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A model for non-obligate oligomer formation in protein aggregration

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ABSTRACT

Using solvent-exposed intramolecular backbone hydrogen bonds as physico-chemical descriptors for protein packing, a role for transient, non-obligate oligomers in the formation of aberrant protein aggregates is presented. Oligomeric models of the both wild type (wt) and select mutant variants of superoxide dismutase (SOD1) are proposed to provide a structural basis for investigating the etiology of Amyotrophic Lateral Sclerosis (ALS).

1. Introduction

Protein–protein association is essential for a wide variety of cellular processes. Where the complex formed by the interaction of more than one polypeptide chain is the biologically active state then the assembly is termed an obligate oligomer, and represents the protein's quaternary structure. While there exists a wide variety of techniques, including light scattering [1], mass-spectrometry [2] and Nuclear Magnetic Resonance [3], capable of elucidating various aspects of macromolecular structure most of our knowledge of the structural aspects of protein–protein interactions (PPIs) comes from protein crystallography [4]. The Protein data Bank (www.rcsb.org) represents a compilation of 3D protein structures, more than 80% of which were characterized by X-ray crystallography [5]. It has been estimated that monomers represent approximately 25% of the structures deposited in the PDB, with dimers representing a further 15% [6]. While the bias in the data towards soluble proteins is not surprising, the relatively low percentage, less than 7%, of hetero-oligomeric complexes of all sizes is noteworthy.

Given the dominant role of crystallography in protein structure determination it is not surprising that crystal contacts between proteins serve as a common starting point in the analysis of biologically important protein–protein contacts. However it cannot be assumed that the crystallization conditions are an accurate reflection of the biological conditions driving macromolecular assembly and protein function *in vivo*. Additionally the contents of the asymmetric symmetry unit (ASU) may represent multiple copies of the biological state of the protein. Conversely the presumed biological molecule might best be represented by applying crystallographic symmetry to the contents of the ASU. While water mediates many protein functions and plays an important, if not determinant, role in protein folding, the fraction of water crystallized with the protein has been shown to correlate with crystal symmetry. A correlation was also observed between the crystal symmetry and the internal symmetry of the protein oligomer [7]. Thus the oligomeric unit presented by the ASU is, at least to some extent, a product of the experimental conditions employed.

However, there is much that we can infer about macromolecular assemblies from the crystalline state. While studies of the various structural determinants of the binding affinity of protein–protein complexes have covered the gamut of physico-chemical descriptors, analysis of amino acid preferences and secondary structure packing at the interfaces has yielded some of the most useful insights [8,9]. Buried surface are (BSA) remains a primary descriptor of binding affinity, and this has led to the identification of interface "hot spots" [10], or residues that, when substituted by alanine, correlate with a change in the free energy of dissociation, ΔG^0_{diss}. Informatics approaches that score putative protein complexes represent an attempt to enumerate possible assemblies by identifying interfaces as either biologically relevant or simply contacts due to crystal packing forces [11]. Since 2007 the PISA (Protein Interface, Surfaces and Assemblies) protocol, a graph-theoretical approach to identify chemically stable and biologically relevant associations that may potentially be formed in a given crystal packing, has been used in the PDB submission process to aid in quaternary structure determination [12]. Alternatively the user can utilize PISA to independently analyze any PDB entry.

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Uncontrolled oligomerization, in concert with protein misfolding, converts peptides and proteins from their soluble forms into insoluble fibrillar aggregates, that can give rise to a variety of pathological conditions. While molecular chaperones, including the small heat shock proteins (sHsps), play an important role in protecting against protein misfolding and aggregation, for diseases such as Alzheimer's disease (AD), Parkinson's (PD) and Amyotrophic Lateral Sclerosis (ALS), the accumulated protein aggregates eventually overtaxes the heat shock response, leading to apoptosis and neuronal cell death. Not surprisingly an important paradigm driving therapeutic development has been that the formation of these highly organized fibrillary aggregates leads to neurodegeneration and death [13], despite the fact that the relevance of plaques, or extracellular fibrils, to AD pathogenesis remains unclear since substantial neuronal dysfunction is observed prior to the appearance of fibrillary deposits [14]. There is also a growing body of evidence to suggest that these fibrils may be just end-stage products, and that the primary toxic element is a pre-fibrillar oligomer [15]. The failure of therapeutic strategies based on fibril elimination [16,17], is leading to a shift in focus away from deposition and towards aggregation and oligomerization [18]. ALS is linked to the misfolding and aggregation of superoxide dismutase (SOD1), with over 90% of cases sporadic and the remaining familial cases associated with a wide array of inherited mutations. While it is known that oligomeric assemblies of both wild type (wt) and mutant SOD1 are precursors to the larger and detergent-insoluble aggregates, the structural events that trigger oligomerization remain elusive. Furthermore studies have found that mutant, misfolded SOD1 can convert wtSOD1 in a prion-like fashion [19], and that misfolded wtSOD1 can be propagated by release and uptake of protein aggregates [20].

Solvent-exposed intramolecular backbone hydrogen bonds, or dehydrons, have been previously identified as vulnerabilities or structural defects, in the packing of a wide array of proteins [23,24]. Exposure of such dehydrons to an aqueous environment has been shown to weaken protein secondary structures [25,26]. In turn excluding solvent from protein regions containing exposed hydrogen bonds has been implicated as a determinant factor in ligand-protein [27] and protein–protein [28] interactions, as well as protein subunit assembly [29]. This dehydron hypothesis has also been utilized to provide a mechanism of action for sHsp, based on the protection of solvent-exposed backbone hydrogen bonds within the α-crystalline domain [30,31], as well as structural basis for the modulation of SCA3 toxicity by αB-crystalline [32]. This paper seeks to highlight the utility of looking beyond the x-ray crystallographic data when analyzing for protein–protein contacts in putative protein oligomers. Using the protein SOD1 as an example, and focusing on solvent-exposed intramolecular backbone hydrogen bonds as physico-chemical descriptors for protein packing, we will present a role for transient, non-obligate oligomers in the formation of aberrant protein aggregates.

2. Methods

The crystal structures for the wild type of human superoxide dismutase are available from the RCSB (www.rcsb.org) as PDB entry 2C9V [33]. A wide array mutant structures are also available, including G37R (1AZV) [34], G85R (2ZKX) and G93A (2WZ6) [35]. After adding hydrogens these proteins were subjected to a short energy minimization using the CHARMm force field [36]. Protein alignments and superimposition were done using the MODELER protocol as implemented in the Discovery Studio program suite.

The extent of hydrogen bond desolvation is quantified as the number of non-bonded, carbonaceous groups, ρ, contained within a domain centered on the residues linked by the interaction [28]. This desolvation domain is defined as two intersecting spheres of fixed radius centered on the C_α atoms of the linked residues. Dehydrons are then identified as those backbone hydrogen bonds that are underwrapped by non-polar carbonaceous groups, and defined as those interactions with ρ values at or below the average minus one root mean squared deviation. In this work the default values for domain radius, 6.2 Å, and dehydron cutoff, $\rho \leq 19$, were used as per reference 28. The dehydrons for SOD1 are shown as green (in web version) connectors in Fig. 1.

The biological assembly for SOD1 shown in Fig. 1 was predicted by PISA (available at http://www.ebi.ac.uk/pdbe/pisa/) analysis of the pdb entry 2ZKX [12]. PISA enumerates all macromolecular assemblies that may be potentially formed for a given crystal packing. The Gibb's free energy of interaction as well as an entropy cost of oligomerization is calculated as in Ref. [37]. Those complexes with an overall positive free energy of dissociation are identified as chemically stable. Complexes may be misrepresented due to failures in the energy approximation, or in the inferences made from the crystal packing.

ZDOCK is a Fast Fourier Transform rigid docking protocol that searches all possible binding modes in the translational and rotational spaces between two proteins, and evaluates each using an energy scoring function based on shape complementarity [38]. By associating an unfavorable desolvation energy contribution with specified atoms, protein residues can be blocked from being included in binding sites. Results are filtered by clustering poses where the RMSD lies within a specified cutoff of the predicted binding interface. Of the 54,000 docked poses generated for the SOD1 tetramer using the default parameters as implemented in the Discovery Studio program suite from Accelrys Inc. the 2000 top-ranked poses were filtered into 93 clusters. For each cluster an average contact surface area was generated by calculating the change in the solvent accessible surface (SAS) area upon formation of the protein–protein complex for each docked pose. Finally the pose with the largest excluded SAS area, from the cluster with the largest average contact surface area, was selected. This oligomer is shown in Fig. 1.

3. Results and discussion

Analysis of the dehydron pattern for the wtSOD1 monomer is shown in Fig. 1, and reveals that the underwrapped, solvent-exposed backbone hydrogen bonds are located in three relatively well defined regions (circled). One of these regions lies at the dimer interface and is thus dehydrated and stabilized through formation of the asymmetric unit. The other two areas remain exposed in the dimer, raising the possibility that a higher order oligomer that stabilizes the exposed regions through transient protein–protein interactions (PPI) would be favored under biological conditions. The tetramer shown represents the pose from the cluster with the largest average contact surface area, as identified by the ZDOCK protocol, that in turn gives the greatest solvent excluded surface area upon dimer–dimer contact, a value of 1370 $Å^2$. For comparison this is approximately 60% greater than the average excluded SAS area calculated for those poses in the highest occupancy cluster. As can be seen this PPI corresponds perfectly with the two erstwhile exposed regions containing hydrogen bonded vulnerabilities. One of these regions is shielded by contact with the adjacent dimer interface, while the other is “patched” by residue Trp_{32}. In turn the D_2 symmetry of the tetramer ensures that a corresponding Trp_{32} patch is to be found further along the interface. The combination of C_2 point group symmetry and $P2_1$ space group symmetry in 2C9V, also allows for a D_2 tetramer to be generated simply by applying crystallographic symmetry to the dimeric ASU. For the G85R mutant, which crystallizes in the $I2_12_12_1$ space group, the ASU itself