

Semelparity analysis using randomly generated matrix models

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Projection matrix models have been often employed as an effective tool to quantify population dynamics. Elasticity analysis of the matrix models is the most frequently-used analytical method. Silvertown (1996) mapped the elasticities of stasis, growth, and fecundity for 80 plant species in triangle simplex and reported that they were located in specific regions depending on the groups of plants with different life histories and growth forms. While most of the vectors were distributed in the right-half region of the triangle, semelparous species showed a different distribution and the distribution was concentrated on the upper-left region.

To understand and clarify why semelparous species are distributed in the specific regions, we used random matrices and the COMPADRE database. 68 matrices of semelparous species in the database were selected and their elasticity vectors were mapped in the triangle. Furthermore, 3000 random population matrices of semelparous type were generated and their elasticity vectors were mapped. we examined the evolutionary change in the distribution using a population projection matrix model in which the trade-off between fecundity and adult survival was incorporated. The evolutionary trajectory derived from the trade-off model showed that the evolutionary consequence of semelparity was located in the upper-left in triangle simplex.

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