The Structure of Abstracts



Definition: a brief and objective representation of a document



An abstract allows readers to:

determine the content of a document quickly
work out its relevance to them

find the document through relevant keyword searches

decide whether they need to read the entire document





The 4-part structure of an abstract

1. Background



- 1. Background
- 2. Method



- 1. Background
- 2. Method
- 3. Result



- 1. Background
- 2. Method
- 3. Result
- 4. Conclusion



Cel

A Systematic Survey Identifies Prions and Illuminates Sequence Features of Prionogenic Proteins

Simon Alberti,^{1,5} Randal Halfmann,^{1,3,5} Oliver King,^{1,4} Atul Kapila,^{1,3} and Susan Lindquist^{1,2,3,*} ¹Whitehead Institute for Biomedical Research, Cambridge, MA 02142, USA ²Howard Hughes Medical Institute, Cambridge, MA 02139, USA ³Department of Biology, Massachusetts Institute of Technology, Cambridge, MA 02139, USA ⁴Boston Biomedical Research Institute, Watertown, MA 02472, USA ⁵These authors contributed equally to this work *Correspondence: lindquist_admin@wi.mit.edu DOI 10.1016/j.cell.2009.02.044

SUMMARY

Prions are proteins that convert between structurally and functionally distinct states, one or more of which is transmissible. In yeast, this ability allows them to act as non-Mendelian elements of phenotypic inheritance. To further our understanding of prion biology. we conducted a bioinformatic proteome-wide survey for prionogenic proteins in S. cerevisiae, followed by experimental investigations of 100 prion candidates. We found an unexpected amino acid bias in aggregation-prone candidates and discovered that 19 of these could also form prions. At least one of these prion proteins, Mot3, produces a bona fide prion in its natural context that increases population-level phenotypic heterogeneity. The self-perpetuating states of these proteins present a vast source of heritable phenotypic variation that increases the adaptability of yeast populations to diverse environments.

INTRODUCTION

The prion hypothesis posits that biological information can be replicated solely through self-propagating conformations of proteins. Though it was initially conceived to explain baffling neurodegenerative diseases in mammals (Griffith, 1967; Prusiner, 1982), it has since grown to encompass a number of non-Mendelian traits in fungi (Ross et al., 2005b; Shorter and Lindquist, 2005; Shkundina and Ter-Avanesyan, 2007). All known prions, except for the initially discovered disease-causing prion PrP, are benign, and in some cases can confer selectable advantages (Saupe proteins as metastable cellular switches of protein function.

The realization that protein conformational switches could 15 years (Wickner, 1994), yet only a few proteins with this

capacity have been discovered (Shorter and Lindquist, 2005; Du et al., 2008). Most of these have been found in the yeast S. cerevisiae, with the [PS/+] element being the best understood. [PSI+] is caused by an amyloid-like aggregated state of the translation-termination factor Sup35p. In the prion state, the majority of Sup35p molecules are inactive, resulting in increased levels of nonsense suppression (Liebman and Sherman, 1979; Patino et al., 1996) and programmed frameshifting (Namy et al., 2008). This gives rise to RNA stability changes and functionally altered polypeptides and consequently to phenotypes that can be advantageous under diverse conditions (Eaglestone et al., 1999; True et al., 2004). Remarkably, the ability of Sup35p to switch into a prion conformation, and the regulation of that switch by the protein remodeling factor Hsp104p, have been conserved for over 800 million years of fungal evolution (Chernoff et al., 2000; Zenthon et al., 2006).

Three other amyloid-based prions, formed by the functionally diverse proteins Ure2p, Rng1p, and Swi1p, have been described in S. cerevisiae. Ure2p regulates nitrogen catabolism; its prion state, [URE3], attenuates this activity resulting in the constitutive utilization of poor nitrogen sources (Aigle and Lacroute, 1975; Wickner, 1994). The Rng1p protein in its prion state, [RNQ+] (also called [PIN+]), enhances the inducibility of other prions (Derkatch et al., 2000; Bradley et al., 2002). [SWI+], the most recently discovered prion, is caused by an inactive state of the chromatin remodeling factor Swi1p (Du et al., 2008). Intriguingly, [SWI+] represents the first established link between chromatinbased and prion-based epigenetics, although a biological relevance of this connection remains to be elucidated. Indeed, for all of these prion proteins, the putative functionality of their prion forms is highly debated (Nakayashiki et al., 2005).

The conformational duality of amyloid-based prions resides in structurally independent prion-forming domains (PrDs) (Edskes et al., 2000; True and Lindquist, 2000; True et al., 2004). The et al., 1999; Li and Lindquist, 2000; Santoso et al., 2000; Sondself-templating property of prions makes them both conforma- heimer and Lindquist, 2000). These PrDs are modular and can tionally and epigenetically dominant, and positions prion-forming be transferred to other proteins to create novel prions (Li and Lindquist, 2000). They have a very unusual amino acid composition: enriched for polar residues such as glutamine (Q) and asparprovide a means for inheritance of phenotypes dates back agine (N) and depleted of hydrophobic and charged residues. This composition promotes a disordered molten-globule-like The Summary consists of a single paragraph of fewer than 150 words. It should clearly convey the conceptual advance and significance of the work to a broad readership. In particular, the abstract should contain a brief background of the question, a description of the results without extensive experimental detail, and a summary of the significance of the findings. References should not be cited in the Summary.

Background

Background

Method

Background

Method

Result

Background

Method

Result

Conclusion

nature > letters > article



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Published: 08 November 2017

Parallel palaeogenomic transects reveal complex genetic history of early European farmers

Mark Lipson ⊠, Anna Szécsényi-Nagy ⊠, [...] David Reich ⊠

Nature **551**, 368–372(2017) Cite this article

1823 Accesses 83 Citations 268 Altmetric Metrics



Ancient DNA studies have established that Neolithic European populations were descended from Anatolian migrants who received a limited amount of admixture from resident hunter-gatherers. Many open questions remain, however, about the spatial and temporal dynamics of population interactions and admixture during the Neolithic period. Here we investigate the population dynamics of Neolithization across Europe using a high-resolution genome-wide ancient DNA dataset with a total of 180 samples, of which 130 are newly reported here, from the Neolithic and Chalcolithic periods of Hungary (6000–2900 BC, n = 100), Germany (5500– 3000 BC, *n* = 42) and Spain (5500–2200 BC, *n* = 38). We find that genetic diversity was shaped predominantly by local processes, with varied sources and proportions of hunter-gatherer ancestry among the three regions and through time. Admixture between groups with different ancestry profiles was pervasive and resulted in observable population transformation across almost all cultural transitions. Our results shed new light on the ways in which gene flow reshaped European populations throughout the Neolithic period and demonstrate the potential of timeseries-based sampling and modelling approaches to elucidate multiple dimensions of historical population interactions.

> Write About Science

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Background —

Question/— Knowledge gap

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Background ——

Question/ Knowledge gap Approach/ Method

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> Write About

Background — Question/— Knowledge gap Approach/ _____ Method

Results/ _____ discussion

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Write About Science



1. Background – Introduction, Purpose, Importance



- 1. Background Introduction, Purpose, Importance
- 2. Method Design



- 1. Background Introduction, Purpose, Importance
- 2. Method Design
- 3. Results Outcome



- 1. Background Introduction, Purpose, Importance
- 2. Method Design
- 3. Results Outcome
- 4. Conclusion Discussion, Significance



Exercise





THE ASTROPHYSICAL JOURNAL LETTERS

Magnetic Connectivity between the Light Bridge and Penumbra in a Sunspot

Song Feng^{1,2} , Yuhu Miao³, Ding Yuan³, Zhongquan Qu², and Valery M. Nakariakov^{4,5} Published 2020 April 7 • © 2020. The American Astronomical Society. All rights reserved. <u>The Astrophysical Journal Letters, Volume 893</u>, <u>Number 1</u>





Background -----



Background → Question



Background → Question →

Main approach



Background>	A light bridge is a prominent structure commonly observed within a sunspot. Its presence usually triggers a wealth of dynamics in a sunspot and has a lasting impact on sunspot
Question ——	evolution. However, the fundamental structure of light bridges is still not well understood.
Main	In this study, we used the high-resolution spectropolarimetry data obtained by the Solar Optical Telescope on board the Hinode satellite to analyze the magnetic and thermal
approach	structure of a light bridge at AR 12838. We also combined the high-cadence 1700 angstron
	channel data provided by the Atmospheric Imaging Assembly on board the Solar Dynamic
Results/	shift patches at two ends of this bridge: this pattern appears to be the convective motion
	directed by the horizontal component of the magnetic field aligned with the spine of the
	bridge. Paired upward and downward motions imply that the light bridge could have a two
	intensity of the 1700 angstrom bandpass were detected at two ends, which overlapped the
	paired blue- and redshift patches. The oscillatory signals at the light bridge and the
	the photosphere, the periodicity seems to have a common origin from underneath the
	sunspot. Therefore, we infer that the light bridge and penumbra could share a common
	magnetic source and become fragmented at the photosphere by magnetoconvection.



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discussion	intensity of the 1700 angstrom bandpass were detected at two ends, which overlapped the
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	the photosphere, the periodicity seems to have a common origin from underneath the
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Conclusion \rightarrow	magnetic source and become fragmented at the photosphere by magnetoconvection.





ARTICLES https://doi.org/10.1038/s41929-020-00533-6

Shape-selective C-H activation of aromatics to biarylic compounds using molecular palladium in zeolites

Jannick Vercammen[®]¹, Massimo Bocus², Sam Neale², Aram Bugaev[®]³, Patrick Tomkins¹, Julianna Hajek², Sam Van Minnebruggen¹, Alexander Soldatov[®]³, Andraž Krajnc⁴, Gregor Mali[®]⁴, Véronique Van Speybroeck[®]²[™] and Dirk E. De Vos[®]¹[™]



Check for updates

Asymmetric domino electrophilic halocyclizations are highly useful in the synthesis of structurally complex and pharmaceutically important compounds. Although some studies aimed at catalytic and enantioselective polyene cyclizations are documented, the chiral products have been limited to fused rings. Here, we report an efficient and highly enantio- and diastereoselective halocyclization and spiroketalization of olefinic keto-acids. Instead of electron-deficient thiourea, in this study electron-rich thiourea catalysts are crucial for high enantioselectivity. The resulting spiro compounds are privileged cores of many drugs and natural products. Our experimental and computational studies revealed that the reaction proceeded via a double dynamic–kinetic resolution mechanism. We anticipate that this work will stimulate the synthesis of other multifunctional compounds via electrophilic halocyclization.



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