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Letter to Editor
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Modifying Other's Originality without Quote is an Act of Piracy

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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/X***CYP21A1P - XA - RP2 - C4B* - **1/X***CYP21A2* gene array (1/X indicates an uncertain fraction of the gene sequence) [1] and a deletion of the *RP2 - C4B - CYP21A2* - **1/X***TXNB* 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.

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.

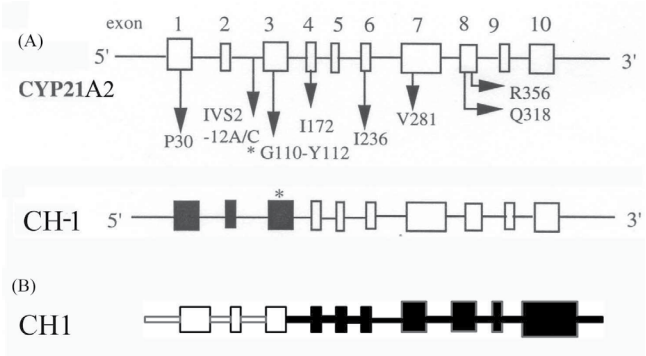

Figure 1: Diagram of the representation of the chimeric *CYP21A1P/CYP21A2* genes used by Lee and New et al. studies. (A) The structure of the functional *CYP21A2* gene containing ten exons indicated by a *white box* [1,5-9]. The *solid* arrows indicate mutations which exist in *CYP21A1P* which showed 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].

Study	Publication	Designation for chimeric *CYP21A1P/CYP21A2*	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.

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

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