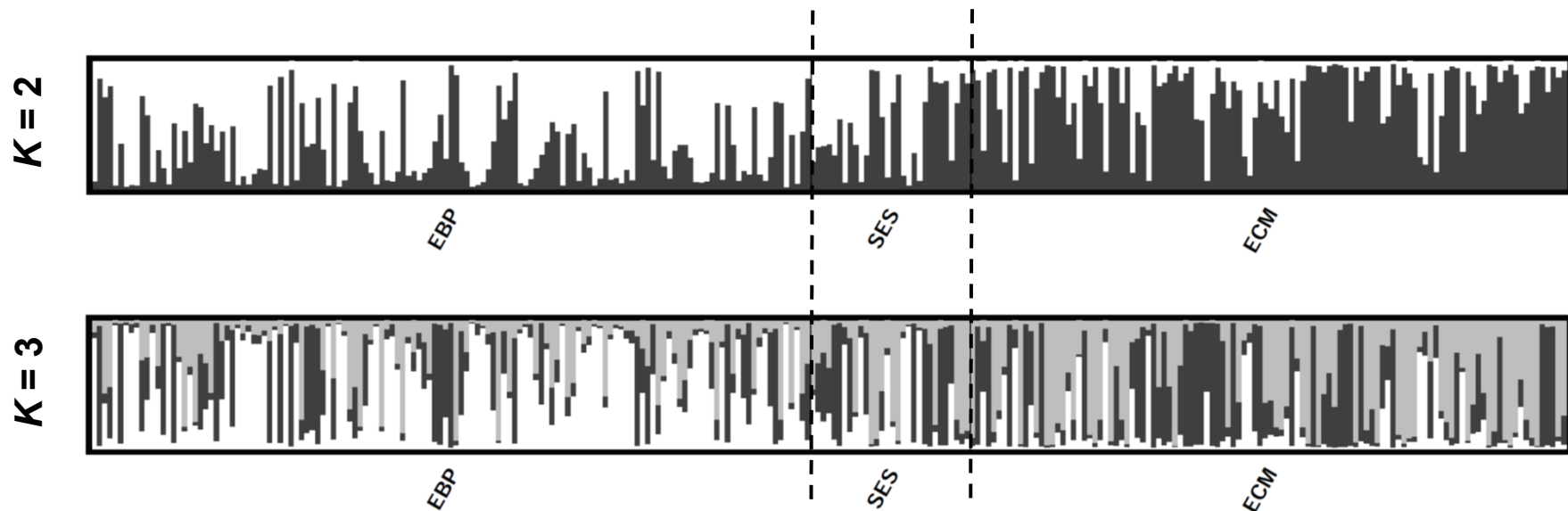


Figure S1. Analysis of *Seseli farrenyi* populations with Structure v. 2.3.4 (Pritchard, Stephens & Donnelly, 2000), using the raw allozyme data (Table S3) generated in the year 2000 and which were employed for producing the study of López-Pujol *et al.* (2002). In this analysis, the dataset is much larger ($N = 277$) as in the year 2000 the total population size was estimated to be around 2000 (López-Pujol, 2000; see also Table 1). As with nSSR, the final image of this analysis was obtained using the programs Clumpp v. 1.1.2 (Jakobsson & Rosenberg, 2007) and Distruct v. 1.1 (Rosenberg, 2004), assuming $K = 2$ and $K = 3$.



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