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O.07- Unraveling the interactome of the HSP70 escort protein 1

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Proteins are macromolecules that are essential to various cellular processes, such as signaling, transport, metabolism, etc. Among the many human proteins, there is the HSP70 escort protein 1, also known as HEP1, which is an essential co-chaperone in maintaining the functional structure and remodeling of supramolecular assemblies of the HSPA1A and HSPA9 proteins. Structurally, HEP1 is formed by a DNL-Type zinc-finger domain that presents a tetra cysteine motif, essential for its interaction with the Zn2+. Besides being present in mitochondria, under heat stress, HEP1 can also be found in the nucleus of eukaryotic cells. Although there is knowledge about HEP1's action on two members belonging to the HSP70 family, its interaction network, as well as the cellular processes in which it is involved, need to be further investigated. This work aimed to study and map the interactome of HEP1. We used the biotin-dependent proximity identification (BioID) by assays with HEK293WT human cells previously transfected with specific plasmids (BioID2 and HEP1-BioID2) and subjected to normal and heat stress growth conditions. Subsequently, analyses through SDS-PAGE, Western blotting, functional assays, and Liquid Chromatography coupled to Mass Spectrometry (LCMS) were performed. Our data suggests HEP1's ability to interact with many cellular proteins (a total of 1924 different proteins), with a greater number of interactors for the heat stress condition than for the normal condition. Additionally, we discovered that HEP1 can interact with several members of the protein quality control (PQC) system, DNA/RNA modulating proteins, as well as different HSP70s, such as HSPA2, HSPA4, HSPA4L, HSPA5, HSPA6 and HSPA8, and those previously reported in the literature, HSPA1A and HSPA9. HEP1 is involved with heat stress response and studies are ongoing to explore and understand the functional implications of its interactions. Keywords: Interactome, HEP1, Molecular chaperone

O.08- Vaginal Microbiota Composition In Women During Climacteric: Implications For Vaginal Health And Disease.

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The human vaginal microbiota plays a crucial role in maintaining vaginal health, which has been investigated by the scientific community. These microbial communities interact with the vaginal epithelium and depend on host tissues for their sustenance. The climacteric is the period of a woman's life marked by the transition from the reproductive to the non-reproductive phase, in which various physiological changes occur, including in her microbiota, which can have an impact on her health and quality of life. Thus, an imbalance in the vaginal microbiota has been associated with as vaginosis, vaginitis, sexually transmitted infections, cervical cancer. Evaluating the vaginal microbiota of climacteric women and the role of the predominant species in maintaining vaginal health. Vaginal samples were collected from 66 individuals, the composition of the vaginal microbial was analyzed by 16S rRNA gene sequencing. No significant difference was found in the microbial composition between the three groups according to alpha and beta diversity. The most prevalent genera were: Lactobacillus, Gardnerella and Prevotella respectively (Reproductive Group: 48.4%, 17.2% and 6.5%; Women in menopausal transition 56.2%, 14.0% and 6.1%; Postmenopausal women 36.0%, 16.0% and 9.5%). In both groups, the most abundant species was Lactobacillus iners (Reproductive 26.7%; Transition 30.9%; Postmenopausal 28.6%). An important finding in all groups was the presence of G. vaginalis as the second most prevalent species, with 10.0% in the menopause transition period. Another relevant finding is the high prevalence of Atopobium vaginae: 6.0% in reproductive group and 3.85 in post-menopause. The most abundant L.iners species in this study can be considered an indicator of the transition between a healthy microbiota and a dysbiotic state. In addition, G. vaginalis has potential as a marker of bacterial vaginosis, due to its primary colonization of the environment and biofilm formation.
Keywords: 16S rRNA sequencing, Vaginal Health, Vaginal Microbiota