Dear Editor,

We read the publication on “Cyclooxygenase-2 (COX-2) gene polymorphisms –765G>C and –1195A>G and mycosis fungoides risk” with a great interest. Sayed et al. [1] found that “The AA genotype in the COX-2 –1195A>G gene polymorphism and the GC genotype in the COX-2 –765G>C gene were significantly more frequent among MF patients compared to controls [1].” We would like to share ideas on this finding. The lack of specific genetic predominance, homozygous polymorphism, in the case of COX-2 –765G>C shows that there might be some additional genetic polymorphisms that might affect the final phenotypic expression, mycosis fungoides (MF) risk. The example of confounding genetic polymorphisms that might relate to MF risk include p53 Arg72Pro polymorphism [2]. In fact, the main pathogenesis process in either COX-2 –765G>C or –1195A>G is the single mutation in the molecule, and this change result in molecular weight change that further affects the final phenotypic expression. This is the same pathogenesis as described in other medical disorders such as Alzheimer’s disease [3].

Key Message
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References