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Patterns of spread and persistence of foot-and-mouth disease types A, O and Asia-1 in Turkey: a meta-population approach

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SUMMARY

Despite significant control efforts, foot-and-mouth disease (FMD) persists in Turkey, and new strains of serotypes A, O and Asia-1 are periodically reported to enter the country from the east. The status of FMD in Turkey is important regionally because the country forms a natural bridge between Asia where the disease is endemic, and Europe which has disease-free status. This study analysed spatial and temporal patterns of FMD occurrence in Turkey to explore factors associated with the disease's persistence and spread. Annual records of FMD distribution in Turkish provinces throughout 1990–2002, grouped by serotype (O, A and Asia 1), were analysed using geostatistical techniques to explore their spatial and temporal patterns. A meta-population model was used to test how disease status, expressed in terms of presence/absence, extinction, and colonization, and measured at the province level throughout the periods 1990–1996 and 1997–2002, could be predicted using province-level data on: ruminant livestock numbers; meat production-demand discrepancy (as a surrogate measure of animal and animal products marketing, i.e. long-distance contagion through the traffic of mainly live animals to urban centres); and the disease prevalence distribution as recorded for the previous year. A drastic overall reduction in FMD occurrence was observed from the period 1990–1996 to 1997–2002 when the disease was shown to retract into persistence islands. FMD occurrence was associated with host abundance, short distance contagion from adjacent provinces, and meat production-demand discrepancies. With FMD retracting into identified provinces, a shift in predictors of FMD occurrence was observed with a lower contribution of short-distance contagion, and a relatively higher association with meat production-demand discrepancies leading to live animal transport over long distances, and hence presenting opportunities for identifying critical-control points. The pattern of persistence differed according to serotype groups and is discussed in relation to their differential affinity to cattle and small ruminant hosts.

INTRODUCTION

Foot-and-mouth disease (FMD) is one of the most economically important diseases of cloven-hooved livestock (mostly cattle, pigs and sheep) because of its

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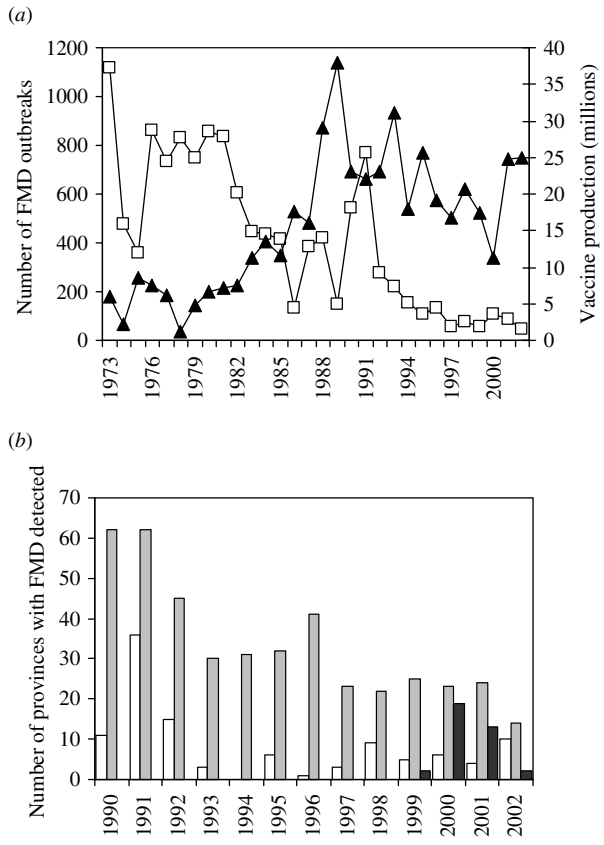

Fig. 1. (*a*) Total number of FMD outbreaks recorded in Turkey between 1973 and 2002 (□) and vaccine production (▲). (*b*) Number of provinces where FMD outbreaks were observed out of a total 80 provinces (all provinces except the Thrace region) between 1990 and 2002, grouped by serotype. □, Type A; ▨, type O; ■, type Asia-1.

potentially very rapid spread and its serious socio-economic impact on the international trade of live animals and animal products [1]. FMD is reported in seven antigenic types (termed *type* or *serotype* throughout the paper), which have a highly uneven but largely stable distribution over decades, and across endemic areas: types O and A have the broadest distribution, type C appears to be confined to the Indian subcontinent, Asia-1 normally occurs in southern Asia, and the SAT serotypes (SAT1, SAT2, SAT3) are normally confined to sub-Saharan Africa [2]. Turkey is particularly important to the continental scale epidemiology of the disease because it forms a bridge along the 'Eurasian ruminant street' [3] stretching from southern Asia where the disease is endemic to Europe where FMD is absent, moreover, three FMD serotypes have been present in Turkey over the last 20 years. Serotypes A and O are endemic and have been observed since the strains were first typed (1952), whereas outbreaks of serotype Asia-1 in 1973, 1984 and more recently in 1999 persisted for less than 3 years on each occasion.

Despite a significant decrease in FMD incidence in the last decade following a rise in vaccine production (Fig. 1*a*), the disease continues to persist in the country and the dynamics of each serotype group is clearly distinct (Fig. 1*b*; there is no cross-immunity between FMD serotypes and the epidemiology of each serotype can thus be analysed separately). Type O is the dominant serotype and persists at a relatively high incidence, type A persists at a much lower incidence and was even not reported in 1994, while the short-term outbreak of the exotic Asia-1 between 1999 and 2002 touched relatively few provinces. Genetic analysis of FMD types O and A viruses isolated from Turkey between 1964 and 2003 indicated that the evolutionary rates observed in FMD type A (1% nucleotide substitution per year) and in type O (0·6% per year) did not explain the nucleotide difference between genetic lineages or sub-lineages identified in Turkish samples (e.g. type A, 18% nucleotide differences between isolates from 1997 and 1995 [4]). The additional fact that Turkish isolates were found to be very close to isolates from the Middle East [4] strongly supports the hypothesis that most, if not all FMD virus strains spreading into Turkey entered the country from the east. In this context, east–west animal movement instigated by the geographical discrepancies between production (mostly in the East) and consumption centres (mostly in the West) have been frequently incriminated as a key risk factor underlying the rapid westward spread of new virus introductions.

Recent advances in the molecular epidemiology of FMD indicate that serotypes or topotypes (genetic lineages observed originally within specific geographic boundaries [5]) differ in basic epidemiological features such as virulence or host specificity [6]. The situation regarding FMD in Turkey in the 1990s thus forms a complex setting in which three different serotypes, each possibly having different basic epidemiological features, fluctuate in a common geographical environment, with the regular entry of new strains that may compensate occasional extinctions. Because the complexity of such a setting, and the significant level of uncertainty regarding critical epidemiological determinants such as the precise distribution of livestock (in particular small ruminants), it was decided to use an inductive approach [7] to explore the pattern of association of the disease with the most significant variables.

We analysed province-level data on FMD outbreaks grouped by serotype (O, A and Asia-1) recorded from 1990 to 2002 in Turkey to characterize their respective spatial and temporal pattern of persistence, and to test how each serotype status, expressed in terms of presence/absence, extinction, and colonization, could be predicted using data on ruminant livestock densities, disease distribution in the nearby provinces in the previous year (as a measure of short-distance contagion), and meat production-demand discrepancy (as a surrogate measure of animal and animal products marketing, i.e. long-distance contagion through traffic of mainly live animals to urban centres). These variables were chosen because the distribution and movement of susceptible animals are strong determinants of FMD dynamics in epidemic conditions [8, 9]. Although FMD shows a high spread rate of invasion in epidemic conditions [9], the effect of short-distance contagion was also tested because in endemic conditions, FMD may smoulder at slow rates as a result of contagion involving alternative hosts and different immunity levels within herds. The analytical framework used to explore the association between FMD distribution and covariates was derived from meta-population ecology [10], following the observation that disease dynamics in a situation close to extinction most closely resembles meta-population dynamics [11].

MATERIALS AND METHODS

Data

Data on monthly numbers of FMD outbreaks per province (85 provinces in total) were compiled by serotype from the monthly summary reports on notifiable diseases produced by the General Directorate of Protection and Control (GDPC) under the Ministry of Agricultural and Rural Affairs (MARA, Turkey). Data on the province-level distribution of livestock (head of cattle, sheep and goats) and people was obtained from the State Institute of Statistics (Turkey). The five provinces of the Thrace region were excluded from the analysis because of the very intensive vaccination scheme carried out in this area. Meat production absolute deficit both for cattle and small-ruminant meat were taken as a surrogate estimate of the disease risk arising from domestic trade in live animals, under the assumption that provinces with a high deficit (e.g. Ankara), or high surplus (e.g. Erzurum) have more movement of live animals. The absolute difference between meat production and demand was estimated for each province. Production was estimated by multiplying livestock numbers and the mean national meat output per animal (bovine meat, 30·81 kg/head per year; ovine meat, 10·63 kg/head per year; caprine meat, 6·66 kg/head per year [12]). Meat demand was estimated by multiplying the number of people and the national demand *per capita* (beef, 4·92 kg/person per year in 2001; mutton and goat meat, 5·24 kg/person per year in 2001 [12]).

Analysis

Spatial and temporal patterns of disease status were studied using inverted correlograms to estimate spatial and temporal autocorrelation [13]. The inverted correlogram is a plot describing the decrease in correlation [increase of the $1-\rho(h)$ function, where h is the distance or time-lag separating observations] as a function of the distance or time-lag between observations. In the presence of spatial or temporal autocorrelation, it is typically a rising curve with lowest values (high ρ) for observations separated by short distances (or short periods of time), which levels off at a distance (or duration) termed the range over which no correlation is observed between observations. In theory, observations separated by a null distance (or period of time) have a spatial autocorrelation coefficient equal to 1, and the correlogram should start at the origin of the axes. This is rarely the case in experimental correlograms, and the value at which the correlogram intercepts the y-axis is termed the nugget, which represents variability at a scale smaller than the minimum lag and measurement error. The difference between the correlogram plateau and the nugget is termed the scale. When autocorrelation was present, spherical models were fitted to the inverted correlograms using a least squares approach [14] and values for the scale, nugget, range and R^2 of the fit were obtained. The spherical model is defined as

$$\rho(d)=\begin{cases} c_0+c[(3d/2a)-(d^3/2a^3)], d\leqslant a \\ c_0+c, d>a \end{cases}$$

where d is the lag distance (or time unit), and c_0, c and a are the nugget, the scale and the range respectively [15]. Spatial autocorrelation was estimated for the number of years for which each province had been infected in a given study period, whereas temporal autocorrelation was estimated for annual disease status at the province level.

Meta-population ecology is not new to disease epidemiology because the assumption of local turnover

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as a consequence of extinction followed by re-colonization applies particularly well to endemic diseases epidemiology ('The derivation of the formula for the minimum amount of suitable habitat required for metapopulation persistence … [in conservation biology] … is identical to that used to determine the proportion of a host population which must be vaccinated in order to eradicate a parasite' [11]). Despite the fact that our province-level data do not form separate sub-populations typically addressed by metapopulation ecology [10], we built a logistic model with a spatial model of contagion derived from metapopulation models to allow the separate exploration of factors that relate to disease persistence in a location once the disease has been established (e.g. production environment), and those related to the establishment of the disease in a new location (short- and long-distance contagion). This logistic model was built in three steps. First, disease status in any given year (present/absent) was tested against all variables simultaneously entered in a multiple logistic regression (SPSS 12·0, SPSS Inc., Chicago, IL, USA). For clarity of presentation of results, only variables significant at the P level of 0·05 were maintained in the model. The variables entered in the model were: the disease status in the previous year (Py), the province surface area (A), the cattle density (Cd), the sheep density (Sd), the goat density (Gd), the buffalo density (Bd), and the absolute difference between production and demand per province for cattle meat (CaMd) and small-ruminant meat (SrMd). Second, the disease status was modelled as a function of the spatial distribution of infected provinces in the previous year as

$$\text{logit}(p_i) = \alpha \sum_{i=1}^{n-1} S_i^{-1} e^{-\beta d_i^2} + \varepsilon,$$

where p is the disease presence probability, n is the number of provinces, S_i^{-1} is the disease status of location i in the previous year (0 or 1), d_i^2 is the square of the distance to location i, α and β are model parameters, and ε is the error term. Third, where both the logistic model and spatial model were found to be significant, a model combining both terms was built, in which the probability of disease presence was estimated as

$$\text{logit}(p_i) = \alpha \sum_{i=1}^{n-1} S_i^{-1} e^{-\beta d_i^2} + f(\text{var}_i) + \varepsilon,$$

where all terms are defined as above, and where $f(\text{var}_i)$ is a linear function of explanatory variables found significant in the simple logistic model. Model parameters were estimated by maximum likelihood. The model significance was tested using the model likelihood ratio [LR(i) which follows a χ^2 distribution with i degrees of freedom where i is the number of independent variables]. McFadden's pseudo-R^2 was estimated to compare the predictive power of models based on the same data subset (i.e. simple logistic model *vs.* spatial model *vs.* combined model), and the percentage of correct predictions of each best-fit model (either using the variables, or combined with the spatial model when significant) was estimated using a classification threshold of 0·5 to allow comparison of models based on different data subsets. This three-step approach was used to model disease status, disease extinction (by using the subset of provinces having reported FMD outbreaks in the previous year), new invasion (by using the subset of provinces with no FMD outbreaks reported in the previous year) for the periods 1990–1996 and 1997–2002 separately for FMD types A and O, and for the period 1999–2002 for FMD type Asia-1.

RESULTS

The first observation was that despite the reduction in disease distribution of FMD types A and O between 1990–1996 and 1997–2002 (Fig. 1), FMD tends to persist in certain locations such as Erzurum or Ankara and that these foci are broadly consistent for all the three serotype groups, including the exotic serotype Asia-1.

A significant *spatial* autocorrelation structure was observed for both types O and A (Fig. 2*a*, *b*). Both serotype groups showed a short-distance spatial structure in the recent time-period 1997–2002 as indicated by the range of the best-fit models of autocorrelation (159 and 190 km for types A and O respectively), and a long-distance spatial dependence in the time-period 1990–1996 with model ranges of 511 km and 533 km for FMD types A and O respectively. FMD type O showed a much stronger spatial autocorrelation in the period 1990–1996 (long-range, low nugget) than in the period 1997–2002 (short range, higher nugget). No spatial autocorrelation was observed in the spatial distribution of number of years of infection by FMD Asia-1 (Fig. 2*c*).

Correlograms of FMD occurrences showed almost no evidence of *temporal* autocorrelation in FMD type A (Fig. 2*d*), whereas a strong *temporal* autocorrelation (1–4 years) was observed for FMD type O

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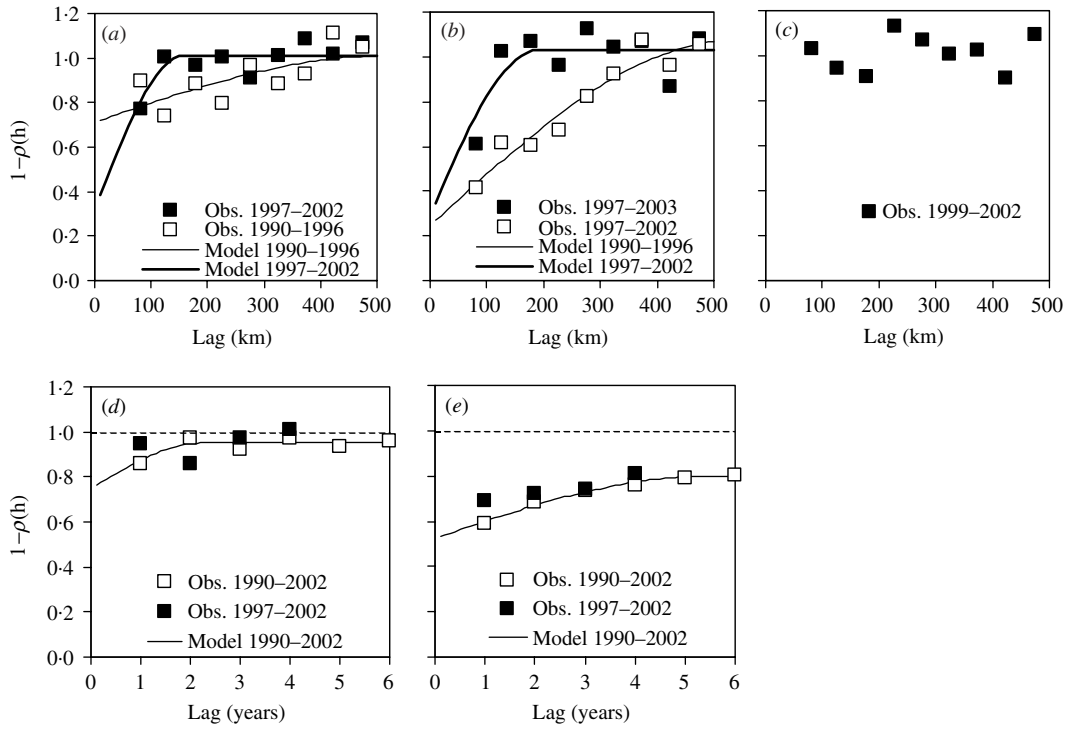

Fig. 2. Spatial inverted correlograms of number of years of infection by FMD in Turkey for the periods 1990–1996 and 1997–2002 for FMD types A and O (*a*, *b*), and 1999–2002 for type Asia-1 (*c*) with their respective best-fit spherical model [type A (1990–1996): range 511 km, nugget 0·711, scale 0·298, R^2 0·495; type A (1997–2002): range 159 km, nugget 0·321, scale 0·691, R^2 0·677; type O (1990–1996): range 533 km, nugget 0·245, scale 0·828; R^2 0·933; type O (1997–2002): range 190 km, nugget 0·290, scale 0·743, R^2 0·637]. Temporal inverted correlograms of Turkish provinces' infection status by FMD in the periods 1990–2002 and 1997–2002 with their spherical model for FMD type A (*d*) (range 2·27 years, nugget 0·751, scale 0·202, R^2 0·730) and type O (*e*) (range 5·42 years, nugget 0·525, scale 0·273, R^2 0·982) respectively (FMD Asia-2 is not presented because the time-series was too short for temporal analysis).

indicating that for this serotype observations separated by up to several years are significantly correlated (Fig. 2*e*). The fact that the correlograms of the whole 1990–2002 period matches that of the 1997–2002 period indicates a stable temporal structure, i.e. over the years there was no structural shift in the pattern of persistence. The fact that the correlogram of FMD type O did not attain the independence value of 1 within the time-span of the analysis (some correlation is still observed for infection status separated by over 4 years) suggests that some provinces constitute predilection sites where the disease is more prone to appear regardless of the history of disease presence.

Results of the logistic models indicated that in FMD type O during 1990–1996, disease status was positively related to the previous year's status, to the province area and to the small-ruminant-meat absolute deficit, and negatively related to the density of goats (see Table). During 1997–2002, a positive association was observed between type O disease status and previous year's status, province area, sheep density, cattle and small-ruminant-meat absolute deficit, whereas a negative association was observed with goat density. Goat density was generally replaced by a positive association with cattle density when it was forced out of the model. Separating the records on disease extinction events from those associated to new disease occurrence, we observed that disease persistence in previously infected provinces was positively related to cattle and small-ruminant-meat absolute deficit during 1997–2002, while new occurrence events were related to the absolute numbers of cattle (as the product of cattle density and province area) either directly during 1997–2002, or interpreted through the negative association with goat density. In both time periods, a significant spatial effect was observed (as indicated also by the significance of the spatial model alone) of adjacent provinces infested in the previous year. The relationship with meat product absolute deficit was fairly stable and remained significant when the most important

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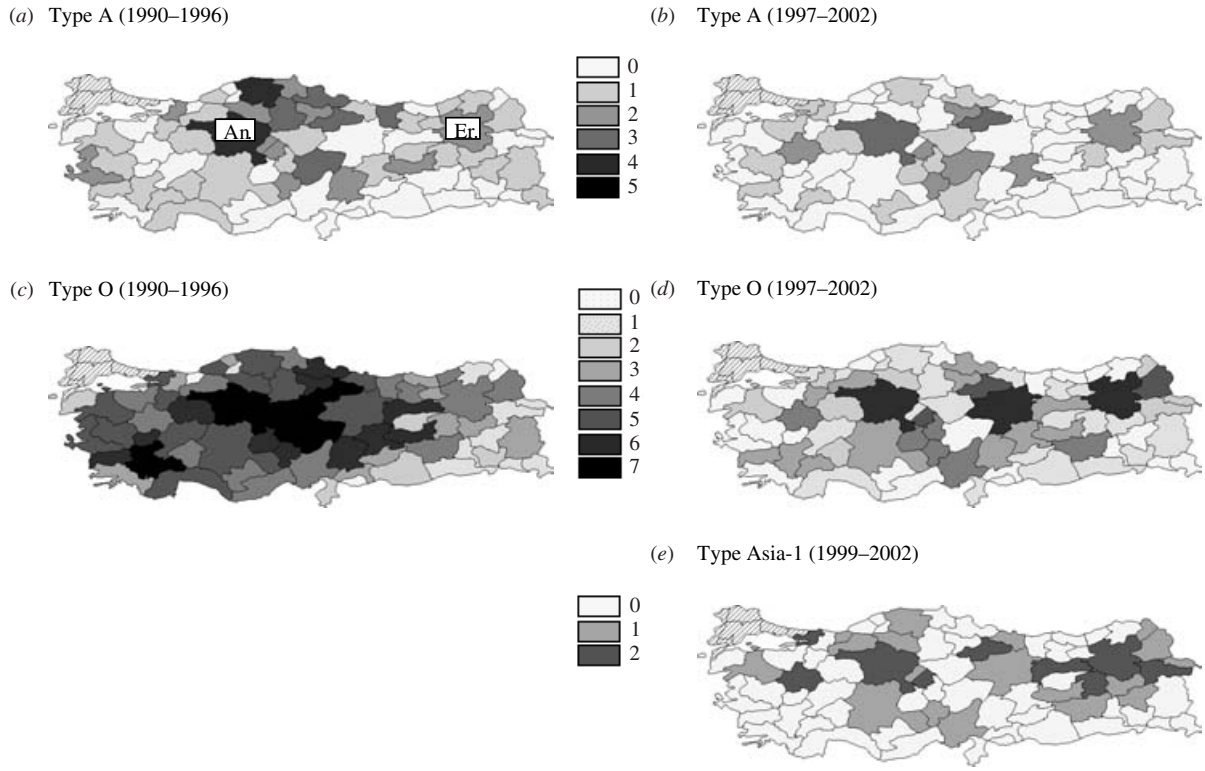

Fig. 3. Distribution of number of years of infection by FMD serotypes in Turkey. (*a*) Type A (1990–1996); An., Ankara province; Er., Erzurum province. (*b*) Type A (1997–2002). (*c*) Type O (1990–1996). (*d*) Type O (1997–2002). (*e*) Type Asia-1 (1999–2002).

production and consumption centres, such as Erzurum and Ankara respectively, were removed from the analysis. FMD type A presence was found to be positively related to the previous year's status and negatively related to goat density for 1990–1996, and positively related to province area and negatively related to goat density for 1997–2002. A significant spatial effect of nearby provinces infested in the previous year was observed during 1990–1996 for FMD type A. Finally, the presence of FMD type Asia-1 was found to be positively related to the production-demand gap in cattle meat, to sheep density, and negatively to goat density, whereas no significant relationship with the nearby provinces infested in the previous year was observed.

DISCUSSION

The increase in vaccine production during the 1980s (Fig. 1*a*), and the change in the mid-1990s from regional vaccination focused on the region south and east of Istanbul, to twice-yearly national campaigns which now effectively cover at least half of the national cattle herd, are believed to be important factors contributing to the marked decrease of FMD incidence between 1990–1996 and 1997–2002. This reduction of FMD incidence appears to have been highly beneficial to Europe since no outbreaks traced to this source have occurred between 1997 and 2003 whereas at least five outbreaks occurred between 1990 and 1996. This reduction does not, however, appear to be homogeneously distributed: type A and particularly type O retract from country-wide aggregates into provinces with a predilection, as illustrated by distribution maps of types A and O during 1990–1996 and 1997–2002 (Fig. 3) and quantified by the shift from long-range spatial autocorrelation observed in types A and O during 1990–1996 to short-range autocorrelation in types A and O during 1997–2002 (Fig. 2). Another shift is observed between 1990–1996 and 1997–2002 for types A and O. In the first period, short-distance contagion from nearby provinces was found to be a significant predictor for both types (Table), whereas for 1997–2002, this effect was found to be much weaker for type O and no longer significant for type A. It is also during 1997–2002 that a significant positive association between type O persistence and production-demand gap in both cattle

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Table. *Logistic model of FMD types A, O and Asia-1 occurrence, extinction and new colonization in Turkey (1990–2002)*

		Variables alone			Spatial model alone			Combined			Pred.
Variables		χ^2	P	R^2	χ^2	P	R^2	χ^2	P	R^2	%*
Type A (1990–1996)											
P/A	Py, **Gd**	19·92	<0·001	0·055	15·30	<0·001	0·042	24·73	<0·001	0·069	86·4
Ext.	—		n.s.			n.s.			—		—
Inf.	**Gd**	5·66	0·017	0·021	5·84	0·015	0·022	9·92	0·006	0·037	88·9
Type A (1997–2002)											
P/A	A, **Gd**	12·66	0·0018	0·049		n.s.			—		91·7
Ext.	—		n.s.			n.s.			—		—
Inf.	A, **Gd**	12·18	0·002	0·052		n.s.			n.s.		92·2
Type O (1990–1996)											
P/A	Py, A, **Gd**, SrMd	95·26	<0·001	0·153	83·46	<0·001	0·134	118·79	<0·001	0·191	74·2
Ext.	—		n.s.		27·47	<0·001	0·088	27·47	<0·001	0·088	72·1
Inf.	A, **Gd**	11·59	0·003	0·051		n.s.			—		73·4
Type O (1997–2002)											
P/A	Py, A, Sd, **Gd,** CaMd, SrMd	77·59	<0·001	0·143	15·16	<0·001	0·027	82·18	<0·001	0·151	74·0
Ext.	CaMd, SrMd	22·07	<0·001	0·101		n.s.			—		63·3
Inf.	A, Cd	12·90	0·0016	0·046	5·856	0·015	0·021	21·97	<0·001	0·077	81·8
Type Asia-1 (1999–2002)											
P/A	Sd, **Gd**, CaMd	14·12	0·002	0·064		n.s.			—		88·0
Ext.	—		n.s			n.s.			—		—
Inf.	A, Cd.	10·45	0·005	0·058		n.s.			—		89·1

P/A, full dataset using (presence/absence); Ext, extinction (subset of provinces infected in the previous year); Inf, new infection (subset of provinces not infected in the previous year); Py, status in the previous year (0/1); A, province area (km²); Cd, cattle density (head/km²), Sd, sheep density (head/km²); Gd, goat density (head/km²); CaMd, cattle meat absolute deficit (kg); SrMd, small-ruminant-meat absolute deficit (kg). Variables with a negative coefficient are in boldface type.

* Percentage of correct prediction of the best model (using the combined model or variables alone when the spatial model is not significant) using a classification threshold of 0·5.

and small-ruminant meat is observed. These results suggest a shift away from spread resulting from direct animal contact between ruminants and leading to short-distance spread between neighbouring provinces, towards an increasingly apparent and relatively more important contribution from long-range FMD jumps dispersal that can be attributed to the transport of animals from production centres to consumer areas. When FMD distribution is widespread, short-distance contagion by animal contact is highly probable and the relative contribution of long-distance contagion through the market chain is minor. With disease incidence decreasing, short-distance contagion through animal contact become less likely, and the relative contribution of long-distance contagion through the market chain increases. The distribution patterns of the exotic serotype Asia-1 confirm this scenario. Asia-1 presents an even lower overall incidence than type A (Fig. 3), and would thus, be expected to show an even lower contribution of spatial effect, with some significant association with meat absolute deficit. This is precisely what is observed, as Asia-1 is marked by a positive association with production-demand gap, an association with host abundance (which was also observed for types A and O), no short-distance spatial effect and no spatial autocorrelation. This trend is illustrated by the distribution of FMD types A and O during 1997–2002 and Asia-1 during 1999–2002, in which the disease appears to persist in certain locations characterized by high net influx or efflux of animals, such as Erzurum or Ankara (Fig. 3).

Apart from the relationships with the distribution of previously infected provinces and with meat production-demand gaps, all other statistically significant factors observed in the logistic models for types A and O are related to cattle abundance, either directly (cattle density and area for type O, 1997–2002) or

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indirectly through the negative association with goat density (the highest goat densities are located in the eastern mountain parts of the country, where cattle are comparatively rare), and a positive association between type O presence and sheep density for 1997–2002 is observed. This type of positive association between disease persistence and host abundance is consistent with predictions of standard epidemiological models [11]. As the clinical signs of FMD are frequently mild or unapparent in small ruminants [16], the probability of detecting the disease is much higher in cattle than small ruminants and explains why cattle density is found to be the main host variable.

There was almost no evidence of temporal autocorrelation in FMD type A, whereas a strong temporal autocorrelation over as much as 4 years was observed for FMD type O (Fig. 2*d*, *e*). This results indicates that, along with its higher quantitative persistence, type O persists broadly in the same provinces from year to year, whereas the pattern of type A is much less predictable and only relates to cattle abundance. Findings from phylogenetic analysis of FMD samples collected in Turkey throughout 1990–2002 indicated that each type A sublineage disappears before a new one is established, whereas several type O sublineages may coexist for several years [4]. The pattern of persistence of both types is clearly very different. Type A frequently goes extinct at province level (type A became extinct in 52 out of 71 infected provinces during the 1990–1996 period and in 24 out of 28 during 1997–2002) and needs a flow of new introductions to persist at the scale of the country. In comparison, type O shows a much lower rate of extinction at province level (74 out of 262 during 1990–1996 and 82 out of 158 during 1997–2002). It is hypothesized that higher persistence in FMD type O in Turkey relates to a higher host-affinity of type O towards small ruminants. Sheep form an ideal reservoir for FMD allowing the persistence of infections in cattle: they are abundant (2·58 sheep per cattle on average in Turkey), they are frequently in contact with cattle through mixed farming, they show very little clinical signs of infection allowing the disease to remain unseen [16], and they are not targeted by vaccination. Several examples have implicated sheep in the spread of FMD (e.g. the 2001 Asia topotype O in the United Kingdom [17] or Ireland [18] and the 1999 type O epidemic in Morocco [19]) even if type O appears unable to maintain itself in sheep alone [20]. Under this hypothesis, local extinction of type O in mixed cattle/sheep livestock systems would take considerably more time than extinction of type A. In our results, the possible implication of sheep in type O persistence and spread was suggested by the significant relationship between type O distribution and small-ruminant-meat absolute deficit (1990–1996 and 1997–2002) and sheep density (1997–2002). This hypothesis is also consistent with the observation that among the samples examined at the SAP Institute (Ankara), the proportion of outbreaks in small ruminants *vs*. cattle was significantly lower for type A than for type O, even when the virus was relatively widespread in cattle [4]. The significant reduction in sheep populations in Turkey over the 1990s might also reduce opportunity for short-distance spread and have accelerated local extinction (a higher rate of extinction was observed for type O during 1997–2002 than 1990–1996).

Even if little is known about host affinity of the FMD virus, especially at the serotype or topotype level, host specificity appears central to understanding subtle patterns of persistence and spread of FMD. Despite the rapid evolution of the FMD virus, characterized by high mutation rates and quasi-species dynamics [21], and the fact that minor changes in the genome may change host affinity [22], the failure of type Asia-1 to establish persistence following several introductions, and the relatively short persistence of each type A topotype in Turkey suggests that each topotype may position itself distinctly in terms of its virulence in the range of host species, calling for better experimental quantification of FMD serotypes and topotypes host affinity.

The modelling approach used here is helpful in that it allows the exploration of the main statistical association between FMD presence in space and time and covariates. However, it is based on several straightforward assumptions (e.g. short-distance spread, meat deficit as a surrogate variable for trade) that would require more detailed epidemiological and covariate data, and a more elaborate model structure, to be carefully assessed and quantified.

However, the trends and patterns explored in this study provide three important results. First, FMD type O, which was the most widespread serotype in the early 1990s in Turkey, retracts into persistence islands, and this process occurs along a shift in the main predictors of its presence, from short-distance contagion from adjacent provinces towards a relatively higher association with meat-products absolute deficit, as surrogate estimates of market-chain-related

animal movements. This pattern is also observed to a lesser extent in the less frequent FMD type A, and is consistent with the pattern observed for the exotic FMD type Asia-1. Second, with all three serotypes at low incidence in the period 1996–2002, the geographical distribution of persistence foci is broadly consistent among the three serotypes (Fig. 3), and is associated with meat production-demand gaps for types O and Asia-1. Given that FMD lineages belonging to each serotype group behave independently in geographical terms, this result implies that the persistence islands identified indicate places to which any FMD lineage would be most likely to spread under the current systems of control. Third, our results suggest that a higher affinity of FMD type O towards sheep could explain its higher persistence in Turkey. Further reduction in incidence and risk should follow intense investigation of the identified persistence islands and invasion pathways, and the identification of control measures to address persistence in these regions and efflux to free areas.

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