MAYO CLINIC
Mayo Medical Laboratories

1-800-533-1710

TACIF

Transmembrane Activator and CAML Interactor (TACI) Gene, Full Gene Analysis

Patient ID	Patient Name		Birth Date	Gender	Age
SA00055096	SAMPLEREPORT, TACIF		1966-06-10	F	46
Order Number	**Client Order Number**	**Ordering Physician**	**Report Notes**		
SA00055096	SA00055096	UNKNOWN, PROVIDER			
Account Information		**Collected**			
C7028846 DLMP Rochester		15 Mar 2013 03:39			

TACI, Full Gene Sequence

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Reason for Referral

MCR

CVID, splenomegaly, autoimmune thrombocytopenia with no family history.

Method

MCR

Fluorescent DNA sequence analysis was used to test for the presence of mutations in the 5 exons, exon-intron boundaries, and the 5' and 3' UTR of the TACI gene.

Result

MCR

This individual was shown to have one copy of the following mutation in the TACI gene: g. 24216, c.310T>TC, p.C104R in exon 3 of the TNFRSF13B (TACI) gene.

Interpretation

MCR

This mutation is one of the most common TACI mutations reported in CVID patients. The mutation is within the extracellular (EC) domain of the TACI receptor in the second cysteine-rich domain (CRD). This residue is highly conserved and reported studies indicate that this mutation - C104R abolishes binding of the ligands -BAFF and APRIL to the TACI receptor. B cells from these patients have been shown to be unable to produce immunoglobulins in response to APRIL (ligand) stimulation. Further, the heterozygous C104R mutation has been shown to have a dominant-negative effect (Garibyan et al, JCI, 2007). The reported CVID phenotype of the patient matches what has been described to be associated with TACI mutations (splenoemgaly, AITP). Recommend evaluation of B cell immunophenotyping analysis (test number 88800) to assist in classification of the CVID phenotype. Additional literature references for TACI mutations in CVID can be provided on request.

TACI mutations have been reported to account for 8–15% of CVID cases depending on the study population assessed. The majority of TACI mutations are sporadic though some familial mutations (autosomal dominant and autosomal recessive) have been reported. Present evidence seems to suggest that homozygous TACI mutations are associated with CVID and/or selective IgA deficiency, while the clinical significance of heterozygous mutations remains controversial, though these have also been reported in some CVID and IgA-deficient patients. It is possible that TACI may be a disease-associated gene rather than a disease-causing gene. The underlying genetic defect or molecular basis has not been identified in the majority (75–80%) of CVID patients. It may be reasonable to regard most cases of CVID as oligogenic, i.e., the phenotype results from the contribution of more than a single gene defect.

ADDITIONAL INFORMATION

Laboratory developed test.

Reviewed By

MCR

Yvonne Philo

TACI Gene Sequencing

MCR

Performed

Received: 15 Mar 2013 03:39 **Reported:** 13 Jun 2013 12:48

Performing Site Legend

Code	Laboratory	Address
MCR	Mayo Clinic Dept. of Lab Med and Pathology	200 First Street SW, Rochester, MN 55905