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Comparison of the Full Catalytic Cycle of Hydroformylation Mediated by Mono- and Bis-Ligated Triphenylphosphine–Rhodium Complexes by Using DFT Calculations

Ivo Jacobs, Bas de Bruin,* and Joost N. H. Reek*[a]

The coordination mode of triphenylphosphine to rhodium is considered to be important for the outcome of hydroformylation catalysis. The difference in reactivity between mono- and bis-ligated rhodium species has not been investigated systematically, mostly because it is impossible to obtain pure mono-ligated rhodium under hydroformylation conditions. Therefore, we performed detailed computational studies to get an insight into the effect of the coordination of triphenylphosphine to rhodium on hydroformylation catalysis. The DFT-calculated cat-

alytic pathway of the monophosphine-based catalyst shows a lower free energy barrier ($24.5 \text{ kcal mol}^{-1}$) compared to the pathway of the bisphosphine catalyst ($28.9 \text{ kcal mol}^{-1}$). This confirms that monophosphine catalysts have an intrinsically higher activity than bisphosphine catalysts and indicates that the rate enhancement seen with the tetraphenylporphyrin-based catalyst reported by our group previously is at least partly due to the monocoordination enforced by this encapsulating ligand.

Introduction

Hydroformylation can be considered as the flagship reaction of homogeneous catalysis: it is applied commercially on a multi-million ton per year scale, but also studied in detail at the fundamental level.^[1] Both terminal and internal olefins are used as feedstock to produce various products. Terminal olefins are more reactive, and selectivity issues are less challenging. Two aldehyde products can be formed from primary olefins: the linear (L) or the branched (B) aldehyde (Figure 1). There is

Figure 1. Hydroformylation yields two products: linear (L) and branched (B) aldehydes.

a large market for the linear aldehyde, and many industrial processes aim for this product. In some of the processes, the aldehydes are further reacted to produce either alcohols or acids. There is an increasing demand in recent years for

branched aldehydes, after linear aldehydes.^[2] For example, isobutyraldehyde, which is a precursor of isobutyric acid and neopentyl glycol, is a product that is prepared by the hydroformylation of propene. Although nowadays several catalysts can produce the linear aldehyde in high selectivity, catalysts that mainly produce branched aldehydes from aliphatic alkenes are scarce, and selectivities are still rather low.

In 2001 we reported an encapsulated hydroformylation catalyst that forms by self-assembly from *meta*-trispyridylphosphine and three zinc tetraphenylporphyrin building blocks. The encapsulated monophosphine rhodium catalyst self-assembles upon mixing the ligands with $\text{Rh}(\text{acac})(\text{CO})_2$ ($\text{acac} = \text{acetylacetonato}$) under a syngas atmosphere (Figure 2).^[3] This complex is an active hydroformylation catalyst that preferentially produces the branched aldehyde product from terminal alkenes. It even operates at temperatures as high as 80°C , although under these conditions higher CO pressures are required to prevent the formation of bisphosphorus-ligated complexes.^[3c] Next to terminal olefins, the catalyst can also be used to hydroformylate internal olefins with unequaled selectivity, preferably forming the most internal product.^[4] In all experiments, the encapsulated catalyst showed higher activity with respect to the parent triphenylphosphine-derived catalyst.

From detailed studies it is already known for a long time that bisphosphine-ligated rhodium complexes (and trisphosphine) give a much higher selectivity for the linear product,^[5] and therefore high concentrations of ligands are used in commercial applications. Although bulky monodentate phosphite ligands have been used,^[6] which lead to monophosphorus-ligated rhodium complexes that are active, bulky phosphine ligands that lead to exclusive monocoordination have not been

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Figure 2. Porphyrin capsule enables the formation of mono-ligated rhodium species.

reported.^[7] As such, the supramolecular ligand system shown in Figure 2, in which the phosphine donor is embedded, is the only system that shows such exclusive monocoordination. Matt et al. recently reported a cyclodextrin-based phosphine ligand that also leads to the exclusive formation of mono-ligated rhodium complexes under hydroformylation conditions, which resulted in the enantioselective hydroformylation of styrene.^[8]

Because the properties of mono-ligated phosphine rhodium catalysts are not known experimentally, it is impossible to determine whether the high activity and unusual selectivity are the result of confinement effects or of the coordination to rhodium. To improve our understanding of how the coordination affects catalytic performance in the case of the triphenylphosphine-modified rhodium system, we performed a DFT study that compares mono- and bis-ligated rhodium species. This should facilitate the better understanding of the operational mode of supramolecular systems.

The catalytic cycle of rhodium-catalyzed hydroformylation is depicted in Figure 3. Three stages can be distinguished: In the first stage, a rhodium hydride species reacts with an olefin to form a rhodium alkyl species. In the second stage, this rhodium alkyl species reacts with CO to form a rhodium acyl species. Finally, in the third stage, the acyl species reacts with hydrogen to form the product aldehyde and the rhodium hydride is reformed. This mechanism is well established and has been extensively corroborated by using both experimental (spectroscopic) and theoretical methods.^[5,9,10]

The kinetics of the hydroformylation reaction catalyzed by phosphine-modified rhodium are in most cases dominated by the reactions of the first stage. This results in the rate equation in a first order in olefin, a negative order in CO, and a zero order in hydrogen. From the kinetics alone it cannot be determined which individual step is rate determining, because all three possibilities give the same rate equation. Spectroscopic evidence shows that hydride species **1** is the resting state.^[5b] The olefin coordination is rate determining if Xantphos is used as a ligand,^[11] and several studies show that hydride migration is irreversible (for triphenylphosphine, but not for the BISBI or Xantphos ligand),^[12] but there is no direct experimental evi-

dence that shows exactly which step is rate determining. However, several computational studies concluded that hydride migration is rate determining.^[11,13,16a] Some systems exhibit a different kind of kinetics, which is dominated by the third stage. This is called type II kinetics and displays first order in hydrogen, zero order in olefin, and negative order in CO. In this case, **7** is the resting state, and one of the reactions leading from it up to the release of product must be

Figure 3. Catalytic cycle of the rhodium-catalyzed hydroformylation with triphenylphosphine as a ligand. L can be CO or PPh₃ in any combination.

rate determining. This type of kinetics is less common, and mostly encountered only with bulky phosphite ligands.^[5b] Breit's phosphinine system may also fall under this category.^[14]

The reactivities of mono- and bisphosphine complexes have been compared earlier in computational studies of the hydroformylation reaction, most recently by Hirst and Carbo.^[15] The full catalytic cycle has never been investigated in any of the computed models, though. In most cases, only the first stage of the reaction was taken into account. We considered it important to perform calculations on the full catalytic cycle by using the same computational model throughout, accounting for all relevant transition states and all possible changes on the potential energy surface on migrating from the bisphosphine to the monophosphine cycles and thus allowing a proper comparison with kinetic data from experimental studies. This information is important to find out whether the changed behavior seen in the case of the encapsulated rhodium complex is only due to the enforced monocoordination or if other effects play a role.

Herein, we report DFT calculations on the entire catalytic cycle of hydroformylation mediated by mono- and bis-ligated rhodium species. These calculations show that the pathways are similar and that the rate-determining step in all cases is the hydride migration. It also became clear from these calculations that attractive van der Waals interactions between the triphenylphosphine ligands, as well as between the ligands and the substrate, are important, which is in line with a previous report by Kumar and Jackson.^[16] Because these interactions are not taken into account in (uncorrected) DFT calculations, DFT-D3 dispersion-corrected calculations were needed to get a better estimate for the energy difference between mono- and bis-triphenylphosphine complexes. Therefore, the rate-determining transition states **TS-3** were recalculated with dispersion corrections to arrive at more realistic overall reaction barriers.

Results and Discussion

General

Several papers have appeared that report DFT calculations on (parts of) the hydroformylation catalytic cycle.^[17] In all these reports, model ligands such as PH_3 or PF_3 (which is the better model for PPh_3) have been used to reduce the calculation time. For our calculations, we decided to use the full PPh_3 ligand because we also wanted to take into account steric hindrance in bisphosphine complexes, as it could have a strong influence on the difference between the bisphosphine pathway and the monophosphine pathway. Because we were primarily interested in activity, ethene was used as the substrate model initially. However, upon comparing the monophosphine and bisphosphine complexes, ethene was not found to be a good model, and to correct this, all propene variants of the rate-limiting transition state **TS3** were also built and calculated.

For DFT calculations, we used the B3LYP functional with Stuttgart–Dresden basis sets with ECPs (ECP=effective core potential) for rhodium and phosphorus, and Pople basis sets for the rest, in Gaussian 03. This combination of functional and basis sets has previously been shown to give accurate results.^[18] Because Grimme's dispersion corrections are not implemented in Gaussian 03, the relevant structures for which we wanted to investigate the effect of dispersion corrections were reoptimized in Turbomole Version 6.5 at the b3-lyp, def2-TZVP disp3 (DFT-D3) level of theory. A small-core ECP pseudo-potential was used for rhodium. The def2-TZVP basis set used was slightly larger but otherwise similar to 6-311G**.

Here, we will first discuss the catalytic cycle of the bisphosphine rhodium complexes and then compare that with the catalytic cycle of the monophosphine complex.

Formation of the active complex

The $\text{Rh}(\text{acac})(\text{CO})_2$ precursor can be converted to various rhodium complexes under catalytic conditions. A schematic overview of the complexes identified with high-pressure IR spectroscopy (under various conditions) and their connecting equilibria is presented in Figure 4. As known from the Rossi and

Figure 4. Representation of the equilibria of rhodium complexes before substrate addition. DFT-calculated free energies are given in kcal mol^{-1} . Dispersion-corrected energies are given in parentheses.

Hoffmann study,^[19] the stronger sigma-donating ligands prefer to occupy the axial positions. Therefore, in all complexes the hydride ligands reside at the axial position and structures with the hydride in the equatorial plane are not even minima on the potential energy surface. Phosphine ligands are much less strong sigma donors and thus do not have a preference for the axial position as compared to CO.

The monophosphine complexes are predicted to be lower in energy than the bisphosphine complexes if regular DFT without dispersion corrections is used (Figure 4). This finding contradicts experimental observations.^[20] This is mostly due to the absence of attractive dispersive interactions in regular DFT, which leads to an underestimation of the stability of bisphosphine complexes, especially if they are situated in the *cis* position with respect to one another. Some of the complexes were therefore reoptimized by using Grimme's dispersion corrections (D3 version, implemented as disp3 in the Turbomole program package). The results are presented in Figure 4. These calculations show that there are significant attractive van der Waals interactions between the phosphines, and the non-dispersion-corrected calculations clearly underestimate the stability of bisphosphine complexes. In general, these errors are expected to be similar for subsequent steps in a reaction sequence starting from either mono- or bisphosphine rhodium complexes, and thus as long as no PPh_3 association/dissociation occurs in the sequence the DFT-calculated reaction pathways should benefit from error cancellation. However, **ee1** is $0.6 \text{ kcal mol}^{-1}$ lower in energy than **ea1**, as predicted by the uncorrected calculations, which matches well with the **ee1/ea1** ratio of 85:15 observed in NMR experiments by Brown and Kent.^[10e] The dispersion-corrected calculations predict **ea1** to be $1.7 \text{ kcal mol}^{-1}$ lower in energy than **ee1**, which could be an effect of overcorrection for van der Waals interactions if gas phase calculations are compared to condensed phase experi-

ments. Ultimately approximately 2 kcal mol^{-1} error in the energy difference between **ee1** and **ea1** is better than approximately 10 kcal mol^{-1} error in the energy difference between monophosphine and bisphosphine. Because the dispersion effects are significant, we evaluated the barriers for all key transition states both with and without dispersion corrections (vide infra).^[21] In the following section, we compare the catalytic cycles that start from **ee1/ea1** with those that start from **a1/e1**.

Catalytic cycle with the bisphosphine rhodium complex as a catalyst

The (noncorrected) DFT-calculated free energy profile of the first two steps of the bisphosphine pathway is shown in Figure 5. The resting state of the triphenylphosphine-ligated catalyst is the five-coordinated rhodium hydride complex **1**.

Figure 5. Energy diagram of the first stage of the catalytic cycle with the bisphosphine catalyst until substrate coordination. Red line is for the **ea** complex, and the black line is for the **ee** complex.

This hydride complex exists as a mixture of two isomers, which are indicated by the position of phosphine ligands (*e*=equatorial and *a*=axial), and **ea1** is $0.6 \text{ kcal mol}^{-1}$ higher in energy than **ee1**. The equilibrium between **1** and **2** is characterized by a late transition state (Rh–C distance is 3.1 and 3.2 Å for **TS-ee1** and **TS-ee3-c**, respectively). The calculated free energy barriers for CO dissociation from **ee1** and **ea1** were 13.8 and $17.5 \text{ kcal mol}^{-1}$, respectively. The reverse reactions, CO binding to **tP2** and **cP2** to form **ee1** and **ea1**, have lower free energy barriers (10.3 and $7.4 \text{ kcal mol}^{-1}$, respectively).

In the square planar complexes, the *trans* complex **tP2** is 7 kcal mol^{-1} lower in energy than the *cis* complex **cP2**, which can be due to steric hindrance between the two triphenylphosphine ligands. In **cP2** the square planar complex is significantly distorted, with a P–Rh–P angle of 104° .

After coordination of ethene, the five-coordinated ethene complex is obtained. In this substrate-associated complex, both isomers **ee3** and **ea3** are close in energy. The rhodium–olefin interactions are underestimated in DFT calculations, and therefore the energies of these alkene intermediates are probably a few kcal mol^{-1} lower.^[22,23]

The energy profile of hydride migration steps are depicted in Figure 6, and the Berry pseudorotation-like mechanism is further clarified in Figure 7 (for transition state **TS-ee3-c**). Migratory insertion of the olefin into the Rh–H bond of **ee3** leads to the formation of the square planar *cis*-coordinated bisphosphine alkyl complex **cP4** via low barrier transition state

Figure 6. Energy diagram of the hydride migration reaction with the bisphosphine complex. The way different pathways connect the intermediates is shown at the bottom.

Figure 7. Migratory insertion steps involving the bisphosphine hydrido-rhodium carbonyl-olefin complex **ee3**, which results in the square planar *cis*-bisphosphine alkyl-rhodium carbonyl complex **cP4**. Bond distances are given in Å.

TS-ee3-c ($\Delta G^\ddagger = 11 \text{ kcal mol}^{-1}$). For **ea3**, two pathways are possible because the olefin can rotate toward either the phosphine ligand or CO. The former has a lower barrier ($\Delta G^\ddagger = 13 \text{ kcal mol}^{-1}$) and results in the formation of **tP4**.

In line with findings in the literature, the hydride migration is here predicted to have the highest overall barrier and is thus the rate-determining step. The transition state **TS-ee3-c** corresponds to the lowest energy pathway in this rate-determining step and lies $28.9 \text{ kcal mol}^{-1}$ above the corresponding resting state, **ee1**.

From Figure 7 it becomes clear that the distance between the two phosphine ligands changes in the hydride migration

step, and it is therefore necessary to investigate the effect of dispersion corrections for this reaction. The dispersion-corrected free energy barriers are listed in Table 1 and compared with

Table 1. Free energy barriers for the rate-determining bisphosphine transition states from **ee1/ea1** with ethene as a substrate.

	$\Delta G^\ddagger$ [kcal mol ⁻¹]	
	DFT (for ee1)	DFT-D3 (for ea1)
TS-ea3-c	35.9	30.6
TS-ea3-t	31.5	26.8
TS-ee3-c	28.9	25.8

the noncorrected values. The DFT-D3 barriers are 3–6 kcal mol⁻¹ lower than the DFT barriers, but the relative order remains the same. The lower DFT-D3 barriers are partly explained by stronger ethene binding in the transition states, as close contacts between the substrate and the aryl groups of the catalyst lead to favorable interactions, which are taken into account by including dispersion corrections.

For comparison, the corresponding propene transition states were also calculated. For each of the ethene transition states, four corresponding propene transition states can be drawn, which leads to 12 transition-state structures. Six of them lead to the linear product and six to the branched product. Because dispersion is important, we evaluated these transition states both at the DFT and at the DFT-D3 level. The results of these calculations are summarized in Table 2. Dispersion corrections

Table 2. Free energy barriers for the rate-determining bisphosphine transition states from **ee1/ea1** with propene as a substrate.

	$\Delta G^\ddagger$ [kcal mol ⁻¹]	
	DFT (for ee1)	DFT-D3 (for ea1)
TS-p-ea3-c-B	39.9	32.7
TS-p-ea3-c-B	45.4	36.8
TS-p-ea3-c-L	40.9	32.6
TS-p-ea3-c-L	41.9	33.5
TS-p-ea3-t-B	38.0	30.8
TS-p-ea3-t-B	40.4	31.9
TS-p-ea3-t-L	35.7	28.9
TS-p-ea3-t-L	36.8	30.7
TS-p-ee3-c-B	34.7	29.4
TS-p-ee3-c-B	35.1	30.1
TS-p-ee3-c-L	32.3	28.2
TS-p-ee3-c-L	35.0	28.7

stabilize both the transition states and the minima. Like in the case of ethene, the barriers are lowered if dispersion corrections are applied. The barriers are lowered more in the case of propene, which can be expected because the larger propene benefits more from stronger van der Waals interactions (thus reducing unfavorable steric interactions) in the transition state.

Notably, the lowest transition state for ethene has the same structure as the lowest transition state for propene for both the linear and the branched pathway (Figure 8). The lowest barrier for the formation of the linear product is $1.2 \text{ kcal mol}^{-1}$

Figure 8. Lowest transition-state structures for the a) branched (TS-p-ee3-c-B) and b) linear (TS-p-ee3-c-L) reactions are almost identical.

lower than the lowest barrier for the formation of the branched product. This corresponds to a modest rate difference of a factor of 9,^[24] which corresponds qualitatively with the reported selectivities of triphenylphosphine-modified rhodium catalysts.^[25]

The energy profile of the second stage of the catalytic cycle are depicted in Figure 9. In the first step, CO coordinates to the square planar complex to form the more stable five-coordinated rhodium species. As expected, this step is exothermic for all complexes.

Figure 9. Energy diagram of the second stage of the catalytic cycle with the bisphosphine catalyst. Red line is for the **ea** complex, and the black line is for the **ee** complex.

The next step in the catalytic cycle involves the migratory insertion of CO into the metal–alkyl bond to form the rhodium acyl species. According to the calculated pathway, the mechanism is best described by the migration of the alkyl species to CO (Figure 10). During this reaction step, the ligands rotate in such a way that the *trans*-bisphosphine acyl complex **tp6** is formed from the **ea**-alkyl complex **ea5**. Similarly, the *cis*-bisphosphine acyl **cp6** is formed from the **ee**-alkyl complex **ee5**. The formation of the four-coordinate acyl complex is exothermic. The formation of a C–C bond clearly compensates for

Figure 10. Mechanism of the CO insertion of the **ea**-alkyl complex, which results in the *trans*-acyl complex. Bond distances are given in Å.

the formation of a relatively unfavorable unsaturated four-coordinate rhodium complex. The energy barrier is low (≈ 14 kcal mol $^{-1}$) for the **ea** species, and even a bit less for the **ee** species. After the acyl formation step, CO is coordinated to the complex to form the five-coordinate acyl species. This is less energetically favorable than one would expect, mainly owing to entropy contributions. Also, there is a significant energy barrier between the four- and five-coordinated species.

Experimentally it is not clear whether the final reaction with hydrogen occurs via an oxidative addition–reductive elimination pathway or via a concerted metathesis-like mechanism. In our calculations, we could not find a pathway that supports the concerted mechanism. Instead, if the rhodium acyl complex is approached by hydrogen, oxidative addition occurs with relatively low energy barriers (< 20 kcal mol $^{-1}$).

The oxidative addition of hydrogen to the four-coordinated rhodium acyl complexes can occur in two ways for each complex: one in which both hydride atoms are situated in the *cis* position of the acyl species and one with one hydrogen atom in the *cis* position and one hydrogen atom in the *trans* position of the acyl species. The latter geometry is expected to be energetically less favorable because two strong sigma donors (a hydride and the acyl species) are coordinated *trans* with respect to one another. This is confirmed by the calculations, showing that the *trans* complex is 3–8 kcal mol $^{-1}$ higher in energy (Figures 11 and 12). In addition, the barriers leading to the rhodium(III) intermediates with *cis* and *trans* hydrogen atoms are higher. We therefore assume that the *cis*–*trans* hydride complexes do not play a role here.

An analysis of the energy profiles reveals that the lowest energy pathway for the last stage of the reaction also involves a change in coordination geometry. The *trans*-biphosphine acyl is transformed into the *cis*-biphosphine hydride after the reductive elimination of the product aldehyde. Interestingly, the *cis*-biphosphine acyl is also preferably converted to the *cis*-biphosphine hydride during the elimination step, which means that the catalytic cycle ends with the *cis*-biphosphine hydride. After coordination of CO, which leads to the **ea** rest-

Figure 11. Energy diagram of the third stage of the catalytic cycle with the biphosphine catalyst via the *cis*–*cis* dihydride species (with respect to the acyl species). The way different pathways connect the intermediates is shown at the bottom.

Figure 12. Energy diagram of the third stage of the catalytic cycle with the biphosphine catalyst via the *cis*–*trans* dihydride species (with respect to the acyl species).

ing state complex, a reorganization should occur to form the slightly more favorable **ee** complex.^[26]

Catalytic cycle with the monophosphine rhodium complex as a catalyst

The mechanism and energy profile for the pathway of the monophosphine rhodium complex are similar to those for the pathway of the biphosphine analogue. Thus, we will not discuss the pathway in detail, but instead focus the discussion on the differences between the two pathways.

The energy diagram of the first stage is depicted in Figure 13. The pathway starting from **e1** involves the expected low barrier CO dissociation and alkene coordination. The only significant difference with the biphosphine pathway is that the back reaction from **tCO2** to **a1** is without barrier on the enthalpy surface. Therefore, the free energy barrier $\Delta G^\ddagger$ cannot be accurately evaluated. Based on entropy comparisons,^[27] the estimated free energy of **TS-a1** amounts to approximately 18 kcal mol $^{-1}$.

Figure 13. Energy diagram of the first stage of the catalytic cycle with the monophosphine catalyst until substrate coordination.

The free energy of activation for the hydride migration step (Figure 14) is similar for monophosphines and bisphosphines: 11.8 and 13.1 for mono-P compared with 11.0 and 13.0 for bis-P. The lowest energy pathway is the one in which the phosphine configuration is retained: migrating from **e3** to **cCO4** via

Figure 14. Energy diagram of the hydride migration reaction with the monophosphine complex. The way different pathways connect the intermediates is shown at the bottom.

TS-e3-c. Importantly, the overall energy barrier calculated from the resting state up to this transition state significantly differs for the mono- and bisphosphorus complexes. This barrier, which controls the rate of the reaction, amounts to 24.5 kcal mol⁻¹, which is lower than the corresponding barrier for the bisphosphine complex (28.9 kcal mol⁻¹). This result is in agreement with the higher reactivity observed for the monophosphine coordination complex in the supramolecular capsule. The origin of this energy difference seems to lie mostly in the substrate coordination step (2 to 3), which is 6 kcal mol⁻¹ more endergonic for the bisphosphine complex. This is not surprising because the bisphosphine complex is more electron-rich than the monophosphine complex.

The overall energy barriers of the non-dispersion-corrected calculations are compared with those of the dispersion-corrected calculations in Table 3. Again the barriers decrease by a few

Table 3. Free energy barriers for the rate-determining monophosphine transition states from **a1** with ethene as a substrate.

	$\Delta G^\ddagger$ [kcal mol ⁻¹]	
	DFT	DFT-D3
TS-a3-c	26.9	24.3
TS-e3-c	25.5	22.9
TS-e3-t	28.0	23.6

kcal mol⁻¹. The difference between corrected and noncorrected calculations is smaller than that in the case of bisphosphines, which is expected because there are less internal steric and van der Waals interactions.

The same trend is also seen in the case of propene as a substrate (Table 4). The DFT and DFT-D3 barriers differ slightly more than that in the case of ethene and slightly less than that in the case of bisphosphines with propene. This is all as

Table 4. Free energy barriers for the rate-determining monophosphine transition states from **a1** with propene as a substrate.

	$\Delta G^\ddagger$ [kcal mol ⁻¹]	
	DFT	DFT-D3
TS-p-a3-c-B	32.2	27.5
TS-p-a3-c-B	32.2	27.7
TS-p-a3-c-L	30.6	26.8
TS-p-a3-c-L	30.7	26.8
TS-p-e3-c-B	32.0	26.9
TS-p-e3-c-B	32.2	27.6
TS-p-e3-c-L	31.8	28.0
TS-p-e3-c/t-L	29.5	26.3
TS-p-e3-t-B	31.6	27.5
TS-p-e3-t-B	33.6	27.9
TS-p-e3-t-L	31.6	28.1

expected taking into account the amount of internal steric interactions: The more sterically crowded bisphosphine system benefits more from the inclusion of attractive van der Waals forces. The lowest transition states for the linear and branched products are depicted in Figure 15. Notably, they exactly correspond with the lowest transition states in the case of the bisphosphine pathway. Also in this case, the lowest transition state corresponds with the linear product; however, the difference between linear and branched products is smaller than that in the case of bisphosphines. The difference is 0.6 kcal mol⁻¹, and this corresponds to a rate difference of factor of 3.^[23] This means that the calculations support the observation that bisphosphine rhodium complexes give a higher linearity than the monophosphine rhodium complexes. Long-range interactions play an important role in this because the uncorrected calculations predict the linear barrier to be 2.5 kcal mol⁻¹ lower. As shown in Figure 15, a long-range substrate–ligand interaction exists in the branched transition state, which is not present in the linear transition state. The energy differences indicate that this is a stabilizing interaction. This striking

Figure 15. Structures of the lowest transition states for the a) branched (TS-p-e3-c-B) and b) linear (TS-p-e3-c-t-L) products.

difference does not occur in the case of the bisphosphine pathway.

The energy diagram of the second stage of the catalytic cycle is depicted in Figure 16. CO coordinates to the unsaturated square planar complex to form the five-coordinated com-

Figure 16. Energy diagram of the second stage of the catalytic cycle with the monophosphine catalyst.

plex. This binding of CO to complex **4** is energetically less favorable than we found for the bisphosphine analogue, but it follows a similar pathway. Interestingly, CO insertion follows a slightly different pathway. The transition states TS-a5 and TS-e5 are similar in structure (Figure 17), which differ only in the way the phosphine ligand is rotated. Both these transition states subsequently lead to the same product, eCO6. The energy barriers for these transition states are significantly higher than those for the bisphosphine pathway, but because these energy barriers are after the rate-determining step this does not affect the overall rate. The binding of CO to the square planar complexes **6** to form the saturated 18-electron species is slightly more favorable than we observed for the bisphosphine, but otherwise it is similar.

For hydrogenolysis (Figures 18 and 19), the pathway is similar to that of the bisphosphine complexes; however, the free energy of activation of the oxidative addition reaction is significantly lower for the monophosphine complexes. This is surprising because oxidative addition normally becomes faster as

TS-a5

TS-e5

Figure 17. Structures of TS-a5 and TS-e5 differ only in the way the tri-phenylphosphine ligand is rotated as compared to the rest of the complex.

Figure 18. Energy diagram of the third stage of the catalytic cycle with the monophosphine catalyst via the *cis-cis* hydride species. The way different pathways connect the intermediates is shown at the bottom.

Figure 19. Energy diagram of the third stage of the catalytic cycle with the monophosphine catalyst via the *cis-trans* hydride species.

complexes become more electron rich.^[28] However, if we look at van der Waals models of the transition states leading to the six-coordinated complexes, it becomes clear that steric influences are likely important here (Figure 20). The final reductive

Figure 20. van der Waals representation of a) TS-cP6-cc and b) TS-cCO6-cc, showing that steric hindrance is most likely important for the oxidative addition of hydrogen.

elimination shows similar barriers and pathways for the mono- and bis-P complexes. The *cis-trans* hydrogen complexes and the associated transition states are again energetically unfavorable, and therefore the reaction has to proceed via the *cis-cis* complex. Starting from **cCO6**, the most favorable route is via **TS-cCO6-cc** and **TS-ccH-cCO8-t**, which then regenerates **tCO2**.

The configuration of the complex does not change in the path from hydride migration up to CO insertion (for the lowest energy pathway), but it does in the final hydrogenolysis step. Thus, for the mono-coordinated complex, there is an overall change in the coordination mode during the catalytic cycle. The pathway that is slightly higher in energy but still relevant for the overall reaction involves a change in configuration in the hydride migration step; that is, similar to that observed for the bisphosphine pathways, the reaction ends with the higher energy resting state and a reorganization may occur before it enters the next catalytic cycle.

Our results are in line with the previously published theoretical work on hydroformylation: The hydride complex is the resting state of the reaction, and the hydride migration step is associated with the highest barrier. The former is supported by spectroscopic evidence, whereas the latter is in line with the kinetic data (see the Introduction). The absolute barriers found herein are slightly different from those published earlier, which is clearly due to the difference in method used for the calculation as well as the difference in ligands used. In one of the more recent studies, for example, by Jensen et al.^[13] (one that explicitly used triphenylphosphine, although only mono-ligated), a value of 105 kJ mol⁻¹ (25 kcal mol⁻¹) was found for the overall barrier for the reaction from the hydride resting state to the hydride migration rate-limiting transition state. This corresponds well with the 25.5 kcal mol⁻¹ value we found without dispersion corrections for the monophosphine complex. Jensen et al. found a value of 74 kJ mol⁻¹ (18 kcal mol⁻¹) for the overall barrier for the reaction from the five-coordinated acyl to the release of the product. This corresponds qualitatively with the 19.7 kcal mol⁻¹ value that we found (**TS-ccH-cCO8-t-e7**). Hirst and Carbo^[15] recently compared the reaction barrier of ethene hydroformylation using phosphine ligands with both mono- and bis-ligated triphenylphosphines and found values

of 22.4 and 25.9 kcal mol⁻¹, respectively, which correspond well with the values found herein.

Conclusions

We have reported here, for the first time, DFT calculations on the entire catalytic cycle of the hydroformylation reaction mediated by both mono- and bis-triphenylphosphine rhodium complexes involving the entire molecular structure. For both catalytic cycles, we found similar pathways, and according to these DFT calculations the rate-determining step is in both cases associated with the migratory insertion of the olefin into the Rh–H bond. By using these energy profiles, type I kinetics is observed in both cases, which is found experimentally for 1-octene under standard conditions.^[5b]

The key hydride migration step of the process was investigated in detail by comparing ethene and propene substrates, and we also investigated the effect of dispersion corrections. The relative energies of the resting states (**1**) are not predicted correctly without dispersion corrections. In contrast to experimental observations, the uncorrected DFT energies suggest that monophosphine complexes are lower in energy. Dispersion-corrected (DFT-D3) calculations suggest that bisphosphine complexes are lower in energy, which is in line with experimental observations. With dispersion corrections, the overall barrier for ethene hydroformylation with the bisphosphine catalyst is predicted to be 3.0 kcal mol⁻¹ lower than that for ethene hydroformylation with the monophosphine catalyst. With propene as the model substrate, the overall barrier is predicted to be only 1.9 kcal mol⁻¹ lower for the monophosphine pathway. In addition, the trend in selectivity that is predicted for the hydroformylation of propene mediated by the mono- and bisphosphine complexes is correct: For the bisphosphine complex, the linear reaction is predicted to be nine times faster than the branched reaction, whereas for the monophosphine complex, the linear reaction is predicted to be only three times faster than the branched reaction. This supports the calculated pathways and applied computational models.

The porphyrin-encapsulated catalysts were 10 times more active than the nonencapsulated analogues. The present calculations suggest that this increase in rate is most likely a consequence of the change from bisphosphine to monophosphine coordination. The overall energy barrier for the reaction is 1.9 kcal mol⁻¹ lower for the monophosphine complex, which roughly corresponds with a rate enhancement by a factor of 30.^[23] The selectivity of these monophosphine complexes as predicted by these calculations, however, favors the linear product, which means that the steric hindrance imposed by the capsule plays an important role in directing the selectivity toward the branched aldehyde. It is difficult to obtain precise experimental (kinetic) data on the use of monophosphine-ligated rhodium complexes in hydroformylation because these complexes so far have been obtained in a mixture of complexes. The present computational data nicely demonstrate that the high reaction rates observed for the trispyridylphosphine–porphyrin-based catalysts are mostly due to the coordi-

nation, whereas the selectivity of these catalysts is more controlled by the confined space created around the active site.

Experimental Section

The uncorrected DFT calculations were performed with Gaussian 03.^[29] Minima on the potential energy surface were characterized by being stationary points without negative eigenvalues. Transition states were characterized by having one negative eigenvalue. Eigenvector following (called IRC in Gaussian), was used to confirm which minima were connected by the transition states. The B3LYP functional was used in all cases. For rhodium and phosphorus, the SDD basis set was used (SDDAll was specified for phosphorus; see Gaussian 03 manual) so as to prevent Gaussian 03 from actually using the D95V basis set; see the manual) with ECPs, and for phosphorus, an extra *d* function with an exponent of 0.386 was added.^[30] For the ligands directly attached to rhodium (CO, ethene, hydrogen, and everything originating from these), the 6-311G** basis set was used, and for the phenyl groups on the triphenylphosphine ligands, 6-31G* was used.

The DFT-D3 dispersion-corrected geometry and transition-state optimizations were performed with the Turbomole program package^[31] coupled to the PQS Baker optimizer^[32] via the Bopt package^[33] at the b3-lyp level.^[34] We used the def2-TZVP basis set^[35] (small-core pseudopotentials on rhodium^[36]) and Grimme's dispersion corrections (disp3 version).^[37] Scalar relativistic effects were included implicitly through the use of rhodium ECPs. All minima (no imaginary frequencies) and transition states (one imaginary frequency) were characterized by calculating the Hessian matrix. Zero point energy and gas phase thermal corrections [entropy and enthalpy, 298 K, 1 bar (1 bar = 100 kPa)] from these analyses were calculated accordingly by using standard thermodynamic relations.

A simple conformational study was performed at the PM3 level for **ee1** and **ea1**, which assured us that any error stemming from conformational freedom of the triphenylphosphine ligands would be smaller than 2 kcal mol⁻¹ because almost all minima were within that range. This error was probably well within the accuracy of the calculations (for details, see the Supporting Information). Conformational freedom of the alkyl and acyl substituents was expected to give even lower errors.

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