

Characterizing the dynamics of stationary vegetation boundaries

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The vegetation of landscapes consists of patches and intervening boundaries. Boundaries are often considered as the hotspots of vegetation changes, since several plant species reach the limit of their local distribution at the boundaries. Therefore, the dynamics of boundaries can be a sensitive indicator of environmental changes and can help to understand the mechanism of landscape scale pattern changes.

The dynamics of boundaries is usually described by their positional movements. Positional boundary dynamics has three main types: stationary, directional and shifting. A boundary is stationary, i.e. stable in position, if strong and stable abiotic parameters maintain them over long periods of time. Directional dynamics means the unidirectional translocation of boundaries due to abiotic or biotic drivers, while shifting dynamics takes place if these factors fluctuate in time.

In my study, I aimed to refine this scheme by analysing the dynamics of two vegetation complexes. The first one was located in Bugacpuszta, a landscape dominated by sand dune ranges with xeric plant communities on dunes and mesic ones in dune slacks. The other location was the Turjánvidék, which is a mosaic of wet meadows and steppe fragments. In both cases, the emergence of boundaries is dependent on topography-driven differences in water supply; therefore stationary boundary dynamics is expected to prevail. However, in the first case the mesic patches gradually lost the majority of their water supply in the last few decades, meaning that a key environmental factor had a directional trend. In the Turjánvidék, the average water supply is still satisfactory, but its inter-annual variations have become much larger, which can be considered as a shifting effect.

In Bugac, the vegetation of a 55-m and a 30-m transect were monitored between 1999 and 2013 using contiguous grids of quadrats. Presence/absence data of all plant species was recorded and the data were analysed with the split moving window technique. The method identifies the position of boundaries and the contrast the boundaries bridge between the patches. Five significant boundaries could be detected along the transects over the years. I tested the dynamics of their position and contrast using linear regressions. According to the results, positions did not follow the retraction of the groundwater, but the contrast between the adjacent patches showed significant trends: two boundaries disappeared and one new one appeared, which could be explained by the increasing proportion of xeric species and by the opening up of the vegetation.

In the Turjánvidék, I surveyed the vegetation along thirteen permanent, 40 m long transects. The surveys were performed in a wet year (in 2013) and in a dry year (in 2014). After performing the split moving window analysis, the boundary parameters were compared between the two years using t-tests. The results indicated that the position of the boundaries did not react to the differences of water availability, but the wet and dry patches became more similar to each other in the dry year, which could be traced back to the higher proportion of xeric species in the wet patches in 2014.

Thus, it can be concluded that even strong directional or shifting environmental processes cannot elicit positional changes in stationary boundaries; therefore positions are not recommended for bioindication in these cases. On the other hand, contrast changes sensitively indicated the reactions of the vegetation. This also means that landscapes with stationary boundaries can also be dynamic, but the typical pattern changes are not patch expansion vs. shrinking but patch fusion and division, which should be taken into consideration in a variety of ecological and nature conservation applications.

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Genetic investigations in neurodegenerative disorders

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Genetic investigations are useful tools to identify genes, which directly or indirectly play a role in the pathomechanisms of diseases and thereby indicating useful therapeutic interventions. The aim of our research group was to investigate different single nucleotide polymorphisms (SNPs) in multiple sclerosis (MS), amyotrophic lateral sclerosis (ALS) and Parkinson's disease (PD). As a first step a biobank in the Department of Neurology, Szeged was established. Necessary ethical and biobank licenses were obtained and sample collections were started. Parallel with the collection of blood samples, databases belonging to the samples (age, sex, disease onset, etc.) were created. DNA purification from whole blood was performed using a simple salting out technique developed by Miller. To distinguish the alleles of the examined genes fluorescent labeled Taqman probes or restriction fragment length polymorphism techniques were applied. For statistical evaluation of the data SPSS software version 20 was utilized.

In case of MS chemokine receptor V polymorphism rs333 was studied, since earlier results about its involvement in the pathomechanism of MS were controversial. We investigated the receptor and its deletion in a large MS (428) and control (831) population from Hungary and Serbia. There was no significant difference in genotype (OR=1.092, 95% CI=0.807-1.478, p=0.568 for wt/wt (wt=wild type allele) vs wt/ Δ 32, Δ 32/ Δ 32 (Δ 32= Δ 32 base pair deletion allele)) or allele frequency (OR=0.914, 95% CI=0.692-1.207, p=0.525). Neither the deletion