



Regulated expression of *Gemin5*, *Xrn1*, *Cpeb* and *Stau1* in the uterus and ovaries after superovulation and the effect of exogenous estradiol and leptin in rodents

Abhishek Shetty¹ · Thejaswini Venkatesh² · Rie Tsutsumi³ · Padmanaban S. Suresh⁴

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Abstract

The aim of this study was to evaluate whether *Gemin 5*, *Cpeb*, *Xrn1*, and *Stau1* expression in rodent ovaries and uterine tissues is dependent on gonadotropins, steroid hormones, and leptin in the superovulation and ovariectomized mouse models of menopause. Treatment of pregnant mare serum gonadotropin-primed rats with human chorionic gonadotropin (hCG) significantly induced *Stau1* and *Gemin 5* messenger RNA expression in rat ovaries. *Gemin 5* expression in ovaries was sustained at relatively high levels at 12 h and 24 h post hCG treatment compared to *Stau1*, suggesting its role in follicle development, ovulation, and luteogenesis in rat ovaries. Induced expression of *Stau1* and *Gemin 5* in the uterine tissue post hCG treatment at 12 h and 24 h—the duration between ovulation and post-ovulation—suggests their regulation by hCG and/or ovarian steroids, which are required for pregnancy establishment and maintenance. *Cpeb* expression was significantly higher ($p < 0.05$) in the uterine tissues after combined treatment of estradiol and leptin at 4 h. Further, the significant upregulation of uterine *Gemin 5* and *Xrn1* by the synergistic activities of leptin and estradiol at 40 h in ovariectomized mice establishes them as targets of cross-talk. Although these are preliminary data, the combination of *Gemin 5*, *Cpeb*, *Xrn1*, and *Stau1* transcript alterations in rodent ovaries and uterine tissue displayed in two different experimental models underscore their importance as therapeutic targets for anovulation or in overcoming endometrial homeostasis disturbances during pregnancy due to obesity.

Keywords Ovaries · Superovulation · Ovariectomy · *Gemin 5*

Introduction

Messenger RNAs (mRNAs) form complexes with RNA binding proteins (RBPs) in the cytoplasm, and the type of complex formed with specific RBPs controls translation of these bound mRNAs [1]. These transient mRNA complexes also contain micro RNAs, and were initially identified as

cytoplasmic foci, such as processing bodies (P-bodies) and stress granules by microscopy [1]. Various proteins involved in mRNA degradation, translational repression, mRNA surveillance, and RNA-mediated gene silencing colocalize in these cytoplasmic foci [1]. The roles of P-bodies—that are highly dynamic—and stress granules, have been studied by various researchers in a variety of eukaryotic cells. P-bodies contain decapping enzymes and exonucleases that alter mRNA stability and turnover according to the specific cellular context [1]. Recently, Youn et al. identified many proteins that colocalize in P-bodies [2]. Among these proteins, cytoplasmic polyadenylation element binding protein (CPEB), XRN1 (5′–3′ exoribonuclease I), STAU1 (double-stranded RNA-binding protein Staufen homolog 1), and *Gemin 5* (Gem-associated protein 5) regulate polyadenylation-induced translation, mRNA decay, mRNA localization, and inhibition of both cap-dependent and internal ribosome entry site (IRES)-driven translation initiation [3]. *Cpeb* knockout mice exhibit progressive oocyte loss and infertility [4]. Ovulation, a key female reproductive event, is a highly

✉ Padmanaban S. Suresh
surepadman@gmail.com; surepadman@rediffmail.com

¹ Department of Biosciences, Mangalore University, Mangalagangothri, Mangalore, Karnataka 574 199, India

² Department of Biochemistry and Molecular Biology, Central University of Kerala, Kasargod, Kerala 671 316, India

³ Department of Nutrition and Metabolism, Institute of Biomedical Sciences, Tokushima University Graduate School, 3-18-15, Kuramoto-cho, Tokushima City 770-8503, Japan

⁴ School of Biotechnology, National Institute of Technology, Calicut, Kerala 673 601, India