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The 8<sup>th</sup> Meeting of the Immunology of Diabetes Society (IDS-8)

Program & Abstracts



Vol.52 Suppl. October 2005

PUBLISHED BIMONTHLY BY The JAPAN ENDOCRINE SOCIETY

http://square.umin.ac.jp/endocrine

## A POSSIBLE IMPLICATION OF SOLUBLE CTLA-4 IN TYPE 1 DIABETES

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Background/Rational: Type 1 diabetes is a polygenic organ-specific autoimmune disease caused by the destruction of insulin-producing  $\beta$ -cells in the pancreas. Genetic linkage and association studies have suggested CTLA4 as a candidate gene for the diabetes susceptibility locus IDDM12. Although the genetic association has been confirmed several times, a biological defect of CTLA-4 expression and/or function in T1D patients has not been demonstrated to date. CTLA-4 is a surface receptor expressed on T cells upon activation and which is constitutively expressed on regulatory T cells. While CTLA-4 is a negative regulator of T cell reactivity, the role of this molecule in the function of regulatory T cells is still elusive. Alternative mRNA spliced form of CTLA4, coding for a shorter soluble protein (ligand-binding) (sCTLA-4) but lacking the trans-membrane domain, exist in human, mouse and rat and it has been shown to be decreased in individuals carrying the disease-associated haplotype of CTLA4. Higher levels of sCTLA4 have been previously demonstrated in other autoimmune diseases like thyroiditis and LES as well as in asthma.

Aim: The aim of this pilot study was to investigate serum levels of sCTLA-4 in patients affected by T1D (n=14) compared with healthy individuals (n=22) and patients with thyroiditis (ATD) (n=24).

Methods: Serum sCTLA-4 levels were measured using a commercially available ELISA kit following the manufacturer recommendations.

Results: Surprisingly, we found higher levels of serum sCTLA-4 in T1D patients compared to healthy controls, (mean 1,84 $\pm$ 1,14  $\,$  ng/ml vs. 0,16 $\pm$  0,84 ng/ml, respectively. p=0,005) and we confirmed the increased levels in ATD.

Conclusions: These preliminary results reinforce a possible role for CTLA-4 in T1D and ATD. We speculate that the sCTLA-4 binding to B7 surface receptors on dendritic cells may interfere with inhibition of pathogenic self-reactive T cells or with the suppressive function of regulatory cells. Larger studies using high throughput technology and correlation with susceptibility CTLA4 genotypes together with functional studies are underway to clarify the biological significance of these results.