

## The multifaceted role of transglutaminase in neurodegeneration: Review article

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Received December 15, 2003

Accepted January 15, 2004

Published online July 6, 2004; © Springer-Verlag 2004

**Summary.** A critical role for transglutaminase [TGase] has been hypothesized in the pathogenesis of the CAG trinucleotide repeat diseases, characterized by proteins with abnormal expansions of a polyglutamine domain. In the last few years the involvement of TGase in neurodegenerative diseases [NDS], including its role in aggregate formation, has been broadened to include Alzheimer's [AD] and Parkinson's Disease [PD]. It is clear that reduction of TGase activity is beneficial for prolonged survival in mouse models of NDS. The pathological progression of these diseases might reflect in part increases of TGase induced aggregates, or changes in other pathways influenced by increases in TGase activity. Neurodegeneration may be influenced by increased TGase activity affecting apoptosis, modulation of GTPase activity and signal transduction. This review will focus on the leading hypotheses in relation to both old and new experimental results.

**Keywords:** Transglutaminase – Neurodegeneration – Huntington disease – Alzheimer's disease – Parkinson's disease – Cystamine

**Abbreviations:** TGase, Transglutaminase; HD, Huntington's Disease; AD, Alzheimer's Disease; PD, Parkinson's Disease; NDS, Neurodegenerative Diseases; Gln, Glutamine; SBMA, spinal bulbar muscular atrophy; htt, Huntingtin; NAC, Non-amyloid component; A $\beta$ , amyloid-beta; APP, amyloid precursor protein

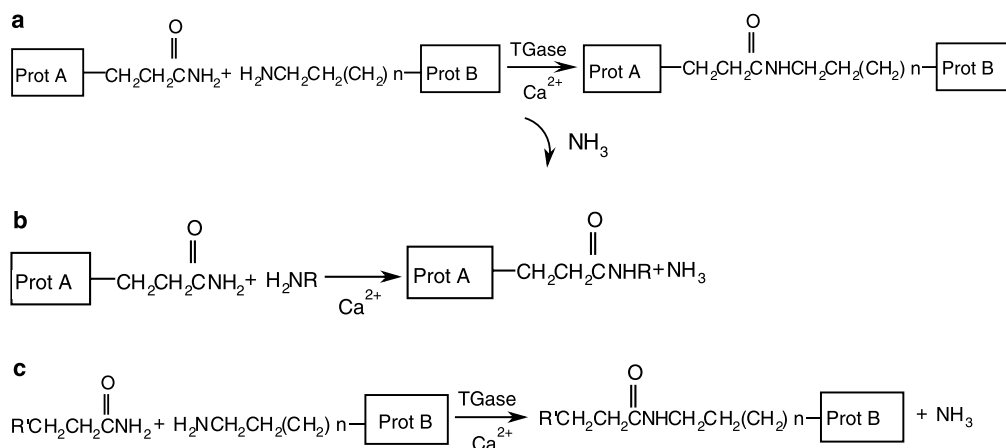
### Transglutaminase and the post-translational modification of proteins

Clarke and collaborators introduced the term Transglutaminase (TGase) in 1957. They described the enzymatic transamidation of proteins in guinea-pig liver (Clarke et al., 1957). Thereafter, Pisano and colleagues demonstrated that transamidation occurs through cross-linking of proteins through an acyl-transfer reaction between the  $\gamma$ -carboxamide group of peptide-bound glutamine (Gln) and the  $\epsilon$ -amino group of peptide-bound lysine, resulting in an  $\tilde{\epsilon}(\gamma$ -glutamyl)lysine isopeptide bond (Fig. 1a) (Pisano et al., 1968).

This enzymatic activity required the binding of  $\text{Ca}^{2+}$ , but at higher concentrations than the physiological range associated with most intracellular processes (Burgoyne and Weiss, 2001). Interestingly, in most NDS, there is evidence for increased intracellular  $\text{Ca}^{2+}$  concentration, which can be associated with neuronal loss (Lue et al., 1996; Peterson and Goldman, 1986; Ito et al., 1994; Gibson et al., 1996).

A number of competitive inhibitors are available, which block the crosslinking of proteins mediated by TGase. The inhibitor becomes incorporated into the protein substrate and blocks either the acceptor or the donor site. In the case of an amine incorporation, the competitive inhibitor is a primary amine that binds to the acceptor (Fig. 1b), and in the case of acylation the inhibitor is a Gln-containing peptide which blocks the donor (Fig. 1c).

Selkoe provided the first description relating neurodegeneration and TGase activity in 1982. He hypothesized that TGase is involved in NDS, including Parkinson's Disease (PD), Huntington's Disease (HD) and Alzheimer's Disease (AD), because they all might involve aggregate formation in neurons undergoing degeneration. Selkoe and colleagues reported for the first time, that TGase was present and active in brain (Selkoe et al., 1982). Their experiments demonstrated that brain TGase covalently cross-linked brain proteins into insoluble polymers *in vitro*. However, paired helical filaments, one of the types of aggregates present in AD, did not form under the specific *in vitro* conditions. That observation, in part, left open the question of TGase involvement in aggregate



**Fig. 1.** TGase mediated chemical reactions: **a** Crosslinking of two different proteins where protein A serves as an acceptor while protein B serves as a donor. The product is a covalent bond between protein A and B. Protein A and B are not necessarily two different proteins, resulting in a third possibility where the covalent bond is formed within the same protein. **b** Incorporation of a primary amine or a diamine into protein A results in the future interaction with any other protein containing a potential lysine donor. **c** Acylation of protein B in the presence of a peptide that contains a glutamine residue as an acceptor

formation in NDS, and may have discouraged further research on TGase in NDS for another decade!

After the ensuing decade of inattention to the role of TGase in NDS, a series of landmark discoveries in the early 90's by Fischbeck and colleagues working on bulbar spinal muscular atrophy (SBMA), and Gussella and colleagues working on HD, showed that expanding polyglutamine repeats were at the center of the genetic basis of a group of diseases called the trinucleotide repeat diseases. Expanding stretches of CAG trinucleotide repeats, encoding Gln in different proteins were found to be the basis of the pathology of SBMA, HD and soon thereafter six other NDS (La Spada et al., 1991; Gusella et al., 1983). In 1993 Howard Green hypothesized that TGase cross-linking of polyglutamine stretches in the huntingtin protein (htt) was critical for the pathogenesis of HD (Green et al., 1993). Since Green's hypothesis, a series of experiments undertaken in humans, animal, and *in vitro* cell culture models have supported this idea. The possible role of TGase in other NDS that are not caused by an expanding CAG repeat encoding polyglutamine, has been rekindled. Interest in the role of TGase in PD and in AD has sparked new studies in these diseases.

#### Aggregated proteins in NDS serve as substrates for TGase activity

TGase substrates are commonly found in neuronal aggregates in other NDS. Non-amyloid component (NAC), a target for TGase, is a fragment of alpha-synuclein that is present in an aggregated form in Lewy bodies of PD

patients (Arima et al., 1998) and in amyloid plaques of AD patients (Wirths et al., 2000). Interestingly, aggregated NAC is more toxic than its monomer (El-Agnaf et al., 1998; Forloni et al., 2000). In addition to NAC, TGase mediated protein-aggregation in NDS, including the domains which participate in this intramolecular process, was shown for amyloid-beta ( $A\beta$ ), the major component of amyloid plaques in AD, (Rasmussen et al., 1994).  $A\beta$  oligomerization is catalyzed via TGase (Ikura et al., 1993; Dudek and Johnson, 1994; Ho et al., 1994). Finally, Tau, the major component of the paired helical filaments, forms insoluble and filamentous oligomeric products in the presence of TGase *in vitro* (Dudek and Johnson, 1993; Appelt and Balin, 1997).

Htt was first demonstrated as an excellent glutamyl-donor substrate for TGase *in vitro* (Kahlem et al., 1996; Cooper et al., 1997; Gentile et al., 1998; Karpuj et al., 1999; Karpuj et al., 2002a). In 1999 we demonstrated that TGase could cross-link soluble mutated htt and transform it into an insoluble aggregated conformation, which is a principal feature of HD (Karpuj et al., 1999). In HD patients a truncated version of the mutated htt is present as a nuclear inclusion in neurons (Davies et al., 1997; DiFiglia et al., 1997; Becher et al., 1998). These inclusions are also present in the cytoplasm (Lunkes et al., 2002). *In vitro* experiments demonstrate that more TGase catalyzed aggregates form, when shorter htt constructs, containing 135 or fewer amino acids are used than when the full-length htt constructs are employed. This dependence on the length of the htt construct is particularly evident, when the polyglutamine domain of htt exceeds the pathologic

threshold of polyQ36. In addition, TGase itself was found to be associated with these htt aggregates *in vitro* (Karpuj et al., 1999). Moreover, additional biochemical support for TGase mediated aggregates comes from the laboratory of Professor Howard Green. Green and colleagues showed recently that mutated htt polymers are resistant to denaturation by formic acid, which further suggests the participation of covalent bonds (Iuchi et al., 2003).

### **TGase activity is elevated in NDS in brain**

Besides these *in vitro* experiments, there are *in vivo* results that further indicate a role for TGase in NDS. Immunohistochemistry revealed the co-localization of TGase with amyloid plaques and neurofibrillary tangles in the brains of AD patients (Gilad and Varon, 1985; Miller and Anderton, 1986; Appelt and Balin, 1996; Johnson et al., 1997; Kim et al., 1999; Lesort et al., 1999). In addition to the physical proximity of TGase to aggregated proteins, there is evidence for a link between aggregate formation and TGase activity. For example aggregate formation of alpha-synuclein inclusions in cells is augmented by a calcium ionophore, and prevented by a TGase inhibitor (Junn et al., 2003). Similar findings were reported for htt by Igarashi and coworkers in 1998.

Furthermore, TGase was found to be co-localized with alpha-synuclein in the halo of Lewy bodies, in postmortem brain tissue of PD patients (Junn et al., 2003). TGase activity is elevated in the affected areas of AD brains, compared to controls [reference]. This is in agreement with the fact that there are more  $\epsilon(\gamma\text{-glutamyl})\text{lysine}$  linkages in insoluble proteins in AD brain tissue. Moreover, elevation of two different TGase isoforms-TGase 1 and 2 expression was evident in AD (Kim et al., 1999). TGase activity was also increased in brains and cerebrospinal fluid of HD patients (Karpuj et al., 1999; Lesort et al., 1999; Jeitner et al., 2001), and TGase is found in htt aggregates *in vivo* (Zainelli et al., 2003). Whether this increased activity of TGase modulates the progress of the disease, or is a result of the disease progression itself is still an enigma.

### **Inhibition or ablation of TGase activity prolongs survival of NDS in mouse models**

Interference with TGase, either by gene-targeted deletion of TGase, or competitive inhibition of its substrate, prolongs the lifespan in various animal models of HD (Karpuj et al., 2002a; Dedeoglu et al., 2002; Mastroberardino et al., 2002). It is important to note that these maneuvers, effectively impairing TGase activity to some degree, were

not able to completely reverse HD-like pathology in animal models of HD. It should be noted, however, that for these fatal models of HD, any prolongation in survival is significant. Moreover, the animal models for HD are an extreme model of the disease, with the poly Q domains exceeding those found in juvenile onset HD, thus possibly setting a higher barrier for any successful therapeutic approach. Therefore, clinical trials in humans, using approaches that interfere with TGase activity might have more favorable results, compared to the stringent animal models. Similar studies with PD and AD animal models should be conducted in order to assess the general effect on prolongation of survival due to reduction of TGase activity in NDS involving aggregate formation.

### **Is prolongation of survival after interference with TGase associated with reduction in aggregate formation?**

As for other NDS that are associated with aggregate formation, it remains unclear whether aggregates are involved in HD pathogenesis, or whether they may have a protective function by sequestering aggregated htt (Ordway et al., 1997; Saudou et al., 1998; Yamamoto et al., 2000; Orr and Zoghbi, 2000; Chen et al., 1996). Three different papers address this question in HD animal models (Karpuj et al., 2002b; Dedeoglu et al., 2002; Mastroberardino et al., 2002). While it is clear from all these studies that inhibition of TGase activity prolongs NDS survival, their conclusions are controversial with respect to its effect on aggregate formation. In our own work (Karpuj et al., 2002a, b), no effect on the number or size of aggregates was observed, when cystamine is used to compete for the TGase substrate. In contrast, Dedeoglu and colleagues demonstrate a reduced number of aggregates using the same TGase inhibitor. These contrasting results might be explained by the fact that Dedeoglu et al. started the treatment prenatally, via oral feeding of the pregnant mothers, or at 21 days (i.p.), while Karpuj et al. started at 7 weeks of age (i.p.). This might have important implications for the timing of therapeutic trials directed at reducing TGase activity. As in most degenerative conditions, more robust results might be expected when earlier intervention is instituted. The fact that survival can be prolonged even when treatment is started at 7 weeks, a time when disease is manifest, indicates that impairment of TGase activity is a formidable and encouraging strategy.

The study by Mastroberardino et al. (2002) demonstrated that targeted disruption of the TGase gene in HD transgenic mice increased the number of aggregates. The

R6/1 mice used in their model of HD, obtained from Jackson Laboratories, has a longer incubation time for disease, than the R6/2 mice used by Karpuj et al. and Deodoglu et al. In contrast to their studies with cystamine where survival was prolonged by about 20%, deletion of TGase prolonged the life span in 12%. It is possible that aggregate formation may proceed along different pathways in mice where the gene for TGase is deleted. Perutz and we have argued that aggregate formation might be due in part to TGase induced cross-links, as well as to hydrogen bonded beta sheets (Karpuj et al., 1999; Perutz, 1999; Karpuj et al., 2002b). The two processes need not be mutually exclusive.

In summary, while inhibition of TGase activity appears clearly associated with prolonged survival in all mouse models of HD, there is no clear association of this effect with effects on aggregate formation. This suggests that the reduced life-span in these animals is not related to aggregate formation, and that the effect of TGase inhibition is probably mediated through alternative pathways, not involved in aggregate formation.

#### **Alternative mechanisms for prolonged survival by interference with TGase activity**

Evidence for alternative pathways that are involved in the prolongation of survival following competition for TGase substrate, was described in our studies with cystamine. Using DNA microarrays, mice treated with cystamine showed elevated transcription of neuro-protective genes, including DnaJ and osteopontin (Karpuj et al., 2002b). Inhibition of TGase activity also alters the level or location of other essential proteins in neurons that serve as a substrate for TGase. For example glyceraldehyde 3-phosphate dehydrogenase and the alpha-ketoglutarate dehydrogenase complex are both inactivated by TGase 2 in the presence of glutamine donors (Cooper et al., 1997a; Gentile et al., 1998). Alterations in these metabolites can modulate cerebral energy metabolism (Gibson et al., 2000). Yet, another possibility is that the elevation of TGase activity influences other critical and potentially pathogenic pathways. Such pathways regulated in part by TGase activity involve apoptosis, and signal transduction (Huo et al., 2003; Nakaoka et al., 1994).

#### **Future goals**

Interference with TGase prolongs the survival of several NDS raising several interesting points, worthy of future attention:

Several experiments indicate, in cell culture and in *in vivo* models (Junn et al., 2003; Igarashi et al., 1998; Dedeoglu et al., 2002), that TGase inhibitors down-regulate protein aggregation in NDS. It is important to note that these inhibitors might also have an effect on the down-regulation of caspase-another key enzyme involved in NDS (Ientile et al., 2003; Sanchez Mejia and Friedlander, 2001). It would be interesting to use RNAi or other techniques to inhibit the expression of TGase or specific caspases. Down-regulation of each of them separately in neuronal cell cultures or in primary cultures might reveal contrasting effects of each of these two enzymes on neurodegeneration. The confluence of these two enzymatic pathways, TGase and caspase, might become apparent, since caspase cleaves Htt into the truncated isoform that is present in aggregates of HD patients (Kim et al., 2001). These capase cleaved fragments of htt, might serve a better substrate for TGase.

Since neurodegeneration occurs mainly in brain cells and progresses as we age, it would be interesting to compare TGase activity in mouse CNS neurons to neurons in the periphery at various ages. It would be exciting to generate different transgenic mice which express TGase in a tissue specific manner and cross these mice with the various mouse models for NDS. This could shed more light on the direct effect of TGase on NDS *in vivo*. Similarly it would be useful to use conditional knock in and knock out mice to see whether delayed changes in TGase activity might modulate disease. Thus temporal and spatial control of TGase activity in various models of NDS will provide important insights into the role of this critical enzyme in these devastating diseases. It would be interesting as well to test the role of TGase in other trinucleotide repeat diseases where glutamine expansions play a pathogenic role.

As previously mentioned, there are protein aggregates which are associated with a specific NDS, but in each disease these aggregates contain a mixture of various proteins. In HD it is evident that the polyglutamine repeats in the htt protein serve as one of the substrates for TGase. Since TGase crosslinks Lysines and Glutamines, it is still open where the Lysine donor comes from. Might it be essential, to have another protein, as the lysine donor, associated with htt that initiates the cascade of aggregation (an intermolecular cross-linking)? Or is it sufficient to have htt aggregates (cross-linked with intramolecular or intermolecular bonds)? Are other proteins in these aggregates simply 'chaperones' in aggregation process? This would favor the observation that chaperone molecules and ubiquitinated proteins are associated with aggregates in these diseases.

A good way to explore for which proteins are present in the aggregates would be to use labeled TGase inhibitors.

For example if one uses an amine donor peptide with biotin (Fig. 1b R = Biotin) then immunoprecipitation of the crosslinked product with avidin would presumably fish out the putative interacting proteins which might be involved in these aggregates. It would be interesting to perform this experiment in an inducible cell line and add the inhibitors before and after the induction of the aggregates in the presence or absence of TGase, and to compare at the same time the size of aggregates.

It is intriguing that the targeted gene disruption of three major proteins involved in neurodegenerative diseases, htt, alpha-synuclein, and amyloid precursor protein (APP, which is the precursor of A $\beta$ ) does not result in death. That might indicate that the loss of these proteins to cellular metabolism, when they aggregate, is *not* causing neurodegeneration. On the other hand these proteins, htt, alpha synuclein and APP, may serve as seeding material to other proteins that are essential to the cell milieu and which might be recruited by TGase into these aggregates. One such protein is the transcriptional corepressor C-terminal binding protein (Kegel et al., 2002). Finding other interacting proteins present in these aggregates might be important. Once the proteins that comprise aggregates are identified, it would be productive to explore whether over and underexpressing this protein might rescue a neuron from degeneration.

The therapeutic potential of TGase modulation must be explored. The ubiquity of TGase catalyzed reactions in physiological processes such as blood coagulation, make the development of specific inhibitors a high priority. But other wide ranging enzyme systems like cyclooxygenases, metalloproteases and HMG coA reductase can be inhibited with beneficial results in the clinic.

If TGase is indeed involved directly in the process of neurodegeneration it would be interesting to understand how it contributes to the specificity of each neurodegenerative conditions. For example neurodegeneration in AD, PD and HD involve very different regions of brain with very different clinical pictures. Different isoforms of TGase or specific cofactors of TGase in these selective areas might explain this phenomenon. Understanding the role of TGase in the pathogenesis of neurodegeneration will undoubtedly teach us a great deal about pathogenesis, and may help in the design of therapies for these devastating conditions.

## Acknowledgements

This work was supported in part by grants from the NIH, from the Hereditary Disease Foundations, and from the Human Frontiers Program.

The authors would like to thank Dr. Christian Essrich for his constructive comments and insights in the preparation of this review.

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