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substituted with the non-phosphorylatable amino-acid alanine in all heptads. Cells carrying this allele were similar to <italic>lsk1</italic>Δ in the SIN, and were unable to complete cytokinesis upon perturbation of the cell division machinery. We conclude that Ser-2 phosphorylation is necessary for regulation of cytokinesis.

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A Cyclin-Dependent Kinase that Promotes Cytokinesis through Modulating Phosphorylation of the Carboxy Terminal Domain of the RNA Pol II Rpb1p Sub-Unit

Jim Karagiannis¹, Mohan K. Balasubramanian¹,².

Abstract

In *Schizosaccharomyces pombe*, the nuclear-localized kinase, Lsk1p, promotes cytokinesis by positively regulating the Septation Initiation Network (SIN). Although a member of the cyclin-dependent kinase (CDK) family, neither a cyclin partner nor a physiological target has been identified. In this report we identify a cyclin, Lsc1p, that physically interacts and co-localizes with Lsk1p. Furthermore, *lsk1Δ*, *lsc1Δ*, as well as kinase-dead *lsk1-K306R* mutants, display highly similar cytokinesis defects. Lsk1p is related to CDKs that phosphorylate the carboxy-terminal domain (CTD) of the largest sub-unit of RNA polymerase II (Rpb1p). Interestingly, we find that Lsk1p and Lsc1p are required for phosphorylation of Ser-2 residues found in the heptad repeats of the CTD. To determine if Rpb1p could be a physiological target, we replaced the native *rpb1* gene with a synthetic gene encoding a Rpb1p protein in which Ser-2 was substituted with the non-phosphorylatable amino-acid alanine in all heptads. Cells carrying this allele were similar to *lsk1Δ* mutants: They were viable, displayed genetic
Abstract

Cancer is recognized to be a family of gene-based diseases whose causes are to be found in disruptions of basic biologic processes. An increasingly deep catalogue of canonical networks details the specific molecular interaction of genes and their products. However, mapping of disease phenotypes to alterations of these networks of interactions is accomplished indirectly and non-systematically. Here we objectively identify pathways associated with malignancy, staging, and outcome in cancer through application of an analytic approach that systematically evaluates differences in the activity and consistency of interactions within canonical biological processes. Using large collections of publicly accessible genome-wide gene expression, we identify small common sets of pathways – Trka Receptor, Apoptosis response to DNA Damage, Ceramide, Telomerase CD40L and Calcineurin – whose differences robustly distinguish diverse tumor types from corresponding normal samples, predict tumor grade, and distinguish phenotypes such as estrogen receptor status and p53 mutation state. Pathways identified through this analysis perform as well or better than phenotypes used in the original studies in predicting cancer outcome. This approach provides a means to use genome-wide characterizations to map key biological processes to important clinical features in disease.

Terms

doi:10.1371/journal.pone.0000425
XHTML (2) vs HTML (5)

XHTML for machine-created documents
Micro/macroformats

Standard document layout - maps to NLM DTD
Microformats for DOI, PMID, other identifiers
COinS
RDFa?
Colony PCR reactions confirming the integration of <i>rpbl-12xCTD</i> and <i>rpbl-12xS2ACTD</i> constructs. Cells of <i>rpbl-12xS2ACTD cdc14-118</i> double mutants are inviable at 30°C due to cytokinesis failure. (A) Cells of the indicated genotypes were cultured at 25°C for 2 days on agar plates, followed by shifting to 30°C for 5 hours. The proportion of cells containing multiple nuclei was calculated by manual inspection.

Mutation of Ser-2 to Glutamate in the heptad repeats of the carboxy-terminal domain of Rpblp is lethal in <i>S. pombe</i>. The mean percentage of cells (+/- standard deviation) displaying the indicated number of nuclei five hours after shift from 25°C to 30°C is shown.

We would like to thank Makoto Kimura and Akira Ishihama for the pREP41-<i>fcpl</i> plasmid used in this study as well as K. Gull for helpful discussions.

This work was supported by research funds from Temasek Life Sciences Laboratory. JK is a recipient of a Singapore Millennium Foundation fellowship.
Distributed conversations

Postgenomic
Normalised URLs to identify articles
By hook or by crook? Morphometry, competition and cooperation in rodent sperm.

BACKGROUND: Sperm design varies enormously across species and sperm competition is thought to be a major factor influencing this variation. However, sperm traits is still poorly understood. The sperm of most murid rodents are characterised by an apical hook of the sperm head that varies markedly in extent. The woodmouse Apodemus sylvaticus (Muridae), the highly reflected apical hook of sperm is used to form sperm groups, or “trains,” which exhibited increased velocity compared to individual sperm.

METHODOLOGY/PRINCIPAL FINDINGS: Here we use a comparative study of murine rodent sperm and demonstrate that sperm cooperation are likely to be general adaptations to sperm competition in rodents. We found that species with relatively larger testes, and therefore more intense, more reflected apical sperm hook. In addition, we show that sperm groups also occur in rodents other than the European woodmouse.

CONCLUSION: Sperm cooperation is more widespread than assumed so far and highlight the importance of diploid versus haploid selection in the evolution of sperm.

PLoS One / Postgenomic mashup

Chris Surridge has an interesting post over at the PLoS blog about the comments (or the lack thereof) on PLoS One papers. He mentions one particular discussion thread associated with it on Gene Expression but no real comments on the...

Swim Sperm, Swim Together, Swim Like the Wind!

It would appear that today will be Sex Day at Pure Pedantry. So be it. I didn't know this but mouse and rat sperm have funny shaped hooks at their sperm from a variety of mouse and rat species (click to enlarge). A) Variation...
Introduction

Sperm vary enormously in size and shape across taxa\(^1\). This variation is largely unexplained, but is thought to be determined by three factors: (i) phylogeny\(^2\); (ii) mode of fertilisation (internal vs external\(^3\)); and (iii) post-copulatory sexual selection i.e., sperm competition and cryptic female choice\(^4\). There is strong empirical
citation...
Citations

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Clathrin light chain: importance of the conserved carboxy terminal domain to function in living cells.

Wang J, Wang Y, O'Halloran TJ

Traffic. 2006 Jul ; 7(7): 824-32

Clathrin triskelions assemble into coats capable of packaging membrane and receptors for transport to intracellular destinations. A triskelion is formed from three heavy chains bound to three light chains. All clathrin light chains (clc) contain an acidic amino terminal domain, a central coiled segment, and a carboxy terminal domain conserved in amino acid sequence. To assess their functional contribution in vivo, we expressed tagged segments of the Dictyostelium clcA in clc-minus Dictyostelium (clc null) cells. We examined the ability of these clcA fragments to rescue clathrin phenotypes, to cluster into punctae on membranes, and to bind to the heavy chain. When expressed in clc null cells, a clcA fragment containing the acidic amino terminal domain and the central coiled domain bound heavy chain but was dispensable for clathrin function. Instead, the carboxy terminal domain of clcA was a critical determinant for association with punctae, for clathrin function and for robust binding to the heavy chain. A 70 and 49 amino acid carboxy terminal fragment was necessary and sufficient for full function, and for localization into punctae on intracellular membranes. A shorter 34 amino acid carboxy terminal fragment could distribute into punctae but failed to rescue developmental deficiencies. These results reveal the importance of the carboxy terminal domain of the light chain in vivo.
References


Fission yeast Clp1p phosphatase regulates G2/M transition and coordination of cytokinesis with cell cycle progression.
Background: In Saccharomyces cerevisiae the mitotic-exit network (MEN) functions in anaphase to promote the release of the Cdc14p phosphatase from the nucleolus. This release causes mitotic exit via inactivation of the cyclin-dependent...
At the same time, the bill establishes a common fund comprising up to 5% of the agency's total budget.

But it is, says NIH director Elias Zerhouni, “a renewed vote of confidence in the NIH and really a turning point.”

But two events occurred last week that, between them, have the potential to mark a turning point for the world's largest biomedical research agency.

David Obey (Democrat, Wisconsin), a long-time champion of the NIH, will be chairing the relevant subcommittee of the House of Representatives, as well as the full appropriations committee.

For many biomedical researchers, funding levels represent the clearest indication of whether goodwill has been restored.

Given this sort of backing, and last week's events, it is beginning to look as if the NIH could enjoy a happier and more productive new year than might have been envisaged just a few months ago.

His sentencing on 22 December, along with new, tighter agency rules, may begin to disperse the cloud that has been hanging over the agency as a result of the actions of a few dozen NIH researchers.

In particular, the bill requires the NIH director to submit biennial reports to Congress, detailing the work of its 19 institutes and centres, and justifying their priorities.

In this regard, the omens are good, particularly given the allocation of critical committee positions in the new Congress.
Data/Text Mining

Document visualisation
Search indexing
Citation visualisation
Semantic search

Machine-readable: semantic abstracts; understanding
bioperl-db-1.5.2_100/scripts/biosql/load_seqdatabase.pl - 3 identical

```perl
182:    --format embl
    # Bio::ClusterIO stream with -format => 'unigene'
    --format ClusterIO::unigene
```

search.cpan.org/.../bioperl-db-1.5.2_100.tar.gz - Artistic - Perl

bioperl-1.4/Bio/Cluster/UniGene.pm - 5 identical

```perl
60:    unigene_id() - set/get unigene_id
```

```perl
26:    $stream = Bio::ClusterIO->new('-file' => "Hs.data",
    '-format' => "unigene");
    # note: we quote -format to keep older perl's from complaining.
```

freshmeat.net/.../bioperl-1.4.tar.gz - Artistic - Perl - More from bioperl-1.4.tar.gz »

bioperl-1.5.1/Bio/ClusterIO/unigene.pm - 5 identical

```perl
1:    # unigene.pm,v 1.23.2.1 2005/10/09 15:16:20 jason Exp
    # BioPerl module for Bio::ClusterIO::unigene
    #
19:    Bio::ClusterIO::unigene - UniGene input stream
```

bioperl.org/DIST/bioperl-1.5.1.tar.bz2 - Artistic - Perl - More from bioperl-1.5.1.tar.bz2 »

bioperl-1.2.3/Bio/Cluster/UniGenel.pm - 6 identical

```perl
108:    Function: Returns the title associated with the object.
    Example: $title = $unigene->title or $unigene->title($title)
    Returns: A string
```

```perl
126:    Function: Returns the gene associated with the object.
    Example: $gene = $unigene->gene or $unigene->gene($gene)
    Returns: A string
```

search.cpan.org/.../bioperl-1.2.3.tar.gz - Artistic - Perl - More from bioperl-1.2.3.tar.gz »
Abstract

In *Schizosaccharomyces pombe*, the nuclear-localized kinase, Lsk1p, promotes cell division by regulating the **Septation Initiation Network (SIN)**. Although a member of the **cyclin** family, neither a **cyclin** partner nor a physiological target has been identified. In this study, we found that Lsc1p, that physically interacts and co-localizes with Lsk1p. Furthermore, *lsk1Δ*, *lsclΔ*, and *lsk1-K306R* mutants, display highly similar **cytokinesis** defects. Lsk1p is related to **CDK** carboxy-terminal domain (CTD) of the largest sub-unit of RNA polymerase II (Rpb1p).

Lsk1p and Lsc1p are required for **phosphorylation** of Ser-2 residues found in the heptad repeats of Rpb1p. To determine if Rpb1p could be a physiological target, we replaced the native *rpb1* gene encoding a Rpb1p **protein** in which Ser-2 was substituted with the non-phosphorylatable Ser-1 in all heptads. Cells carrying this allele were similar to *lsk1Δ* mutants: They were unable to interact with the **SIN**, and were unable to complete **cytokinesis** upon perturbation of the **machinery**. We conclude that **Ser-2** **phosphorylation** of the CTD heptads plays a novel role in the regulation of **cytokinesis**.

Terms

doi:10.1371/journal.pone.0000433
Avoid PDF

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Zip archive including supplementary data
rel=offline-resource
Able to extract data
**Figure S3**

*rpb1-12xS2ACTD cdc14-118* double mutants are inviable at 30°C due to cytokinesis indicated genotype were freshly streaked to YES plates and incubated for 24 hours at 30°C. Cells of the indicated genotype were grown to mid-log phase at 24°C and then shifted to 32°C being fixed and stained with DAPI (nuclei) and aniline blue (cell wall/septa). Bar, 10 microns.

(1.52 MB TIF)

**Figure S4**

Mutation of Ser-2 to Glutamate in the heptad repeats of the carboxy-terminal domain *pombe*. (A) Heterozygous diploid strains bearing the *rpb1-12xS2ECTD* mutation were selected individual asci were then separated and grown on YES plates for 3 days at 32°C. The plating displaying the observed 2:2 segregation of viable to inviable progeny are shown. (B) For the colony morphology observed when inviable spores were examined by brightfield microscopy.
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Table 3. Mean percentage of cells (±standard deviation) displaying the indicated number of septa five hours after shift from 24°C to 34°C (n=3).
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doi:10.1371/journal.pone.0000433.t003
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   - Multiway SLCA-based Keyword Search in XML Data

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   - SPARQ2L: Towards Support For Subgraph Extraction Queries in RDF Databases

10. Amr El Abbadi (University of California, Santa Barbara)
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Open Data/ Collaboration

Shared institutional /funding repositories while worked on. Opened up to public once published. Linked by DOI from papers, with granularity (fragment identifiers/MPEG7?) Access to data - high bandwidth or sneakernet
Collaboration

Shared workspace and data
Wiki for collaborative knowledge store
Electronic notebooks (structured)
Google Docs for editing papers
Zotero + Connotea or similar

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Assessing Contribution

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h-index
Open source software
Reputation
Identity
Ownership of ideas