Evaluation of factors affecting the performance of the ‘Higher Taxa Approach’ (HTA) for assessing richness and composition in bee communities

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Environmental studies and ecological monitoring often require identification of species present in a habitat. Species-level identification might require substantial time, money, and taxonomic knowledge, , especially when small-bodied taxa, such as insects, are considered. Many groups of insects are considered good indicators for biodiversity and environmental condition, thus high importance is attached to developing tools for their rapid mapping. Since many field studies and surveys are limited in time and resources there is a growing need to develop cost-effective surrogates for direct species evaluation.

One of the surrogates proposed is the 'Higher Taxa Approach' (HTA), according to which specimens are identified to a higher taxonomic level (genus, sub-family etc'). Richness and composition patterns of these higher taxonomic levels are believed to indicate species-level patterns. Since the identification of specimens to Genus, and further yet to higher taxonomic levels, is usually much faster and far less demanding in terms of taxonomical expertise, this approach is believed to be cost-effective for indicating species-level patterns. The HTA had been extensively tested in a variety of ecosystems, taxa, spatial scales and statistical approaches. Studies examining the reliability of the HTA at small scales (tens of kilometers), especially those focusing on species-rich taxa, led to mixed conclusions, and a general pattern is yet to be considered. Importantly, to date, there are very few studies which investigated the factors affecting HTA performance.

Bees (superfamily Apoidea) are of great importance to man due to their crop pollination services. In light of a continuous decline in the number of honeybee colonies around the world in the last few decades there is growing concern over periods of pollination shortages and efforts are made to find alternative pollination agents.. In recent years, a large number of studies demonstrated the contribution of wild bees to crop pollination, given adequate environmental conditions. Consequently, there is growing need to investigate bee diversity patterns and the effects of land-use on wild bees. These studies are based on species-level identification of bees, which required experts’ knowledge and take long. Thus, the taxonomic identification is often a "bottleneck" in the process and a major limiting factor in conducting bee surveys. In addition to their ecological importance, bees are good model taxa for examining the reliability of the HTA in local scales. Bees have a limited foraging range (hundreds of meters to a few kilometers) and tight species-habitat interactions that create a variety of bee communities in adjacent habitats. Moreover, since bees are a species-rich taxon and since there is a wide range in the number of species nested within different genus they provide the suitable platform to quantitatively test the effects of different factors on the reliability of the HTA.

In this study I investigated the reliability of the HTA as a surrogate for direct species evaluation in bee studies, and to evaluate different factors which may influence the HTA reliability. The study used data sets from three climate regions: Desert- central Arava, Israel; Mediterranean- Judean foothills, Israel; Temperate- central New Jersey and Pennsylvania, USA. In each of this climate zones, a range of natural and human-influenced habitats were sampled.

I used two commonly applied measures of surrogacy . The first was the ability of HTA to prioritize sites for conservation based on species richness and composition (applying a complementarity approach). The second measure of surrogacy used was the ability of higher taxa to indicate the similarities between species communities of different sites or habitats, a most commonly used test in HTA studies. Only a few studies examined the factors influencing the performance of HTA. In this study, I tested two possible factors that may influence the success of HTA - species distribution within higher taxonomic levels and, phylogenetic relatedness between species. Lastly, I developed and tested a novel method which combines the use of body size data in addition to taxonomic classification.

Higher taxa richness in a given site is strongly correlated with species richness. Yet, there were biases in site prioritization when using subfamily richness; some sites which ranked high in subfamily richness were poor in species richness and vice versa. Results of the complementary-based site selection showed that using genus level data to select a network of sites for conservation worked well compared to other suggested surrogates. On the other hand, the use of data at the subfamily level produced mixed results and should thus be evaluated prior to application.

The degree of similarity in community composition between sites calculated at species level was strongly correlated with the similarity calculated at the genera level, but less so when calculated at the subfamilies level. One factor influencing these correlations is the ratio between the number of species and the number of groups in the higher taxonomic levels: the more species in the higher taxa, the weaker is the correlation. Another factor that seems to reduce the reliability of HTA is the presence of even a small number of species-rich groups. In addition we found that assigning species to higher taxonomic levels at random did not affect HTA performance in this test, suggesting that ecological similarity between related species does not influence HTA in this test.

When using genus level data we found that incorporating species-level data for small number of species rich genera, dramatically improve HTA performance. In addition, combing body size categories at higher taxa data, improved HTA success in identifying similarity in community structure between sites.

The results of this study, which are based on large data sets covering a variety of bio-climate regions and habitats, suggest that for bees, the HTA can efficiently replace direct species data in local-scale ecological research and monitoring programs. In general, genus-level data was reliable in prioritizing sites for conservation, based on both species richness and on complementarity in species composition across sites. In contrast, using subfamily data showed mixed results that might lead to erroneous results. Furthermore, in most cases, using data on both genus and subfamily levels, successfully described the differences observed between habitats. At the same time, high species/higher taxa ratio, as well as the present of few species' rich groups, decreased the performance of HTA. Therefore HTA should be used with caution in sites where, according to previous studies, this ratio was high. In order to overcome this problem, it is possible to identify a small number of species-rich groups or add a subdivision according to body characteristics.

This study shows that the HTA efficiently indicates patterns of richness and composition in bee community, and is expected to perform well also in taxa with similar species distribution properties. In addition, this study shows that previous knowledge of the community characteristics in a given area, in terms of species distribution in higher taxonomic levels and the present of extremely species' rich groups, could be valuable for accessing the expected reliability of HTA.