



Änderungen der Beiträge des ÖEG-Kolloquiums 2020 in Wien, 14.03.2021

Two in one: Diapause und Voltinismus des Buchdruckers

MARTIN SCHEBECK, NINA DOBART, GREGORY J. RAGLAND, AXEL SCHOPF &
CHRISTIAN STAUFFER

Numerous insect species express diapause, in order to match their life-cycles with environmental conditions. By entering diapause, insects cease reproduction and direct development, suppress metabolic rate and enhance resistance against external stressors. In addition, diapause extends generation time and influences voltinism, i.e. the number of generations per year. We describe facultative and obligate diapausing individuals of the most common European spruce bark beetle, *Ips typographus*, and report their geographic distribution. Laboratory experiments at different photoperiodic conditions with Central and Northern European beetles were conducted. Egg numbers and gonad size were used to evaluate diapause expression. Under long-days, Central European females did not enter diapause. Under short-days, individuals expressed a photoperiod-regulated diapause. In Northern European beetles, short-days, long-days and extra-long-days induced diapause in *I. typographus*. Our results show that beetles entered a photoperiod-insensitive, i.e. obligate, diapause. Obligate diapausing individuals were also present in Central European locations. Our findings help to understand the life-cycle, phenology and voltinism of the most important European forest pest and will improve management strategies.

Anschrift der Verfasser

Dr. Martin SCHEBECK, MMSc; DI Dr. Nina DOBART; Univ.-Prof. Dr. Axel SCHOPF;
Univ.-Prof. DI Dr. Christian STAUFFER, Department für Wald- und Bodenwissenschaften,
Universität für Bodenkultur Wien, BOKU. Peter-Jordan-Straße 82/I, A-1190 Wien, Austria

Ass.-Prof. Gregory J. RAGLAND: Department of Integrative Biology,
University of Colorado-Denver. 1151 Arapahoe, Denver, CO 80204, USA

E-Mails: martin.schebeck@boku.ac.at, dobart@gmx.at, gregory.ragland@ucdenver.edu,
axel.schopf@boku.ac.at, christian.stauffer@boku.ac.at

Prey-RNA allows to differentiate between scavenging and active predation in predatory insects

Die Analyse von Beute-RNA ermöglicht zwischen Aasfraß und aktiver Predation in räuberischen Insekten zu unterscheiden

VERONIKA NEIDEL, DANIELA SINT, CORINNA WALLINGER & MICHAEL TRAUGOTT

Molecular gut content analysis facilitates studying generalist predators as natural enemies of invertebrate crop pests in farmland. However, not all their feeding interactions are necessarily the result of active predation as many predators, e.g. ground beetles (Coleoptera: Carabidae), frequently engage in scavenging, the opportunistic consumption of prey remains. For prey-DNA detection in gut content, the type of a feeding interaction is inconsequential: active predation and scavenging are detectable equally well. If trophic data is solely based on DNA-detections, the proportion of scavenging in the diet of a predator thus remains unknown, potentially leading to an overestimation of a natural enemy's contribution to pest regulation. Here, we propose a new approach, combining prey-DNA and prey-RNA detection, as RNA is only expressed in living organisms, is less stable than DNA and should thus degrade faster after death than DNA. Therefore, we hypothesize that prey-RNA is less likely to be detected in case of scavenging. To test our assumption, feeding experiments were conducted: fresh and 24 h-dead fruit flies (*Drosophila melanogaster*) were fed to carabids (*Harpalus rufipes*) to simulate predation and scavenging, respectively. Carabids' gut content was screened for the presence and relative amount of fly DNA and RNA at different time points of digestion. At 0–12 hrs after fresh prey consumption, the average signal strengths of *Drosophila*-specific PCR products of RNA were 71–96 % that of DNA. To our knowledge, this is the first example of successful prey-RNA detection in the gut content of a consumer, challenging the common believe that RNA cannot persist in gut content. After carrion consumption, the difference in signal strength between RNA and DNA was more pronounced, with RNA producing signals of just 15–30 % the strength of DNA, 0–12 hrs after feeding. Contrary to our assumption, prey-RNA was detectable in both feeding types, but less frequently and on average with a lower relative amount in scavengers than in predators. Our findings demonstrate that prey-RNA allows to discriminate between scavenging and predation in recent feeding events, providing a novel approach to study the respective importance of carrion and fresh prey for predatory arthropods using molecular gut content analysis. The combination of RNA and DNA detections will help to better estimate the prevalence of scavenging in field-collected predatory arthropods and thus significantly improve the prediction of their regulatory potential.

Anschrift der VerfasserInnen:

Veronika NEIDEL, Daniela SINT, Corinna WALLINGER, Michael TRAUGOTT,
Applied Animal Ecology, Department of Zoology, University of Innsbruck,
Technikerstraße 25, Innsbruck 6020, Austria. E-Mail: veronika.neidel@uibk.ac.at

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