

**Ukens innhold (klikk på sidetallet, så kommer du dit direkte ...)**

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**John og Hilary Birks med *Perspective* i *Science***

John og [Hilary](#) gratuleres herved med *perspective*-artikkelen "The rise and fall of forests" i *Science*. Det sier seg selv at BIOs JIF-konkurranse hermed har fått en helt ny leder (JIF for *Science* er 29,0). Artikkelen er ikke lenger enn at de fleste har tid til å lese den, og den kan åpnes [her](#)! At den er trykket som *perspective* betyr at redaktørene av *Science* har henvendt seg til John og Hilary og bedt dem om å sette et nytt forskningsresultat i perspektiv. *Science* viser med dette at tidsskriftet betrakter disse forskerne som ledende internasjonale autoriteter i fagfeltet paleoøkologi.



**Birks, HJB & HH Birks 2004. The rise and fall of forests. *Science* 305, 484-485**

Etter denne artikkelen ser 10-på-topp-lista slik ut: (alle BIO-artikler fra i år ligger [her](#).)

#	JIF	F-gr	Referanse
1	29.0	EECRG	Birks, HJB & HH Birks 2004. The rise and fall of forests. <i>Science</i> 305, 484-485.
2	11.2	EVØ	Skorping A, Jensen KH. 2004. Disease dynamics: all caused by males? <i>Trends Ecol. Evol.</i> 19: 219-220.
3	10.5	CSG	Futterer O, Angelov A, Liesegang H, Gottschalk G, Schleper C, Schepers B, Dock C, Antranikian G, Liebl W 2004. Genome sequence of <i>Picrophilus torridus</i> and its implications for life around pH 0. <i>Proc. Natl Acad Sci. USA</i> 101: 9091-9096
4	5.6	EMO	Irimia, A; Vellieux, FMD; Madern, D; Zaccari, G; Karshikoff, A; Tibbelin, G; Ladenstein, R; Lien, T; Birkeland, NK. 2004. The 2.9 angstrom resolution crystal structure of malate dehydrogenase from <i>Archaeoglobus fulgidus</i> : Mechanisms of oligomerisation and thermal stabilisation. <i>J. mol. Biol.</i> 335: 343-356.
5	5.4	FSG	Falk, K; Aspehaug, V; Vlasak, R; Endresen, C. 2004. Identification and characterization of viral structural proteins of infectious salmon anemia virus. <i>J. Virol.</i> 78: 3063-3071.

## Forkortelse på navnene til forskergruppene

AAØ	Akvatisk atferdsøkologi	FSG	Fiskesykdomsgruppen
AIB	Anvendt og industriell biologi	MAS	Mikroalgers og soppers fysiologi og anvendelse
CSG	Christa Schlepers gruppe	MBD	Marin biodiversitet
DBF	Fiskenes utviklingsbiologi	MIØ	Mikrobiell økologi
EECRG	Ecological and Environmental Change	MOD	Modelleringsgruppen
EMO	Ekstremofile mikroorganismer	SKJ	Gruppe for skjelettforskning
EVØ	Evolusjonær økologi	SYS	Systematikk-gruppen
FIBER	Fish Biology, Ecology and Reproduction	ØEF	Økosystem-effekter av fiske

## Andre nye artikler fra BIO

Levsen A, Alvik T, [Grotmol S](#) 2004. Neurological symptoms in tricolor sharkminnow *Balantiocheilos melanopterus* associated with *Myxobolus balantiocheili* n. sp infecting the central nervous system. DISEASES OF AQUATIC ORGANISMS 59: 135-140

**Abstract:** A new species, *Myxobolus balantiocheili*, is described from the central nervous system of wild and cultured tricolor sharkminnow *Balantiocheilos melanopterus* from Thailand. The infection was associated with emaciation and severe neurological symptoms, including sudden uncoordinated darting, rolling and pitching. Whitish cysts of varying shape, measuring 70 to 500 µm, were located in the brain, spinal cord and in the meninx, and were sometimes accompanied by haemorrhages. In the brain, most cysts were located in the medulla oblongata and the mesencephalon. Cysts with a segmental distribution were observed in the meninx of the spinal cord. Single di- to hexasporic pansporoblasts, and free mature spores, were frequently seen in both the white and grey matter of the brain and spinal cord, mostly associated with blood vessels. Mature spores varied in shape from oval to ellipsoid, measuring  $12.3 \pm 0.59$  (range 10.6 to 13.3) x  $10.0 \pm 0.47$  (9.2 to 10.9) x  $6.9 \pm 0.20$  (6.7 to 7.1) µm. Spore size and morphology, in addition to fish-host species and apparently narrow tissue tropism, clearly distinguishes this new *Myxobolus*. No marked inflammatory response or gliosis was associated with the lesions, but compression and degeneration of the nervous tissue surrounding large cysts was observed. We suggest that the high temperature of the fish hosts' tropical habitat may have increased the rate of development and the virulence of *M. balantiocheili*.



Rowlands WL, Dickey-Collas M, [Geffen AJ](#), Nash RDM 2004. Abundances of *Metridia lucens* in the western Irish Sea . J. mar. BIol. Ass. UK 84: 617-618.

**Abstract:** Interannual and spatial differences in the abundance of *Metridia lucens* are reported from the Irish Sea from 1996 to 2001. In most years the abundance in spring is very low (<50 m(2)), however in 2001 the abundance was high and this enabled a rare study of the vertical distribution of *M. lucens* in coastal waters. The vertical distribution differs with time of day and water column structure. Abundances were always higher in stratified deeper waters compared with mixed or coastal waters.



Myklestad Å, Sætersdal M 2004. The importance of traditional meadow management techniques for conservation of vascular plant species richness in Norway. BIOLOGICAL CONSERVATION 118: 133-139

**Abstract:** Using information from a regional survey of vascular plants of 130 sites in western Norway, a selection of sites based on a heuristic iterative complementarity-based nature reserve selection procedure was performed. The results indicate that conservation of traditionally managed hay meadows is of major importance as they contributed 60.1% of all native species recorded; afforested grasslands (deciduous woodlands < 70 years old) contributed 26.8%, whereas artificially fertilized hay meadows and intensively cultivated grasslands taken together contributed 13.1% of the species. The species composition of the meadows was significantly nested. Thus, if you conserve the most species-rich meadows, you also conserve most of the species in the less species-rich meadows. Nestedness in meadows was significantly correlated with within-meadow habitat diversity and soil pH. The most species-rich meadows were traditional meadows, characterized by high habitat diversity and high soil pH. These meadows will support nearly all species including habitat specialists and regionally rare species, whilst artificially fertilized hay meadows only support the generalist subset, i.e. common species. Area was not significantly correlated with nestedness suggesting that it is more important to cover many habitats than to preserve large traditional meadows just because they are large.

[Åse Myklestad](#) disputerte ved BIO i juni. Hun er nå ulønnet medlem av EECRG-gruppa. Siden hun bruker BIO (Bot inst) som adresse, framkommer hennes publikasjoner som våre. Tusen takk!

Myklestad Å. 2004. Soil, site and management components of variation in species composition of agricultural grasslands in western Norway. GRASS AND FORAGE SCIENCE 59: 136-143

**Abstract:** A partitioning of the total variance in species composition of grasslands associated with increasing fertilizer inputs (unfertilized pastures, artificially fertilized hay meadows and intensively cultivated grassland) in western Norway was undertaken. The partitioning was carried out with (partial) constrained ordinations (canonical correspondence analysis) and associated Monte Carlo permutation tests. Explained variation was high (0.651), with soil chemistry, management and site explaining 0.271, 0.228 and 0.052 of the variation, respectively, and the interaction between soil and management explaining 0.100 of the variation. However, much of the measured soil chemistry was considered to be an effect of management. The soil chemistry variable explaining most variation was extractable P content, associated with high soil extractable P contents in the intensively cultivated grassland due to high fertilizer applications. However, soil extractable P content did not explain differences in species composition when grasslands with smaller differences in fertilizer inputs (meadows vs. pastures) were compared. Total soil C and N contents and C:N ratios explained significant variation between all grassland types. Lowest levels of these variables were measured in the grassland with the highest fertilizer inputs, suggesting that total soil N content cannot be used as a predictor of fertility. Significantly higher soil N contents were measured in grasslands of low productivity, probably due to a low decomposition rate of stress-tolerant plants and the consequent low availability of soil N and accumulation of soil organic matter. Ellenberg N values reflected soil chemical differences in this study with high Ellenberg N values reflecting high Ca, Mg and P contents and pH values and low total C and N contents and C:N ratios.

Sandvik SM, Heegaard E, Elven R, [Vandvik V](#) 2004. Responses of alpine snowbed vegetation to long-term experimental warming. *ECOSCIENCE* 11: 150-159

**Abstract:** In order to assess the influence of experimental warming on individual species response, species composition and richness, and the abundance of ramets in a wet late-melting snowbed, we established 20 open-top chambers (OTCs) permanently for 5 y (six growing seasons) at Finse, southwest Norway. *Salix herbacea*, *Saxifraga stellaris*, *Omalotheca supina*, *Cerastium cerastoides*, and *Epilobium anagallidifolium* increased in the experimentally warmed plots, while there was no significant response in *Carex lachenalii*, *Deschampsia alpina*, *Poa alpina*, *Juncus biglumis*, *Saxifraga rivularis*, or *Veronica alpina*. Species composition changed significantly with time both in the OTCs and in the control plots. Although invasion rates slightly increased in the OTCs compared to the controls, differences in overall species composition or richness were not significant between the OTCs and the control plots during the 5-y study. Our results suggest that vegetation change is going on naturally and that the effect of this change overrides the effect of the temperature treatment. We conclude that increased plant growth will result in denser vegetation in a warmer future. Whether the higher net invasion will result in more diverse vegetation is yet unclear, as the processes take more time than allowed for in this study.



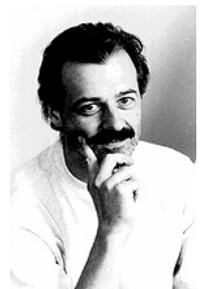
Karlsbakk E 2004. A trypanosome of Atlantic cod, *Gadus morhua* L., transmitted by the marine leech *Calliobdella nodulifera* (Malm, 1863) (Piscicolidae). *PARASITOLOGY RESEARCH* 93: 155-158.

**Abstract:** The fish leech, *Calliobdella nodulifera*, transmitted a trypanosome while feeding on laboratory-reared cod (*Gadus morhua*). The flagellate body length increased from 43µm 17 days post-infection (d.p.i.) to 57 µm 113 d.p.i. Characteristic features are cell striation, a nearly central nucleus and a short (3.5 µm) distance from the kinetoplast to the posterior end (PK). Following growth, the trypanosomes became increasingly slender, with fewer striae and a shorter flagellum, while the PK was unaffected. The trypanosomes differ morphologically from *Trypanosoma murmanensis* transmitted by the leech *Johanssonia arctica*.

*Engil Karlsbakk er forsker i [fisksykdomsgruppa](#). De to neste artiklene kommer fra samme gruppe.*

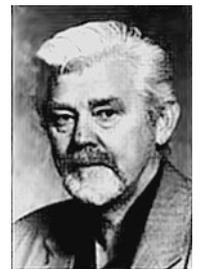
Fridell F, Devold M, [Nylund A](#) 2004. Phylogenetic position of a paramyxovirus from Atlantic salmon *Salmo salar*. *DISEASES OF AQUATIC ORGANISMS* 59: 11-15

**Abstract:** A paramyxovirus has been isolated from Atlantic salmon *Salmo salar* suffering from epitheliocystis. This virus does not cause any mortality when used to challenge disease-free salmon, but has been associated with 2 cases of mortality in salmon farms in Norway. Atlantic salmon paramyxovirus (ASPV) has been suggested as a name for the virus. The ASP virus is a slow-growing virus in cell cultures (rainbow trout gill cells: RTgill-W1). Little is known about its importance and its phylogenetic position is uncertain. Hence, the need for a fast and



sensitive diagnostic method for studying the prevalence of this virus in salmon farms and for more basic knowledge about its identity were the motivation for this study. A partial nucleotide sequence (816 bp) from the large protein (L protein) gene of the ASP virus has been sequenced from 2 different isolates. The putative amino acid sequence has been compared with the L protein of other paramyxoviruses. This sequence gives strong support to a relationship between the ASP virus and members of the subfamily Paramyxovirinae, genus *Respirovirus*.

[Hordvik I](#), Torvund J, Moore L, [Endresen C](#) 2004. Structure and organization of the T cell receptor alpha chain genes in Atlantic salmon. MOLECULAR IMMUNOLOGY 41: 553-559  
**Abstract:** A cDNA fragment of the T cell receptor (TCR) alpha chain mRNA in Atlantic salmon (*Salmo salar*) was amplified by PCR and used as a probe to isolate a full-length clone from a leukocyte cDNA library. Additionally, a genomic lambda clone comprising the TCR alpha chain constant region (C $\alpha$ ) gene and flanking regions was isolated and partially sequenced. The C $\alpha$  gene consists of three exons corresponding to the immunoglobulin (Ig) domain, the hinge region and the transmembrane peptide/cytoplasmic tail, and two exons corresponding to the untranslated tail of the mRNA. Remnants of a transposase gene and a partial duplication of the C $\alpha$  gene were found nearby the intact gene. One J segment was found 1.5 kb upstream of the C $\alpha$  gene. Twenty-six other J elements were identified among cDNA fragments covering the V/J/C $\alpha$  junction. Representatives of five V $\alpha$  gene families were identified by PCR amplification of genomic DNA fragments. PCR amplification of C $\alpha$  fragments from another individual revealed a slightly different C $\alpha$  gene which most likely represents an allelic variant.



Kurabachew M, Enger Ø, [Sandaa RA](#), Skuce R, Bjorvatn B 2004. A multiplex polymerase chain reaction assay for genus-, group- and species-specific detection of mycobacteria. DIAGNOSTIC MICROBIOLOGY AND INFECTIOUS DISEASE 49: 99-104  
**Abstract:** We developed and evaluated a single-step, multiplex polymerase chain reaction (PCR) assay for distinguishing (1) between the *Mycobacterium tuberculosis* complex (MTBC) and mycobacteria other than tuberculosis (MOTT) and (2) between *M. tuberculosis* and *M. bovis* species. The assay targeted the 16S and the 23S rDNA to distinguish between MTBC and MOTT species, and the *oxyR* gene to distinguish between *M. tuberculosis* and *M. bovis* strains. Clinical samples and reference strains (N = 156) comprised 93 strains of *M. tuberculosis*, 44 of *M. bovis*, 1 *M. africanum* strain, and 18 strains representing 9 different species of MOTTs. MOTTs generated only a single PCR product of about 2.5 kilobase; however, all of the MTBC strains produced a 118 base pair (bp) fragment and an additional 270 bp fragment was obtained for *M. tuberculosis* and *M. africanum* when the primer pair oxyRT13-2.11oxyRMT-1 was used. When oxyRTB2.1 loxyRMB-1 primers were used, the 270 bp fragment was obtained for only *M. bovis*. The assay needed as little as 1 pg of purified genomic DNA to make a positive identification.



Ruth-Anne Sandaa og Øyvind Enger. Bildet er fra [Schrödingers katts](#) webside.

## Utlysning av midler til Biodiversitet-forskning med finansiering fra European Science Foundation

EUROCORES programmet EuroDIVERSITY.

### 1. Understanding biodiversity change

- Ecological, evolutionary and socio-economic processes that drive biodiversity change, and the interplay between these processes.
- Causes and predictive value of biodiversity patterns, including macroecological and other emergent properties of complex systems across levels of biological organisation.
- Effects of genetic biodiversity within and among species on population, community and ecosystem processes.

### 2. Understanding impacts of biodiversity change on ecosystem services

- Impacts of biodiversity changes (including biological invasions) on ecosystem functioning, stability and services, and their underlying mechanisms.
- Functional role of microbial biodiversity in ecosystems.

- Consequences of food-web and non-trophic interactions for ecosystem functioning.
  - Spatial processes across systems, metacommunities, and the dynamics of biodiversity and ecosystem processes at landscape to regional scales.
3. Exploring the interface between biological and social systems
- Socioeconomic consequences of changes in ecosystem services driven by biodiversity; assessment of opportunities for, and limits to, substitution between these services and man-made capital.
  - Identifying the basis of social choice (values, incentives) for the conservation, restoration and management of biodiversity.
  - Dynamics of coupled social and ecological systems: effects of cross-scale interactions and mismatch between ecological processes, socio-economic processes and management institutions

Obs! Rent deskriptive biodiversitet studier er ikke relevante for denne utlysningen.

Prosjektet bør involvere partnere fra minst 2 ESF-medlemsland og vare i 3 år (men med mulighet for kortere og lengre perioder)

Søknadsprosessen i 2 runder. Frister:

- **30. September:** 1-2 sider prosjektskisse (+ budsjett, partnerbeskrivelse, CVer, osv.)
- 1. februar 2005: detaljert prosjektbeskrivelse, der sammenslåing av flere initiativer kan bli anbefalt

Det er ikke publisert føringer om størrelse på prosjektet. Et trygt utgangspunkt kan være å satse på prosjekttypen vi kjenner fra EUs FP4 og FP5, men her går det an å være kreativ !!!

[http://www.esf.org/esf\\_article.php?language=0&activity=7&domain=3&article=435&page=1097](http://www.esf.org/esf_article.php?language=0&activity=7&domain=3&article=435&page=1097)

*Clelia*

## Sjømat for alle

Professor **Ragnar Nortvedt** minner om at konferansen *Sjømat for alle* gjennomføres i Grieghallen 2.-3. september under temaet "Innovasjon krever marked". På fiskeflåten ved Fisketorget arrangeres "Sjømatens festmiddag" torsdag 2. september. Det vil dessuten bli folkefest på flåte ved fisketorget 3.- 4. september. For fullstendig program og påmelding til konferanse og festmiddag, se [www.sjomat.no](http://www.sjomat.no)

