

Nucleolar dominance, a locus-level regulation of ribosomal DNA expression, in *D. melanogaster* females

Duoja Li^{1,2}, Natalie Warsinger-Pepe^{1,3}, Yukiko M. Yamashita^{1,4,5}

¹Life Sciences Institute ²Molecular, Cellular and Developmental Biology ³Department of Molecular and Integrative Physiology ⁴Cell and Developmental Biology ⁵Howard Hughes Medical Institute, University of Michigan, Ann Arbor

Abstract

Ribosomal DNA (rDNA) codes for the catalytic RNA components of ribosomes and is organized in tandem repeats of in eukaryotic genomes. In *Drosophila*, rDNA loci are on the X and Y chromosomes where each locus contains ~200-250 copies. A large-scale regulation of rDNA expression called nucleolar dominance, where rDNA locus is entirely silenced or activated, operates to regulate the dosage of rRNA. In male *D. melanogaster*, Y rDNA is preferentially transcribed while the entire X rDNA locus is silenced. In females, both rDNA loci are transcribed in larval brains. Previous studies were unable to characterize female nucleolar dominance in other tissues and developmental stages due to technical limitations. Here we identify sequence variation in an X rDNA locus and utilize these sequence differences with fluorescent in situ hybridization to characterize nucleolar dominance in females. We expand on previous studies and show that nucleolar dominance does not occur in X/X females in multiple tissues and throughout development. Using various chromosome complements and compound chromosomes, we found that nucleolar dominance is not limited to Y chromosome or male cells. This study begins to unravel factors dictate the rDNA expression pattern in both female and male and will help us understand how nucleolar dominance occurs.

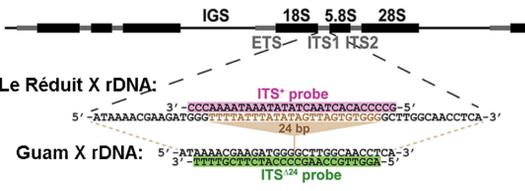
Introduction

rDNA codes for essential RNA catalytic components of ribosomes, and its transcription is important for ribosome functions [1]. Thus, the regulation of rDNA transcription is critical to meet cellular metabolic demand. Nucleolar dominance was originally found to occur in interspecies hybrids [2-5], and has been shown to occur within a species [6-8]. In male *D. melanogaster*, previous studies found that Y rDNA dominates over X rDNA expression [6, 8]. Utilizing SNPs between X and Y rDNA loci and RNA in situ hybridization, we found that Y rDNA dominance is established developmentally [9]. In female *D. melanogaster*, both X rDNA loci are expressed in larval neuroblasts [3, 9]. However, due to the high sequence homology, no SNPs were found between X rDNA loci, limiting the understanding of nucleolar dominance in females. This study expands on the knowledge of female nucleolar dominance to various tissues and developmental stages using RNA in situ and explored potential factors impacting nucleolar dominance.

Methods

RNA in situ hybridization

- RNA in situ hybridization used from Natalie et al. (2020) [9], modified from Levesque et al. (2013) [10].



DNA fluorescence in situ hybridization (DNA FISH)

- relative rDNA size was quantified using a modified protocol from Lu et al. (2018) [11].



Results

Figure 1. Co-dominance occurs in X/X females throughout development

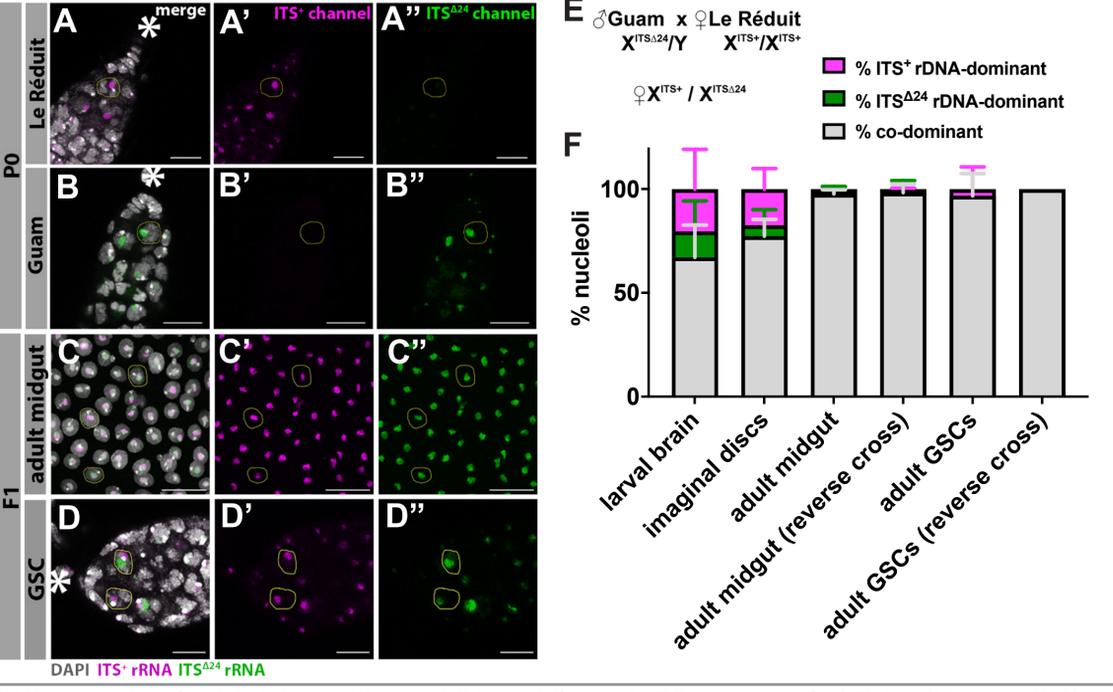


Figure 2. Zhr1 rDNA is silenced in female cells with Guam X

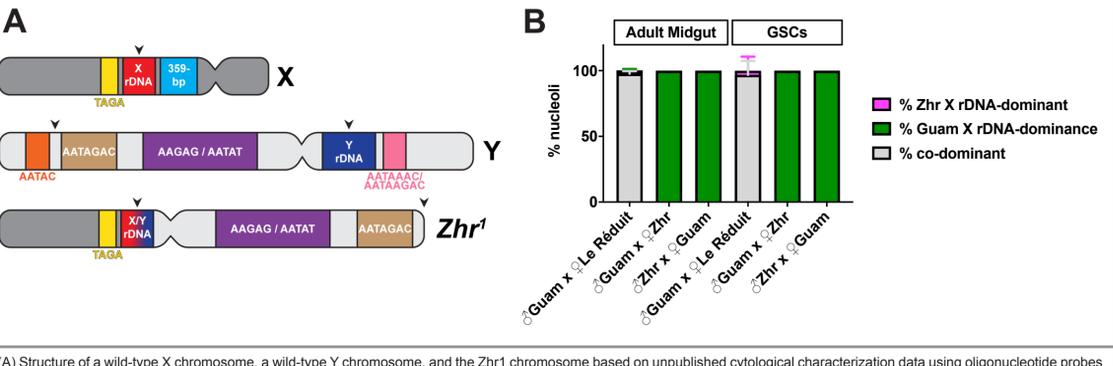


Figure 3. Guam X rDNA can dominate in male and female somatic cells

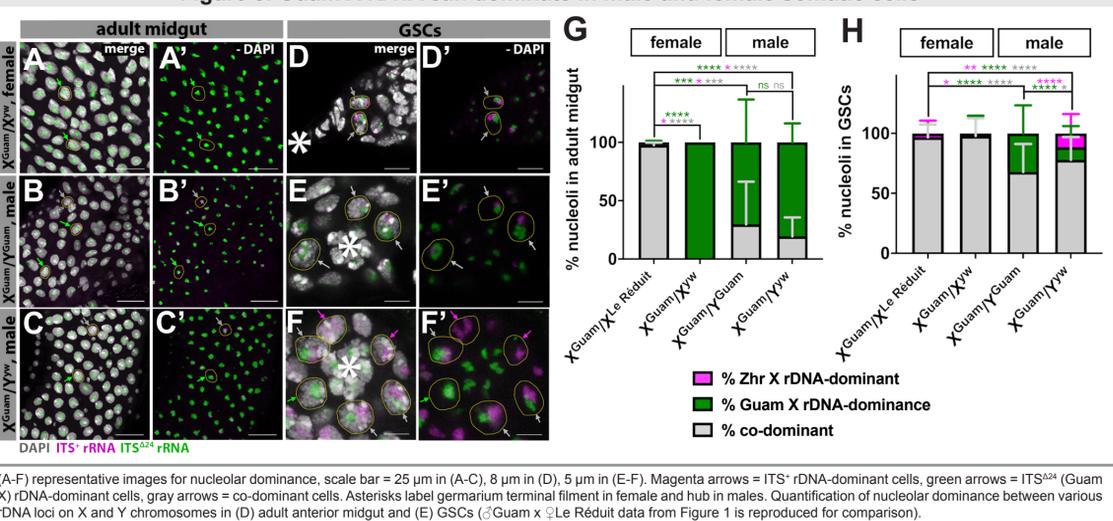
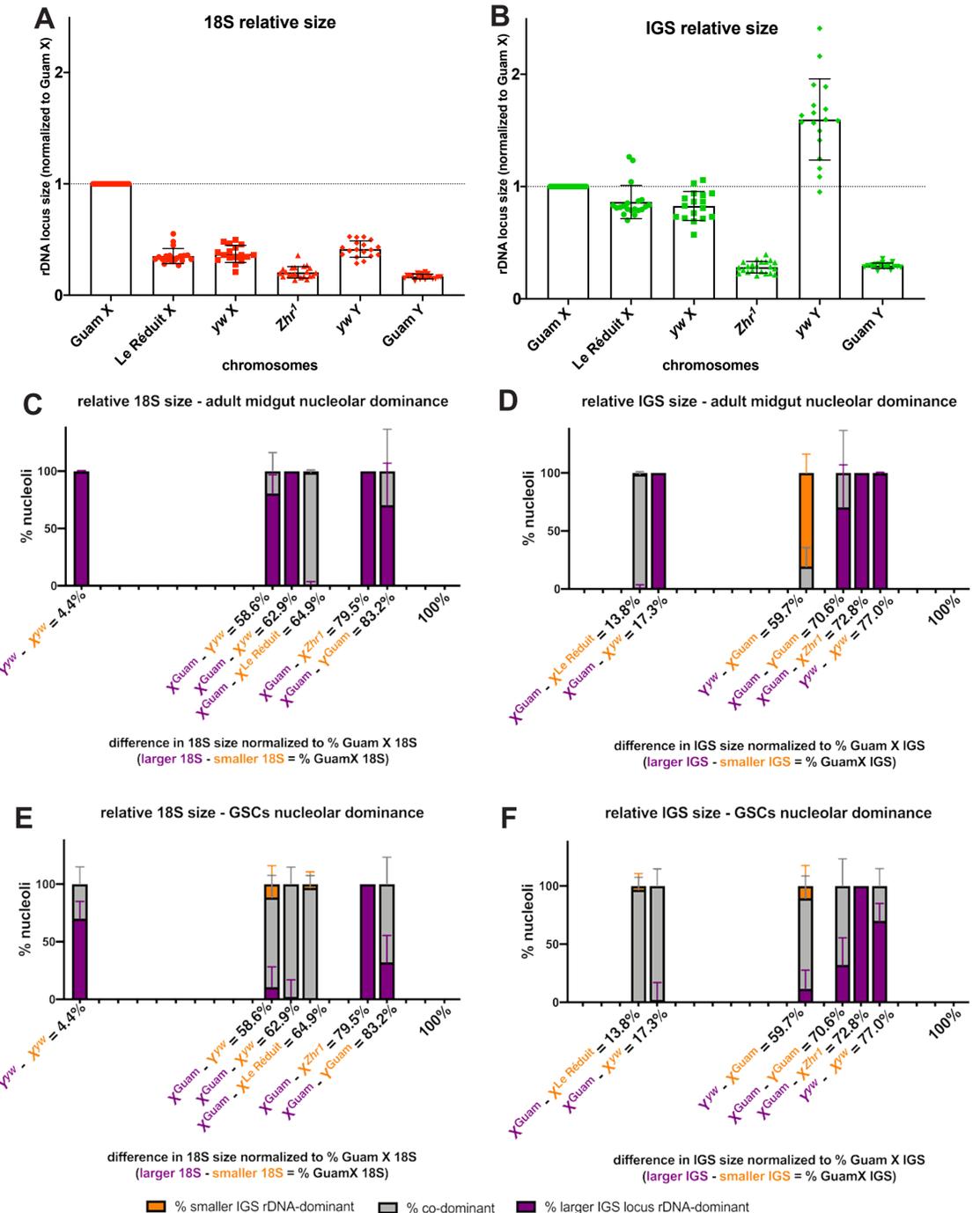


Figure 4. Relative rDNA size varies across chromosomes and strains



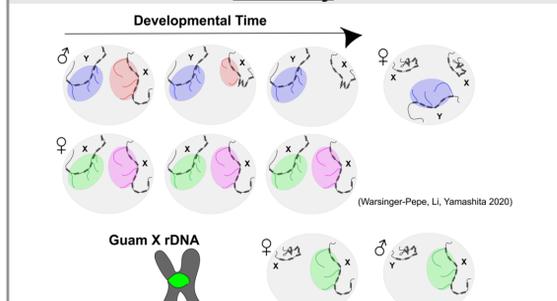
Discussion

We characterized nucleolar dominance in female *D. melanogaster*, expanding on our previous knowledge to other tissue types and developmental stages. Using a compound chromosome and various chromosome complements, we identified an X chromosome that is able to dominate over both X and Y rDNA loci. Our data suggests that rDNA size may play a tissue-specific role in establishing dominance. Furthermore, our data suggests that elements within the Guam X rDNA may strongly dictate its ability to dominate over other rDNA loci. What these elements are and how they influence nucleolar dominance await future investigation.

Reference

- Grewal, S.S., et al. (2005). PMID: 15723055
- Chen, Z.J., L. Comai, and C.S. Pikaard (1998). PMID: 9843986
- Durica, D.S. and H.M. Krider (1977). PMID: 408210
- Honjo, T. and R.H. Reeder (1973). PMID: 4763983
- Navashin, M., Chromosome Alterations Caused by Hybridization and Their Bearing upon Certain General Problems. CYTOLOGIA, 1934. 5(2): p. 169-203.
- Greil, F. and K. Ahmad (2012). PMID: 22649076
- Lewis, M.S., J.M. Cheverud, and C.S. Pikaard (2004). PMID: 15238541
- Zhou, J., et al (2012). PMID: 22665801
- Warsinger-Pepe, N., D. Li, and Y.M. Yamashita (2020). PMID: 32122935
- Levesque, M.J., et al. (2013). PMID: 23913259
- Lu, K.L., et al. (2018). PMID: 29436367
- Ferree, P.M. and D.A. Barbash. (2009). PMID: 19859525

Summary



Acknowledgement

Thank you to the Yamashita lab members for PhD and scientific discussion, especially to Dr. Yukiko Yamashita and PhD candidate Natalie Warsinger-Pepe for extensive mentorship and training, and to biology undergraduate program co-sponsor Dr. Steven Clark.