

Microbial Hydroxylation of Hydroxyprogesterones and α -Glucosidase Inhibition Activity of Their Metabolites

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Microbial transformation of 11α -hydroxyprogesterone (**1**) with *Cunninghamella elegans*, *Gibberella fujikuroi*, *Fusarium lini*, and *Candida albicans* yielded $11\alpha,15\alpha,16\alpha$ -trihydroxypregn-4-ene-3,20-dione (**3**), 11α -hydroxy- 5α -pregnane-3,20-dione (**4**), $6\beta,11\alpha$ -dihydroxypregn-4-ene-3,20-dione (**5**), 11α -hydroxypregna-1,4-diene-3,20-dione (**6**), $11\alpha,17\beta$ -dihydroxyandrost-4-en-3-one (**7**), and $11\alpha,15\alpha$ -dihydroxypregn-4-ene-3,20-dione (**8**). On the other hand, microbial transformation of 17α -hydroxyprogesterone (**2**) with *Cunninghamella elegans* and *Fusarium lini* yielded $11\alpha,17\alpha$ -dihydroxypregn-4-ene-3,20-dione (**9**), and 17α -hydroxypregna-1,4-diene-3,20-dione (**10**). The structures of the metabolites **3**–**10** were deduced on the basis of spectroscopic methods. Compound **3** was identified as a new metabolite, which exhibited a promising inhibitory activity against the α -glucosidase enzyme.

Key words: 11α -Hydroxyprogesterone, 17α -Hydroxyprogesterone, Microbial Transformation, *Cunninghamella elegans*, *Candida albicans*, *Fusarium lini*, *Gibberella fujikuroi*, α -Glucosidase Inhibition