On the basis of our findings, we propose a model in which the absence of a strong **Sp3** site within the context of the promoter, as in the **G allele**, could change the balance of the basic **transcription complex** toward enhanced transcription. (e.g., through altered **acetylation** or **phosphorylation**).

基於我們的發現，我們在缺乏牢固的**Sp3地點**的催化物脈絡提議一個模式, 就像在**G對偶基因**中，可以基於增大的副本改變基本複製綜合體的平衡。(例如：經由改變的**乙酰化作用**或**磷酸化作用)**

From an evolutionary perspective, sequence comparison with the **CTGF orthologues** of other species suggests that the C allele, the more prevalent allele in humans, has evolved recently.

從進化的觀點，其他品種的**CTGF同源基因**連串對照下暗示**C對偶基因**(普遍於人類品種的對偶基因)近來已逐步進化。

Although this finding requires confirmation through more extensive study, it implies that there is strong positive selection and the possibility of advantages for this **repressor site** in humans.

儘管這個發現需要更廣泛的研究來驗證，它暗示了在人類當中這個**壓抑物區**有很多有利的可能性和穩固且正面的淘汰。