**Materials and Methods**

This case-control study was approved by the Dermatology Research Ethics Committee, Faculty of Medicine, Cairo University. The patients and controls were consecutively recruited from the Dermatology Outpatient Clinic, Cairo University Hospital, and written informed consents were signed by participants before starting the study.

The study included 70 patients with various stages of mycosis fungoides (MF). Each patient was subjected to complete history taking and full clinical examination to detect the extent and type of MF. Diagnosing MF in our department depends mainly on constellation of clinical and histopathological features as described in the literature [12]. Immunohistochemical staining with anti-CD3, CD5, CD7, CD4, CD8, or CD30 monoclonal antibodies and TCR gene rearrangement studies are done only for selected cases when indicated. Staging of MF was further completed by lymph node examination and biopsy (when indicated). Laboratory investigations (complete blood picture, liver and kidney function tests, fasting and 2-hour postprandial blood sugar levels, and lactate dehydrogenase expression) as well as radiological investigations (chest X-ray and abdominal ultrasound) were carried out. Accordingly, staging of MF was determined in each patient following the TNM staging system [12]. The control group comprised 100 apparently healthy volunteers. Individuals with past or present history of hematopoietic or solid malignancies were excluded from the control group.

*DNA Extraction*

Venous blood samples (2 mL) were collected in the morning into EDTA vacutainer tubes used for genomic DNA extraction. Extraction of genomic DNA from whole blood was carried out using spin column-based purification with the QIA gene extraction kit.

*Genotyping of –765G>C and –1195A>G Polymorphisms*

Restriction fragment length polymorphism PCR analysis was used to amplify the COX-2 polymorphisms (–765G>C and –1195A>G) according to the method described in the literature [12]. The following primers were used to amplify the target fragments containing these two polymorphisms: 5′-TCTCACCCTCA-CATGCTCCT-30 (forward) and 5′-TCTTTTCTGTCCACTTTTCCAA-3 (reverse) for COX-2 –1195A>G; 5′-ATGAGGAGAATTTACCTTTCGC-3 (forward) and 50′-TTTTGTGGAATGAAATAGCTACCT-3 (reverse) for COX-2 –765G>C.

The PCR was performed in a total volume of 25 µL using 10 pmol of each primer, 1.5 mM HgCl2, 200 µM dNTPs, and 2 U of Taq DNA polymerase. The conditions were as follows; 35 cycles, each consisting of denaturation at 94˚C for 30 s, annealing at 61˚C for 30 s, and extension at 72˚C for 30 s. The reaction cycles were preceded by 5 min of denaturation at 94˚C and were followed by 7 min of extension at 72˚C.

The PCR products were confirmed by electrophoresis on 2% agarose gel and visualized by ethidium bromide staining.

SPSS computer program (version 20; SPSS Inc., Chicago, IL, USA) was used for data analysis. *p* < 0.05 was considered significant.