

## Chapter 04

# Modifying Others Originality without Quote is an Act of Piracy

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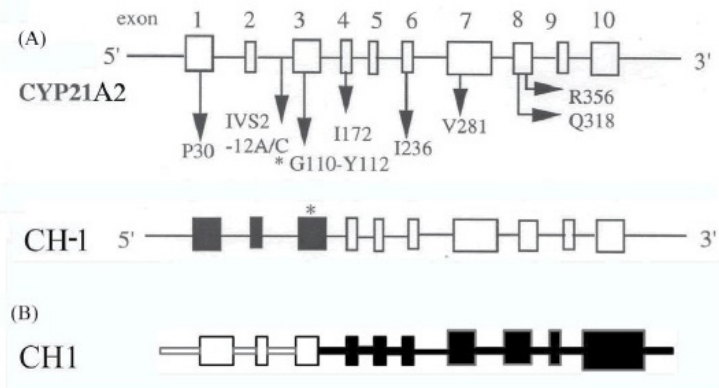
## Abstract

A defective *CYP21A2* gene downstream of the *TNXB* gene in congenital adrenal hyperplasia (CAH) falls into three categories: (a) small-scale conversions of *CYP21A1P*, (b) spontaneous mutations, and (c) chimeric RCCX modules that include the chimeric *CYP21A1P/CYP21A2* and *TNXA/TNXB* genes [1]. Most of the *CYP21A2* mutations identified so far were a result of small-scale conversions of the *CYP21A1P* (up to 11 for *CYP21A1P*) during both meiosis and mitosis [2], which account for about 70%-80% of all CAH cases. The Chimeric *CYP21A1P/CYP21A2* and *TNXA/TNXB* genes, which result from unequal cross-over (or deletions) during meiosis [2] and occur in ~20% of CAH alleles in most populations [1,3] respectively reflect the deletion of the *1/XCYP21A1P - XA - RP2 - C4B - 1/XCYP21A2* gene array (1/X indicates an uncertain fraction of the gene sequence) [1] and a deletion of the *RP2 - C4B - CYP21A2 - 1/XTXNB* gene array [1]. Their deletion range is about a 26- or 32-kb gene sequence which depends on whether C4B is the long or short gene (more commonly shown in the literature as being 30 kb). In fact, these different types of large-gene deletions in the RCCX region are generally considered to represent one event in many studies.

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I read with interest the recent article by New et al. [4], in which the authors described an analysis of 1,507 CAH families. They showed CYP21A2 gene deletion with 9 phenotypes of the chimeras, designating them CH1, CH2, CH3, CH4, CH5, CH6, CH7, CH8, and CH9 [4] in figure configuration (as attached Figure 1 in the context). However, by examining the figure, the word abbreviation of “CH” representing “Chimeric CYP21A1P/CYP21A2” was originally used by the Lee’s study [1,5-8]. Furthermore, there were more modifications of the figure configuration from Lee’s studies such as font including “CH-1” style (Lee’s study) (Figure 1A) having been changed into “CH1” (Figure 1B) and configuration of exons representation for the CYP21A1P and CYP21A2 genes as black boxes and white boxes respectively (in Lee’s study) (Figure 1A) having been modified into CYP21A1P and CYP21A2 genes as white boxes and black boxes respectively (Figure 1B). Moreover, the figure legend’s statement “To date, nine types of chimera (CH1-CH9) with different junction site have been identified” did not cite its origin from the paper published by Chen et al’s study [10]. Most seriously, I have found out that they did not do chimera study and there was no citation for these two references. Therefore, these point-out issues (Table 1) do not seem to be created or studied by the New et al’s group [4] and may have been perceived mistakenly as the New et al’s originality thereafter.



**Figure 1:** Diagram of the representation of the chimeric *CYP21A1P/CYP21A2* genes used by Lee and New et al. studies. (A) The structure of the functional *CYP21A2* gene containing ten exons indicated by a white box [1,5-9]. The solid arrows indicate mutations which exist in *CYP21A1P* which showed the black box. CH-1 represents a chimeric *CYP21A1P/CYP21A2s* as described in Lee studies [1,5-9]. 707-714delGAGACTAC in *CYP21A1P* is marked by an asterisk (\*). (B) The structure of the functional *CYP21A2* gene indicated by a black box and the white box represents a nonfunctional *CYP21A1P* gene in New et al. study [4].

**Table 1:** Study on chimeric *CYP21A1P/CYP21A2* gene in congenital adrenal hyperplasia.

Study	Publication	Designation for chimeric <i>CYP21A1P/CYP21A2</i>	Ref.
Lee HH*	+	CH-1 to CH-5	[1,5-9]
Chen et al.	+	CH-1 to CH-9	[5]
New et al.	-	CH1 to CH9	[4]

\*There were more than 10 articles related with chimeric *CYP21A1P/CYP21A2* gene study in the past 10 years.

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