Revised text on EMS analysis:

*EMS methods*

To determine whether spatial patterns of biodiversity across meadows are consistent with metacommunity processes operating at the landscape scale, we applied the elements of metacommunity (EMS) framework (Leibold and Mikkelson 2002, Presley et al 2010). This analysis first tests for coherence in species distributions across meadows by comparing observed species distributions with expected distributions based on a null model. If positive coherence is identified, spatial patterns can be further tested to identify patterns consistent with individualstic species distributions across the landscape (a Gleasonian model of species distributions), or clumped species distributions (Clementsian structure), or random, providing insight to possible types of community structure (Liebold and Mikkelson 2002, Presley et al 2010, Henriques-Silva et al 2014?). We analyzed metacommunity structure for the 9 meadows sampled in July 2012 using the R package Metacom. We used a null model that fixed species richness within sites (‘fixed row) but allowed composition to vary based on their marginal probabilities (method = “R1”).

*EMS results*

Across all sites in midsummer, elements of metacommunity structure (EMS) analysis suggested a checkerboard pattern of species distribution among meadows. For all epifaunal taxa (30 taxa), EMS suggested negative coherence (86 embedded absences relative to 56.17 +6.53 expected by the null model, z = - 4.57, P <0.01). For grazers only (17 taxa), we observed a similar pattern of negative coherence (29 embedded absences relative to 16.42 +3.76 expected by the null model, z = - 3.35, P <0.01).