild-type enzymes. The ligand is able to assume a number of different conformations, but none of them is able to trigger acylation. Notably, migration of the acetyl from the phenol to the carboxylate group does occur, however, as already mentioned, the anhydride form is unable to trigger acylation of Ser 530.

In conclusion, our theoretical study has led to a reasonable mechanistic hypothesis for acetylation of cyclooxygenase by aspirin, which is consistent with previous experimental findings

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by other investigators. In particular, Ser530 appears to be acetylated under intramolecular general base catalysis provided by the vicinal carboxylate group of aspirin; it is widely accepted that solvolysis of acetylsalicylate both by water and alcohols occurs by the same mechanism.[24–26] Moreover, a transition state with the same geometry proposed by Minor and Schowen[29] was found, and the key role of Tyr385 was confirmed by site-directed mutagenesis.[10] Future challenges include the more precise determination of the reaction free energy profile by extensive conformational sampling by QM/MM MD, possibly using a higher level of QM theory. Also, an estimate of the energetic cost of the 5 Å upward diffusion after the initial ion pairing to Arg120 to assume the pro-acylating starting conformation found by simulated annealing should be made. Finally, the adaptability of the protocol described herein to other irreversible COX inhibitors must be assessed.

Computational Methods

All molecular models were built using standard bond lengths and angles with the MOE software package.[30] MM and QM/MM computations were performed with CHARMM (version c33b1)[17] using the CHARMM22 force field. Parameters for aspirin necessary for pure MM calculations were derived from the GAFF force field[31] using the CHARMMGEN facility included in the AMBER 10 suite.[32] Electrostatic charges were fitted through the RESP approach[33] to the ab initio HF/6-31G(d) electrostatic potential computed with GAMESS-US.[34] 3D Coordinates for COX-1 and COX-2 were retrieved from the Protein Data Bank[13] (PDB codes 1Q4G and 1PXX, respectively); hydrogen atoms were added in standard positions and then minimized in CHARMM. All geometry optimizations were carried out using a termination criterion based on gradient (<0.01 kcal mol^{-1}). Docking of aspirin in the active site was accomplished with AutoDock 4.0[16] using the Lamarckian genetic algorithm (default parameters, 200 runs per isoform). Random enzyme–aspirin complexes were generated with an in-house SVL script running in MOE, imposing a distance <3.5 Å between the acetyl carbon and the Ser530 OH group. The complexes were solvated in an octahedral periodic box under PBC, and a preliminary minimization with harmonic constraints on backbone (10 kcal mol^{-1} Å^{-2}) and side chain atoms (2.5 kcal mol^{-1} Å^{-2}) was carried out, while leaving aspirin and hydrogen atoms unconstrained. Equilibration of water was then accomplished, first with self-guided Langevin dynamics, then at constant *p*,*T* (300 K) in order to achieve the correct density in the solvated system, finally at constant *V*,*T* using a Nosè–Hoover thermostat as implemented in CHARMM. A SA protocol was designed where the ligand was heated to 1000 K and then slowly cooled to 300 K in 100 K steps, allowing 5 ps sampling in each temperature window, while protein and bulk water were maintained at 300 K. At the end of each SA run an energy minimization was carried out, and the resulting geometry was used for the following SA cycle. QM/MM calculations were accomplished under SBC at the SCC-DFTB level of theory as implemented in CHARMM;[18] link atoms were used to fill empty valences at the boundary between the MM and the QM regions. 1 ns QM/MM MD were accomplished at constant *V*,*T* (300 K) with a Nosè–Hoover thermostat. The PESs were computed setting sequential constraints on two reaction coordinates while allowing the rest of the system free to relax. The DFT corrections to the potential energy were calculated using PC-GAMESS.[35]

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Keywords: aspirin · acylation · cyclooxygenases · enzyme catalysis · quantum chemistry

[1] A. Burke, E. Smyth, G. A. FitzGerald in *Goodman & Gilman's The Pharmacological Basis of Therapeutics, 11th ed.* (Ed.: L. L. Brunton), McGraw-Hill, New York, **2006**, pp. 671–716.
[2] M. M. Wolfe, D. R. Lichtenstein, G. Singh, *N. Engl. J. Med.* **1999**, *340*, 1888–1899.
[3] L. Lazzarato, M. Donnola, B. Rolando, E. Marini, C. Cena, G. Coruzzi, E. Guaita, G. Morini, R. Fruttero, A. Gasco, S. Biondi, E. Ongini, *J. Med. Chem.* **2008**, *51*, 1894–1903.
[4] P. Tosco, Proceedings of the XIX National Meeting on Medicinal Chemistry, Verona (Italy), September 14–18, **2008**.
[5] D. L. DeWitt, E. A. el-Harith, S. A. Kraemer, M. J. Andrews, E. F. Yao, R. L. Armstrong, W. L. Smith, *J. Biol. Chem.* **1990**, *265*, 5192–5198.
[6] P. J. Loll, D. Picot, R. M. Garavito, *Nat. Struct. Biol.* **1995**, *2*, 637–643.
[7] D. Riendeau, J. A. Mancini, J.-P. Falgueyret, P. J. Vickers, G. P. O'Neill, *J. Biol. Chem.* **1995**, *270*, 29372–29377.
[8] A. L. Blobaum, L. J. Marnett, *J. Med. Chem.* **2007**, *50*, 1425–1441.
[9] L. J. Marnett, *Prostaglandins Other Lipid Mediators* **2002**, *68–69*, 153–164.
[10] G. P. Hochgesang, Jr., S. W. Rowlinson, L. J. Marnett, *J. Am. Chem. Soc.* **2000**, *122*, 6514–6515.
[11] M. Bala, C. N. Chin, A. T. Logan, T. Amin, L. J. Marnett, O. Boutaud, J. A. Oates, *Biochem. Pharmacol.* **2008**, *75*, 1472–1481.
[12] I. Wells, L. J. Marnett, *Biochemistry* **1992**, *31*, 9520–9525.
[13] RCSB Protein Data Bank, http://www.rcsb.org/ (last accessed March 2, 2009).
[14] K. Gupta, B. S. Selinsky, C. J. Kaub, A. K. Katz, P. J. Loll, *J. Mol. Biol.* **2004**, *335*, 503–518.
[15] S. W. Rowlinson, J. R. Kiefer, J. J. Prusakiewicz, J. L. Pawlitz, K. R. Kozak, A. S. Kalgutkar, W. C. Stallings, R. G. Kurumbail, L. J. Marnett, *J. Biol. Chem.* **2003**, *278*, 45763–45769.
[16] a) D. S. Goodsell, A. J. Olson, *Proteins* **1990**, *8*, 195–202; b) G. M. Morris, D. S. Goodsell, R. Huey, A. J. Olson, *J. Comput.-Aided Mol. Des.* **1996**, *10*, 293–304; c) G. M. Morris, D. S. Goodsell, R. S. Halliday, R. Huey, W. E. Hart, R. K. Belew, A. J. Olson, *J. Comput. Chem.* **1998**, *19*, 1639–1662.
[17] B. R. Brooks, R. E. Bruccoleri, B. D. Olafson, D. J. States, S. Swaminathan, M. Karplus, *J. Comput. Chem.* **1983**, *4*, 187–217.
[18] Q. Cui, M. Elstner, T. Frauenheim, E. Kaxiras, M. Karplus, *J. Phys. Chem. B* **2001**, *105*, 569–585.
[19] G. Monard, X. Prat-Resina, A. Gonzàlez-Lafont, J. M. Lluch, *Int. J. Quantum Chem.* **2003**, *93*, 229–244.
[20] M. Watanabe, J. Rosenbusch, T. Schirmer, M. Karplus, *Biophys. J.* **1997**, *72*, 2094–2102.
[21] a) R. Labia, J. Peduzzi, *Biochim. Biophys. Acta* **1978**, *526*, 572–579; b) S. G. Waley, *Biochem. J.* **1985**, *227*, 843–849.
[22] D. Davidson, L. Auerbach, *J. Am. Chem. Soc.* **1953**, *75*, 5984–5986.
[23] M. L. Bender, F. Chloupek, M. C. Neveu, *J. Am. Chem. Soc.* **1958**, *80*, 5384–5387.
[24] A. R. Fersht, . A. J. Kirby, *J. Am. Chem. Soc.* **1967**, *89*, 4857–4863.
[25] T. St. Pierre, W. P. Jencks, *J. Am. Chem. Soc.* **1968**, *90*, 3817–3827.
[26] D. S. Kemp, T. D. Thibault, *J. Am. Chem. Soc.* **1968**, *90*, 7154–7155.
[27] D. M. Friedrich, Z. Wang, A. G. Joly, K. A. Peterson, P. R. Callis, *J. Phys. Chem. A* **1999**, *103*, 9644–9653.

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[28] J. C. Hermann, C. Hensen, L. Ridder, A. J. Mulholland, H.-D. Höltje, *J. Am. Chem. Soc.* **2005**, *127*, 4454–4465.
[29] S. S. Minor, R. L. Schowen, *J. Am. Chem. Soc.* **1973**, *95*, 2279–2281.
[30] MOE version 2007.09, Chemical Computing Group Inc., Montreal (Canada), **2008**.
[31] J. Wang, R. M. Wolf, J. W. Caldwell, P. A. Kollman, D. A. Case, *J. Comput. Chem.* **2004**, *25*, 1157–1174.
[32] AMBER 10, D. A. Case, T. A. Darden, T. E. Cheatham III, C. L. Simmerling, J. Wang, R. E. Duke, R. Luo, M. Crowley, R. C. Walker, W. Zhang, K. M. Merz, B. Wang, S. Hayik, A. Roitberg, G. Seabra, I. Kolossváry, K. F. Wong, F. Paesani, J. Vanicek, X. Wu, S. R. Brozell, T. Steinbrecher, H. Gohlke, L. Yang, C. Tan, J. Mongan, V. Hornak, G. Cui, D. H. Mathews, M. G. Seetin, C. Sagui, V. Babin, P. A. Kollman, University of California, San Francisco (USA), **2008**.
[33] J. Wang, P. Cieplak, P. A. Kollman, *J. Comput. Chem.* **2000**, *21*, 1049–1074.
[34] M. W. Schmidt, K. K. Baldridge, J. A. Boatz, S. T. Elbert, M. S. Gordon, J. H. Jensen, S. Koseki, N. Matsunaga, K. A. Nguyen, S. J. Su, T. L. Windus, M. Dupuis, J. A. Montgomery, *J. Comput. Chem.* **1993**, *14*, 1347–1363.
[35] A. A. Granovsky, PC GAMESS/Firefly version 7.1.E, http://classic.chem.msu.su/gran/gamess/index.html/ (last accessed March 2, 2009).
[36] ShareGrid project, http://dcs.di.unipmn.it/ (last accessed March 2, 2009).
[37] W. L. DeLano, The PyMOL Molecular Graphics System, DeLano Scientific LLC, Palo Alto (USA) **2008**; http://www.pymol.org/ (last accessed March 2, 2009).

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P. Tosco, L. Lazzarato*

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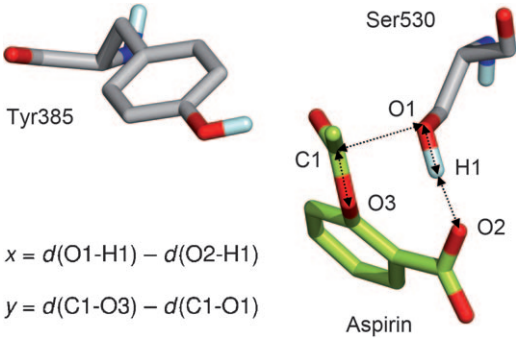
Mechanistic Insights into Cyclooxygenase Irreversible Inactivation by Aspirin



$x = d(\text{O1-H1}) - d(\text{O2-H1})$

$y = d(\text{C1-O3}) - d(\text{C1-O1})$

A mechanistic hypothesis for the acetylation of cyclooxygenase (COX) by aspirin is proposed on the basis of a QM/MM study. This mechanism is consistent with previous experimental findings by other investigators. Ser530 appears to be acetylated under intramolecular general base catalysis provided by the carboxylate moiety of aspirin, while Tyr385 plays a crucial role in orienting and polarizing the acetyl group.

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