PHYSARUM NEWSLETTER

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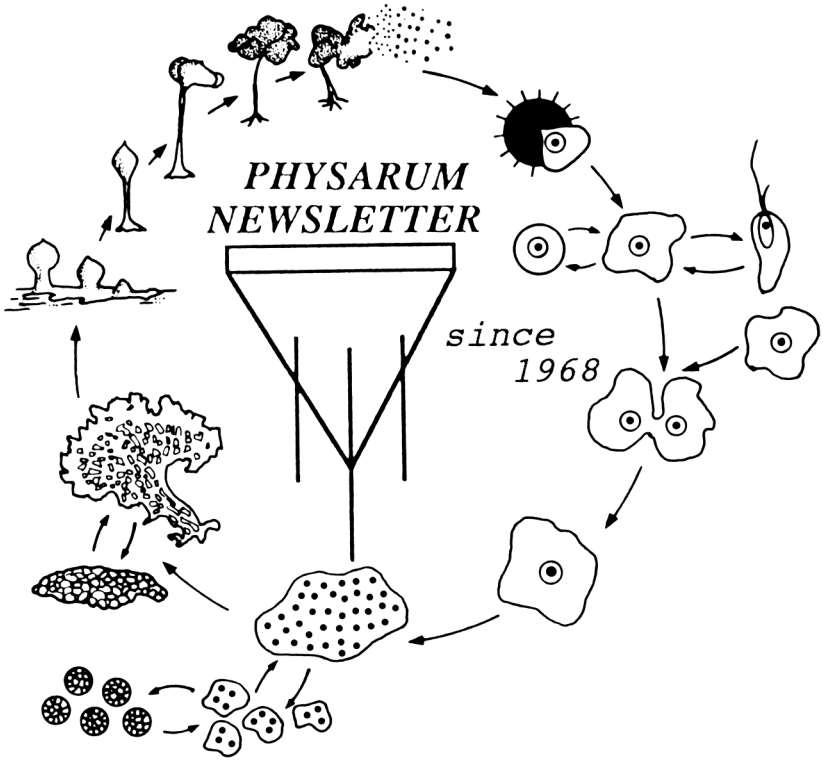

PHYSARUM NEWSLETTER

Volume 38, Number 1 December, 2006

The ***PHYSARUM*** **NEWSLETTER** (**PNL**) is published on a non-profit basis. It is intended to inform researchers and other interested readers about recent discoveries concerning Physarum polycephalum and other myxomycetes. **PNL** is published once or twice yearly with titles and abstracts of recent publications, notices of events (primarily meetings) of interest to its readership, etc. Brief reviews or papers describing research results, special techniques for culturing the organism, and/or technical details that might not otherwise be published are welcome and may be sent to any of the members of the editorial group:

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Financial support of the **PNL** derives from contributions by the readership. We request contributions ($10 US) be made in the form of checks made payable to **M. R. Adelman**; please use the "note" section of the check to indicate that it is for **PNL**.

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*The Physarum Newsletter (**PNL**) was established during the 1968 Physarum Conference held in Madison, Wisconsin, as a publication that would provide a forum for scientists interested in research involving myxomycetes. The format for **PNL** was established by the first editor, **Oddar F. Nygaard**. From its inception **PNL** has provided its readership with a survey of the literature dealing with Physarum and other myxomycetes. In 1971 Nygaard was succeeded as editor of **PNL** by his colleague at Case Western Reserve University, **Thomas E. Evans**. Evans expanded the size and distribution of **PNL** and, under his direction, **PNL** became a coordinating center for organizing biennial meetings of Physarum scientists. When the timely distribution of **PNL** to readers in Europe became a problem, **Richard Braun** agreed to handle European distribution from Lausanne. In 1983, **Henry Aldrich** (Department of Microbiology & Cell Science, University of Florida) became editor; he managed the production and distribution of **PNL** for five years before transferring these responsibilities to **Claude Nations** (Biological Sciences, Southern Methodist University). Nations enlisted associate editors **Ulrike** and **Friedhelm Achenbach** (Germany) and **Fumio Sawada** (Japan); this not only facilitated more rapid distribution of **PNL** but also encouraged international participation of the readership in the continuing development of **PNL**. In March 1991, with the retirement of Sawada, **Shigeyuki Kawano** took over the post of Associate Editor in Japan. With the retirement of Nations, **Mark R. Adelman** took over as Editor of **PNL** in early 1993. In 2000 **Eggehard Holler** took over from the Achenbachs, joining Kawano as Associate Editors.*

*Modified from C. Nations, **PNL** 24:1 1992*

EDITOR'S CORNER

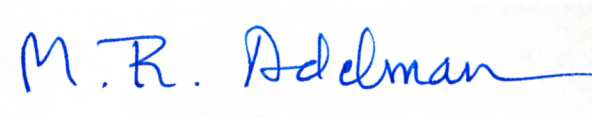
The preparation of this issue of PNL is truly a bittersweet task. After serving as Editor for over a decade, I am, as previously announced, stepping down (in preparation for my retirement from the faculty at USUHS). Hence this will be the last issue of PNL that I will prepare. Although none of you has indicated a willingness to take on this 'labor of love', it is STILL my hope that this will NOT be the last issue of PNL. [Until the matter is resolved, I will transfer all archival material to Tom Evans, who has graciously offered to arrange for our records to be preserved at Case Western Reserve University.] At a point where the availability of the complete *Physarum* genome (see page 1) brings promise of a re-invigoration of research on 'our' organism, it seems to me especially important that we maintain a means of communication amongst members of the *Physarum* cummunity as a whole. While it is now exceedingly easy for individuals and small groups to remain in daily (even hourly) contact, I have always thought that the PNL served a unique purpose in that it allowed (and thus urged) all who work on *Physarum* a relatively simple means of maintaining some overview sense of the variety of questions that we all have been exploring. It was for much the same reason that I always found *Physarum* Workshops to be so valuable and enjoyable. And, just as I expect those workshops to be 'reborn' in the near future, so I expect that some version of PNL will re-appear. When these cherished entities 'excyst', it will probably be in altered format and, hopefully, with renewed energy and sense of purpose.

With that presumed future in mind, I have taken the liberty of preparing this issue of PNL in a fully digital format for the first time. Since 1993 I have carried on the tradition of producing each issue of PNL by the venerable 'copy - cut&paste-duplicate-snailmail' method, even though I recognized how thoroughly unmodern and inefficient that approach had become. It was always fun to gather together the year's worth of accumulated reprints, read (or skim) those not read, number and file them, make a copy of the first page, then cut and paste the abstracts, etc. And to do a literature search for papers that you had not sent me and/or I had not 'found' in my own, quite-targeted, weekly literature searches. In the past few years we have all slipped away from the old ways. Very few of you have been sending me reprints (whether hard copy or Emailed pdf versions). And I have long since ceased to do my own regular searches, first because I already have more to read than I can ever hope to 'finish' and, second because computerized literature searches are so easily done a month or so before the abstracts are needed. But I had retained the old way of actually printing out a copy of each 'found' treasure, then doing the cut/paste, etc. For this issue, all has been done without any such printing, cutting, pasting and so forth. The cutting and pasting was of the digital files our library (LRC) sent me. You will each receive this PNL by Email as pdf. But, since I do not have Email addresses for each of you, and because some of the adresses I have may be inaccurate, AND as one final act of defiance of the new, I will also send you each a hardcopy by snailmail! I still find much pleasure in the scholarly act of doing such a 'global' search, selecting according to some theme(s) and informing my colleagues of the results. It can be done more efficiently than it has been done in the past, and perhaps this version will prove a sufficient stimulus to one of you to take up the mantle!

Alternatively, perhaps our website (see page 2) is the appropriate mode by which to effect the kind of communication that PNL has achieved. Perhaps a portion of that website [or its successor(s)] should/will be a BLOG (or a series of BLOGS!). It is up to those of you who carry on with *Physarum* research to think about and make such decisions. I have indicated my intention to continue maintaining our website for several more years; but I would be delighted if someone expressed tne desire to share that 'labor of love', or even take it over! So please consider yourselves empowered - or challenged…

Another aspect of the nature of this task is the fact that I have transmitted to you a number of issues with pieces in memorium of colleagues who are no longer with us. In this issue I have the bittersweet pleasure of including an 'In Memorium' of Professor Noburô Kamiya (page 4). Professor Kamiya was a pioneer in what many of us used to call 'primitive motility'. I had the pleasure of working for him when I was an undergraduate, still have - and cherish - a photocopy of his masterful monograph on Protoplasmic Streaming, and was distressed - after learning of his death some years ago - at my inability to find an obituary suitable for inclusion in PNL. In this issue, thanks to his son, Ritsu Kamiya, I am able to send you a suitable 'In Memorium' of Professor Kamiya. There is a kind of symmetry - and a sense of continuity - in this that I find quite satisfying and that I know would please not just Professor Kamiya and the many *Physarum* workers who came before him, but will also please the many like me who recall him. And, I hope, it should serve to remind the many who may not know of his work that we are all part of a continuum, a community that owes much to one another but also to *Physarum*.

The brisk chilly airs of another December are upon us here in Bethesda. The various year-end holidays and celebrations approach. We make plans and have great hopes for the new year. I wish you all - as always - the very best in all of your endeavors.



Physarum Genome Project Update

There has been a LOT of progress! As you know, we decided to use our website as a resource by which the community could be kept informed of this progress and several Emails have been posted there. Lead by Jonatha Gott and Gerard Pierron, a series of "progress reports" are being posted, aimed at showing those of us who are not genomics experts, how to use the available data. This will, in my opinion, serve as an invaluable impetus, helping non-experts try out ways in which to use the genomic data (and tools) to answer a series of questions that have resided in our individual "to-do"lists for varying periods of time. I may even do some (primitive) data-mining myself!! I urge each of you to check out the Genomics page from time to time, not only to see what is being done, but also to see if you might want to use some of these newly-available (to the *Physarum* community) tools. The direct URL is:

http://www.educationalassistance.org/Physarum/Genome/Genome.html

*PHYSARUM*PLUS - OUR WEBSITE

If you haven't taken a look out our Website recently, why not take the time to do so now. The URL remains the same:

http://www.educationalassistance.org/Physarum/PhysarumPlus.html

[**NOTE: The old URL (http://bicmra.usuhs.mil/Physarum/PhysarumPlus.html) will remain active until I retire from USUHS, but it has, for some time now, redirected people to the 'new' one (above). If you 'google' *Physarum*, one or both of these apear at, or near, the top of the hits list!]

We continue to get queries from students, and the numbers are increasing, albeit not as fast as I would like. One of my goals remains to attract a few more young scientists to work on *Physarum*; our website is an important part of that effort. As always, I welcome any suggestions for improving the site and would be delighted to add any materials you care to send me. As Jonatha Gott has observed, once the *Physarum* Genome Project is more complete, progress in using that data will require the establishment of an internet-accessible database. While, in principle, this could be done as an adjunct to ***Physarum*Plus**, I agree with the working group proposal to establish "our" genome database as a spin-off from Dictybase. The site would of course be cross-linked with ***Physarum*Plus**.

Now, I ask your suggestions, contributions, and input on several aspects of ***Physarum*Plus**. As you know, I've chosen to keep the format very simple, so that our site is accessible to as many browsers as possible (right now I'm routinely checking with OmniWeb, Safari, Firefox, Netscape, and Internet Explorer, and would appreciate any suggestions you have as to other browsers I should add to my "routine test" list). In order to maximize the likelihood of cross-platform (and browser) compatibility, I continue to do everything in "pure" html, even though this is a bit time-consuming and limits (for me at least) the number of "bells and whistles" - something I personally regard as a plus! But I would welcome suggestions as to changes in format or "look", especially from those of you who have hands-on experience in setting up and maintaining websites. My goal is to "grow" the site and improve it over the next few years so that, when I step down as webmaster, it can easily be taken over by someone else; perhaps even wrapped into the genomic database website that will have been established in collaboration with the Dictybase folks.

There seem, to me, to be several elements of the website that require attention:

1. The ***Physarum* Life Cycle** section is in need of updating and expansion. I think a section on "ecology" would be desirable (if no one contributes, I'll take a cut at this, so **beware**!). And each of the major sections that I quickly put together several years ago need to be fleshed out, especially with the judicious addition of referenced articles. What I would like to see is several "expert contributions" written expressly for the site, containing references (URLs would be great), and attributed to the respective authors.

2. The **Images of *Physarum*** and **Movies of *Physarum*** pages should be expanded. Please send me any pictures you have that could be added to the site: a scanned image in jpeg format, with a brief caption would be great. And what about some movies or animations?? Send them as a Quicktime file or, if you only have the stuff on videotape, send that: I have capacity for converting videotape segments to Quicktime movies. Do any of you have facilities for converting motion picture film to digital format? If so, would you be willing to undertake the conversion of a limited number of films to digital so they could be put on the website? I believe we can increase the attractiveness of the site a LOT if we add more visual information, and movies are great in this regard.

3. If you have a job opening, please send me a notice of it. A simple Email (with a link to an internet version of the job offering if such exists) will get the ball rolling: I can usually post such a listing to the **Positions Available** section within 24 hours!

4. We should expand the section on **Experimental Protocols and Technical Tips**. I will be posting many of my 'protocols' documents here, once I retire and have a bit more time. Please send me yours. And, in a related matter, please give me some feedback on the following: We all have files of projects that never got finished (or published). Some of the information we have would be very valuable to potential new colleagues, but they have no access to it. What about setting up a new folder, with a title something like **Unfinished Business: Projects Someone Else Might Like to Take On**?

5. As our membership expands (and, with the genome project as a driving force, it ***will***), we need to continually update listings, cull old members who are no longer interested, and reach out to even more workers, including those who publish work involving *Physarum*, but do not regard themselves as Physarologists. Take a moment to check your own listing in the **Membership List**, scan the list to see if there are names of any who might best be eliminated, and send me suggestions of some folks I should contact to see if they'd like to be listed as members of our community.

BOTTOM LINE: ***Physarum*Plus** is OUR billboard. Help me make it better and more useful. It can pay dividends for all of us

In Memorium: NOBURÔ KAMIYA

Professor Noburô Kamiya, the former president of the Japan Society for Cell Biology and a member of the Japan Academy, passed away on January 10, 1999 in Osaka after suffering from serious anemia for one and a half years. Kamiya was born in Tokyo on July 23, 1913. In 1938, after graduation from the Department of Botany at the Imperial University of Tokyo , he was appointed as an exchange student of the DAAD (Deutscher Akademischer Austauschdient) and worked in the laboratory of Professor Ernst Kuster, a world-famous experimental cytologist, at the University of Giessen in Germany. He extended his knowledge on the structure and behavior of cells of lower plants in the living state. Unfortunately his stay in Giessen was interrupted suddenly by the outbreak of World War II. He was urged to leave Germany with other Japanese, and on September 4, 1939, he was on a refugee boat which left Bergen, Norway for Yokohama via New York and the Panama Canal.

He described his very interesting experiences in the prefatory article in the Annual Review of Plant Physiology, Plant Molecular Biology in 1989. Instead of returning to Japan he decided to continue his research work in the United States and left the refugee boat at New York. He immediately posted a letter to Professor William Seifriz at the University of Pennsylvania asking about the possibility of working in his laboratory. To his great joy Professor Seifriz warmly accepted the young Japanese scientist with whom he was not acquainted.

It was in the laboratory of Seifriz that Kamiya encountered his lifelong companion organism, a slime mold *Physarum polycephalum*. He had a keen interest in the very active cytoplasmic movement observed in the plasmodium of this organism, and in only 3 months after his arrival in the United States, succeeded for the first time in measuring the motive force of this cytoplasmic streaming by means of his now famous double-chamber method, the first of his many elegant techniques. His astonishing achievement came at a time when other scientists were interested only in the velocity of cytoplasmic streaming. Kamiya began to understand cytoplasmic streaming in plant cells in terms of the motive force which is most fundamental in the mechanics of cell motility.

His happy time in the United States was again interrupted when war broke out with Japan in December 1941. However, even as a citizen of a hostile country, he was permitted to remain in the same home of Mrs. Collins on the campus of Haverford College. Under quite limited laboratory conditions, Kamiya constructed a simple but elegant measuring system to demonstrate the twisting of the plasmodial strand with alternation of clockwise twisting with a counterclockwise one. This was another interesting aspect of the dynamic nature of the protoplasm of this slime mold in addition to the shuttle streaming.

In June 1942, Kamiya was repatriated by an exchange boat between the USA and Japan. On returning to Japan, he taught for several years as a lecturer at the University of Tokyo (renamed from the Imperial University of Tokyo). In 1949, he was appointed professor of the Biology Department of Osaka University, a new department established by Professor Shiro Akabori, a famous biochemist. He chaired the Laboratory of Cell Physiology for 28 years. During this time he and his coworkers demonstrated that the motive force of the cytoplasmic streaming in the slime mold is driven by ATP as in the

case of muscle contraction and extracted from the plasmodium a contractile protein named plasmodial myosin B which is sensitive to ATP and capable of superprecipitation. He extended his work to the rotational cytoplasmic streaming in characean cells, and demonstrated that the force driving the streaming is a sliding force generated at the boundary between the inner surface of the immobile chloroplast layer and the streaming endoplasm. His premise that the structure responsible for the streaming should be at the sol-gel interface was confirmed by the finding of actin bundles by his pupils. He further succeeded in measuring the motive force of the rotational cytoplasmic streaming by another of his very sophisticated methods. He also measured water permeability of characean cells very accurately by using the transcellular osmosis method, and found the polar nature of the plasma membrane, the endoosmotic permeability being higher than the exoosmotic one. The osmoregulatory capacity of characean cells was also demonstrated by means of ligation of the cell with silk thread after transcellular osmosis. In addition to the fruitful achievements in his own research, he brought up about 30 graduate students who later worked in various fields of plant cell biology including cell motility, cell differentiation and membrane physiology as leading scientists not only in Japan but also internationally.

In September 1977, the year of his retirement from Osaka University, he was appointed professor of the new National Institute for Basic Biology and placed in charge of the "Laboratory of Cell Mechanism", and became chairman of the Department of Cell Biology. Besides being the chairperson responsible for the establishment of the new cell biology center in Japan, he concentrated on clarifying the mechanism of contraction and relaxation of the plasmodial strand by means of a mechano-electric transducing device, which measured the unidirectional tension of a plasmodial strand under isotonic or isometric contraction with the change between the two being instantaneous. With this method, he and his group clarified several important aspects of cell dynamics of protoplasm, that is, cyclic changes of cytoskeletal structures, the possible existence of a catch mechanism known in molluscan catch muscle, rhythmic changes in cytosolic ATP and Ca2+ concentrations, and pH. One major achievement was the first successful preparation of synthetic actomyosin thread of non-muscle cell origin from myosin and actin extracted from *Physarum* plasmodium. This thread could generate a tension which was dependent on ATP.

One of Kamiya's unique talents was his ingenuous methodology which was based on his philosophy to observe cells and measure cell activities with minimal disturbance. His methods were sometimes very simple, since he knew how efficient simple techniques could be for finding the answers to open questions, but in many cases, they were very sophisticated. The simple techniques included cutting, Iigation, vacuolar perfusion and effusion of endoplasm, a hammer method for dislodging chloroplasts from the cortical gel in characean cells. The sophisticated methods and devices included a double-chamber manometer and osmometer, a mechano-electric transducing device, a video centrifuge microscope, a shadow printing method for determination of velocity distribution of cytoplasmic streaming, agar capillary methods for measuring the viscosity of the endoplasm, a compression method for measuring the motive force of characean cytoplasmic streaming, and a chamber for differential treatments of characean cells.

Kamiya was not only a pioneer in the investigation of the cell motility phenomena in non-muscle cells but also a plant physiologist displaying great originality in both ideas and methodologies. If we compare one of his monographs, "Protoplasmic Streaming" in

1959 with the book by A.J. Ewart in 1903 entitled "On the Physics and Physiology of Protoplasmic Streaming", we are amazed at the difference in the contents between the two books. The monograph is abundant in new physico-chemical results obtained by using the unique techniques developed by Kamiya himself. We have the impression that there was a blank in research in the field of plant cell motility of a half century which was suddenly filled. It was indeed a benchmark monograph and laid the basis for modern research in plant cell biology, as demonstrated by the fact that it was nominated to Citation Classics, Nov. 20, 1989. This monumental contribution was followed by many approaches with fruitful results and heralded a new era for functional cell biology in plants. Professor Kamiya also published many reviews such as those in Annu. Rev. Plant Physiol. in 1960 and in 1981 and many scientific publications over 50 years.

Kamiya served as President of the Japanese Society of Plant Physiologists for two years (1972-73), President of the Japan Society for Cell Biology (1974-77) and President of the International Federation of Cell Biology (1985-88). He received many honorary degrees and awards. His fame and elegant personality attracted many scientists from all over the world; short visits by famous scientists like J. Bonner, H. Burstroem, V.A. Engelhargt, H. Huxley, A. Katchalsky, L.C. Pauling and K.V. Thimann and long stays by younger scientists like R.D. Allen, J.C.W. Chen and C. Gicquard.

Ritsu Kamiya, his eldest son and professor of Biology at the University of Tokyo , disclosed in his address to those who came to the funeral that his father, just three days before death, expressed his wish to write a monograph on the slime mold. His mind was clear until thirty minutes before his final everlasting sleep.

Masashi Tazawa
The University of Tokyo

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*****The editor is extremely grateful to Prof. Ritsu Kamiya for providing the OCR conversion of a scanned image of Prof. Tazawa's tribute to Noburô Kamiya [originally published in the journal of the Japan Society for Cell Biology (Cell Structure and Function 24, 55-57, 1999)], and for obtaining Prof. Tazawa's permission to include it here.*

ABSTRACTS OF RECENT ARTICLES

Int J Biochem Cell Biol. 2006;38(12):2164-72

A cDNA cloned from Physarum polycephalum encodes new type of family 3 beta-glucosidase that is a fusion protein containing a calx-beta motif. Maekawa A, Hayase M, Yubisui T, Minami Y. Department of Biochemistry, Okayama University of Science, 1-1 Ridai-cho, Okayama 700-0005, Japan. The microplasmodia of Physarum polycephalum express three types of beta-glucosidases: secretory enzyme, a soluble cytoplasmic enzyme and a membrane-bound enzyme. We are interested in the physiological role of three enzymes. We report the sequence of cDNA for membrane beta-glucosidase 1, which consists of 3825 nucleotides that includes an open reading frame encoding 1248 amino acids. The molecular weight of membrane beta-glucosidase 1 was calculated to be 131,843 based on the predicted amino acid composition. Glycosyl hydrolase family 3 N-terminal and C-terminal domains were found within the N-terminal half of the membrane beta-glucosidase 1 sequence and were highly homologous with the primary structures of fungal beta-glucosidases. Notably, the C-terminal half of membrane beta-glucosidase 1 contains two calx-beta motifs, which are known to be Ca(2+) binding domains in the Drosophila Na(+)/Ca(2+) exchanger; an RGD sequence, which is known to be a cell attachment sequence; and a transmembrane region. In this way, Physarum membrane beta-glucosidase 1 differs from all previously identified family 3 beta-glucosidases. In addition to cDNA for membrane beta-glucosidase 1, two other distinctly different mRNAs were also isolated. Two sequences were largely identical to cDNA for membrane beta-glucosidase 1, but included a long insert sequence having a stop codon, leading to truncation of their products, which could account for other beta-glucosidase forms occurred in Physarum poycephalum. Thus, the membrane beta-glucosidase is a new type family 3 enzyme fused with the Calx-beta domain. We propose that Calx-beta domain may modulate the beta-glucosidase activity in response to changes in the Ca(2+) concentration.
PMID: 16914364 [PubMed - in process]

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Trends Microbiol. 2006 Jun;14(6):249-53.

Acetate kinase: not just a bacterial enzyme. Ingram-Smith C, Martin SR, Smith KS. Department of Genetics and Biochemistry, Clemson Univer sity, Clemson, SC 29634-0318, USA. The bacterial enzymes acetate kinase (AK) and phosphotransacetylase (PTA) form a key pathway for synthesis of the central metabolic intermediate acetyl coenzyme A (acetyl-CoA) from acetate or for generation of ATP from excess acetyl-CoA. Putative AK genes have now been identified in some eukaryotic microbes. In Chlamydomonas reinhardtii and Phytophthora species, AK forms a pathway with PTA. AK has also been identified in non-yeast fungi but these fungi do not have PTA. Instead, AK forms a pathway with D-xylulose 5-phosphate phosphoketolase (XFP), a pathway that was also previously found only in bacteria. In Entamoeba histolytica, neither PTA nor XFP was found as a partner for AK. Thus, eukaryotic microbes seem to have incorporated the 'bacterial' enzyme AK into at least three different metabolic pathways. Publication Type: Review
PMID: 16678422 [PubMed - indexed for MEDLINE]

Int J Syst Evol Microbiol. 2006 Jun;56(Pt 6):1449-58.
Phylogenetic position of Multicilia marina and the evolution of Amoebozoa. Nikolaev SI, Berney C, Petrov NB, Mylnikov AP, Fahrni JF, Pawlowski J. Department of Evolutionary Biochemistry, AN Belozersky Institute of Physico-Chemical Biology, Moscow State University, Russia. Recent molecula r phylogenetic studies have led to the erection of the phylum Amoebozoa, uniting naked and testate lobose amoebae, the mycetozoan slime moulds and amitochondriate amoeboid protists (Archamoebae). Molecular data together with ultrastructural evidence have suggested a close relationship between Mycetozoa and Archamoebae, classified together in the Conosea, which was named after the cone of microtubules that, when present, is characteristic of their kinetids. However, the relationships of conoseans to other amoebozoans remain unclear. Here, we obtained the complete small-subunit (SSU) rRNA gene sequence (2746 bp) of the enigmatic, multiflagellated protist Multicilia marina, which has formerly been classified either in a distinct phylum, Multiflagellata, or among lobose amoebae. Our study clearly shows that Multicilia marina belongs to the Amoebozoa. Phylogenetic analyses including 60 amoebozoan SSU rRNA gene sequences revealed that Multicilia marina branches at the base of the Conosea, together with another flagellated amoebozoan, Phalansterium solitarium, as well as with Gephyramoeba sp., Filamoeba nolandi and two unidentified amoebae. This is the first report showing strong support for a clade containing all flagellated amoebozoans and we discuss the position of the root of the phylum Amoebozoa in the light of this result.
PMID: 16738126 [PubMed - indexed for MEDLINE]

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FEBS J. 2006 Mar;273(5):1046-55.
Stage specific expression of poly(malic acid)-affiliated genes in the life cycle of Physarum polycephalum. Spherulin 3b and polymalatase. Pinchai N, Lee BS, Holler E. Institut fur Biophysik und Physikalische Biochemie der Universitat Regensburg, Germany. Polymalic acid is receiving interest as a unique biopolymer of the plasmodia of mycetozoa and recently as a biogenic matrix for the synthesis of devices for drug delivery. The acellular slime mold Physarum polycephalum is characterized by two distinctive growth phases: uninucleated amoebae and multinucleated plasmodia. In adverse conditions, plasmodia reversibly transform into spherules. Only plasmodia synthesize poly(malic acid) (PMLA) and PMLA-hydrolase (polymalatase). We have performed suppression subtractive hybridization (SSH) of cDNA from amoebae and plasmodia to identify plasmodium-specific genes involved in PMLA metabolism. We found cDNA encoding a plasmodium-specific, spherulin 3a-like polypeptide, NKA48 (spherulin 3b), but no evidence for a PMLA-synthetase encoding transcript. Inhibitory RNA (RNAi)-induced knockdown of NKA48-cDNA generated a severe reduction in the level of PMLA suggesting that spherulin 3b functioned in regulating the level of PMLA. Unexpectedly, cDNA of polymalatase was not SSH-selected, suggesting its presence also in amoebae. Quantitative PCR then revealed low levels of mRNA in amoebae, high levels in plasmodia, and also low levels in spherules, in agreement with the expression under transcriptional regulation in these cells.
PMID: 16478477 [PubMed - indexed for MEDLINE]

Exp Parasitol. 2006 Apr 16; [Epub ahead of print]
Naegleria fowleri: A free-living highly pathogenic amoeba contains trypanothione/trypanothione reductase and glutathione/glutathione reductase systems. Ondarza RN, Hurtado G, Tamayo E, Iturbe A, Hernandez E. Center of Research on Infectious Diseases, National Institute of Public Health, Cuernavaca, Morelos, Mexico 62508, Mexico; Department of Biochemistry, Faculty of Medicine, National Autonomous University of Mexico (UNAM), University City, Mexico 04510, Mexico; Center for Marine Biotechnology and Biomedicine, Scripps Institution of Oceanography, University of California San Diego (UCSD), La Jolla, CA 92093-0204, USA. This paper presents definitive data showing that the thiol-bimane compound isolated and purified by HPLC from Naegleria fowleri trophozoites unequivocally corresponds by matrix assisted l aser-desorption ionization-time-of-flight MS, to the characteristic monoprotonated ion of trypanothione-(bimane)(2) [M(+)H(+)] of m/z 1104.57 and to the trypanothione-(bimane) of m/z 914.46. The trypanothione disulfide T(S)(2) was also found to have a molecular ion of m/z 723.37. Additionally HPLC demonstrated that thiol-bimane compounds corresponding to cysteine and glutathione were present in Naegleria. The ion patterns of the thiol-bimane compounds prepared from commercial trypanothione standard, Entamoeba histolytica and Crithidia luciliae are identical to the Naegleria thiol-bimane compound. Partially purified extracts from N. fowleri showed the coexistence of glutathione and trypanothione reductases activities. There is not doubt that the thiol compound trypanothione, which was previously thought to occur only in Kinetoplastida, is also present in the human pathogens E. histolytica and N. fowleri, as well as in the non-pathogenic euglenozoan E. gracilis. The presence of the trypanothione/trypanothione reductase system in N. fowleri creates the possibility of using this enzyme as a new "drug target" for rationally designed drugs to eliminate the parasite, without affecting the human host. PMID: 16620809]

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J Math Biol. 2006 Aug;53(2):273-86.
Mathematical model for rhythmic protoplasmic movement in the true slime mold. Kobayashi R, Tero A, Nakagaki T. Department of Mathematical and Life Sciences, Hiroshima University, Higashi Hiroshima, 739-8526, Japan. ryo@math.sci.hiroshima-u.ac.jp The plasmodium of the true slime mold Physarum polycephalum is a large amoeboid organism that displays "smart" behavior such as chemotaxis and the ability to solve mazes and geometrical puzzles. These amoeboid behaviors are based on the dynamics of the viscoelastic protoplasm and its biochemical rhythms. By incorporating both these aspects, we constructed a mathematical model for the dynamics of the organism as a first step towards understanding the relation between protoplasmic movement and its unusual abilities. We tested the validity of the model by comparing it with physiological observation. Our model reproduces fundamental characteristics of the spatio-temporal pattern of the rhythmic movement: (1) the antiphase oscillation between frontal tip and rear when the front is freely extending; (2) the asynchronous oscillation pattern when the front is not freely extending; and (3) the formation of protoplasmic mounds over a longer time scale. Both our model and physiological observation suggest that cell stiffness plays a primary role in plasmodial behaviors, in contrast to the conventional theory of coupled oscillator systems. PMID: 16770610 [PubMed - in process]

Appl Environ Microbiol. 2006 Apr;72(4):2428-38.

Biodiversity of amoebae and amoeba-resisting bacteria in a hospital water network. Thomas V, Herrera-Rimann K, Blanc DS, Greub G. Center for Research on Intracellular Bacteria, Institute of Microbiology, CHUV Hospital, Bugnon 46, 1011 Lausanne, Switzerland. Free-living amoebae (FLA) are ubiquitous organisms that have been isolated from various domestic water systems, such as cooling towers and hospital water networks. In addition to their own pathogenicity, FLA can also act as Trojan horses and be naturally infected with amoeba-resisting bacteria (ARB) that may be involved in human infections, such as pneumonia. We investigated the biodiversity of bacteria and their amoebal hosts in a hospital water network. Using amoebal enrichment on nonnutrient agar, we isolated 15 protist strains from 200 (7.5%) samples. One thermotolerant Hartmannella vermiformis isolate harbored both Legionella pneumophila and Bradyrhizobium japonicum. By using amoebal coculture with axenic Acanthamoeba castellanii as the cellular background, we recovered at least one ARB from 45.5% of the samples. Four new ARB isolates were recovered by culture, and one of these isolates was widely present in the water network. Alphaproteobacteria (such as Rhodoplanes, Methylobacterium, Bradyrhizobium, Afipia, and Bosea) were recovered from 30.5% of the samples, mycobacteria (Mycobacterium gordonae, Mycobacterium kansasii, and Mycobacterium xenopi) were recovered from 20.5% of the samples, and Gammaproteobacteria (Legionella) were recovered from 5.5% of the samples. No Chlamydia or Chlamydia-like organisms were recovered by amoebal coculture or detected by PCR. The observed strong association between the presence of amoebae and the presence of Legionella ($P < 0.001$) and mycobacteria ($P = 0.009$) further suggests that FLA are a reservoir for these ARB and underlines the importance of considering amoebae when water control measures are designed.
PMID: 16597941 [PubMed - indexed for MEDLINE]

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Med Chem. 2005 Nov;1(6):575-90.

Isolation of bioactive natural products from myxomycetes. Ishibashi M. Graduate School of Pharmaceutical Sciences, Chiba University, Chiba 263-8522, Japan. mish@athenaeum.p.chiba-u.ac.jp The Myxomycetes (true slime molds) are an unusual group of primitive organisms that may be assigned to one of the lowest classes of eukaryotes. As their fruit bodies are very small and it is very difficult to collect much quantity of slime molds, few studies have been made on the chemistry of myxomycetes. Cultivation of the plasmodium of myxomycetes in a practical scale for natural products chemistry studies is known only for very limited species. Here is described a review on the recent results on isolation of bioactive natural products from myxomycetes obtained in these two years in the laboratories. Spore germination experiments were studied of hundreds of field-collected myxomycetes collected in Japan and succeeded in laboratory culture of plasmodia of several myxomycetes in a practical scale for natural products chemistry studies. As a result, pyrroloiminoquinones, polyene yellow pigments, and a peptide lactone from cultured plasmodia of Didymium iridis, Physarum rigidum and P. melleum, respectively were isolated. New naphthoquinone pigments, cycloanthranilylprolines, tyrosine-kinase inhibitory bisindoles, and a cytotoxic triterpenoid aldehyde lactone were also isolated from field-collected fruit bodies of Cribraria purpurea, Fuligo candida, Tubifera casparyi, and Tubifera dimorphotheca, respectively. Publication Type: Review
PMID: 16787341 [PubMed - indexed for MEDLINE]

Int J Biol Macromol. 2006 Aug 15;39(1-3):37-44.

Use of the myosin motor domain as large-affinity tag for the expression and purification of proteins in Dictyostelium discoideum. Kollmar M. Abteilung NMR basierte Strukturbiologie, Max-Planck-Institut fur Biophysikalische Chemie, Am Fassberg 11, D-37077 Gottingen, Germany. mako@nmr.mpibpc.mpg.de The cellular slime mold Dictyostelium discoideum is increasingly be used for the overexpression of proteins. Dictyostelium is amenable to classical and molecular genetic approaches and can easily be grown in large quantities. It contains a variety of chaperones and folding enzymes, and is able to perform all kinds of post-translational protein modifications. Here, new expression vectors are presented that have been designed for the production of proteins in large quantities for biochemical and structural studies. The expression cassettes of the most successful vectors are based on a tandem affinity purification tag consisting of an octahistidine tag followed by the myosin motor domain tag. The myosin motor domain not only strongly enhances the production of fused proteins but is also used for a fast affinity purification step through its ATP-dependent binding to actin. The applicability of the new system has been demonstrated for the expression and purification of subunits of the dynein-dynactin motor protein complex from different species.

PMID: 16516959 [PubMed - indexed for MEDLINE]

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Mycologia. 2006 Mar-Apr;98(2):223-32.

Species richness and ecological characterization of myxomycetes and myxomycete-like organisms in the canopy of a temperate deciduous forest. Schnittler M, Unterseher M, Tesmer J. University of Greifswald, Botanical Institute and Botanical Garden, D-17489 Greifswald, Germany. martin.schnittler@uni-greifswald.de The ecological community of myxomycetes and myxomycete-like organisms (MMLO) in the canopy of living deciduous trees was studied in a riparian deciduous forest at Leipzig, Germany. A systematic survey carried out with a total of 146 moist chamber cultures resulted in 386 records of 37 taxa, with 32 myxomycetes, two myxobacteria, two protostelids and the fruit body forming ciliate Sorogena stoianovitchae, the latter recorded for the first time for Europe. With 94% of all cultures positive for MMLO, these organisms are present consistently in the investigated sections of white-rotten twigs attached to living trees at 10-30 m above the ground. Our sampling recovered a majority of the likely species, with 37 out of the 42-45 predicted according to a species-accumulation curve and two other estimators of species richness. Nonmetric multidimensional scaling revealed pH, water-holding capacity and stage of decay to explain most of the variation in species distribution. Arcyria cinerea and Perichaena depressa as the most common species occurred in 32% and 29% of all samples, respectively. Viewing the sampled twigs as habitat islands and a single spore as sufficient to establish a population, a simulation program assuming a random spore rain estimated an average of 0.4 and 0.35 spore hits per twig as necessary to explain the observed frequencies. This is matched by the potential productivity of the substrate. All fruit bodies from the cultured twigs would be able to create a spore rain of 86 (A. cinerea) or 40 (P. depressa) spore hits per twig when dispersed evenly over the plot. The terminal fall velocity of spores was measured, revealing that it took about 5 h for a spore to land (30 m) in still air and indicating high dispersal ability for canopy-inhabiting MMLO.

PMID: 16894967 [PubMed - in process]

Mycologia. 2006 Jan-Feb;98(1):144-8.
A new ballistosporous species of Protostelium. Spiegel FW, Shadwick JD, Hemmes DE. Department of Biological Sciences, University of Arkansas, Fayetteville 72701, USA. fspiegel@uark.edu During surveys of the protostelids of the Hawaiian Islands and the South Island of New Zealand, an undescribed species of Protostelium was discovered fruiting on collections of substrates found in several sites on the southern and western parts of the island of Hawaii and from one site near Port Elizabeth, New Zealand. The new species, P. okumukumu, has a sporocarp with a bipartite stalk that supports a single, spherical spore. The basal portion of the stalk is straight and rigid. The upper part of the stalk is a nearly spherical apophysis. The junction between the stalk base and the apophysis is flexible such that the spore and apophysis swing back and forth as a unit. Spores are forcibly discharged from the stalk, and only the straight base of the stalk is left behind. Amoebae typical of the taxon Protostelium germinate from the spores, and when an amoeba differentiates into a prespore cell, it becomes lozenge shaped (nearly ellipsoid) in top view, as is typical for species of Protostelium. This represents the seventh species of protostelids described to have forcible spore discharge, and the possibility of forcible discharge needs to be examined in several other species. PMID: 16800313
[PubMed - indexed for MEDLINE]]

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FEBS J. 2006 Jun;273(12):2789-800.
RNA reprogramming of alpha-mannosidase mRNA sequences in vitro by myxomycete group IC1 and IE ribozymes. Fiskaa T, Lundblad EW, Henriksen JR, Johansen SD, Einvik C. Department of Molecular Biotechnology, RNA Research group, Institute of Medical Biology, University of Tromso, Norway. Trans-splicing group I ribozymes have been introduced in order to mediate RNA reprogramming (including RNA repair) of therapeutically relevant RNA transcripts. Efficient RNA reprogramming depends on the appropriate efficiency of the reaction, and several attempts, including optimization of target recognition and ribozyme catalysis, have been performed. In most studies, the Tetrahymena group IC1 ribozyme has been applied. Here we investigate the potential of group IC1 and group IE intron ribozymes, derived from the myxomycetes Didymium and Fuligo, in addition to the Tetrahymena ribozyme, for RNA reprogramming of a mutated alpha-mannosidase mRNA sequence. Randomized internal guide sequences were introduced for all four ribozymes and used to select accessible sites within isolated mutant alpha-mannosidase mRNA from mammalian COS-7 cells. Two accessible sites common to all the group I ribozymes were identified and further investigated in RNA reprogramming by trans-splicing analyses. All the myxomycete ribozymes performed the trans-splicing reaction with high fidelity, resulting in the conversion of mutated alpha-mannosidase RNA into wild-type sequence. RNA protection analysis revealed that the myxomycete ribozymes perform trans-splicing at approximately similar efficiencies as the Tetrahymena ribozyme. Interestingly, the relative efficiency among the ribozymes tested correlates with structural features of the P4-P6-folding domain, consistent with the fact that efficient folding is essential for group I intron trans-splicing.
PMID: 16817905 [PubMed - indexed for MEDLINE]

Mycologia. 2006 Jan-Feb;98(1):51-6.
Mitochondrial inheritance patterns in Didymium iridis are not influenced by stage of mating competency. Scheer MA, Silliker ME. Nova Southeastern University College of Osteopathic Medicine, Fort Lauderdale, Florida 33328, USA. To test whether the timing of transition to mating competency affected mitochondrial transmission patterns in D. iridis. Reciprocal crosses were made by combining mating compatible strains that differed in their competency to mate. The results were compared to crosses where both mating strains were competent at the time of combining and crosses where somatic fusion of plasmodia was allowed. The results show that the mating competency of the parental strains at the time of confronting a compatible mate does not affect mitochondrial transmission patterns, mating efficiency or the likelihood of biparental inheritance. However the timing of plasmodial formation is delayed when precompetent and competent strains are mated compared to when both strains are competent at the time of mixing. We also observed that somatic fusion of plasmodia did not appreciably increase the incidence of biparental inheritance compared to crosses where individual plasmodia were isolated. These results provide additional evidence of the variable nature of mitochondrial inheritance in D. iridis within crosses and between mating trials.
PMID: 16800304 [PubMed - indexed for MEDLINE

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Curr Genet. 2006 Apr;49(4):259-71.
Identification of a putative mitochondrial RNA polymerase from Physarum polycephalum: characterization, expression, purification, and transcription in vitro. Miller ML, Antes TJ, Qian F, Miller DL. Department of Cell and Molecular Biology, The University of Texas at Dallas, 2601 N. Floyd Road, Richardson, TX 75080, USA. Mitochondrial RNA polymerases (mtRNAPs) are necessary for the biogenesis of mitochondria and for proper mitochondrial function since they transcribe genes on mtDNA for tRNAs, rRNAs, and mRNAs. The unique type of RNA editing identified in mitochondria of Physarum polycephalum is thought to be closely associated with transcription, and as such, RNA editing activity would be expected to be closely associated with the mtRNAP. In order to better characterize the role of mtRNAPs in mitochondrial biogenesis and to determine the role of the Physarum mtRNAP in RNA editing, the cDNA of the Physarum mtRNAP was identified using PCR and degenerate primers designed from conserved motifs in mtRNAPs. This amplification product was used to screen a cDNA library for the cDNA corresponding to the Physarum mtRNAP. A cDNA corresponding to a 3.2 kb transcript containing a 997 codon open reading frame was identified. The amino acid sequence inferred from the open reading frame contains motifs characteristic of mtRNAPs. To confirm that a cDNA for an RNA polymerase had been isolated, the cDNA was expressed in E. coli as an N-terminal maltose binding protein (MBP) fusion protein. The fusion protein was purified by affinity chromatography and shown to have DNA-directed RNA polymerase activity. This functional mtRNAP will be useful for in vitro studies of mitochondrial transcription and RNA editing.
PMID: 16402203 [PubMed - indexed for MEDLINE]

Biochim Biophys Acta. 2006 May-Jun;1763(5-6):510-21.

Structure, function and evolution of the mitochondrial division apparatus. Kuroiwa T, Nishida K, Yoshida Y, Fujiwara T, Mori T, Kuroiwa H, Misumi O. Laboratory of Cell Biology and Frontier Project Life's Adaptation Strategies of Environmental Change, Department of Life Sciences, College of Science, Rikkyo University, 3-34-1 Nishiikebukuro, Toshima-ku, Tokyo 171-8501, Japan. tsune@rikkyo.ne.jp Mitochondria are derived from free-living alpha-proteobacteria that were engulfed by eukaryotic host cells through the process of endosymbiosis, and therefore have their own DNA which is organized using basic proteins to form organelle nuclei (nucleoids). Mitochondria divide and are split amongst the daughter cells during cell proliferation. Their division can be separated into two main events: division of the mitochondrial nuclei and division of the matrix (the so-called mitochondrial division, or mitochondriokinesis). In this review, we first focus on the cytogenetical relationships between mitochondrial nuclear division and mitochondriokinesis. Mitochondriokinesis occurs after mitochondrial nuclear division, similar to bacterial cytokinesis. We then describe the fine structure and dynamics of the mitochondrial division ring (MD ring) as a basic morphological background for mitochondriokinesis. Electron microscopy studies first identified a small electron-dense MD ring in the cytoplasm at the constriction sites of dividing mitochondria in the slime mold Physarum polycephalum, and then two large MD rings (with outer cytoplasmic and inner matrix sides) in the red alga Cyanidioschyzon merolae. Now MD rings have been found in all eukaryotes. In the third section, we describe the relationships between the MD ring and the FtsZ ring descended from ancestral bacteria. Other than the GTPase, FtsZ, mitochondria have lost most of the proteins required for bacterial cytokinesis as a consequence of endosymbiosis. The FtsZ protein forms an electron transparent ring (FtsZ or Z ring) in the matrix inside the inner MD ring. For the fourth section, we describe the dynamic association between the outer MD ring with a ring composed of the eukaryote-specific GTPase dynamin. Recent studies have revealed that eukaryote-specific GTPase dynamins form an electron transparent ring between the outer membrane and the MD ring. Thus, mitochondriokinesis is thought to be controlled by a mitochondrial division (MD) apparatus including a dynamic trio, namely the FtsZ, MD and dynamin rings, which consist of a chimera of rings from bacteria and eukaryotes in primitive organisms. Since the genes for the MD ring and dynamin rings are not found in the prokaryotic genome, the host genomes may make these rings to actively control mitochondrial division. In the fifth part, we focus on the dynamic changes in the formation and disassembly of the FtsZ, MD and dynamin rings. FtsZ rings are digested during a later period of mitochondrial division and then finally the MD and dynamin ring apparatuses pinched off the daughter mitochondria, supporting the idea that the host genomes are responsible for the ultimate control of mitochondrial division. We discuss the evolution, from the original vesicle division (VD) apparatuses to VD apparatuses including classical dynamin rings and MD apparatuses. It is likely that the MD apparatuses involving the dynamic trio evolved into the plastid division (PD) apparatus in Bikonta, while in Opisthokonta, the MD apparatus was simplified during evolution and may have branched into the mitochondrial fusion apparatus. Finally, we describe the possibility of intact isolation of large MD/PD apparatuses, the identification of all their proteins and their related genes using C. merolae genome information and TOF-MS analyses. These results will assist in elucidating the universal mechanism and evolution of MD, PD and VD apparatuses. Publication Type: Review
PMID: 16690143 [PubMed - indexed for MEDLINE]

Tsitologiia. 2005;47(1):89-98.
[Light and electron microscopic investigation of Pelomyxa prima (Gruber, 1884) (Peloflagellatea, Pelobiontida)] [Article in Russian] Frolov AO, Chistiakova LV, Malysheva MN, Gudkov AV. Cell organization of a multinuclear pelobiont Pelomyxa prima has been studied at the light and electron microscopic le vels. Motile individuals demonstrate a characteristic drop-like or pyriform shape and reach 550 microkm in length. The cell cover is represented by a well-developed, morphologically differentiated glycocalyx 80-100 nm thick. The cytoplasm contains many structural vacuoles. The nuclei are of vertical type, numbering up to several nuclei in large individuals. Numerous cytoplasmic microtubules are associated with the external membrane of the nuclear envelope. Separate non-motile flagella are distributed throughout the cell surface, being more numerous in the posterior body end and uroidal zone of the protist. Basal bodies of the flagella are extremely long, being deeply immersed into the cytoplasm. These bodies are surrounded by a muff of electron-dense material, with numerous microtubules radiating from it. A compact bundle of microtubules starts from the base of a basal body axially into the cytoplasm. Besides, a band-like lateral microtubular rootlet is present. The number of microtubules in the axoneme of undulipodia is unstable. Neither mitochondria, nor Golgi complex were found. Two species of bacterial endocytobionts are present in the cytoplasm in considerable numbers.
PMID: 16602249 [PubMed - indexed for MEDLINE]

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J Eukaryot Microbiol. 2005 Nov-Dec;52(6):461-75.
Actin-based motility in the net slime mould Labyrinthula: evidence for the role of myosin in gliding movement. Preston TM, King CA. Biology Department, University College London, Gower Street, WC1E 6BT, United Kingdom. t.preston@ucl.ac.uk In contrast to crawling movement (e.g. in amoebae and tissue cells) the other major class of substratum-associated motility in eukaryotes, gliding, has received relatively little attention. The net slime mold Labyrinthula provides a useful laboratory model for studying this process since it exhibits a particular kind of gliding in its plasmodial stage. Here nucleated spindle cells glide along self-established cytoplasmic trackways in a predominantly unidirectional manner, at 1-2 microm/s. These trackways, upon which gliding is dependent, are held by filopodial tethers some distance off the well-developed reticulopodial mesh anchoring the plasmodium onto the substratum. Reflection interference microscopy resolves this matrix in live plasmodia. The axially disposed cytoskeletal elements of the trackways are revealed by rhodamine-labelled phalloidin to be rich in F-actin. A weft of peripheral, rapidly extending filopodia (50 microm/min) typifies the expanding regions of the plasmodium. Here spindle cells are recruited before emigrating into newly differentiated trackways. Immunoblotting whole plasmodia or a sucrose-soluble cytoplasmic extract reveals a single actin-positive band of Mr 48 kDa. Polyclonal antibodies to two distinct myosin peptide sequences identify a single myosin HC (Mr 96 kDa) in immunoblots. Gliding was reversibly blocked by 10 mM 2,3-butanedione-2-monoxime, a myosin ATPase inhibitor, but it was insensitive to the actin-binding drugs cytochalasin D and phalloidin. We suggest that the force (>50 pN) for gliding motility results from interaction of myosin molecules, associated with the spindle cells, with trackway F-actin via the bothrosomes.
PMID: 16313437 [PubMed - indexed for MEDLINE]

Cell Motil Cytoskeleton. 2006 Feb;63(2):77-87.
Regulation of levels of actin threonine phosphorylation during life cycle of Physarum polycephalum. Shirai Y, Sasaki N, Kishi Y, Izumi A, Itoh K, Sameshima M, Kobayashi T, Murakami-Murofushi K. Department of Biology, Ochanomizu University, Bunkyo-ku, Tokyo 112-8610, Japan. yukih@cc.ocha.ac.jp Under various environmental stresses, the true slime mold Physarum polycephalum converts into dormant forms, such as microcysts, sclerotia, and spores, which can survive in adverse environments for a considerable period of time. In drought-induced sclerotia, actin is threonine phosphorylated, which blocks its ability to polymerize into filaments. It is known that fragmin and actin-fragmin kinase (AFK) mediate this phosphorylation event. In this work, we demonstrate that high levels of actin threonine phosphorylation are also found in other dormant cells, including microcysts and spores. As the threonine phosphorylation of actin in microcysts and sclerotia were induced by drought stress but not by other stresses, we suggest that drought stress is essential for actin phosphorylation in both cell types. Although characteristic filamentous actin structures (dot- or rod-like structures) were observed in microcysts, sclerotia, and spores, actin phosphorylation was not required for the formation of these structures. Prior to the formation of both microcysts and sclerotia, AFK mRNA expression was activated transiently, whereas fragmin mRNA levels decreased. Our results suggest that drought stress and AFK might be involved in the threonine phosphorylation of actin. Copyright (c) 2005 Wiley-Liss, Inc.
PMID: 16374832 [PubMed - indexed for MEDLINE]

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J Biol Chem. 2005 Dec 16;280(50):41458-64.
Structural evidence for non-canonical binding of Ca2+ to a canonical EF-hand of a conventional myosin. Debreczeni JE, Farkas L, Harmat V, Hetenyi C, Hajdu I, Zavodszky P, Kohama K, Nyitray L. Department of Biochemistry, Eotvos Lorand University, Budapest H-1117, Hungary. We have previously identified a single inhibitory Ca2+-binding site in the fi rst EF-hand of the essential light chain of Physarum conventional myosin (Farkas, L., Malnasi-Csizmadia, A., Nakamura, A., Kohama, K., and Nyitray, L. (2003) J. Biol. Chem. 278, 27399-27405). As a general rule, conformation of the EF-hand-containing domains in the calmodulin family is "closed" in the absence and "open" in the presence of bound cations; a notable exception is the unusual Ca2+-bound closed domain in the essential light chain of the Ca2+-activated scallop muscle myosin. Here we have reported the 1.8 A resolution structure of the regulatory domain (RD) of Physarum myosin II in which Ca2+ is bound to a canonical EF-hand that is also in a closed state. The 12th position of the EF-hand loop, which normally provides a bidentate ligand for Ca2+ in the open state, is too far in the structure to participate in coordination of the ion. The structure includes a second Ca2+ that only mediates crystal contacts. To reveal the mechanism behind the regulatory effect of Ca2+, we compared conformational flexibilities of the liganded and unliganded RD. Our working hypothesis, i.e. the modulatory effect of Ca2+ on conformational flexibility of RD, is in line with the observed suppression of hydrogen-deuterium exchange rate in the Ca2+-bound form, as well as with results of molecular dynamics calculations. Based on this evidence, we concluded that Ca2+-induced change in structural dynamics of RD is a major factor in Ca2+-mediated regulation of Physarum myosin II activity. PMID: 16227209 [PubMed - indexed for MEDLINE]

Acta Biochim Biophys Sin (Shanghai). 2005 Nov;37(11):767-72.
Function of c-Fos-like and c-Jun-like proteins on trichostatin A-induced G2/M arrest in Physarum polycephalum. Li XX, Lu J, Zhao YM, Huang BQ. Institute of Genetics and Cytology, Northeast Normal University, Changchun 130024, China. The homologs of transcription factors c-Fos and c-Jun have been detected in slime mold Physarum polycephalum during progression of the synchronous cell cycle. Here we demonstrated that c-Fos-like and c-Jun-like proteins participated in G2/M transition by the regulation of the level of Cyclin B1 protein in P. polycephalum. The study of antibody neutralization revealed that interruption of the functions of c-Fos-like and c-Jun-like proteins resulted in G2/M transition arrest, implicating their functional roles in cell cycle control. When G2/M transition was blocked by histone deacetylase inhibitor trichostatin A, changes in c-Fos- and c-Jun-like protein levels, and hyperacetylation of c-Jun-like protein, were observed. The data suggest that in P. polycephalum, c-Fos- and c-Jun-like proteins may be the key factors in the regulation of histone acetylation-related G2/M transition, involving the coordinated expression and hyperacetylation of these proteins.
PMID: 16270156 [PubMed - indexed for MEDLINE]

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Cell Motil Cytoskeleton. 2005 Jul;61(3):172-88.
Characterization of Amoeba proteus myosin VI immunoanalog. Dominik M, Klopocka W, Pomorski P, Kocik E, Redowicz MJ. Department of Muscle Biochemistry, Nencki Ins titute of Experimental Biology, Polish Academy of Sciences, Warsaw, Poland. Amoeba proteus, the highly motile free-living unicellular organism, has been widely used as a model to study cell motility. However, molecular mechanisms underlying its unique locomotion and intracellular actin-based-only trafficking remain poorly understood. A search for myosin motors responsible for vesicular transport in these giant cells resulted in detection of 130-kDa protein interacting with several polyclonal antibodies against different tail regions of human and chicken myosin VI. This protein was binding to actin in the ATP-dependent manner, and immunoprecipitated with anti-myosin VI antibodies. In order to characterize its possible functions in vivo, its cellular distribution and colocalization with actin filaments and dynamin II during migration and pinocytosis were examined. In migrating amoebae, myosin VI immunoanalog localized to vesicular structures, particularly within the perinuclear and sub-plasma membrane areas, and colocalized with dynamin II immunoanalog and actin filaments. The colocalization was even more evident in pinocytotic cells as proteins concentrated within pinocytotic pseudopodia. Moreover, dynamin II and myosin VI immunoanalogs cosedimented with actin filaments, and were found on the same isolated vesicles. Blocking endogenous myosin VI immunoanalog with anti-myosin VI antibodies inhibited the rate of pseudopodia protrusion (about 19% decrease) and uroidal retraction (about 28% decrease) but did not affect cell morphology and the manner of cell migration. Treatment with anti-human dynamin II antibodies led to changes in directionality of amebae migration and affected the rate of only uroidal translocation (about 30% inhibition). These results indicate that myosin VI immunoanalog is expressed in protist Amoeba proteus and may be involved in vesicle translocation and cell locomotion.
PMID: 15909304 [PubMed - indexed for MEDLINE]

Protist. 2005 Aug;156(2):191-202.
The testate lobose amoebae (order Arcellinida Kent, 1880) finally find their home within Amoebozoa. Nikolaev SI, Mitchell EA, Petrov NB, Berney C, Fahrni J, Pawlowski J. Department of Evolutionary Biochemistry, A. N. Belozersky Institute of Physico-Chemical Biology, Moscow State University, Moscow, Russia. s-nikol@yandex.ru Testate lobose amoebae (order Arcellinida Kent, 1880) are common in all aquatic and terrestrial habitats, yet they are one of the last higher taxa of unicellular eukaryotes that has not found its place in the tree of life. The morphological approach did not allow to ascertain the evolutionary origin of the group or to prove its monophyly. To solve these challenging problems, we analyzed partial small-subunit ribosomal RNA (SSU rRNA) genes of seven testate lobose amoebae from two out of the three suborders and seven out of the 13 families belonging to the Arcellinida. Our data support the monophyly of the order and clearly establish its position among Amoebozoa, as a sister-group to the clade comprising families Amoebidae and Hartmannellidae. Complete SSU rRNA gene sequences from two species and a partial actin sequence from one species confirm this position. Our phylogenetic analyses including representatives of all sequenced lineages of lobose amoebae suggest that a rigid test appeared only once during the evolution of the Amoebozoa, and allow reinterpretation of some morphological characters used in the systematics of Arcellinida.
PMID: 16171186 [PubMed - indexed for MEDLINE]

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Protoplasma. 2005 Apr;225(1-2):77-84.
Characterisation of the Rac/PAK pathway in Amoeba proteus. Klopocka W, Moraczewska J, Redowicz MJ. Department of Molecular and Cellular Neurobiology, Nencki Institute of Experimental Biology, Warsaw, Poland. Molecular mechanisms underlying the unique locomotion of the highly motile Amoeba proteus still remain poorly understood. Recently, we have shown that blocking the endogenous amoebal Rac-like protein(s) leads to distinct and irreversible changes in the appearance of these large migrating cells as well as to a significant inhibition of their locomotion. To elucidate the mechanism of the Rac pathway in Amoeba proteus, we tested the effects of blocking the endogenous myosin I heavy chain kinase (MIHCK), one of the Rac effectors in Acanthamoeba castellanii and Dictyostelium discoideum, with anti-MIHCK antibodies in migrating amoebae, as well as the effect of inhibiting Rac and MIHCK on the actin polymerisation process. Antibodies against A. castellanii MIHCK detected an A. proteus protein with a molecular mass (ca. 95 kDa) similar to the A. castellanii kinase. The cellular distribution of MIHCK in A. proteus was very similar to those of Rac-like protein in amoebae and MIHCK in A. castellanii. Amoebae microinjected with anti-MIHCK antibodies moved slower and protruded fewer wide pseudopodia (5-6) than the control cells (9-10), resembling to some extent the phenotype of cells microinjected with anti-Rac antibodies. The in vitro studies indicate that the A. proteus Rac-like protein, but not the MIHCK isoform, is engaged in the regulation of the nucleation step of the actin polymerisation process. These observations suggest that MIHCK may be one of the effectors for Rac in these extremely large cells.
PMID: 15948264 [PubMed - indexed for MEDLINE]

Bioorg Khim. 2005 May-Jun;31(3):259-68.
[Isolation and characterization of the ALP1 protease from Aspergillus fumigatus and its protein inhibitor from Physarium polycephalum] [Article in Russian] Davies DA, Kalinina NA, Samokhvalova LV, Malakhova GV, Scott G, Volynskaia AM, Nesmeianov VA. It is known that Aspergillus fumigatus secretes a serine protease ALP1 of the subtilisin family in the presence of extracellular protein substrates. We found conditions of A. fumigatus culturing that provide a high ALP1 activity inside cells without induction by extracellular proteins. The identity of the properties of the secreted and intracellular enzymes was shown. A thermostable protein inhibitor of the ALP1 protease was isolated from the plasmodium of the myxomycete Physarum polycephalum. Its molecular mass is 32-33 kDa. The inhibitor inhibits the ALP1 protease activity with IC50 of 0.14 microM. This protein was also shown to be a less efficient inhibitor of the activity of HIV-1 protease (IC50 2.5 microM). The English version of the paper: Russian Journal of Bioorganic Chemistry, 2005, vol. 31, no. 3; see also http://www.maik.ru.
PMID: 16004384 [PubMed - indexed for MEDLINE]

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Eur Biophys J. 2005 May;34(3):262-72.
Acto-myosin cytoskeleton dependent viscosity and shear-thinning behavior of the amoeba cytoplasm. Marion S, Guillen N, Bacri JC, Wilhelm C. Unite de Biologie Cellulaire du Parasitisme, INSERM U389, Institut Pasteur, Paris, France. The mechanical behavior of the human parasite Entamoeba histolytica plays a major role in the invasive process of host tissues and vessels. In this study, we set up an intracellular rheological technique derived from magnetic tweezers to measure the viscoelastic properties within living amoebae. The experimental setup combines two magnetic fields at 90 degrees from each other and is adapted to an inverted microscope, which allows monitoring of the rotation of pairs of magnetic phagosomes. We observe either the response of the phagosome pair to an instantaneous 45 degrees rotation of the magnetic field or the response to a permanent uniform rotation of the field at a given frequency. By the first method, we concluded that the phagosome pairs experience a soft viscoelastic medium, represented by the same mechanical model previously described for the cytoplasm of Dictyostelium discoideum [Feneberg et al. in Eur Biophys J 30(4):284-294 2001]. By the second method, the permanent rotation of a pair allowed us to apply a constant shear rate and to calculate the apparent viscosity of the cytoplasm. As found for entangled polymers, the viscosity decreases with the shear rate applied (shear-thinning behavior) and exhibits a power-law-type thinning, with a corresponding exponent of 0.65. Treatment of amoeba with drugs that affect the actin polymer content demonstrated that the shear-thinning behavior of the cytoplasm depends on the presence of an intact actin cytoskeleton. These data present a physiologic relevance for Entamoeba histolytica virulence. The shear-thinning behavior could facilitate cytoplasm streamings during cell movement and cell deformation, under important shear experienced by the amoeba during the invasion of human tissues. In this study, we also investigated the role of the actin-based motor myosin II and concluded that myosin II stiffens the F-actin gel in living parasites likely by its cross-linking activity.
PMID: 15711811 [PubMed - indexed for MEDLINE]

Nature. 2005 May 5;435(7038):43-57.
The genome of the social amoeba Dictyostelium discoideum. Eichinger L, Pachebat JA, Glockner G, Rajandream MA, Sucgang R, Berriman M, Song J, Olsen R, Szafranski K, Xu Q, Tunggal B, Kummerfeld S, Madera M, Konfortov BA, Rivero F, Bankier AT, Lehmann R, Hamlin N, Davies R, Gaudet P, Fey P, Pilcher K, Chen G, Saunders D, Sodergren E, Davis P, Kerhornou A, Nie X, Hall N, Anjard C, Hemphill L, Bason N, Farbrother P, Desany B, Just E, Morio T, Rost R, Churcher C, Cooper J, Haydock S, van Driessche N, Cronin A, Goodhead I, Muzny D, Mourier T, Pain A, Lu M, Harper D, Lindsay R, Hauser H, James K, Quiles M, Madan Babu M, Saito T, Buchrieser C, Wardroper A, Felder M, Thangavelu M, Johnson D, Knights A, Loulseged H, Mungall K, Oliver K, Price C, Quail MA, Urushihara H, Hernandez J, Rabbinowitsch E, Steffen D, Sanders M, Ma J, Kohara Y, Sharp S, Simmonds M, Spiegler S, Tivey A, Sugano S, White B, Walker D, Woodward J, Winckler T, Tanaka Y, Shaulsky G, Schleicher M, Weinstock G, Rosenthal A, Cox EC, Chisholm RL, Gibbs R, Loomis WF, Platzer M, Kay RR, Williams J, Dear PH, Noegel AA, Barrell B, Kuspa A. Center for Biochemistry and Center for Molecular Medicine Cologne, University of Cologne, Joseph-Stelzmann-Str. 52, 50931 Cologne, Germany. The social amoebae are exceptional in their ability to alternate between unicellular and multicellular forms. Here we describe the genome of the best-studied member of this group, Dictyostelium discoideum. The gene-dense chromosomes of this organism encode approximately 12,500 predicted proteins, a high proportion of which have long, repetitive amino acid tracts. There are many genes for polyketide synthases and ABC transporters, suggesting an extensive secondary metabolism for producing and exporting small molecules. The genome is rich in complex repeats, one class of which is clustered and may serve as centromeres. Partial copies of the extrachromosomal ribosomal DNA (rDNA) element are found at the ends of each chromosome, suggesting a novel telomere structure and the use of a common mechanism to maintain both the rDNA and chromosomal termini. A proteome-based phylogeny shows that the amoebozoa diverged from the animal-fungal lineage after the plant-animal split, but Dictyostelium seems to have retained more of the diversity of the ancestral genome than have plants, animals or fungi. PMID: 15875012 [PubMed - indexed for MEDLINE]

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J Biomed Opt. 2006 Mar-Apr;11(2):024014.
Doppler flow imaging of cytoplasmic streaming using spectral domain phase microscopy. Choma MA, Ellerbee AK, Yazdanfar S, Izatt JA. Duke University, Department of Biomedical Engineering, Durham, North Carolina 27708, USA. mac32@duke.edu Spectral domain phase microscopy (SDPM) is a function extension of spectral domain optical coherence tomography. SDPM achieves exquisite levels of phase stability by employing common-path interferometry. We discuss the theory and limitations of Doppler flow imaging using SDPM, demonstrate monitoring the thermal contraction of a glass sample with nanometer per second velocity sensitivity, and apply this technique to measurement of cytoplasmic streaming in an Amoeba proteus pseudopod. We observe reversal of cytoplasmic flow induced by extracellular CaCl2, and report results that suggest parabolic flow of cytoplasm in the A. proteus pseudopod.
PMID: 16674204 [PubMed - indexed for MEDLINE]

Biofizika. 2005 Jul-Aug;50(4):704-12.
[Synchronization of mechanochemical auto-oscillations within the Physarum polycephalum plasmodium by periodical external actions] [Article in Russian] Teplov VA, Mitrofanov VV, Romanovskii IuM. Amoeboid locomotion of huge unicellular organism, the Physarum polycephalum plasmodium, is stipulated by endoplasmic flow, which is produced by spatially highly coordinated rhythmic contractions of the ectoplasm. To describe the self-organization of the plasmodial contractile activity, we proposed a mathematical model, which is based on the hypothesis of positive feedback between the deformation of the cytoskeleton and release of a chemical regulator of the active contraction. A nonautonomous analogue of this model was used to study the synchronization of mechanochemical auto-oscillations by periodic gradient of the external pressure. Numerical computations of the system of differential equations obtained revealed a dependency of the synchronization band on the amplitude of the external pressure oscillations. On the basis of this dependence and experimental data on the band of synchronization of the shuttle endoplasmic flow by the periodic gradient of temperature obtained with the help of the laser Doppler anemometer, relative efficiency of external synchronizing action of temperature and pressure was evaluated.
PMID: 16212064 [PubMed - indexed for MEDLINE]

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Curr Genet. 2005 Feb;47(2):100-10.
Rearrangements in the Physarum polycephalum mitochondrial genome associated with a transition from linear mF-mtDNA recombinants to circular molecules. Nomura H, Moriyama Y, Kawano S. Laboratory of Plant Life Systems, Department of Integrated Biosciences, Graduate School of Frontier Sciences, University of Tokyo, Bldg. FSB-601, 5-1-5 Kashiwanoha, Kashiwa, Chiba, 277-8562, Japan. Although mitochondrial DNA (mtDNA) is transmitted to progeny from one parent only in Physarum polycephalum, the mtDNAs of progeny of mF+ plasmodia vary in structure. To clarify the mechanisms associated with the mitochondrial plasmid mF that generate mtDNA polymorphisms, 91 progeny of four strains (KM88 x JE8, KM88 x TU111, KM88 x NG111, Je90) were investigated using RFLP analysis, PCR, and pulse-field gel electrophoresis (PFGE). Nine mtDNA rearrangement types were found, with rearrangements occurring exclusively in the mF regions. PFGE revealed that, in the groups containing rearranged mtDNA, the linear mF-mtDNA recombinants had recircularized. Sequencing the rearranged region of one of the progeny suggested that the mF plasmid and the mtDNA recombine primarily at the ID sequences, linearizing the circular mtDNA. Recombination between the terminal region of the mF plasmid and a region about 1 kbp upstream of the mitochondrial/plasmid ID sequence results in a rearranged circular mtDNA, with variations caused by differences in the secondary recombination region.
PMID: 15688251 [PubMed - indexed for MEDLINE]

Bioconjugate Chem. 2006, 17 (2), 317-326.

Polycefin, a New Prototype of a Multifunctional Nanoconjugate Based on Poly(-L-malic acid) for Drug Delivery. Bong-Seop Lee, Manabu Fujita, Natalya M. Khazenzon, Kolja A. Wawrowsky, Sebastian Wachsmann-Hogiu, Daniel L. Farkas, Keith L. Black, Julia Y. Ljubimova, and Eggehard Holler*. *Institut für Biophysik und physikalische Biochemie der Universität Regensburg, Germany, Maxine Dunitz Neurosurgical Institute, Cedars-Sinai Medical Center, Los Angeles, California 90048, Department of Surgery, Cedars-Sinai Medical Center, Los Angeles, California, and Arrogene, Inc., Tarzana, California 91356.* A new prototype of nanoconjugate, Polycefin, was synthesized for targeted delivery of antisense oligonucleotides and monoclonal antibodies to brain tumors. The macromolecular carrier contains: 1. biodegradable, nonimmunogenic, nontoxic -poly(L-malic acid) of microbial origin; 2. Morpholino antisense oligonucleotides targeting laminin 4 and 1 chains of laminin-8, which is specifically overexpressed in glial brain tumors; 3. monoclonal anti-transferrin receptor antibody for specific tissue targeting; 4. oligonucleotide releasing disulfide units; 5. L-valine containing, pH-sensitive membrane disrupting unit(s), 6. protective poly(ethylene glycol); 7. a fluorescent dye (optional). Highly purified modules were conjugated directly with N-hydroxysuccinimidyl ester-activated -poly(L-malic acid) at pendant carboxyl groups or at thiol containing spacers via thioether and disulfide bonds. Products were chemically validated by physical, chemical, and functional tests. In vitro experiments using two human glioma cell lines U87MG and T98G demonstrated that Polycefin was delivered into the tumor cells by a receptor-mediated endocytosis mechanism and was able to inhibit the synthesis of laminin-8 4 and 1 chains at the same time. Inhibition of laminin-8 expression was in agreement with the designed endosomal membrane disruption and drug releasing activity. In vivo imaging showed the accumulation of intravenously injected Polycefin in brain tumor tissue via the antibody-targeted transferrin receptor-mediated endosomal pathway in addition to a less efficient mechanism known for high molecular mass biopolymers as enhanced permeability and retention effect. Polycefin was nontoxic to normal and tumor astrocytes in a wide range of concentrations, accumulated in brain tumor, and could be used for specific targeting of several biomarkers simultaneously.

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Cell Struct Funct. 2005 Feb;29(5-6):159-64.

Class-specific binding of two aminoacyl-tRNA synthetases to annexin, a Ca2+- and phospholipid-binding protein. Shirakawa T, Nakamura A, Kohama K, Hirakata M, Ogihara S. Graduate School of Science, Biological Science, Osaka University, Japan. Annexins are a family of Ca2+/phospholipid-binding proteins that have diverse functions. To understand the function of annexin in Physarum polycephalum, we searched for its binding proteins. Here we demonstrate the presence of two novel annexin-binding proteins. The homology search of partial amino acid sequences of these two proteins identified them as aminoacyl-tRNA synthetases (ARSs). Furthermore, antibody against aminoacyl-tRNA synthetases cross-reacted with one of two proteins. Our results imply the interaction between intracellular membrane dynamics and protein translation system, and may give a clue to understand the mechanism of some myositis diseases, which have been known to produce autoantibodies against ARSs.
PMID: 15840947 [PubMed - indexed for MEDLINE]

Biochem Biophys Res Commun. 2006 Mar 24;341(4):1119-27.
Screening for beta-poly(L-malate) binding proteins by affinity chromatography. Gottler T, Holler E. Institut fur Biophysik und Physikalische Biochemie, Universitat Regensburg, D-93040 Regensburg, Germany. Poly(beta-L-malic acid) is a cell type-specific polymer of myxomycetes (true slime mold s) with the physiological role to organize mobility of certain proteins over the giant multinucleated plasmodia. We have developed an affinity chromatography employing 1,6-diamino-n-hexane-Sepharose-coupled poly(malic acid) to identify such proteins in cellular extracts of Physarum polycephalum. Molecular masses were measured by SDS-PAGE and non-denaturing PAGE after silver staining and/or Western blotting. Protein complexes/subunits were detected by 2-dimensional non-denaturing PAGE/SDS-PAGE. A simplified gel shift experiment displayed binding to fragmented calf thymus DNA. Nuclei were richest in poly(malate) binding proteins followed by cytoplasm and membranes. A protein of 370 kDa dissociated into 11 subunits of 11-29 kDa, indicative of a highly complex protein. This and other proteins displayed binding to nucleic acid in gel shift experiments. Poly(malate) is considered a structural and functional equivalent of long contiguous aspartate repeats in proteins of eukaryotes.
PMID: 16476581 [PubMed - indexed for MEDLINE]

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Phys Rev E Stat Nonlin Soft Matter Phys. 2005 Jan;71(1 Pt 1):010902.
Inertia of amoebic cell locomotion as an emergent collective property of the cellular dynamics. Nishimura SI, Sasai M. Department of Complex Systems Science, Graduate School of Information Science, Nagoya University, Nagoya 464-8601, Japan. Amoebic cells are ubiquitous in many species and have been used as model systems to study the eukaryotic cellular locomotion. We construct a model of amoebic cells on two-dimensional grids, which describes sensing, cell status, and locomotion in a unified way. We show that the averaged position of simulated cells is described by a second-order differential equation of motion and that the mechanical pushing at the initial moment boosts the cell movement, which continues after the cell is released from the pushing. These "inertialike" features suggest the possibility of Newtonian-type motions in chemical distributions of the signaling molecule. We show, as an example, the possibility of rotating motion in a "centripetal" distribution. The observed inertial motion is an emergent collective dynamics, which is controlled by diffusive and chemical processes in the cell. Publication Type:Evaluation Studies
PMID: 15697573 [PubMed - indexed for MEDLINE]

Protist. 2005 Dec;156(4):425-32.
A plastid in the making: evidence for a second primary endosymbiosis. Marin B, Nowack EC, Melkonian M. Botanisches Institut, Lehrstuhl I, Universitat zu Koln, Gyrhofstrasse 15, 50931 Koln, Germany. birger.marin@uni-koeln.de One of the major steps in the evolution of life was the origin of photosynthesis in nucleated cells underpinning the evolution of plants. It is well accepted that this evolutionary process was initiated when a photosynthetic bacterium (a cyanobacterium) was taken up by a colorless host cell, probably more than a billion years ago, and transformed into a photosynthetic organelle (a plastid) during a process known as primary endosymbiosis. Here, we use sequence comparisons and phylogenetic analyses of the prokaryotic rDNA operon to show that the thecate, filose amoeba Paulinella chromatophora Lauterborn obtained its photosynthetic organelles by a similar but more recent process, which involved a different cyanobacterium, indicating that the evolution of photosynthetic organelles from cyanobacteria was not a unique event, as is commonly believed, but may be an ongoing process.
PMID: 16310747 [PubMed - indexed for MEDLINE]

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Nucleic Acids Res. 2006 Jan 1;34(Database issue):D423-7.
dictyBase, the model organism database for Dictyostelium discoideum. Chisholm RL, Gaudet P, Just EM, Pilcher KE, Fey P, Merchant SN, Kibbe WA. dictyBase, Center for Genetic Medicine, Feinberg School of Medicine, Northwestern University, Chicago, IL 60611, USA. chisholm@northwestern.edu dictyBase (http://dictybase.org) is the model organism database (MOD) for the social amoeba Dictyostelium discoideum. The unique biology and phylogenetic position of Dictyostelium offer a great opportunity to gain knowledge of processes not characterized in other organisms. The recent completion of the 34 MB genome sequence, together with the sizable scientific literature using Dictyostelium as a research organism, provided the necessary tools to create a well-annotated genome. dictyBase has leveraged software developed by the Saccharomyces Genome Database and the Generic Model Organism Database project. This has reduced the time required to develop a full-featured MOD and greatly facilitated our ability to focus on annotation and providing new functionality. We hope that manual curation of the Dictyostelium genome will facilitate the annotation of other genomes.
PMID: 16381903 [PubMed - indexed for MEDLINE]

J Cell Biol. 2005 Jun 6;169(5):719-24.
De novo formation of basal bodies in Naegleria gruberi: regulation by phosphorylation. Kim HK, Kang JG, Yumura S, Walsh CJ, Cho JW, Lee J. Department of Biology, Yonsei University, Seoul 120-749, Korea. The de novo formation of basal bodies in Naegleria gruberi was preceded by the transient formation of a microtubule (MT)-nucleating complex containing gamma-tubulin, pericentrin, and myosin II complex (GPM complex). The MT-nucleating activity of GPM complexes was maximal just before the formation of visible basal bodies and then rapidly decreased. The regulation of MT-nucleating activity of GPM complexes was accomplished by a transient phosphorylation of the complex. Inhibition of dephosphorylation after the formation of basal bodies resulted in the formation of multiple flagella. 2D-gel electrophoresis and Western blotting showed a parallel relationship between the MT-nucleating activity of GPM complexes and the presence of hyperphosphorylated gamma-tubulin in the complexes. These data suggest that the nucleation of MTs by GPM complexes precedes the de novo formation of basal bodies and that the regulation of MT-nucleating activity of GPM complexes is essential to the regulation of basal body number.
PMID: 15939759 [PubMed - indexed for MEDLINE]

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BioSystems (2006), doi:10.1016/j.biosystems.2006.09.016
Robot Control with Biological Cells. Soichiro Tsuda, Klaus-Peter Zauner, Yukio-Pegio Gunji.
At present there exists a large gap in size, performance, adaptability and robustness between natural and artificial information processors for performing coherent perception-action tasks under real-time constraints. Even the simplest organisms have an enviable capability of coping with an unknown dynamic environment.
Robots, in contrast, are still clumsy if confronted with such complexity. This paper presents a bio-hybrid architecture developed for exploring an alternate approach to the control of autonomous robots. Circuits prepared from amoeboid plasmodia of the slime mold *Physarum polycephalum* are interfaced with an omnidirectional hexapod robot. Sensory signals from the macro-physical environment of the robot are transduced to cellular scale and processed using the unique micro physical features of intracellular information processing. Conversely, the response form the cellular computation is amplifed to yield a macroscopic output action in the environment mediated through the robot's actuators.

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