Do enzymes sleep and work?

Hans Engelkamp, a Nikos S. Hatzakis, a Johan Hofkens, a⁎ Frans C. De Schryver, b Roeland J. M. Nolte a⁎ and Alan E. Rowan a⁎

DOI: 10.1039/b516013h

Single-enzyme studies suggest that dynamic disorder is a general characteristic of enzyme catalysis.

Enzymes, the ubiquitous catalysts of Nature, are remarkable molecular constructs, which determine the patterns of chemical transformations. For more than a century scientists have been studying enzyme activity in bulk, aqueous solution, at the so-called ensemble level and a great wealth of information has been obtained. Using techniques by which the average activity of a large number of enzyme molecules (say \( y \approx 10^{15} \)) is measured, many general principles have been discovered, including Michaelis–Menten kinetics, the occurrence of pH and temperature optima, allosteric interaction, etc. Numerous studies have also looked at the ensemble synergistic action of enzymes. Enzymes in their natural environment, the cell, often interact with numerous neighbouring proteins, and their catalytic activity generally depends upon their environment and their role in the catalytic cycle. In ensemble measurements, only the average value of an observable parameter is detected, and no information is obtained about what precisely the contribution of individual molecules to the overall studied process is. Moreover, the concentration of intermediate steady states is often too small to be detected.

Pioneering experiments in 1961 by Rotman showed the possibility of detecting the activity of single β-D-galactosidase molecules in oil-dispersed water droplets. Enzymatic hydrolysis of the pro-fluorescent 6-hydroxyfluoran-13-D-galacto-pyranoside substrate yielded the fluorescent compound 6-hydroxyfluoran. By analyzing the increase in the fluorescence intensity of the individual droplets with the help of Poissonian statistics, the number of active enzymes in each droplet could be determined, which in several droplets amounted to exactly one. The most interesting outcome of these very first single-enzyme experiments was the observation from thermal denaturation studies that thermal inactivation of the enzyme leads to a mixture of fully-active and completely inactive enzyme molecules; in stark contrast to studies at the ensemble level, in which only an average decrease in activity was measured.

Rotman’s analysis included the assumption that each active enzyme molecule exhibits the same activity. It became apparent in 1995 that this is not necessarily the case for enzymes when it was shown that the activity of individual lactate dehydrogenase molecules can vary by a factor of four. The origin of such activity differences (‘static disorder’) may lie in the presence of several active conformations of the enzyme, which remain stable for extended periods of time. Similar results were obtained for single molecules of alkaline phosphatase for which it was shown that the activity range can span an order of magnitude. It was also observed that partial thermal

Hans Engelkamp studied Chemistry at the Radboud University Nijmegen and received his Ph.D. in 2003 on the hierarchical transfer of stereochemical information in supramolecular architectures from phthalocyanines with Professor R. J. M. Nolte. After three years in industry (Philips Semiconductors) he returned to his Alma Mater to work on single molecule enzymology.

Nikos S. Hatzakis studied Chemistry at the University of Crete in Greece and received his Ph.D. with Professor I. Smonou in 2003 on the use of lipases and esterases for the stereoselective transformations of natural and non-natural substrates. Since 2004 he has been working as a post-doctoral fellow at the Radboud University Nijmegen (groups of Professor A. Rowan and Professor R. Nolte) in the fields of single molecule enzymology and the construction and study of biohybrid structures.
degradation of a bulk sample of alkaline phosphatase divides the population into active and inactive molecules. Again, the individual activity of the surviving enzymes remained the same, very similar to the early results of Rotman with β-D-galactosidase.3

Moving on from time-averaged ensemble measurements to time-averaged single enzyme studies allows for the detection of static disorder, i.e. differences in activity of individual enzyme molecules. The actual measurement, in most cases the fluorescence intensity of the formed product, is still an ensemble measurement in the sense that millions of product molecules are detected.

The detection of dynamic disorder, i.e. time-dependent fluctuations, requires the measurement of the single-enzyme kinetics in real-time, that is, turnover by turnover. In order to achieve this, it is necessary to measure the formed product at the individual chromophore level.7

The detection of a single chromophore in water has only been possible since the early 1990s, when advanced optical instrumentation became available.8 One of the first examples of truly real-time enzyme kinetics was the observation in real-time of the binding of fluoro- rescently labelled ATP and ADP to single myosin molecules.9 Using a total internal reflection microscope, single fluorescently labelled myosin molecules were imaged and individual ATP

Johan Hofkens received his Master’s degree in Chemistry from the University of Leuven in 1988, which was followed by a Ph.D. in Sciences from the same university in 1993. After postdoctoral research with Professor Masahara at Osaka University and Professor Barbara at the University of Minneapolis, he rejoined the University of Leuven where he was in charge of the Single Molecule Unit in the group of Prof. De Schryver. In 2005 he was appointed Research Professor at the University of Leuven. His research interests are fast spectroscopy, single molecule spectroscopy, and optics.

Johan Hofkens

Frans De Schryver obtained the degree of Doctor in Sciences from the University of Leuven in 1964. He was appointed Docent (1969), Professor (1973) and Full Professor (1975) and became an Emeritus Professor in October 2004. He was the Head of the Department of Photochemistry and Spectroscopy at the University of Leuven, specializing in time and space resolved (photo)chemistry, including microscopy. Frans De Schryver is a member of the Koninklijke Vlaamse Academie van België voor Wetenschappen en Kunsten and has received several awards including the Research Award of the Alexander von Humboldt Foundation (1993), the Chaire Bruylants Award (1997), the Porter Medal (1998), the Francqui Chair (1998), the Havinga Medal (1999), the Förster Memorial Lecturer (1999), the Frontiers in Biochemistry Award (2000), the Max-Planck-Forschungspreis für Chemie (2001), the International Award of the Japanese Photochemical Society (2002) and the Medal of the University of Groningen (2005).

Roeland J. M. Nolte received his Ph.D. from the University of Utrecht in 1973. After a postdoctoral stage with Prof. Donald J. Cram at the University of California Los Angeles he joined the Faculty of Science of the University of Utrecht. In 1987 he moved to the Radboud University Nijmegen to become a Full Professor of Organic Chemistry. Since 2003 he has held a special chair as a Royal Netherlands Academy of Arts and Science Professor. Roeland Nolte is director of the Institute for Molecules and Materials at the Radboud University Nijmegen and is Chairman of the Board of Chemical Communications.

Roeland J. M. Nolte

Alan E. Rowan completed his Ph.D. study at the University of Liverpool in the field of Physical Organic Chemistry in 1990. He then departed to New Zealand for a post-doctoral stage at the University of Otago. In 1993 he returned to Europe to take up a TMR Fellowship at the Radboud University Nijmegen in the field of Supramolecular Chemistry in the group of Prof. R. J. M. Nolte. Since then he has become Lecturer, Senior Lecturer, and recently Professor of Molecular Materials at the Radboud University Nijmegen.

Alan E. Rowan
resulting FADH2 is then reoxidized by form but not in its reduced form. The is naturally fluorescent in its oxidized 

A sample of flavin adenine dinucleotide known to be accompanied by the reduction of cholesterol by cholesterol oxidase is 

This phenomenon is the fact that the fluctuates in time. One manifestation of the turnovers in real-time and not only as a time-average led to the finding that the rate of the enzymatic reaction slowly fluctuates. The recorded thermodynamic fluctuations in the activity of horseradish peroxidase enzyme at the single-turnover level. 

The method described by Xie et al., although very elegant, has some important drawbacks. By observing the cofactor, which is prone to photobleaching, the amount of data that can be collected from one enzyme is limited. Furthermore, the actual product formation and release are not observed. These problems can be avoided by using a pro-fluorescent substrate that is converted into a fluorescent product by the enzyme of interest. The first example of this approach was reported by Rigler and coworkers. They recorded the thermodynamic fluctuations in the activity of horseradish peroxidase enzyme at the single-turnover level. 

The Cal B enzyme clearly exhibits on–off behaviour, which, after hydrolysis, is converted into the fluorescent BCECF acid. The Cal B enzyme was adsorbed onto a hydrophobic cover slip and positioned in the focus of a confocal microscope (Fig. 3). Using such an approach we were able to measure the single-enzyme activity as a function of substrate concentration on one single enzyme molecule for very long periods of time, even up to 6 hours. Just as reported in the literature for cholesterol oxidase and horseradish peroxidase, substrate hydrolysis by Cal B was detected by fluorescence imaging with a confocal microscope. As the product, once released from the enzyme, diffuses away from the focal volume very quickly, only the fluorescence of the enzyme–product complex is observed. This enables the separate analysis of the oxidation of the substrate and the dissociation of the enzyme–product complex.

In classical Michaelis–Menten kinetics, these two distinct processes are regarded as one step. Interestingly, the measured data showed single-exponential product dissociation kinetics, but a large distribution of rates for the enzyme to form the enzyme–product complex.

As part of our studies on the design of new building blocks for the construction of nano-sized self-assembled systems, we have recently developed a new class of amphiphilic macromolecules, so-called giant amphiphiles, which consist of an enzyme head group (e.g. a lipase) connected to one or two hydrophobic polymeric tails. Within this project, we became interested in studying the activity of single lipase enzymes and polymeric derivatives of these biomolecules. We studied at the single enzyme level the kinetics of the lipase B from Candida Antarctica catalyzed hydrolysis of a non-fluorescent substrate, viz. BCECF-AM (Fig. 3), which, after hydrolysis, is converted into the fluorescent BCECF acid. The Cal B enzyme was adsorbed onto a hydrophobic cover slip and positioned in the focus of a confocal microscope (Fig. 3). Using such an approach we were able to measure the single-enzyme activity as a function of substrate concentration on one single enzyme molecule for very long periods of time, even up to 6 hours. Just as reported in the literature for cholesterol oxidase and horseradish peroxidase, substrate hydrolysis by Cal B was detected by fluorescence imaging with a confocal microscope. As the product, once released from the enzyme, diffuses away from the focal volume very quickly, only the fluorescence of the enzyme–product complex is observed. This enables the separate analysis of the oxidation of the substrate and the dissociation of the enzyme–product complex.

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are catalytically active. These results indicated that this enzyme has bursts of top activity for ~ 30 ms and then is inactive for 970 ms (Fig. 4). This intriguing behaviour can be better imaged as an enzyme which effectively ‘sleeps’ for 97% of the time and is awake and active for only 3% of its day. Although such an image is an attractive concept the real situation is one in which the enzyme is slowly moving through a landscape of conformations, each with its own specific activity. However within this family of enzyme conformations only a few exhibit a high catalytic activity. The measured bulk activity is therefore an average of short periods of top-activity and periods of inactivity, a finding which never could have been deduced from ensemble measurements. This breathing clearly demonstrates the fundamental importance of studying individual enzyme behaviour and the single molecule turnover, particularly when one wishes to find out the real reason why directed evolution results in more active enzymes.

In further studies we also increased the substrate concentration during the experiment and showed for the first time that the kinetics of an individual Cal B enzyme molecule exhibit Michaelis–Menten-like properties, saturating at a certain substrate concentration, very similar to the ensemble behaviour (Fig. 5). The average $k_{cat}$ and $K_m$ values calculated from the saturation curve amount to $4 \text{s}^{-1}$ and $2.5 \times 10^{-7} \text{M}$, respectively. Interestingly, the top activity derived from our single-enzyme measurements, the actual maximum rate, amounts to $k_{fast} = 125 \text{s}^{-1}$, almost two orders of magnitude higher.

The above experiments had several minor drawbacks in that the process of absorbing the enzyme to the surface is uncontrolled and only a limited number of enzymes remain active. To overcome this problem we have recently constructed an enzyme protein heterodimer consisting of a Lipase (TLL) and a commonly used coating protein (BSA), which acts as a “protein foot”. Deposition of this protein dimer resulted in all the bound enzymes remaining active and exhibiting comparable behaviour. Upon the addition of the pro-fluorescent substrate 5-(and-6)-carboxy-fluorescein diacetate, again a clustering of events was observed, which when further analysed revealed a clear memory effect. In contrast to the earlier work of Xie in which the memory observed in the glucose oxidase lasted only for a couple of events, for TLL–BSA, the lipase enzyme remembers considerably more, approximately 20 events. This does not mean that the TLL is cleverer than glucose oxidase, it simply carries out more catalytic conversions in the same time period, before it “forgets” and the geometry changes. These memory effects further support the concept of a landscape of conformations, which fits the model of a fluctuating enzyme.

As the results presented above indicate, exciting progress has been made in the field of single-molecule enzymology. There are however considerable questions that remain, such as: why are some enzymes or perhaps all enzymes only active a fraction of the time?; how could one restrict the conformation landscape such that the enzyme comes back more quickly to, or remains in the active conformation and why hasn’t Nature done this already? One could argue that having periods of inactivity is Nature’s approach for removing the energy generated during the catalytic reaction. Possibly, the conformational changes leading to the inactive conformations are actually caused by the necessity to dissipate the cumulated energy produced
Investigating this question and other questions will require the simultaneous measurement of protein dynamics with single-pair Fluorescence Resonance Energy Transfer (FRET) and enzyme kinetics at the single-turnover level, as a function of substrate concentration. One elegant way of doing this would be the use of a non-fluorescent substrate, which upon the enzymatic conversion is transformed into a fluorescent product, which can act as an excitation energy donor to an acceptor located at a strategic position with respect to the active site on the enzyme. By following the emission from the acceptor and the donor simultaneously, enzyme activity can be directly correlated to slow conformational changes in the enzyme. Intermolecular single-pair FRET studies have been carried out before on different systems, viz. donor-labelled Staphylococcal nuclease and acceptor-labelled DNA substrate.18 In our case using a fluorescent product as donor would have the advantage of (i) diminishing the degree of bleaching of the chromophore which is attached to the enzyme, as it is only excited when a product is formed, and (ii) the ability to observe the enzymatic turnovers directly.

Enzymes in Nature are susceptible to all kinds of regulation mechanisms by external stimuli. They show substrate selectivity, act at an optimum pH and temperature, show inhibition, activation, denaturation and most importantly display allosteric behaviour. In addition to all of the above, they do their work in biological cells which are literally crowded with all kinds of molecules, balancing numerous simultaneously occurring processes. The newly developed single-molecule techniques open the way to unravel in detail the pathways by which enzymes operate, complementing in this way the vast amount of data that has already been gathered from ensemble measurements. An excellent example of work in this direction is the recent study by van Oijen and coworkers on the behaviour of the multi-enzyme T7 replication fork.19 In this scanning probe approach the individual contributions and synergy between the multiple protein components in the replication system could be resolved. The fact that single enzyme experiments can now be carried out for long periods of time during the enzymatic reaction.17
is especially rewarding, since it will lead to more insight into how enzymatic reactions are coupled in space and in time. As scanning probe microscopy has revolutionized the field of material science, it is without doubt that single enzyme studies in real time will have a similar effect in the field of enzymology.

Acknowledgements

The research described in this article was carried out as part of the EC Sisitomas network (IAAP-V-03) and the EC STREP project Bioscope.

Notes and references


Fig. 5 Michaelis–Menten behaviour of a single Cal B enzyme molecule. Plot of the number of fluorescent events in a time-interval of 20 minutes as a function of the substrate concentration. Saturation is reached at approximately 600 nM. The red line is the fitted Michaelis–Menten curve for $k_{\text{cat}} = 4 \, \text{s}^{-1}$ and $K_{\text{m}} = 2.5 \times 10^{-7} \, \text{M}$. 

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