

ANTIMICROBIAL ACTIVITY OF CERVICAL *LACTOBACILLUS* ISOLATES

Viktoriya Nazarova¹, Almagul Kushugulova¹

¹Laboratory of Human Microbiome and Longevity “National Laboratory Astana” Nazarbayev University, Kabanbay Batyr Ave., 53, Astana, 010000, Republic of Kazakhstan;

*Corresponding author: semeykz@gmail.com

Persistent HPV infection is the primary cause of cervical cancer, inducing precancerous cellular changes that may progress to malignancy if untreated. HPV types 16 and 18 are responsible for most cases. Extensive research demonstrates correlations between HPV infection and vaginal microbiome composition. Bacterial communities are classified into five community state types (CSTs): CSTs I, II, III, and V are dominated by *Lactobacillus crispatus*, *L. gasseri*, *L. iners*, and *L. jensenii*, respectively, while CST IV exhibits greater microbial diversity. A causal relationship exists between CST IV and increased HPV infection risk, with HPV-positive patients showing reduced lactobacilli levels and increased microbial diversity.

Methods: Vaginal swabs from 400 HPV-positive and HPV-negative patients were cultured on MRS medium. From 235 catalase-negative, Gram-positive isolates, antimicrobial activity was assessed using deferred antagonism against eleven standard test strains including *E. coli*, *E. faecalis*, *S. aureus*, *C. albicans*, and *C. glabrata*.

Vaginal swabs from 400 HPV-positive and HPV-negative patients were cultured on MRS medium. From 235 catalase-negative, Gram-positive isolates, antimicrobial activity was assessed using deferred antagonism against eleven standard test strains including *E. coli*, *E. faecalis*, *S. aureus*, *C. albicans*, and *C. glabrata*.

Of 235 lactobacilli cultures tested, antimicrobial activity was demonstrated by 151 cultures (64.3%) against *E. coli*, with inhibition zones ranging up to 33.5 mm (cultures 297-8 and 127-4). Against *E. faecalis*, 139 cultures (59.1%) showed activity, with maximum zones of 36.5 mm (cultures 316-1 and 316-3). For *S. aureus*, 141 cultures (60.0%) exhibited antimicrobial effects, with the largest inhibition zone of 36.5 mm (culture 282-2). Antifungal activity was markedly lower: only 52 cultures (22.1%) were active against *C. albicans*, with maximum zones of 16.5 mm (cultures 127-1 and 127-3), while merely 14 cultures (6.0%) demonstrated activity against *C. glabrata*, achieving maximum inhibition zones of 16 mm (culture 107-4). The data

reveal significantly higher antimicrobial efficacy against Gram-positive and Gram-negative bacteria compared to fungal pathogens

Lactobacilli demonstrated strong antimicrobial activity against bacterial pathogens but limited antifungal effects. These findings suggest lactobacilli may protect against pathogenic microorganisms by maintaining cervicovaginal microbiome balance, potentially reducing HPV infection risk and cervical cancer development.

The author gratefully acknowledges the Laboratory of Human Microbiome and Longevity as well as laboratory mentors for providing experimental materials and technical support.

Keywords: antimicrobial activity, test strain, method of deferred antagonism

References:

1. Dareng EO, Ma B, Famooto AO, Akarolo-Anthony SN, Offiong RA, Olaniyan O, Dakum PS, Wheeler CM, Fadrosch D, Yang H, Gajer P, Brotman RM, Adebamowo CA. Prevalent high-risk HPV infection and vaginal microbiota in Nigerian women. *Epidemiology and Infection*, 144(1):123-137 (2016).
2. Reimers LL, Mehta SD, Massad LS, Burk RD, Xie X, Ravel J, Cohen MH, Palefsky JM, Weber KM, Xue X, Anastos K, Minkoff H, Atrio J, D'Souza G, Ye Q, Colie C, Zolnik CP, Spear GT, Strickler HD. The cervicovaginal microbiota and its associations with human papillomavirus detection in HIV-infected and HIV-uninfected women. *Journal of Infectious Diseases*, 214(9):1361-1369 (2016).
3. Di Paola M, Sani C, Clemente AM, Iossa A, Perissi E, Castronovo G, Tanturli M, Rivero D, Cozzolino F, Cavalieri D, Carozzi F, De Filippo C, Torcia MG. Characterization of cervico-vaginal microbiota in women developing persistent high-risk Human Papillomavirus infection. *Scientific Reports*, 7(1):10200 (2017).
4. Chen Y, Hong Z, Wang W, Gu L, Gao H, Qiu L, Di W. Association between the vaginal microbiome and high-risk human papillomavirus in-

fection in pregnant Chinese women. *BMC Infectious Diseases*, 19(1):677 (2019).

5. Mitra A, MacIntyre DA, Ntritsos G, Smith A, Tsilidis KK, Marchesi JR, Bennett PR, Kyrgiou

M. The vaginal microbiota associates with the regression of untreated cervical intraepithelial neoplasia 2 lesions. *Nature Communications*. 11(1):1999 (2020).