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Technical note

Local spatial autocorrelation map of ovine proteins in Europe

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Abstract

Local spatial autocorrelation (SA) is used to analyse six blood protein polymorphisms: haemoglobin, albumin, esterase A, carbonic anhydrase, protein-X and transferrin from 26 European ovine populations. Local SA is a useful technique for exploring the distribution of ovine allele frequencies and identifying hotspots (localities with positive local SA) and coldspots (negative local SA). The local SA map of joint analysis reveals that there are areas of significant protein heterogeneity in Europe.

Keywords: Sheep; Protein polymorphism; Local spatial autocorrelation; Map

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1. Introduction

Local spatial autocorrelation (SA) measures the dependence of the value of a variable in a locality, given the values of that variable in neighbouring localities (Sokal et al., 1998a). Local SA allows the detection of local areas which present spatial heterogeneity and reveal hotspots and coldspots, that is, local SA areas that are highly positive and negative, respectively (Getis and Ord, 1992; Anselin, 1995; Ord and Getis, 1995, 2001). When several variables are studied in each locality, the joint analysis of local SA can help to infer the causes of the spatial heterogeneity.

This technique has been used in different species of animals (Sokal et al., 1998b; Pomeroy et al., 2001; Smith et al., 2004) and man (Rosenberg et al., 1999; Sokal and Thomson, in press). Similar studies have not been carried out on domesticated species.

The aim of this study was to analyse the allele frequencies of some ovine protein polymorphisms using local SA. The production of a local SA map can reveal areas of significant protein heterogeneity and contribute to our understanding of ovine evolutionary processes.

2. Materials and methods

The data on the allele frequencies of the protein polymorphisms were obtained from the literature. Those populations for which there was no information available on a minimum of 10 allele frequencies, a number large enough for exploring variable data using local SA (Sokal et al., 1998a), were ruled out. Thus, the analysis was restricted to 26 European ovine populations, 6 loci transmitted independently: haemoglobin beta (*HBB*), protein-X (*X*), esterase (*ES*), transferrin (*TF*), carbonic anhydrase (*CA*) and albumin (*ALB*), and 10 allele frequencies (Table 1). The frequencies of the rare variants of these loci were rejected. The populations are situated in an area roughly bounded by 1°W–27°E and 37°N–54°N. The number of individuals studied for each locus fluctuated between 7536 and 12,414.

For each population and each of the 10 allele frequency surfaces local SA was calculated using the Moran

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Table 1
Populations studied

Populations	Location	*HBB B*	*X p*	*ES a*	*TF A*	*TF B*	*TF C*	*TF D*	*TF E*	*CA S*	*ALB S*	Author index[a]
1	Hungary	0.874	0.706	0.816	0.212	0.147	0.170	0.402	0.051	0.990	0.994	4, 5
2	Hungary	0.902	0.737	0.979	0.023	0.139	0.326	0.480	0.023	0.986	1.000	5
3	Italy	0.861	0.717	0.932	0.127	0.201	0.105	0.485	0.047	0.992	0.998	17
4	Italy	0.849	0.683	0.924	0.198	0.190	0.103	0.395	0.114	0.978	0.998	17, 19
5	Italy	0.858	0.701	0.931	0.192	0.200	0.104	0.407	0.097	0.992	1.000	16
6	Italy	0.679	0.727	0.934	0.140	0.294	0.125	0.370	0.015	0.957	1.000	3, 18
7	Italy	0.934	0.407	0.942	0.054	0.321	0.246	0.349	0.029	1.000	1.000	19
8	Italy	0.956	0.705	0.945	0.111	0.253	0.226	0.327	0.081	0.985	1.000	19
9	Italy	0.809	0.781	0.958	0.103	0.126	0.197	0.539	0.026	0.924	1.000	19
10	Italy	0.788	0.649	0.986	0.131	0.081	0.205	0.466	0.101	0.990	1.000	15, 18
11	Italy	0.706	0.675	0.955	0.099	0.237	0.138	0.480	0.041	0.946	1.000	18
12	Netherlands	0.270	0.990	0.510	0.230	0.190	0.340	0.050	0.190	1.000	1.000	1
13	Netherlands	0.517	0.890	0.953	0.130	0.233	0.230	0.260	0.110	0.990	1.000	1
14	Netherlands	0.710	0.990	0.990	0.030	0.020	0.160	0.640	0.010	1.000	1.000	1
15	Netherlands	0.600	0.570	0.950	0.250	0.160	0.200	0.280	0.110	0.990	1.000	1
16	Slovakia	0.790	0.752	0.867	0.242	0.180	0.230	0.256	0.092	0.980	0.969	7, 8, 12
17	Spain	0.963	0.490	0.760	0.060	0.339	0.221	0.222	0.158	0.956	0.978	13, 14
18	Spain	0.850	0.441	0.988	0.129	0.298	0.051	0.498	0.024	0.995	1.000	13, 14
19	Spain	0.817	0.696	0.904	0.233	0.177	0.173	0.380	0.037	1.000	0.993	13, 14
20	Spain	0.919	0.689	0.890	0.394	0.192	0.081	0.333		1.000	1.000	13, 14
21	Spain	0.859	0.686	0.775	0.204	0.155	0.238	0.270	0.113	0.980	0.998	13, 14
22	Spain	0.916	0.772	0.871	0.134	0.114	0.281	0.317	0.149	0.973	0.996	13, 14
23	Spain	0.668	0.591	0.818	0.178	0.157	0.123	0.461	0.081	0.930	0.989	6, 9, 10, 11
24	UK	0.920	0.620	0.800	0.200	0.170	0.490	0.130	0.010	1.000	1.000	2
25	UK	0.870	0.010	0.740	0.171	0.300	0.040	0.470	0.019	1.000	1.000	2
26	UK	0.140	0.960	0.800	0.730	0.010	0.050	0.090	0.120	1.000	1.000	2

[a] Author index refers to that of the papers listed in Appendix A.