

# A comparative analysis of hierarchically organized grooming patterns in hamsters

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## Introduction

Structural organization is a fundamental feature of animal behavior. It is usually a result of evolution or learning and is expressed in hierarchically organized successions of behavioral acts (“behavioral patterns”). Analysis of such patterns opens a possibility to interpret animal behavior, categorize it and to trace its history and evolution. However, the analysis of behavior structure and its transformations is a complicated task that requires development of new specific algorithms similar to those used for the study of morphological traits and DNA sequences.

## Proposed approach

Our approach to behavior structure analysis is based on a functional systems theory (FST) [2-4]. According to the FST, behavioral continuum is separated into individual behavioral acts, each based on a discrete functional system [3]. Functional systems are dynamically self-organized aggregates of neural and peripheral elements that cooperate to achieve an adaptive result for a behaving organism [2]. Achievement of the result of a particular system terminates its activity and initiates self-organization processes for the next functional system [8]. Changes in dynamics of animal behavior at the moments of such critical transitions (“breakpoints”) allowed us to develop motion analysis algorithms that isolate elementary behavioral units from a behavioral continuum [6]. Our next step, followed in the current work, was to reveal and reconstruct a natural structure of behavioral continuum as consisting of hierarchically organized patterns of behavioral acts (“systemic quanta” of behavior [9]).

To develop the new tools for detection and comparative analysis of such behavioral patterns we used highly organized rodent grooming behavior. The main features of grooming behavior are high level of movement stereotypy and fixed successions of discrete grooming acts, which can be defined as evolved actions sequences possessing syntactic rules [5]. Grooming patterns show intraspecies stability and interspecies variability in wide spectrum of taxons. These characteristics and possibility to induce this behavior under experimental conditions and to assess it quantitatively resulted in our selection of grooming as a model for analysis of behavior structure.

## Experiments

We performed comparative structural analysis of grooming in several species of Palaearctic hamsters (subfamily *Cricetinae*) belonging to five taxons with known phylogenetic connections between them: *Phodopus campbelli*, *Mesocricetus auratus*, *Cricetulus griseus*, *Cricetus migratorius* and *Allocricetulus evermanni*. Grooming behavior was induced in animals by water immersion. Each animal was videotaped during 15-min test session under room light in a glass chamber with two side mirrors. The video tracking of animal’s movements was carried out using “Easy Track” software developed in our lab [1]. The subsequent segmentation of grooming continuum into

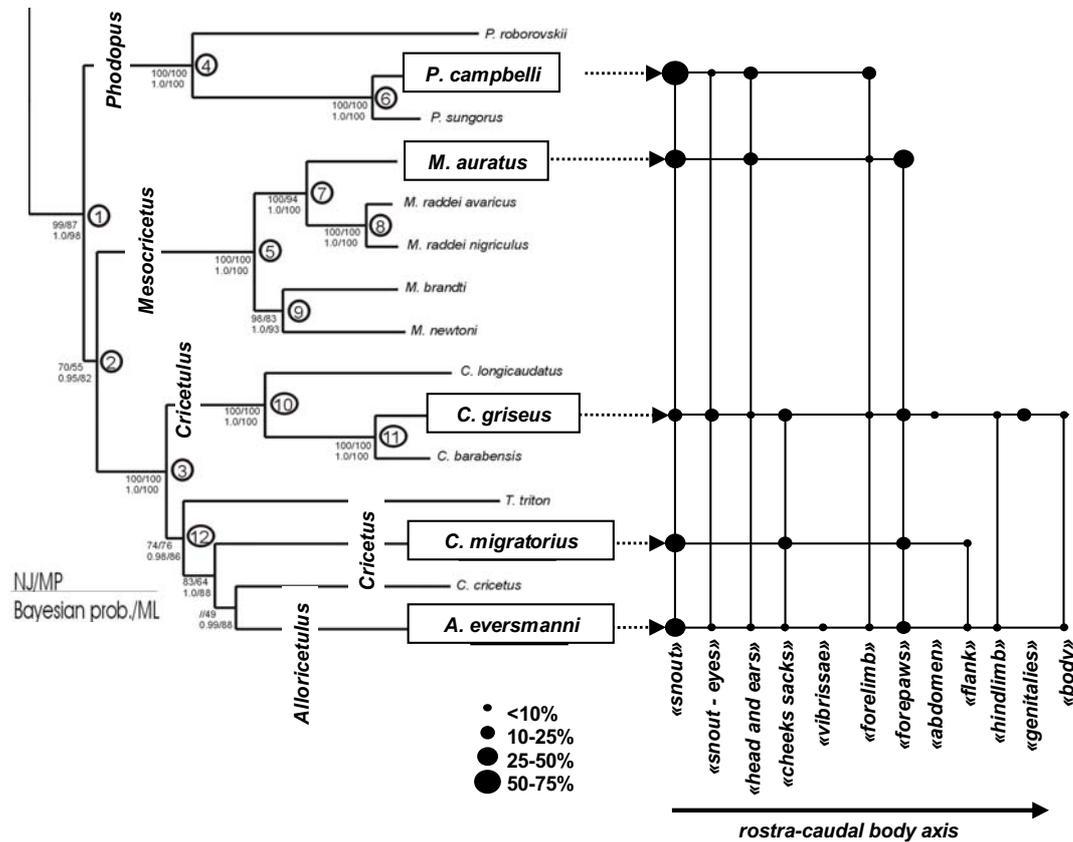
single behavioral acts was performed automatically by “Segment Analyzer” software developed in our lab [6]. In total we detected 24 different grooming acts which were defined as combinations of movement category (licking, washing, biting etc.) and category of body region to which movement was confined (“hand licking”, “forelimb biting”, “snout washing”, etc.). Acquired successions were analyzed by the Theme software to reveal the hierarchy-organized grooming T-patterns [7].

A comparative analysis of grooming patterns uncovered both differences and similarities between sequences of grooming acts in five species. Major difference was in the strategies of transitions from face and head grooming to other body regions. Another pronounced difference was in the probabilities of substitution of single movement category within a similar body region T-pattern (“biting” vs. “licking”, “washing” vs. “fast washing” etc.). On the other hand, strong similarities were found in cheeks sacks grooming patterns in all studied palearctic hamsters. Next we performed a classification of behavioral patterns according to different order of the studied taxons: subfamily-specific, species-specific and individual grooming patterns. All observed species displayed similar simple subfamily-specific patterns during face and head grooming (“snout washing – fast snout washing”, “snout - eyes washing - fast snout washing”, “snout washing - head and ears washing”, “snout washing – forepaws licking”, etc.). Structural analysis also showed that different species of hamsters had numerous individualities in fixed actions programs of grooming behavior including amount of different pattern types, pattern length, pattern hierarchy levels, directions of body regions transitions and body regions attractors for particular patterns.

The results of our subfamily-specific and species-specific analysis suggest that evolution of grooming behavior in Palaearctic hamsters consisted in: (a) appearance of novel grooming patterns, (b) expansion of grooming patterns along the rostra-caudal body axis, (c) elaboration of face and a head grooming behavior, (d) involvement of forepaws in hard-fixed actions programs and (e) substitution of forelimbs to forepaws use in functionally similar patterns (see Figure 1).

## Conclusion and future work

We conclude that functional systems approach to analysis of behavior allows to reveal structure highlights fundamental features in the organization of grooming behavior. It allowed us to detect the “systemic quanta” of grooming behavior, reveal their grouping into fixed actions programs, describe these patterns quantitatively and apply to them a comparative phylogenetic analysis. In future we intend to use this approach to reconstruct the evolution of separate functional systems of grooming behavior based on comparison of subfamily-, species-specific and individual hierarchically organized patterns of behavioral acts in palearctic hamsters and knowledge of phylogenetic connections between the examined taxons.



**Figure 1.** A rostra-caudal expansion of species-specific grooming patterns topography (B) in concordance with molecular-genetic tree of phylogenetic connections between the examined taxons (A).

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