Diminished ovarian reserve (DOR) women: The role of rescue-in vitro maturation (Rescue-IVM)

Nurul Yaqin Mohd Nor1,2, Mohammad Mahmoud Mohammad Ramadneh1,3, Muhammad Azrai Abu1, Abdul Kadir Abdul Karim1, Mohd Faizal Ahmad1

[1]Department of Obstetrics and Gynaecology, Faculty of Medicine UKM, Kuala Lumpur, Malaysia, [2]Department of Obstetrics and Gynaecology, Kuliyyah of Medicine, International Islamic University Malaysia, Kuantan, Pahang, Malaysia, [3]Department of Obstetrics and Gynaecology, Arrawdha General Hospital, Dammam, Saudi Arabia

ABSTRACT

Background and Objective: (Rescue-IVM) is not routinely practiced due to limited evidence. The procedure is incorporated in the IVF procedure of women with (DOR) to improve pregnancy rates. We aim to consolidate the role of Rescue-IVM in DOR women in our centre. **Methods:** A cohort study conducted between July 2021 and July 2022, consisted of two groups: 1) Normal Ovarian Reserve (NOR) and 2) DOR defined as Anti-Mullerian Hormone (AMH) <1.2 ng/mL and antral follicle count (AFC) <5, based on POSEIDON criteria. Concurrent IVF rescue IVM was performed according to the local protocol. The duration of IVM culture depending on stage of oocytes maturation. The result of oocyte maturation rate (OMR), fertilization index (FI) and number of normally cleaved embryos were analysed. **Results:** A total of 157 women underwent 164 cycle of IVF-rescue IVM (NOR 119, DOR 45). The duration of fertility and follicle oocyte index (FOI) were comparable among groups. The total number of collected oocytes for NOR and DOR groups were 975 and 89. Both the OMR (60% vs. 58.57%) (p=0.314) and FI (41.6% vs. 38.3%) (p=0.477) are higher in DOR than NOR. The number of normally cleaved embryos is statistically significant in DOR (16.6% versus 5%) (p=0.06) with a lower number needed to treat (NNT) in DOR group using rescue-IVM strategy (1:169) than in the NOR (1:909). **Conclusion:** With this promising outcome, rescue-IVM can be incorporated with concurrent IVF and considered a good strategy for managing DOR women.

Expression of HOXA10 in endometriotic women following modulation of gonadotropin-releasing hormone receptor

Lazim Nurunnajah[1], Elias Marjanu Hikmah[1,2], Syafruddin Saiful Effendi[3], Sutaji Zulazmi[1,2], Abu Mohammad Azrai[1], Abdul Karim Abdul Kadir[1], Ugusman Azizah[4], Mokhtar Mohd Helmy[4], Ahmad Mohd Faizal[1]

[1]Advanced Reproductive Centre (ARC) HCTM, Department of Obstetrics & Gynaecology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Bandar Tun Razak, Cheras, Kuala Lumpur, Malaysia, [2]Faculty of Medicine & Health Sciences, Universiti Sains Islam Malaysia, Nilai, Seremban, Negeri Sembilan, Malaysia, [3]UKM Medical Molecular Biology Institute (UMBI), Universiti Kebangsaan Malaysia, Bandar Tun Razak, Cheras, Kuala Lumpur, Malaysia, [4]Department of Physiology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Bandar Tun Razak, Cheras, Kuala Lumpur, Malaysia

ABSTRACT

Introduction: Homeobox A10 (HOXA10) gene plays an important role in developing endometrium. *HOXA10* gene expression is relatively lower in women with endometriosis. The aberrant regulation of the gene affects the endometrial receptivity during the implantation window among these women. Our study examined the changes in *HOXA10* messenger RNA (mRNA) and *HOXA10* protein expression in patients with endometriosis, before and after treatment with a gonadotropin-releasing hormone agonist (GnRHa) by modulating the GnRH receptor. **Methods:** A total of seventeen (n=17) endometriotic women aged between 25 to 45 years old were recruited at the Advanced Reproductive Centre (ARC) HCTM, Malaysia. Paired samples were collected during the luteal phase of the patients, before and after treatment with GnRHa. All thirty-four samples were assessed using real-time PCR (qPCR) and western blot. Fold-change (ΔΔCt) of *HOXA10* was calculated, and statistical analysis was done using Wilcoxon Signed Rank Test in SPSS. **Results:** Nine patients showed positive differences, while the other eight show negative differences in *HOXA10* expression. 65% of patients demonstrated upregulation of *HOXA10,* while the remaining 35% demonstrated downregulation of the gene. Although more patients demonstrated upregulation, but no significant difference was detected (p>0.05). Therefore, the median differences of *HOXA10* Ct values between before and after treatment are likely to be equal to zero. **Conclusions:** This study suggests that treatment with GnRHa will not cause *HOXA10* to be expressed differently either before or after the treatment. These results are preliminary data to see *HOXA10* mRNA and *HOXA10* protein expression and will be further validated with methylation-specific qPCR (MS-qPCR).