

**P2145 *CDR1*, *CDR2*, *SNQ2* and *ERG11* gene expression in *Pdr1* mutants of *Candida glabrata* encountered during multi-centre surveillance of candidaemia in Korea**

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**Background:** Fluconazole-resistance (FR) in *Candida glabrata* most commonly reflects overexpression of the drug efflux transporter genes *CDR1*, *CDR2*, and *SNQ2* via gain-of-function mutations in the transcription factor-encoding gene *Pdr1*. However, any association between *Pdr1* mutation and gene overexpression has not hitherto been assessed in Korea. Thus, we measured the expression levels of *CDR1*, *CDR2*, *SNQ2*, and *ERG11* in *Pdr1* mutants of *C. glabrata* isolated in Korean hospitals, compared to the levels in non-*Pdr1* mutants. We also analysed our results in terms of multilocus sequence typing (MLST) genotypes.

**Materials/methods:** A total of 99 independent *C. glabrata* isolates, including 30 *Pdr1* mutants exhibiting FR (fluconazole minimal inhibitory concentration [MIC] ≥ 64 µg/mL) and 69 non-*Pdr1* mutants lacking FR were analysed. All isolates were recovered during 10-year multicentre surveillance of candidemia in Korean hospitals; their MLST sequence types (ST) were ST7 (n=58) and others (n=41). Real-time PCR was used to quantify the expression levels of the four genes after fluconazole exposure.

**Results:** Of the 99 isolates, the 30 *Pdr1* mutants exhibited higher mean levels of *CDR1* (8.3-fold) and *SNQ2* (1.4-fold) than the 69 non-*Pdr1* mutants (both P < 0.05). However, we found no significant between-group differences in the mean expression levels of *CDR2* or *ERG11*. Of 58 ST7 isolates (the most common genotype in Korea), 19 *Pdr1* mutants exhibited higher mean expression levels of *CDR1* (10.6-fold), *CDR2* (2.3-fold), and *SNQ2* (1.7-fold) than the 39 non-*Pdr1* mutants, but the *ERG11* levels did not differ between the two groups. Of 41 non-ST7 isolates, 11 *Pdr1* mutants exhibited higher mean expression levels of *CDR1* (5.8-fold) than the 30 non-*Pdr1* mutants (P < 0.001), but the expression levels of the other three genes did not differ between the two groups.

**Conclusions:** *CDR1* and *SNQ2* overexpression may be the principal drug-resistance mechanisms of *Pdr1* mutants of Korean *C. glabrata*, and the drug efflux gene expression patterns of *Pdr1* may vary by MLST type.

