Mini Review

Development of new anti-TNF therapy

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We have generated the first TNFR1-selective antagonistic TNF mutant based on structural human TNF variants using our phage display technology. This TNF mutant did not activate TNFR1-mediated responses, although its affinity for TNFR1 was equivalent to human wild-type TNF (wtTNF). The TNF mutant neutralized wtTNF-induced TNFR1-mediated bioactivity without influencing TNFR2-mediated bioactivity. In hepatitis mouse models, the antagonistic TNF mutant significantly blocked liver injury caused by inflammation. These results indicate that antagonistic TNF mutants may be clinically useful for anti-TNF therapy and that phage display libraries of protein ligands can be used to select for receptor subtype-selective antagonists.

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Inflammation is induced by physiological and chemical stimulation and is known to be mediated by the association of many biological factors. Inflammation-mediating proteins, typified by cytokines and chemokines, act in the host defense system by stimulating lymphocytes, macrophages, and endothelial cells to heal external injuries¹). When a productive balance of these mediators collapses, inflammatory exacerbation occurs. Longterm over-expression of cytokines causes autoimmune disease²). Thus, development of therapeutic techniques to remedy the imbalance of cytokine production is necessary.

Tumor necrosis factor- α (TNF) is a major inflammatory cytokine and has a central role in host defense and inflammation³⁾. To exert its biological function, TNF binds to two receptor sub-types, TNFR1 and TNFR2, which form homotrimers by preassembling on the cell surface⁴⁾. Deregulation of TNF pro-

duction promotes TNF-dependent pathologies and correlates with the severity and progression of inflammatory diseases such as rheumatoid arthritis (RA)⁵), inflammatory bowel disease⁶), septic shock⁷) and hepatitis⁸). TNF blocking agents (monoclonal antibodies or soluble receptors) have shown significant clinical efficacy in certain inflammatory diseases. The major impact of TNF blocking agents on the immunological system, however, raises some concerns about the safety of this approach, especially with regard to severe infections⁹), malignancies¹⁰) and immune-mediated diseases¹¹). For example, in rheumatoid arthritis and Crohn's disease, studies indicated a higher incidence of tuberculosis reactivation¹²) and the induction of demyelination¹³.

Although the distinction between the role of TNFR1 and TNFR2 on the immune system remains unclear, TNF secreted from activated immune cells in these diseases predominantly

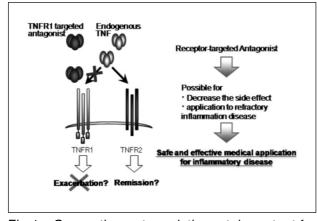


Fig.1 Generation antagonistic protein mutant for receptor targeting

Da phage-display vector has which express the foreign DNA as a fusion protein Phage Library ©Armino acid sequence of expressed rotein is easily obtained by determining the corresponding coding sequence in cDNA oene: Phagemic phagemid DNA vector ③Preparation of cDNA library permit to create a huge diversity of protein library promptly purification can be used to phage displaying receptor @affinity capture binding peptides from a large phage library displaying many different peptide structures

Fig.2 Benefit for engineering protein library using phage display system

activates TNFR1 and accelerates inflammation. In addition, previous studies using animal models of diseases such as arthritis¹⁴⁾ and hepatitis¹⁵⁾ indicated that mainly TNFR1 caused development and exacerbation of inflammation. Moreover, given that in mice lacking the TNFR1 the clinical course of EAE is suppressed both at the pro-inflammatory and the autoimmune phases, the TNFR1 is clearly indicated as an important target for therapy¹⁶⁾. From this perspective, blocking TNFR1 signal transduction may emerge as a powerful and effective therapy for certain inflammatory diseases (Fig.1).

To develop receptor-selective protein ligands, several studies have described useful mutant proteins created by the substitution of amino acids using a site-directed mutagenesis method, as typified by Kunkel's method^{17,18)}. It is difficult, however, to obtain an exhaustive and functional panel of protein mutants using this mutagenesis method. Alternatively, the phage display system is a powerful in vitro technique that enables polypeptides with desired properties to be selected from a large collection of variants encoded by cDNAs in phagemid vectors (Fig.2). Filamentous phage display of peptide or protein variants has been widely used for rapid selection of protein variants that bind with improved affinity and specificity to target molecules¹⁹. The key feature of such selection schemes is that the genotype of a particular variant packaged inside a virion particle is linked to the phenotype of a displayed protein or peptide that has been fused to phage coat proteins, i.e., the gene III protein. Phage particles can be selected by binding to an affinity matrix propagated in E. coli and identified by DNA sequencing. These procedures allow phage libraries to be subjected to a selection step, called "affinity panning". Recovered clones are identified by sequencing and re-grown for further rounds of selection.

Using the phage display system, we previously isolated a lysine-deficient TNF mutant from a protein library in which all six lysine residues in the TNF molecule, including the receptorbinding site, were simultaneously replaced with other amino acids^{19,20)}. This strategy created novel mutant TNFs that exhibited only a slightly different mode of receptor-binding. In the present study, we used the phage display system to isolate novel TNFR1-selective antagonistic TNF mutants that efficiently inhibited a wide variety of TNFR1 mediated effects *in vitro* and *in vivo* without affecting TNFR2-mediated bioactivity.

The selection of amino acids to be altered was based on data from a point mutation study and a TNF structure-function study. Residues (amino acids 89-94) that were shown to contribute to TNFR binding were mapped onto the three-dimensional structure of human TNF. Then, these and other nearby residues were selected for randomization to generate phage libraries (Fig.3). Randomization of each of these residues was performed by PCR with mutated primers in which an NNS codon was incorporated at each randomized position. Each library contained a total of six randomized residues.

To select TNF mutants from phage library that bound strongly to human TNFR1, the mutant TNF phage library was panned against human TNFR1. As a result, we identified ten candidates as TNFR1-selective antagonists and selected the most suitable mutant that possessed the strongest antagonistic activity. To investigate the properties of this antagonistic clone, we examined the binding kinetics and binding specificities of this mutant for TNFR1 and TNFR2 using BIAcore and ELISA techniques, respectively. The antagonistic TNF mutant had an affinity for

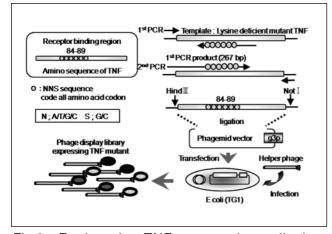


Fig.3 Engineering TNF mutant phage display library

TNFR1 equivalent to wtTNF, but almost no affinity for TNFR2. We also measured the bioactivity of the TNF mutant via TNFRmediating response assays. The antagonistic TNF mutant bound to TNFR1 but did not transmit the death signal. To determine the ability of the TNF mutant to compete with wtTNF, we measured TNFR1-selective responses in the presence of both wtTNF and TNF mutant. The antagonistic TNF mutant inhibited wtTNFinduced cytotoxicity (Fig.4), caspase activation, and NF- κ B activation through TNFR1 in a dose-dependent manner. These results suggest that the antagonistic TNF mutant is a competitive antagonist, inhibiting TNFR1-mediated pathways.

For the therapy of autoimmune disease, TNF blockades (etarnercept, as p75-IgG Fc fusion protein and lenercept as p55-IgG Fc fusion protein) have been developed. However, differences exist in the mechanisms of action of these agents that might confer risks of infection and immunogenisity. There are some reports that tuberculosis disease is a potential adverse reaction from treatment with etanercept. Moreover, antibody formation against lenercept was a significant problem which resulted in significant reduction of the half-life of the receptor. Thus, much is expected from the development of TNF receptor-selective agents that inhibit disease-causing TNF bioactivity without interfering host defense system against infection and antibody formation. In the present report, we generated a receptor-selective antagonistic TNF mutant through the use of phage display. However, there is a possibility of expressing the new function, which binds to another receptor like as TNF receptor superfamily. Therefore, the reasons of showing agonistic or antagonistic activity should be examined via structural analysis of binding sites. We are now analyzing the crystal structures of the complex formed

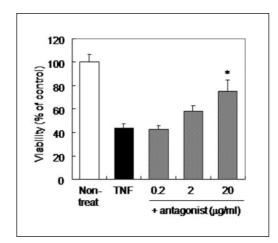


Fig.4 Inhibitory effect of antagonistic mutant TNF on TNF-induced cytotoxicity

Mouse fibrosarcoma L-M cells were treated with wild-type TNF (10 ng/ml). and serial diluted mutant TNF. After 48 hr incubation, ratio of cell death were determined by methylene blue assay.

between the antagonistic TNF mutant and TNFR1 so as to better understand the mechanisms of receptor subtype-selectivity.

While the functions of TNF and its receptors are unclear, their signaling specificities are being examined in many TNF-related studies. In this review, we studied mutant TNF antagonist that bound selectively to TNFR1. The findings from our TNFR1 and TNFR2 study are applicable to the receptors in the TNFR superfamily that do not contain a cytoplasmic death domain. However, we also have produced TNF agonist that binds to TNFR1 and TNFR2. These selective agonists and antagonists are not only therapeutically useful, but also are effective analytical tools for elucidating TNF receptor function. Further functional studies of TNF receptors could uncover interesting receptor biology and may yield additional targets for immunotherapy.

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