

# TRANSCRIPTION OF THREE HERV SEQUENCES IN PEMPHIGUS VULGARIS

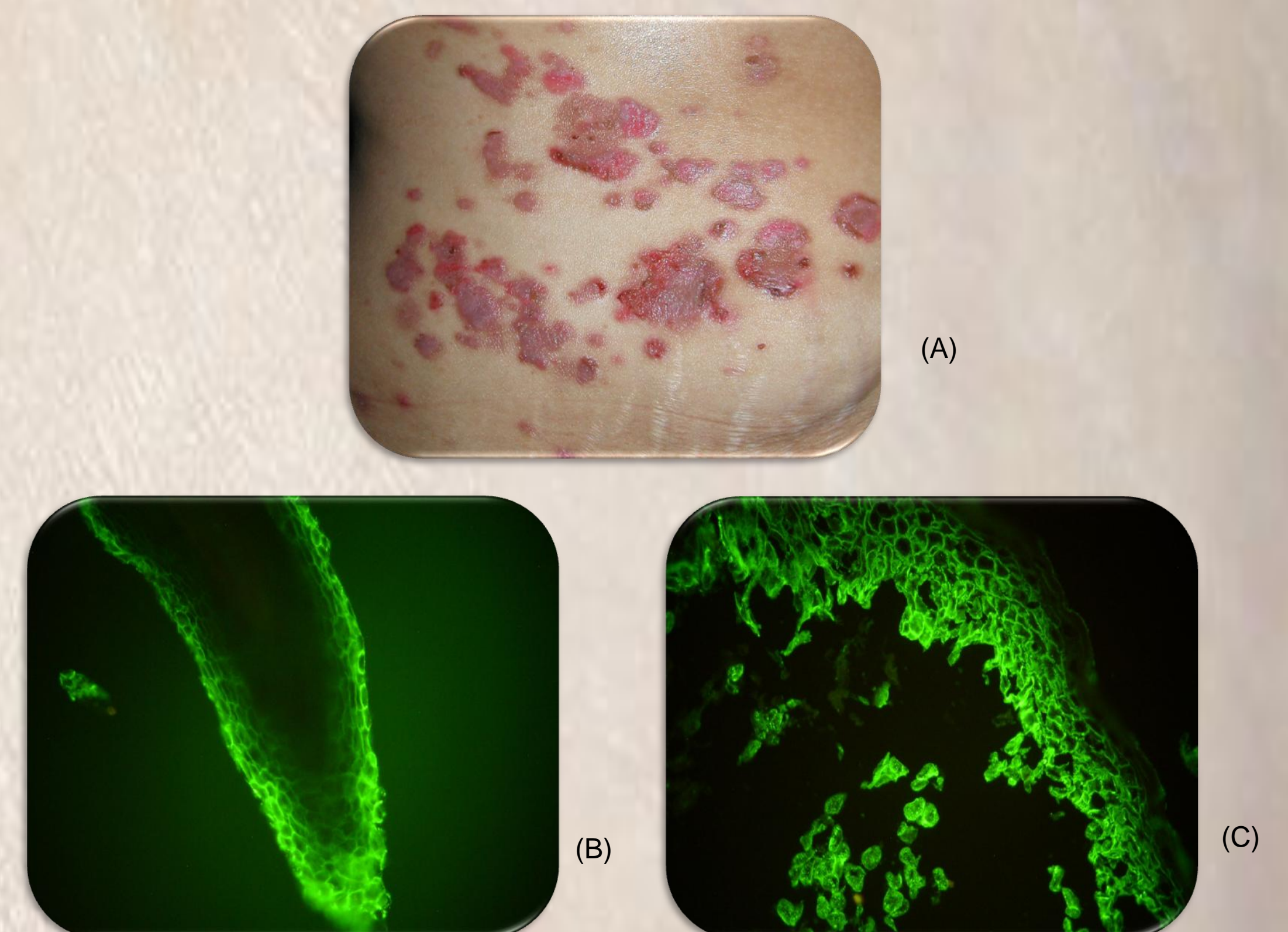
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## INTRODUCTION

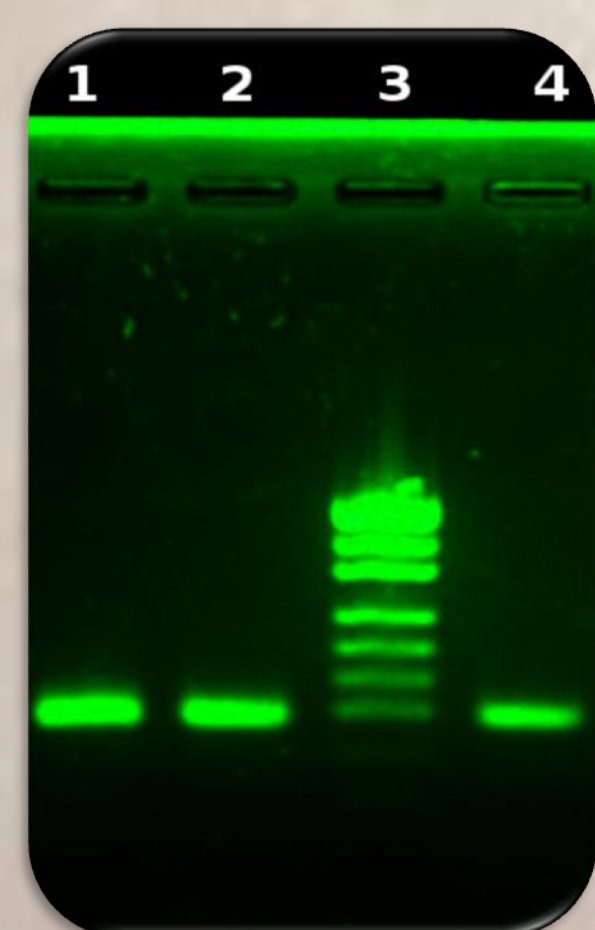
Pemphigus vulgaris (PV) is a chronic, life threatening, autoimmune blistering dermatosis, characterised by autoimmunisation against keratinocyte cell surface membrane proteins, desmosomal cadherins in particular, such as desmoglein-3 and desmoglein-1. Autoantibodies attack these proteins causing separation of adjacent epidermal layers. It is a disease of all races and geographical locations. Both genetic and environmental factors appear to play an important role in the pathogenesis of PV. PV may coexist with HIV infection. Human Endogenous Retroviruses (HERVs) seem to be involved in the pathomechanism of a number of autoimmune diseases including, among others: psoriasis, systemic sclerosis, and lupus erythematosus. Although mostly inactivated, some of these past retroviral infection remnants still possess transcriptionally active open reading frames (ORFs).

## AIM OF THE STUDY

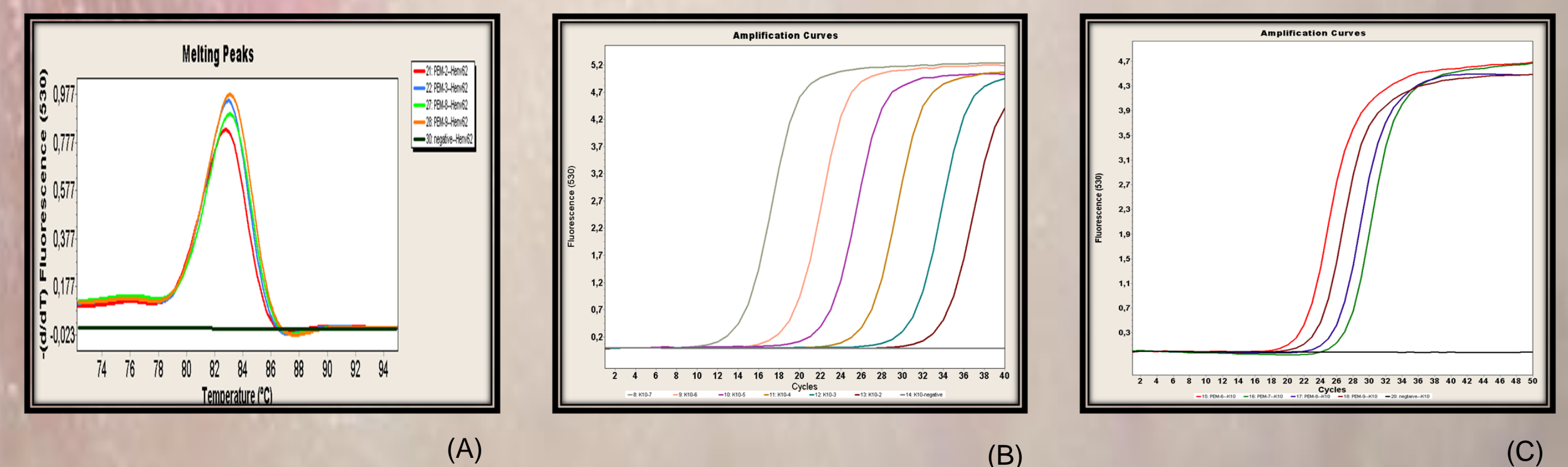
To assess differences in transcription levels of three HERV sequences between PV patients and control group.



**Fig. 1** A case of coexistence of mucocutaneous PV with ITP. Lesions on the trunk (A). DIF of plucked scalp hair (IgG4 pemphigus deposits) (B). DIF of perilesional skin (IgG4 pemphigus deposits) (C). Dsg3 IgG ELISA level 1203 (cut-off - 40), Dsg1 IgG ELISA level 74.59 (cut-off - 41).



**Fig.2** Electrophoresis gel of HERV-K envelope (lane 1), HERV-K10 gag (lane 2) and HERV-H envelope (lane 4); lane 3 - ladder



**Fig. 3** Melting (A), standard (B) and amplification (C) curves of human HERV-H

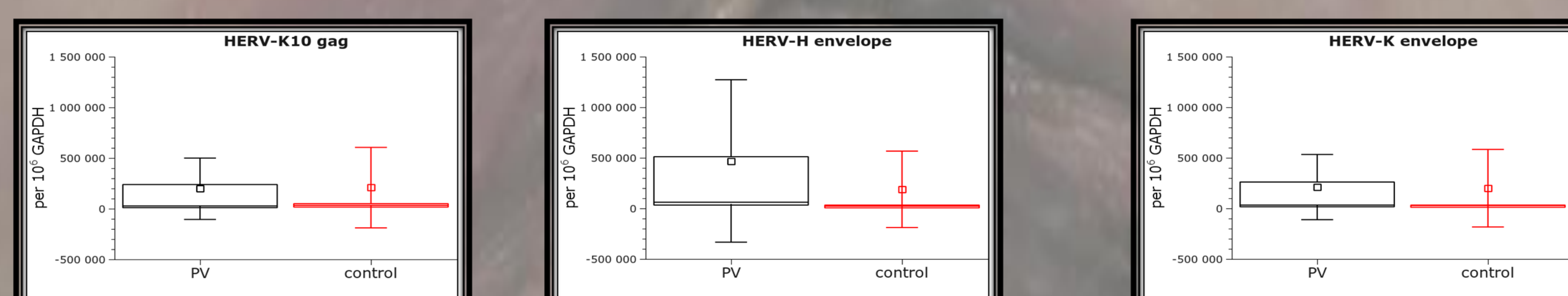
## MATERIALS AND METHODS

Total RNA was isolated from PBMCs of 12 PV patients and 15 healthy volunteers followed by cDNA synthesis by reverse transcription with the use of random hexamer primers. Three different HERV sequences were investigated by Real-Time PCR and normalised to GAPDH gene transcription level. These include: HERV-K envelope (104 bp, HERV ID: 29013, 8p23.1), HERV-K10 gag (103 bp, GenBank: M14123), and HERV-H envelope (101 bp, HERV ID: 10816, 2q24.3). All of the HERVs corresponding to the aforementioned sequences had been previously investigated and reported in other disorders.

## RESULTS AND CONCLUSIONS

Median values of cDNA copies (normalised to GAPDH) in PV patients divided by the same parameter for the control group were 1.22, 0.87, and 2.87 for HERV-K, HERV-K10, and HERV-H respectively. The Two-Sided P-Values of the Two Independent Sample Wilcoxon-Mann-Whitney (U) test were 0.31, 0.85, and 0.03 respectively. The data suggest that there is no statistical evidence for any relevant change in the RNA levels of HERV-K envelope and HERV-K10 gag in PV; however, there is an apparent increase of the HERV-H envelope RNA level.

The significance of HERVs in PV pathogenesis remains unclear. These data indicate frequent elevated levels of HERV-H transcripts in PV, but further investigations are necessary to assess the functional relevance of the HERV-H expression in this dermatosis.



**Fig. 4** Relative expression level of HERV-K10 gag, HERV-H and HERV-K mRNA to GAPDH in PV and control group.