

# Tight Linkage between the Syndrome of Generalized Thyroid Hormone Resistance and the Human c-erbA $\beta$ Gene

S. J. Usala, A. E. Bale, N. Gesundheit, C. Weinberger, R. W. Lash, F. E. Wondisford, O. W. McBride, and B. D. Weintraub

National Institute of Diabetes and Digestive and Kidney Diseases  
(S.J.U., N.G., R.W.L., F.E.W., B.D.W.)  
National Cancer Institute (A.E.B., O.W.M.)  
National Institute of Mental Health (C.W.)  
National Institutes of Health  
Bethesda, Maryland 20892

**Multiple cDNAs belonging to the c-erbA gene family encode proteins that bind T<sub>3</sub> with high affinity. However, the biological functions of these multiple thyroid hormone receptors have not yet been clarified. Generalized thyroid hormone resistance (GTHR) refers to a human syndrome characterized by tissue refractoriness to the action of thyroid hormones; several studies have suggested quantitative or qualitative defects in T<sub>3</sub> binding to nuclear receptors in certain kindreds. To investigate the biological functions of the c-erbA genes, c-erbA $\alpha$  and c-erbA $\beta$ , we tested the hypothesis that an abnormal c-erbA gene product is present in GTHR by examining these genes in members of one kindred. Restriction enzyme analysis failed to identify an abnormal pattern in affected individuals suggesting no rearrangements or large deletions. However, we demonstrated that the gene conferring the GTHR phenotype is tightly linked to the c-erbA $\beta$  locus on chromosome 3. This linkage strongly suggests that the c-erbA $\beta$  gene is important in man as a thyroid hormone receptor and identifies a putative c-erbA $\beta$  mutant phenotype with central nervous system, pituitary, liver, metabolic, and growth abnormalities. (Molecular Endocrinology 2: 1217–1220, 1988)**

## INTRODUCTION

Thyroid hormone action is mediated through the binding of hormone-nuclear receptor complexes to promoter regions of specific genes (1). Recently, two distinct c-erbA cDNAs, isolated from human placental and chicken embryonal libraries, were shown in *in vitro* translation studies to code for proteins that bound T<sub>3</sub>

with high affinity and with the specificity expected for a nuclear T<sub>3</sub> receptor (2, 3). The corresponding genes, c-erbA $\beta$  and c-erbA $\alpha$ , have been localized to chromosome 3p21-25 (4) and chromosome 17q11.2-21 (5), respectively. Subsequently, a c-erbA cDNA, type  $\alpha$ 1, was isolated from a rat brain library and found to be highly homologous to the chicken c-erbA $\alpha$  (6). A second c-erbA $\alpha$  cDNA, type  $\alpha$ 2, was cloned from human testis (7) and kidney (8) libraries, mapped to chromosome 17 (8), and may result from alternative splicing of the same c-erbA $\alpha$  gene (8). However, the particular biological functions of these multiple thyroid hormone receptors have not yet been established. Multiply-sized c-erbA $\beta$  and c-erbA $\alpha$  mRNAs have been reported in several tissues and cell lines, and their relative abundance in various tissues has not been clearly elucidated (2, 6–9). Moreover, one recent study showing differences in antibody recognition of *in vivo* T<sub>3</sub> nuclear receptors and *in vitro* translated products of human c-erbA $\beta$  suggested that the c-erbA $\beta$  protein may not function as an *in vivo* nuclear T<sub>3</sub> receptor (10). Controversy exists, therefore, as to which, if any, of these c-erbA proteins function as physiological thyroid hormone receptors.

Generalized thyroid hormone resistance (GTHR) refers to a syndrome characterized by elevated circulating levels of free thyroid hormones, resistance to thyroid hormone action, and inappropriately normal or elevated levels of thyroid-stimulating hormone (11, 12). Although in the first reported cases the mode of transmission was unclear (13), it now appears that in the majority of cases the syndrome segregates as an autosomal dominant disorder (12). In a less common variant of this syndrome, selective pituitary thyroid hormone resistance, the pituitary gland is more refractory than peripheral tissues to thyroid hormones, and hyperthyroidism results from impaired feedback on TSH secretion (14); an autosomal dominant inheritance pattern has been observed in one kindred (15). The molecular basis for these disorders is heterogeneous and in some patients

probably secondary to receptor abnormalities (16). Defects in nuclear receptor number or affinity as well as impaired nuclear uptake of T<sub>3</sub> have been demonstrated in certain cases (17, 18).

In order to explore more fully the biological functions of the c-erbA $\alpha$  and c-erbA $\beta$  genes we have studied their role in a kindred with generalized thyroid hormone resistance where defective thyroid hormone action is known. It was postulated that if a c-erbA gene product is a functional thyroid hormone receptor, then a relationship might exist between the gene and the GTHR syndrome. We used the candidate gene approach (19) and show that restriction fragment length polymorphisms (RFLPs) of the c-erbA $\beta$  gene are tightly linked to the gene for the clinical phenotype of GTHR.

## RESULTS AND DISCUSSION

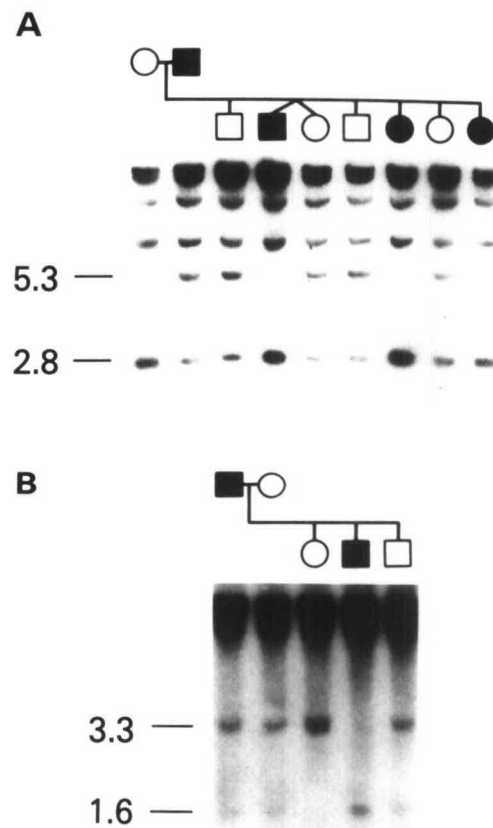
We examined the c-erbA $\beta$  and c-erbA $\alpha$  genes in kindred A (12) with GTHR where a significant decrease in T<sub>3</sub>-binding affinity of salt-extracted fibroblast nuclear receptors was demonstrated in an affected member compared to that in normal subjects ( $0.9 \times 10^{10} \text{ M}^{-1}$  compared to normal range of  $2.5\text{--}8.0 \times 10^{10}$ , Weintraub, B. D., *et al.*, manuscript submitted). Restriction analysis with *Bgl*I, *Bgl*II, *Eco*RI, *Bam*HI, *Pst*I, *Hinf*I, and *Eco*RV, using the human c-erbA $\beta$  cDNA probe (*Materials and Methods*), and *Hind*III, *Eco*RI, and *Pst*I, using a full-length human c-erbA $\alpha$ 1 cDNA probe (Weinberger, C., unpublished data), failed to identify any abnormal bands on Southern blots. This indicated there were no detectable chromosomal rearrangements or large deletions in these c-erbA genes in this kindred (data not shown).

As an alternative method of establishing a relationship between the c-erbA genes and the GTHR trait we performed linkage analysis. Because there existed *in vitro* evidence for a c-erbA $\beta$  receptor DNA binding site which mediated thyroid hormone action (20) we first studied linkage between GTHR and c-erbA $\beta$ . Seventeen family members of kindred A were typed for polymorphisms of the c-erbA $\beta$  gene detected with *Bam*HI and *Eco*RV [Table 1; (21)]. Both RFLPs cosegregated with the GTHR trait (Fig. 1), and sixteen members were informative when haplotyped using the combination of the two RFLPs (fig. 2). Linkage analysis was performed using the program LIPED (22), with the assumptions of complete penetrance, a gene frequency of  $10^{-5}$ , and

**Table 1.** Haplotype Frequencies for RFLPs at the c-erbA $\beta$  Locus

Haplotype	<i>Bam</i> HI Fragment (Kb)	<i>Eco</i> RV Fragment (Kb)	Frequency (n = 68)
A	5.3	1.6	0.26
B	2.8	3.3	0.21
C	2.8	1.6	0.53
D	5.3	3.3	Not observed

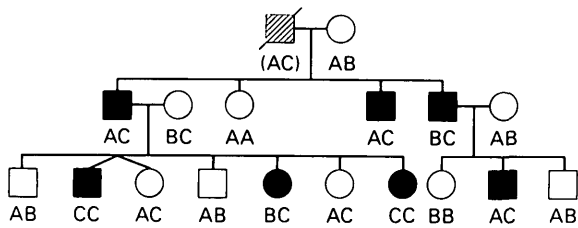
Kb, Kilobase.



**Fig. 1.** Segregation of *Bam*HI and *Eco*RV RFLPs with GTHR in Families from Kindred A

A, Segregation of the *Bam*HI RFLP with GTHR in a nuclear family of kindred A. Affected members are indicated with *solid symbols*. *Squares* represent males; *circles* represent females. The *Bam*HI RFLP consists of a band at 5.3 kilobases or 2.8 kilobases. Note that in the affected father one c-erbA $\beta$  allele is marked by a 5.3 kilobase *Bam*HI band (RFLP) and one c-erbA $\beta$  allele is marked by a 2.8 kilobase *Bam*HI band (RFLP), whereas in the mother both c-erbA $\beta$  alleles are marked by the 2.8 kilobase *Bam*HI band. All the children are informative in that paternal c-erbA $\beta$  alleles, using *Bam*HI RFLPs, can be identified. All unaffected children carry the father's 5.3 kilobase *Bam*HI RFLP and all affected children carry his 2.8 kilobase *Bam*HI RFLP. The father's c-erbA $\beta$  allele marked by the 2.8 kilobase *Bam*HI RFLP segregates with GTHR in this nuclear family. Constant bands occur at 23, 21, 13, and 7.0 kilobases. B, Segregation of the *Eco*RV RFLP with GTHR in a portion of kindred A. The *Eco*RV RFLP consists of a band at 3.3 or 1.6 kilobases. Note the affected father's c-erbA $\beta$  allele marked by the 1.6 kilobase *Eco*RV band segregates with GTHR and the 3.3 kilobase *Eco*RV RFLP segregates with the normal phenotype. The child in lane 5 is not informative since it is uncertain which paternal RFLP he received. Constant bands appear at 15 and 8.9 kilobases. An additional polymorphism with a band at 13.5 kb or 10.5 kb was uninformative in kindred A. The segregation of the *Bam*HI or *Eco*RV RFLPs with GTHR in the other members of kindred A that were haplotyped can be followed in Fig. 2.

equal male and female recombination rates. Table 2 shows the maximum lod score (logarithm of the odds) between the GTHR and c-erbA $\beta$  loci was 3.91 at a recombination fraction of 0 (absolute linkage). This



**Fig. 2.** Haplotyping of kindred A using the *Bam*HI and *Eco*RV restriction fragment length polymorphisms at the c-erbA $\beta$  locus

All individuals were screened for thyroid hormone resistance by measurement of serum T<sub>4</sub>, free T<sub>4</sub>, T<sub>3</sub>, TSH, and free  $\alpha$ -subunit, and through metabolic testing (12). The first generation affected male was identified by history. The daughter in lane 8, Fig. 1A, was erroneously assigned as affected in Ref. 12 because of limited data showing borderline elevated serum T<sub>4</sub> and T<sub>3</sub>. She was reclassified as unaffected before this study based on several additional studies showing normal thyroid hormone and metabolic parameters.

**Table 2.** Pairwise LOD Scores for Linkage between GTHR and c-erbA $\beta$

	Recombination Fraction				
	0.0	0.1	0.2	0.3	0.4
Kindred A	3.91	3.27	2.59	1.76	0.89

score means there is an approximately 1/10,000 probability of the segregation we observed occurring through chance. A lod score of 3.0 or greater is accepted as significant evidence for linkage (23). These data indicate that the gene for GTHR is located close to or is identical with c-erbA $\beta$  on chromosome 3. Although this type of study lacks the resolution necessary to prove identity between the GTHR gene and c-erbA $\beta$ , the close relationship between a gene that codes for a high affinity thyroid hormone binding protein and a syndrome with abnormal thyroid hormone action strongly suggests: 1) the c-erbA $\beta$  gene codes for a physiological thyroid hormone receptor; 2) the syndrome of GTHR in kindred A results from a mutation in the c-erbA $\beta$  gene.

A mutation in the c-erbA $\beta$  gene in kindred A appears to result in abnormalities of thyroid hormone action in many tissues (12). In addition to inappropriate secretion of TSH from the pituitary, affected members of kindred A demonstrated delayed bone age and short stature. Most also displayed mild mental retardation, diminished or inappropriately normal basal metabolic rates, and hepatic resistance to thyroid hormone (relatively low sex hormone binding globulin and relatively high cholesterol).

Thyroid hormone resistance is clinically heterogeneous, and the disorder in some kindreds may be caused by mutations in the c-erbA $\alpha$  gene. It will be interesting to examine whether the gene for selective pituitary resistance to thyroid hormones, in which defective thyroid hormone action is restricted to the pituitary (14), is linked to the c-erbA $\alpha$  gene, which is expressed in relatively high concentrations in the pituitary gland (6). In addition, since a single patient with GTHR

can show subtle variability in the degree of resistance from tissue to tissue (12), it is possible that there are tissue-specific distributions of different thyroid hormone receptors.

Work is in progress to clone and sequence the c-erbA $\beta$  genes of kindred A. It is possible that the putative c-erbA $\beta$  mutant allele is not expressed, and that the resistance to thyroid hormones results solely from a diminished number of c-erbA $\beta$  receptors. However, there is a 3- to 5-fold reduction in the T<sub>3</sub>-binding affinity of the mutant receptor from salt-extracted fibroblasts in kindred A, and the Scatchard plot appeared linear rather than curvilinear as expected for two markedly different affinity components (Weintraub, B. D., *et al.*, manuscript submitted). These observations may mean that the abnormal c-erbA $\beta$  gene is expressed and inhibits the function of the wild type gene product, thus acting as a dominant negative mutation (24). Studies with the estrogen receptor, another c-erbA related protein, have demonstrated that estradiol binding induces a homodimer that shows increased affinity for estradiol (25, 26). If a similar structure exists for the thyroid hormone receptor, the mutant c-erbA gene may produce an inhibitory subunit that in a heterodimer diminishes T<sub>3</sub>-binding affinity and impairs receptor activation. Further characterization of the kindred A mutant c-erbA $\beta$  gene should provide a novel way to study mechanisms of thyroid hormone action in man.

## MATERIALS AND METHODS

DNA was prepared from human leukocytes as follows: 10–20 ml blood were centrifuged at 400  $\times$  g for 5 min and the supernatant was gently removed. The cell pellet was resuspended in 5 vol lysis buffer (0.15 M ammonium chloride, 0.01 M potassium bicarbonate, and 0.1 mM EDTA) and incubated 10–15 min on ice until the solution appeared black. The lysate was centrifuged at 400  $\times$  g for 5 min, the supernatant was removed, and the pellet was resuspended in 20 ml lysis buffer. After 5 min on ice the suspension was centrifuged at 400  $\times$  g for 5 min and the supernatant was removed. The pellet was quickly resuspended in 2–4 ml 10 mM Tris, pH 7.4, 10 mM NaCl, 3 mM MgCl<sub>2</sub>, and an equal volume of 1% sodium dodecyl sulfate (SDS), 0.6 M NaCl, 20 mM Tris, pH 7.4, 10 mM EDTA, 400  $\mu$ g/ml proteinase K, was immediately added. This proteinase K digestion was incubated at room temperature overnight, and then extracted twice with phenol, twice with phenol-chloroform-isoamyl alcohol and twice with chloroform-isoamyl alcohol (24:1). High molecular weight DNA was then obtained by ethanol precipitation and dissolved over 3–4 days in TE at 4 C to a concentration of 0.5–1  $\mu$ g/ $\mu$ l.

DNA (4–6  $\mu$ g) was digested with either *Bam*HI or *Eco*RV at 37 C for 3 h and fractionated by electrophoresis on 0.8% agarose. Gels were soaked for 30 min in 0.4 M NaOH, 0.6 M NaCl and the DNA was transferred overnight to Gene-ScreenPlus (New England Nuclear, Boston, MA) using the solution in a capillary blot procedure (27). Blots were neutralized in 0.5 M Tris, pH 7, 1 M NaCl for 15 min. The c-erbA $\beta$  1.5 kb cDNA probe (phe A12, Ref. 2) was labeled by random priming (Pharmacia oligolabeling kit, Piscataway, NJ) to a specific activity of 1  $\times$  10<sup>9</sup> cpm/ $\mu$ g using 5000 Ci/mmol ( $\alpha$ -<sup>32</sup>P) dCTP (New England Nuclear) and hybridized to the blots overnight at a concentration of 1 ng/ml at 42 C in 50% formamide, 10% dextran sulfate, 1% SDS, and 1 M NaCl. The blots were washed twice in 2 $\times$  SSC (0.3 M sodium chloride,

0.03 M sodium citrate) for 5 min at 25 C, twice in 2× SSC with 1% SDS for 30 min at 65 C, and twice in 0.1× SSC for 30 min at 25 C.

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Address requests for reprints to: Stephen J. Usala, National Institutes of Health, Building 10, Room 8D14, Bethesda, Maryland 20892.

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