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Teaching indicators to unravel the kinetic features of host-guest inclusion complexes
Teaching indicators to unravel the kinetic features of host–guest inclusion complexes†

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Both thermodynamic and kinetic insights are needed for a proper analysis of association and dissociation processes of host–guest interactions. However, kinetic descriptions of supramolecular systems are scarce in the literature because suitable experimental protocols are lacking. We introduce here three time-resolved methods that allow for convenient determination of kinetic rate constants of spectroscopically silent or even insoluble guests with the macrocyclic cucurbit[n]uril family and human serum albumin (HSA) protein as representative hosts.

It has become clear that not only thermodynamic characteristics, e.g., binding affinities, but also the assessment of kinetic parameters [e.g., complexation and decomplexation rates] is required to obtain a full picture of supramolecular systems.3–5 For instance, kinetic rate constants of supramolecular complexes are key parameters for understanding catalysis8 and protein–ligand binding mechanisms,6,9 and stimuli-responsive materials.10,11 The design of out-of-equilibrium systems also requires knowledge of both $K_a$ values and rate constants.12–15 However, except for CEST-active3 or slowly equilibrating systems that can be monitored by NMR (e.g., DOSY, EXSY, inversion recovery),1,16–20 kinetic rate constants of supramolecular systems are experimentally mostly only available for chromophoric or emissive systems.2,4,21–23 These experiments are typically conducted as time-resolved direct host–guest binding titration assays, herein abbreviated as $kin$DBA (Fig. 1a). In some cases, single molecule measurements with nanopores allowed for assessing the kinetic rate constants for complexation and decomplexation of entrapped host–guest complexes.15,24,25

Conversely, binding affinities ($K_a$) of host–guest complexes can be obtained for a wide range of hosts and guests by several different techniques, for instance, through NMR titrations and calorimetric measurements (ITC) as representative direct-binding assays26–28 or competitive-binding assays such as the indicator-displacement assay ($kin$GDA) and kinetic indicator-displacement-assay ($kin$IDA) that are applicable also to spectroscopically silent guests.

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supramolecular repository “SupraBank.org” revealed that only 3% of all entries for CBn–guest complexes included also kinetic rate constants, in agreement with the much larger number of $K_a$ values versus kinetic parameters tabulated in reviews.

Herein, we show three novel competitive approaches through which kinetic rate constants of host–guest complexes, namely the complexation rate ($k_{in}$) and decomplexation rate ($k_{out}$) constants, can be accessed for spectroscopically silent guests. A competitive binding network consisting of a host (H), guest (G), and indicator dye (D) – see Fig. 1 – can be described both by thermodynamic and by kinetic equations (see ESI† for details). The binding affinities of the host-dye (H±D) and host–guest (H±G) complex are denoted as $k_{a}^{HD}$ and $k_{a}^{HG}$, respectively. The complexation & decomplexation rate constants of the H±D and H±G complexes are symbolised by $k_{in}^{HD}$ & $k_{out}^{HD}$ and $k_{in}^{HG}$ & $k_{out}^{HG}$, respectively. Note that an “Sn1”-type, i.e., purely dissociative mechanism for the decomplexation step of the H±G and H±D complexes is implied by kinetic eqn (1)–(3).

\[
\begin{align*}
HG + D & \rightleftharpoons HD + G \\
H + G & \rightleftharpoons HG \\
H + D & \rightleftharpoons HD
\end{align*}
\]

Eqn (3) shows how the thermodynamic and kinetic parameters, i.e., affinity and rate constants, are coupled to each other. The mathematical expression for the background-corrected observable signal intensity $I_t$ at time $t$ is given by eqn (4), assuming that both the host and guest are spectroscopically silent. To kinetically characterize a supramolecular host–guest complex, it is, therefore, the task to obtain $k_{in}^{HD}$ & $k_{out}^{HD}$ by fitting an experimentally obtained signal-time curve of a non-equilibrated competitive binding network involving the host, guest, and dye.

The first, a conceptionally most intuitive method introduced here is the time-resolved guest-displacement assay, $kinGDA$. Fig. 3a shows the $kinGDA$ traces that were obtained when the ultra-high-affinity dye MPCP was added to a solution of spectroscopically silent CB8±nandrolone complex. During the re-equilibration, nandrolone leaves the CB8 cavity, making room for the inclusion of indicator dye MPCP, which is the stronger binding guest. The detectable rate depends on (i) the concentrations of the host, guest, and dye, (ii) the rate constants $k_{in}^{HD}$ and $k_{out}^{HD}$ of the dye, which can be determined by a kinetic direct-binding assay ($kinDBA$) (see Table S3 and Fig. S2, S6–S8, S18, S24, S28, and S33, ESI†), and (iii) on the unknown rate constants $k_{in}^{HG}$ and $k_{out}^{HG}$ of the spectroscopically silent guest. The rate constants $k_{in}^{HG}$ and $k_{out}^{HG}$ can then be extracted from the time-resolved $kinGDA$ curves through a mathematical fitting. Because the goodness of the fit improves when $k_{a}^{HG} = k_{in}^{HG}/k_{out}^{HG}$ is used as an input parameter, prior $k_{a}^{HG}$ determination, e.g., through competitive binding titrations such as GDA or IDA or direct
binding assays (DBA) is recommended. Several host–guest pairs (Fig. S1–S34, ESI) were analysed in this way, see Table 1. Note that the kinetics method is extendable for determining the decomplexation rates of insoluble guests such as estradiol through precomplexation, e.g., see Table 1 for the rate constants k_{HG}^in and k_{HG}^out for the CB7 | estradiol complex and Fig. S16 (ESI) for the kinetic trace and fit. The applicability of k_{HG} | insoluble guests is an asset it shares with the thermodynamic GDA method. The concept is transferable to protein–ligand interactions, as exemplified for human serum albumin (HSA) as a biological important carrier protein31,32 that is commercially available.33,34

Table 1 Experimental k_{HG}, k_{out} and log K_{d} for host–guest and protein–ligand complexes determined by kinGDA, kinitDA and kinitGDA|^PFO in aqueous media

| Guest | Host | k_{HG} | k_{out} | log K_{d} |
|-------|------|--------|--------|----------|
| 4-MBA | CB7f | 3.3 × 10^7 | 6.5 × 10^{-2} | 7.7 |
| Cholesterol | CB7f | 7.0 × 10^7 | 8.7 × 10^{-2} | 5.9 |
| Estradiol | CB7f | 7.0 × 10^7 | 8.7 × 10^{-2} | 6.3 |
| (-)-Fenchone | CB7f | 4.3 × 10^7 | 2.0 × 10^{-2} | 7.5 |
| Norcamphor | CB7f | 1.5 × 10^7 | 9.8 × 10^{-3} | 8.2 |
| Adamantanol | CB7f | 1.7 × 10^7 | 6.6 × 10^{-3} | 10.4 |
| CB8j | 1.2 × 10^7 | 1.97 | 6.8 |
| CB8j | 1.2 × 10^7 | 1.92 | 6.8 |
| CB8j | 6.6 × 10^7 | 3.6 × 10^{-3} | 7.1 |
| CB8j | 4.5 × 10^7 | 4.1 × 10^{-3} | 7.1 |
| CB8j | 2.3 × 10^7 | 2.0 × 10^{-3} | 7.1 |
| CB8j | 2.4 × 10^7 | 2.1 × 10^{-3} | 7.1 |
| CB8j | 3.0 × 10^7 | 3.7 × 10^{-3} | 7.2 |
| CB8j | 2.5 × 10^7 | 3.1 × 10^{-3} | 7.2 |
| CB8j | 1.1 × 10^7 | 6.8 × 10^{-3} | 8.2 |
| CB8j | 1.1 × 10^7 | 7.1 × 10^{-3} | 8.2 |
| CB8j | 1.5 × 10^7 | 1.1 × 10^{-3} | 6.2 |
| CB8j | 1.5 × 10^7 | 1.1 × 10^{-3} | 6.2 |
| CB8j | 6.4 × 10^7 | 5.8 × 10^{-3} | 8.0 |
| CB8j | 6.4 × 10^7 | 5.8 × 10^{-3} | 8.0 |
| CB8j | 2.1 × 10^7 | 5.8 × 10^{-3} | 6.6 |
| methanol | 2.1 × 10^7 | 5.8 × 10^{-3} | 6.6 |
| Phenylbutazone | HSA | 6.6 × 10^6 | 1.0 | 5.8 |

Errors (StDev) from triplicate experiments are ≤ 30% in k_{HG} and k_{out}, see Table S3 (ESI). If not otherwise stated experiments were conducted in deionized water at 25 °C. Minor to no differences in guest binding kinetics have been found for non-desalted and desalted hosts. See Fig. 2 for chemical structures. See Table S3 (ESI) for indicator kinetics. In deionized water with 8.23 μM HCl. DSMI as dye. See ESI for details. 2 H₂O/ethanol (99.9/0.1; v/v) mixture. BE as dye. See ref. 30. In water freshly distilled three times from dilute K₂MnO₄ solution. Desalted CB7/CB8. 6 MIPC as dye. Determined by ITC. 7 CB7 (2 μM), nandrolone (log K_{d}[^M]) = 7.0; 40 2 μM. 9 Dye (2 μM). See ref. 40. 9 Dye (50 μM). 9 Dye (40 μM) likely associative mechanism also present, see text. 11 BE (50 μM) or MDAP (25 μM) in sodium phosphate buffer (50 mM). Calculated using the formula presented in ref. 41. 12 MDAP as dye. In phosphate buffered saline (PBS). 13 Warfarin as dye.

The kinetic trace is recorded and then fitted by a simple exponential decay function

\[ I_t = I_{0} + A \cdot e^{-k_{HG} t} \]

to yield the kinetic parameter k_{HG} | interest (P | signal offset at equilibration to HD | A | amplitude). The k_{HG} | value is then obtained from k_{HG} = k_{out} | k_{in}. In kinGDA | knowledge of the exact concentrations of the involved partners is not needed, thus, kinGDA | can often be the practical choice. However, it is important to note that the applicability of kinGDA | is restricted because k_{HG} | [G]₀ | k_{HG} | [D]₀ is required. Ideally, the kinGDA | traces should overlap upon varying the dye concentration, excluding concentration-induced changes in the binding mechanisms. For most of the CBn–guest complexes, we found that the kinGDA | method is applicable. However, the high dye concentrations required for kinGDA | can cause undesirable associative-binding contributions to H | G decomplexation mechanism. For example, at higher concentrations the dicationic MDAP may form a (transient) ternary complex with charge-neutral CB7 | nandrolone in deionized water, causing an apparent increase in k_{out} (Table 1). This scenario is plausible because the decomplexation rate of CB7 | nandrolone strongly increased in phosphate buffer (Fig. 3d), which implies formation of ternary M | CB7 | nandrolone complexes. (See ref. 37–39 for precedence for M | CBR | G complexes). Thus, ternary dye-CB7 | guest complexes are likely not present in buffered or saline aqueous media and the high dye concentration needed for the kinGDA | method is of no concern (see Table 1).

Finally, a third competitive method, the time-resolved indicator displacement assay (kinitDA), can be employed for obtaining kinetic rate constants. In kinitDA, a pre-equilibrated host-dye pair is mixed with the guest, to which the binding network responds with dye displacement (Fig. 1c). Indeed, comparable results were obtained for kinitDA and kinGDA for the system composed of nandrolone (G), CB7 (H) and berberine (D), see Fig. 3b.

The kinetic methods introduced herein provide meaningful rate constants if the host–guest and host-dye displacement mechanism follow a strict dissociative and not an additional, occasionally observed,36 associative mechanism. Several tests can be adopted to validate a dissociative mechanism. (i) kinitGDA | can be conducted at different dye concentrations and should yield similar k_{HG} | and k_{out} | parameters. (ii) The kinitGDA | method can be compared to the analogous kinitDA setup, see above. In many cases, the competitive methods can circumvent the need for stopped-flow equipment because the equilibration times in the competitive assay format are much longer than in kinDBA. Thus, kinetic characterization of CBn–guest complexes can now also be conducted in laboratories that do not have access to specialized stopped-flow setups. For instance, the kinetic rate constants for the CB7 | steroid and CB8 | steroid complexes can

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be determined in a cuvette equipped with a magnetic stirrer by a standard fluorescence spectrometer. Conversely, explorative $\text{kin}_{\text{GDA}}$ and $\text{kin}_{\text{IDA}}$ experiments for $\beta$-cyclodextrin complexes with high-affinity guests such as adamantanol resulted in equilibrium times that were even too fast (<100 ms at 298 K) for our stopped-flow setup. The investigations of CBn complexes and the protein–ligand complex HSA$\supset$PBZ show that $\text{kin}_{\text{GDA}}$, $\text{kin}_{\text{GDA}}^{\text{PRO}}$, and $\text{kin}_{\text{IDA}}$ yield reliable fits for guest regression rates $\lambda_{\text{GDA}}^\text{亲} \leq 10$ s$^{-1}$. The kinetic rate constants that became available through the use of presented methods were converted alongside literature data to Gibb’s activation energies by Eyring’s equation, see also eqn (S24), (S25) and Table S4 in the ESL† The data displayed in Fig. 4 shows a clear decoupling of thermodynamic and kinetic features for the CBn–guest and HSA–guest complexes compiled, motivating future in-depth analysis of these host–guest inclusion complexes. A first assessment demonstrates that increased thermodynamic stability is not always correlated to an increase in the kinetic inertness of the CBn–guest complexes. In conclusion, it was shown that $\text{kin}_{\text{IDA}}$, $\text{kin}_{\text{GDA}}$, and $\text{kin}_{\text{GDA}}^{\text{PRO}}$ provide an experimental assessment of kinetic rate constants of spectroscopically silent host–guest and protein–ligand pairs. These methods will find use in the supramolecular and protein community due to their ease and scope.

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**Conflicts of interest**

There are no conflicts of interest to declare.

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