Xenopus tropicalis egg extracts provide insight into scaling of the mitotic spindle

Thomas J. Maresca, University of Massachusetts - Amherst
M. D Blower
K. S Brown
T. C Grammer
R. M Harland, et al.

Available at: http://works.bepress.com/thomas_maresca/4/
Xenopus tropicalis egg extracts provide insight into scaling of the mitotic spindle

Katherine S. Brown,1 Michael D. Blower,1 Thomas J. Maresca,1 Timothy C. Grammer,2 Richard M. Harland,2 and Rebecca Heald1

1Department of Molecular and Cell Biology and 2Center for Integrative Genomics, University of California, Berkeley, Berkeley, CA 94720

Introduction

The African clawed frog Xenopus laevis has been instrumental to investigations of both development and cell biology, but the utility of this model organism for genetic and proteomic studies is limited by its long generation time and unsequenced pseudotetraploid genome. Xenopus tropicalis, which is a small, faster-breeding relative of X. laevis, has recently been adapted for research in developmental genetics and functional genomics, and has been chosen for genome sequencing. We show that X. tropicalis egg extracts reconstitute the fundamental cell cycle events of nuclear formation and bipolar spindle assembly around exogenously added sperm nuclei. Interestingly, X. tropicalis spindles were ~30% shorter than X. laevis spindles, and mixing experiments revealed a dynamic, dose-dependent regulation of spindle size by cytoplasmic factors. Measurements of microtubule dynamics revealed that microtubules polymerized slower in X. tropicalis extracts compared to X. laevis, but that this difference is unlikely to account for differences in spindle size. Thus, in addition to expanding the range of developmental and cell biological experiments, the use of X. tropicalis provides novel insight into the complex mechanisms that govern spindle morphogenesis.

Results and discussion

We set out to evaluate the utility of X. tropicalis for in vitro cell biological and biochemical investigations. X. tropicalis eggs

K.S. Brown, M.D. Blower, and T.J. Maresca contributed equally to this paper.

Correspondence to Rebecca Heald: heald@socrates.berkeley.edu

M.D. Blower’s present address is Dept. of Molecular Biology, Massachusetts General Hospital, Boston, MA 02114.

Abbreviations used in this paper: CSF, cytostatic factor; HCG, human chorionic gonadotropin; NuMA, nuclear mitotic apparatus protein; Xnf7, Xenopus nuclear factor 7.
The utility of *X. tropicalis* extracts would be maximized if reagents generated for *X. laevis* could be applied. Fluorescence microscopy revealed that antibodies against *X. laevis* histone H1 (chromatin component; Maresca et al., 2005a), nuclear mitotic apparatus protein (NuMA; spindle pole component; Merdes et al., 1996), and Xenopus kinesin-like DNA-binding protein (Xkid; Funabiki and Murray, 2000) gave identical staining patterns in *X. tropicalis* extracts, compared with *X. laevis* (Fig. 1 B and not depicted). Furthermore, the addition of an inhibitory antibody to Xkid resulted in chromosome congression defects in *X. tropicalis* spindle reactions that were very similar to those observed in *X. laevis* (unpublished data), suggesting that many reagents will be useful in both species. Because *X. laevis* has a pseudotetraploid genome, many genes are present in multiple copies, and without selective pressure, some may be expressed but may not be functional, like one of the Vg1 isoforms (Birsoy et al., 2005). Whether or not the isoforms are functional, there is frequently more than one. *X. laevis* Rae1 (mRNA export factor/spindle regulator; Blower et al., 2005), RCC1 (guanine exchange factor for Ran; Nishitani et al., 1990), and histone H1 were represented by multiple bands on a Western blot, whereas *X. tropicalis* contained a single band for each protein (Fig. 1 C). This suggests that the pseudotetraploid genotype of *X. laevis* contributes to the complexity of the proteome, and the use of *X. tropicalis* could simplify protein analysis.

*X. laevis* biochemistry is not underpinned by genomic information, making identification of proteins by mass spectrometry difficult. To test whether *X. laevis* proteins could be identified using the *X. tropicalis* database, we immunoprecipitated the microtubule-associated developmental regulator Xenopus nuclear factor 7 (Xnf7; Maresca et al., 2005b) from both *X. laevis* and *X. tropicalis* extracts (Fig. 2 A), and then used MALDI mass spectrometry to identify each protein using databases from both species. Xnf7 was identified from both immunoprecipitates using either database (Fig. 2 B), although the number of peptides identified was higher when queried against the database of the same species. Conceptual trypsin digestion of Xnf7 from both species and comparison of the peptides revealed that although the two proteins are highly conserved (Fig. 2 C), only 45% of the peptides have identical masses (not depicted). This analysis suggests that although the *X. tropicalis* database will greatly facilitate the identification of *X. laevis* proteins by mass spectrometry, it will be more efficient to identify homologous *X. tropicalis* proteins.

While validating the use of *X. tropicalis* extracts, we noticed that spindles assembled around *X. laevis* sperm nuclei in *X. tropicalis* extracts were considerably smaller (~30% shorter) than those assembled in *X. laevis* extract (Fig. 3 A). Comparing the fluorescence area of the two types of spindles revealed an approximately threefold difference (unpublished data), indicating a substantially greater microtubule mass in *X. laevis* spindles compared with those of *X. tropicalis*. This prompted us to examine the poorly understood phenomenon of spindle scaling further.

Spindle sizes were extract dependent, suggesting that they may be defined by diffusible cytoplasmic components. To determine whether these factors reflect a balance of activities present in the egg extracts prepared from eggs of *X. tropicalis* and *X. laevis* were 10–20% that of egg extracts after release from CSF arrest, and bipolar spindles when induced to reenter mitosis in metaphase-arrested extracts, interphase nuclei contained single isoforms. Bars, 10 μm.

(∼0.6 mm diam) are approximately one fifth the volume of those of *X. laevis* (1.2 mm diam). To test whether *X. tropicalis* eggs could be used to prepare functional cellular extracts, we collected, dejellied, and crushed unfertilized eggs, which, like those of *X. laevis*, are arrested in metaphase of meiosis II by cytosstatic factor (CSF) activity (Murray, 1991). Metaphase-arrested *X. tropicalis* eggs extracted spindle structures around exogenously added sperm nuclei, entered interphase, and replicated DNA when released from the arrest, and then cycled back into mitosis (Fig. 1 A). Although yields of extract per frog were 10–20% that of *X. laevis, X. tropicalis* egg extracts effectively recapitulated cell cycle events in vitro.

The utility of *X. tropicalis* extracts would be maximized if reagents generated for *X. laevis* could be applied. Fluorescence microscopy revealed that antibodies against *X. laevis* histone H1 (chromatin component; Maresca et al., 2005a), nuclear mitotic apparatus protein (NuMA; spindle pole component; Merdes et al., 1996), and Xenopus kinesin-like DNA-binding protein (Xkid; Funabiki and Murray, 2000) gave identical staining patterns in *X. tropicalis* extracts, compared with *X. laevis* (Fig. 1 B and not depicted). Furthermore, the addition of an inhibitory antibody to Xkid resulted in chromosome congression defects in *X. tropicalis* spindle reactions that were very similar to those observed in *X. laevis* (unpublished data), suggesting that many reagents will be useful in both species. Because *X. laevis* has a pseudotetraploid genome, many genes are present in multiple copies, and without selective pressure, some may be expressed but may not be functional, like one of the Vg1 isoforms (Birsoy et al., 2005). Whether or not the isoforms are functional, there is frequently more than one. *X. laevis* Rae1 (mRNA export factor/spindle regulator; Blower et al., 2005), RCC1 (guanine exchange factor for Ran; Nishitani et al., 1990), and histone H1 were represented by multiple bands on a Western blot, whereas *X. tropicalis* contained a single band for each protein (Fig. 1 C). This suggests that the pseudotetraploid genotype of *X. laevis* contributes to the complexity of the proteome, and the use of *X. tropicalis* could simplify protein analysis.

*X. laevis* biochemistry is not underpinned by genomic information, making identification of proteins by mass spectrometry difficult. To test whether *X. laevis* proteins could be identified using the *X. tropicalis* database, we immunoprecipitated the microtubule-associated developmental regulator Xenopus nuclear factor 7 (Xnf7; Maresca et al., 2005b) from both *X. laevis* and *X. tropicalis* extracts (Fig. 2 A), and then used MALDI mass spectrometry to identify each protein using databases from both species. Xnf7 was identified from both immunoprecipitates using either database (Fig. 2 B), although the number of peptides identified was higher when queried against the database of the same species. Conceptual trypsin digestion of Xnf7 from both species and comparison of the peptides revealed that although the two proteins are highly conserved (Fig. 2 C), only 45% of the peptides have identical masses (not depicted). This analysis suggests that although the *X. tropicalis* database will greatly facilitate the identification of *X. laevis* proteins by mass spectrometry, it will be more efficient to identify homologous *X. tropicalis* proteins.
in both extracts, or a dominant activity in one of the extracts, we combined extracts in different proportions and examined spindle length in the mixed reactions. We found that spindle length had a direct and linear dependence on the proportion of *X. laevis* to *X. tropicalis* extract (Fig. 3 B), suggesting equilibrium behavior of cytoplasmic regulatory activities. Previous work has also demonstrated a role for chromatin mass in determining spindle size (Nicklas and Gordon, 1985). To investigate this phenomenon, we compared spindle length in *X. laevis*, *X. tropicalis*, and mixed extracts using sperm from *X. tropicalis*, whose diploid genome (1.7 × 10⁹ bp) is ~55% that of *X. laevis* (3 × 10⁹ bp; Hirsch et al., 2002), and found that spindles assembled around *X. tropicalis* chromosomes were ~10% shorter in all cases (Fig. 3 B). Therefore, we conclude that although chromatin mass does influence spindle length, soluble cytoplasmic factors are the major determinant in *Xenopus* egg extracts.

To examine whether spindle size regulation is a static or dynamic process, we added fresh extract to preassembled spindles. To *X. tropicalis* extracts containing spindles that had incorporated X-rhodamine–labeled tubulin, we added three volumes of either *X. tropicalis* or *X. laevis* extract containing Alexa Fluor 488 tubulin, and examined spindle length at various time points after mixing. Whereas *X. tropicalis* extract did not affect spindle length over the course of the experiment, addition of *X. laevis* extract caused rapid growth of *X. tropicalis* spindles, by ~5 μm in length within 2 min, and to the size of premixed (75% *X. laevis*, 25% *X. tropicalis*) reactions within 5 min (Fig. 4 A). Reciprocally, the addition of *X. tropicalis* extract to preformed *X. laevis* spindles rapidly shrank them to the size of the premixed controls, whereas addition of *X. laevis* extract did not (Fig. 4 B). The added extract tubulin appeared to incorporate at the plus ends of growing microtubules in the central spindle (Fig. 4, A and B). These results demonstrate that soluble cytoplasmic factors dynamically govern spindle length in *Xenopus* extracts, in agreement with results obtained in *Drosophila* melanogaster cells (Goshima et al., 2005), and indicate that nonmicrotubule spindle matrix elements determining length, if they exist, cannot be purely static structures (Chang et al., 2004).

We found that chromatin bead spindles and asters induced by addition of DMSO or RanGTP were smaller in *X. tropicalis* extracts compared with *X. laevis* extracts (unpublished data). To determine if differences in global microtubule dynamics could account for the differences in spindle and aster size, we measured the parameters of microtubules nucleated from chromosomes in *X. laevis* and *X. tropicalis* extracts (Table I). Overall, although the microtubule growth rate was ~20% slower in the *X. tropicalis* extracts (14.7 μm/min vs. 18.5 μm/min in *X. laevis*; P < 0.015 in t test), catastrophe and rescue frequencies were similar, and the calculated steady-state microtubule lengths were not significantly different (Table I; Verde et al., 1992). Another mode of microtubule turnover in the spindle is poleward microtubule flux, which is when microtubules coordinate polymerize at their plus ends and depolymerize at their minus ends as antiparallel microtubules slide apart (Khodjakov and Kapoor, 2005). We measured these rates using speckle microscopy to mark the spindle microtubule lattice, and found values in both extracts similar to those previously described for *X. laevis*.
Figure 4. Spindle length determination is highly dynamic in Xenopus extracts. (A) Spindles assembled in X. tropicalis extracts containing X-rhodamine tubulin were diluted with three volumes of X. laevis or X. tropicalis extract supplemented with Alexa Fluor 488 tubulin, and fixed for examination at various time points. Quantification of spindle length over time after mixing revealed steady-state spindle lengths were reached within ∼5 min, and they corresponded to those in the premixed control of 75% X. laevis 25% X. tropicalis extract. (B) The same experiment described in A, except that the spindles were assembled in X. laevis extract containing Alexa Fluor 488 tubulin, and diluted with X. tropicalis or X. laevis extract containing X-rhodamine tubulin. Quantification of spindle length over time after mixing is shown. Error bars are the SDs. Bars, 10 μm.

(Table I; 1.79 ± 0.33 μm/min for X. laevis; 2.25 ± 0.25 μm/min for X. tropicalis; Desai et al., 1998). Thus, our results indicate that the coordinated microtubule sliding with balanced plus end polymerization and minus end depolymerization are not significantly different in the two extracts.

What is the underlying cause of spindle size difference in the two extracts? One possibility is that we are unable to make precise enough measurements to distinguish potentially causal differences in the dynamics of microtubules in the two extracts. Alternatively, other microtubule dynamic parameters, such as the frequency of nucleation, pausing, or severing, may generate differences in spindle size (Srayko et al., 2006). Although different in morphology, centrosomal microtubules in the two extracts grew to similar lengths, whereas microtubule structures induced by taxol, DMSO, and RanGTP were significantly smaller in X. tropicalis extracts (unpublished data). An intriguing possibility is that extract factors in the two systems respond differently to microtubule stabilizing/destabilizing agents, including mitotic chromatin. We think that this is possible because we have identified extract factors, such as the microtubule plus-end binding protein Xorbit, whose depletion does not obviously affect centrosomally nucleated microtubules, but strongly destabilizes spindle microtubules (Hannak and Heald, 2006). Extract-dependent changes in the activity of spindle factors or their regulation caused by a different kinase/phosphatase balance or RanGTP signal surrounding chromosomes could locally alter microtubule stability and overall spindle size. The challenge will now be to identify molecules that can account for the observed differences in spindle size in the egg extracts and compare the activities of the orthologous factors between the two Xenopus species.
In conclusion, *X. tropicalis* provides molecular advantages over *X. laevis* as a genetically and proteomically tractable system that can be applied to address cellular biological questions using in vitro approaches. Although it could be expected that the smaller *X. tropicalis* eggs would have smaller spindles, our results show that this is because of a difference in cytoplasmic factors, rather than the size of the cell itself. By comparing cytoplasmic activities that are intrinsic to *X. laevis* and *X. tropicalis* extracts, new insights can be gained into mechanisms regulating cellular morphogenesis.

**Materials and methods**

Preparation of CSF extracts from *X. tropicalis*

CSF-arrested *X. tropicalis* extracts were prepared essentially as previously described for *X. laevis* (Murray, 1991; Desai et al., 1999), with the following exceptions. To induce egg laying, frogs were primed with 10 U of human chorionic gonadotropin (HCG) ~16 h before a hormone boost of 200 U HCG. Laying commenced ~4–5 h after the second HCG injection, and eggs were collected into water at 27–28°C, and eggs were collected into water at 27–28°C. Frogs were also squeezed

**Spindle size determination in mixed extract**

*X. laevis* and *X. tropicalis* extracts were mixed in different proportions and supplemented with either *X. laevis* or *X. tropicalis* sperm nuclei prepared by standard procedures (Murray, 1991) at a concentration of 500 sperm/μl, and X-rhodamine tubulin at 0.125 mg/ml. Cycling reactions were performed, and reactions were diluted into spindle fix (30% glycerol, 1× BRBB, and 0.5% Triton X-100), spun onto coverslips, fixed using a 60×/1.4 NA objective. Speckle movements were tracked on an inverted microscope (BX51; Olympus) and a cooled charge-coupled device camera (Orca II; Hamamatsu), and spindle lengths were measured using MetaMorph software (Molecular Devices). Spindle area measurements were made using thresholded images in MetaMorph. Mixing experiments were performed three independent times by three different investigators, and the results were averaged.

**Immunoprecipitation and mass spectrometry of Xn7**

The Xn7 polyclonal antibody was coupled to protein A dynabeads, as previously described (Maresca et al., 2005b). For immunoprecipitating Xn7, 110 μl of either *X. tropicalis* or *X. laevis* CSF extract was subjected to three successive 45-min incubations on ice with anti-Xn7–coated dynabeads. The beads from each round were pooled and washed extensively with X8 before eluting for 5 min at room temperature into SDS sample buffer and retrieving the beads on a magnet. Half of the supernatant was subjected to SDS-PAGE, the gel was stained with Coomassie blue stain (NuSep), and the indicated bands were excised and subjected to mass spectrometry at the University of California Berkeley Mass Spectrometry Facility.

**Dynamics of spindle size determination**

CSF reactions containing *X. laevis* sperm nuclei and 25 μl of *X. tropicalis* extract (with X-rhodamine tubulin) or *X. laevis* extract (with Alexa Fluor 488 tubulin) were cycled through interphase and back into metaphase by the addition of 25 μl of the same type of extract (no sperm). Once metaphase spindles had assembled, the extract was split into two tubes, each containing 25 μl of the reaction mixture. As a control, 75 μl of the same type of extract supplemented with the other labeled tubulin was added to one of the tubes, while 75 μl of the opposing extract was added to the other 25-μl reaction. Each of the 100-μl reactions were quickly split into 4 separate tubes, and spindles from each condition were diluted and spun down onto coverslips as described in Spindle size determination in mixed extract for imaging and length measurements. All spindle reactions were incubated at ~23°C.

**Microtubule dynamics and flux measurements**

Centrosomes were prepared from KE37 cells as previously described (Chretien et al., 1997) and stored at ~80°C. CSF extracts were prepared as described in the section Preparation of CSF extracts from *X. tropicalis*, and supplemented with either rhodamine tubulin (Cytoskeleton) or Alexa Fluor 488 tubulin (a gift from T. Whitman, University of California, San Francisco, San Francisco, CA) at 0.2 mg/ml. Centrosome reactions consisted of 8 μl of extract plus labeled tubulin, 1 μl of centrosomes, and 1 μl of Oxirase. *X. laevis* extracts were incubated at ~20°C, and *X. tropicalis* extracts were incubated at ~23°C. To image centrosomes, 1 μl of extract was squashed under a 22-mm coverslip and imaged using a 100×/1.3 NA objective. All glassware was base cleaned and stored in 95% ethanol until the time of use. Images were acquired every 3 s for 1–3 min. Microtubule lengths were measured if the microtubule could be followed for at least five successive frames. Microtubule lengths were measured as the distance from the center of the centrosome to the tip of the microtubule. Dynamics measurements were calculated using a custom-made spreadsheet (a gift from R. Tournebize, Institute Pasteur, Paris, France). Calculation of the mean power and mean power were made by manual inspection of raw growth and shrinkage measurements.

**MT flux measurements**

MT flux measurements were made using fluorescence speckle microscopy by incubation of cycled spindles with rhodamine-labeled tubulin at a concentration of 1 μg/ml (Kapoor and Mitchison, 2001). 2 μl of extract was gently squashed under a 22×22-mm coverslip previously outlined using a PAP pen. Images of speckles were collected every 5 s for 2 min using a 60×/1.4 NA objective. Speckle movements were tracked on kymographs to calculate the rate of flux. Measurements were made from at least five separate spindles from three different extracts for both *X. laevis* and *X. tropicalis*.

We thank members of the Heald lab, especially J. Soderholm, for helpful discussions and S. Zhou for mass spectrometry analysis.

This work was supported by National Institutes of Health (NIH) grants to R. Heald (GM057839 and DP1OD00081) and R.M. Harland (GM066841). M.D. Blower is supported by the Damon Runyon Cancer Research Foundation.
References


