



Summary Report

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Spatiotemporal analyses of potato late blight outbreaks in Great Britain 2017-2020

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This document contains a condensed summary, commentary on the datasets used and interpretation of the results of the study. For a full methodology and detailed analysis of results, please refer to the project Final Report.

1. Summary

The GB potato industry requires high quality, robust data on when and where blight is present and the factors that drive its distribution. Information from the blight outbreak sampling supported by AHDB (Fight Against Blight programme (2003–2018)) has been used to investigate why blight strains predominate in certain areas and their rate of spread between locations. This type of information helps improve blight risk assessment, especially in relation to new strains that enter GB.

Through the FAB programme, blight samples collected in the field are sent to a lab and analysed using molecular diagnostic techniques which can split out individual late blight strains. These change over time and recent years have seen new strains (referred to as 36_A2 and 37_A2) arrive in GB and subsequently spread. For the first time, researchers have been able to calculate the speed of spread of the strains. One of the strains shows reduced sensitivity to an important fungicide (fluazinam) – so knowing how quickly a strain might spread is useful information in understanding if it could have reached a particular part of the country and agronomists therefore need to consider submitting samples for testing or revising spray programmes.

Late blight severity is highly dependent on the local weather, so the timing, number and distribution of blight outbreaks reported through the FAB programme obviously varies from year to year. Nevertheless, there were still statistically significant patterns in space and time for early outbreaks, overall incidence, and the distribution of various pathogen genotypes. Together, these analyses provide valuable information on the variable risk posed by late blight across the potato production areas of GB.

Machine learning techniques (neural network models) were used to analyse weather, soil, geology, and topography data to identify the principle factors associated with late blight occurrence. The key findings were:

Early outbreaks

- *Spatial analyses:* Averaged over all years, the statistically significant hot spots (clusters of high incidence) of early outbreaks of disease were generally found in the south of England and Wales, particularly near the coast, whereas a large cold spot (clusters of

low incidence) extends across the production regions of Scotland. This supports the role of climate in the earliest occurrence of outbreaks.

- *Spacetime analyses:* When analysed as a time series, the spatial hot spots of early disease tended to be sporadic: i.e. locations that are on-again off-again hot spots. There were also some sporadic and consecutive hot spots (a run of recent hot spots) of early outbreaks in the Angus / Aberdeenshire regions. This may relate to a warming climate resulting in an increased frequency of early outbreaks in Scotland in recent years.
- *Driving factors:* As expected, the date of first outbreak was later in the north of GB, but only by a matter of weeks. Machine learning was used to develop a model that was 91.2% accurate in predicting low and high levels of incidence of early outbreaks. It identified temperature and precipitation as the most important predictors of early outbreak incidence.
- *Visual aids for decision-making:* Colour-coded maps were produced to show the overall risk of early outbreaks by postcode district, and the week of the year these were most likely to occur.

Spatial spread of disease across the whole season

- Risk of spread of disease among neighbouring postcode districts was highest in the potato growing regions of Tayside, Fife, Lothian, and East Anglia.
- The velocity of spatial spread was calculated from early foci of genotypes 36_A2 and 37_A2 and ranged from 3–17 km per week.
- *Visual aids for decision-making:* A colour-coded map was produced to show the risk of spread of disease among postcode districts.

Overall incidence, 2003-2018

- *Spatial analyses:* Statistically significant hot spots of sampled late blight incidence were found in the Angus, Tayside and Fife regions of Scotland, and in East Anglia, Kent and East Sussex in England. No cold spots were identified.
- *Spacetime analyses:* There were three types of temporal trend identified in the hot spots of incidence: consecutive, sporadic, and new (appearing in the final year). The lack of any persistent hot spots is a consequence of large inter-annual variation in the distribution of disease.
- *Driving factors:* A model was developed that can estimate outbreak risk based on environmental factors. The model revealed a strong positive relationship between density of potato cropping and late blight outbreak risk. Weather also had a strong impact on outbreak risk, particularly temperature, humidity, rainfall and windspeed. Topography (elevation, slope, aspect) had a large impact on outbreak risk, and there was also evidence of an association with soil conditions and geological type.
- *Visual aids for decision-making:* A colour-coded map was produced to show the overall risk of late blight by postcode district.

Pathogen genotypes

- *Spatial analyses:* The mean spatial patterns of the genotypes 13_A2, 6_A1, 8_A1, 37_A2, and 36_A2 were analysed and differences in the central tendency, dispersion, and directional trends of these distributions were observed. The pattern of hot and cold spots varied markedly for each genotype, and some opposing patterns suggested competition and displacement.
- *Spacetime analyses:* Most of the spatial clusters of the pathogen tended to be consecutive hot spots (a run of recent hot spots). The lack of any persistent (long-term)

hot spots or cold spots of any type was due to a large degree of inter-annual variation in genotype distributions. Several new hot spots (hot spots in the final year of analysis) were found for genotypes 36_A2 and 37_A2, in line with their recent invasive spread.

- *Driving factors:* A model was developed to predict the dominant genotype in each postcode district. It identified precipitation and humidity as the most important predictors, suggesting moisture plays an important role in competition among genotypes. The emergence and rapid spread of genotypes 13_A2 and 6_A1 in 2006-2007 was clear but there were few clear patterns to their distribution in the subsequent years. One obvious feature was the local spread of 6_A1 in eastern Scotland in 2011 followed by its dominance in the subsequent years. This indicates the significance of local sources of primary inoculum carried over from the previous season. However, the drivers of the large variation in other genotype distributions between years were not clear and require further investigation.
- *Visual aids for decision-making:* A video was produced to show the changing pattern of genotype distributions each year.

2. Introduction

Although current methods of late blight management are effective, there is clear scope for improvement as there remains a heavy reliance on calendar spray regimes and challenges relating to the timing of the first spray and the position in the spray programme for the chemistry that offers 'premium' blight control. The primary aim of the project was to provide a new understanding of the epidemiology of late blight in GB, and new visual aids to facilitate improved decision-making.

The objectives were:

1. Determine whether the pattern of the earliest outbreaks of disease within each growing season is random, regular, or aggregated, and the spatial scales at which these patterns occur. Identify geographic areas where late blight persistently occurs early in the season. Identify the principle factors associated with early outbreaks of disease.
2. Track the spread of late blight between postal districts over the course of each growing season to determine whether the pattern of outbreaks is random, regular, or aggregated, and the spatial scales at which these patterns occur. Determine the likelihood of spread of late blight among the postal districts of GB. Derive the rate of spatial spread across the landscape.
3. Identify geographic areas where incidence is consistently low or high over multiple growing seasons. Identify the principle factors associated with persistently low and high incidence of disease. Determine the relative risk of late blight occurrence within each postal district.
4. Track the change in the spatial distribution of pathogen genotypes over the duration of the study period. Identify the principle drivers of this change.

Background

Previous AHDB Potatoes-funded work, using samples submitted by Fight Against Blight (FAB) scouts from 2006 to 2018 had shown that British populations of the potato late blight pathogen, *Phytophthora infestans*, had changed markedly over time (Cooke et al., 2009; Cooke et al., 2013; Cooke, 2019). Subsequent AHDB Potatoes-funded work that examined this change using controlled environment experiments to investigate differences among the dominant genotypes in their response to weather conditions (Chapman 2012), although valuable, yielded conflicting results. No single genotype consistently showed dominance in terms of weather-dependent infection criteria, or in terms of competition when multiple isolates infected a plant at the same time. In further AHDB Potatoes-funded work (Dancey et al., 2017; Dancey, 2018; R473 Late Blight Models), a different approach was adopted whereby experimental work was combined with mapping and statistical modelling of existing AHDB Potatoes FAB late blight outbreak data to develop a new national warning system for late blight; the Hutton Criteria. This approach proved successful, leading to significant improvements in the performance of the national warning system, whereas previously the Smith Period showed great spatial variation in predictive power and performed poorly in some regions. The Hutton Criteria, currently deployed by BlightWatch (<https://blightwatch.co.uk/>) play an important role in determining when to start the blight management programme. Although optimal fungicide application timing is important throughout the season, the early sprays are especially critical. Most fungicide chemistry relies on a protectant effect and managing an established infection is thus extremely challenging (Cooke et al., 2011). In this project, we build upon the success of this mapping and modelling work, and extend our analyses of these existing data to answer key epidemiological questions, derive new epidemiological parameters, and produce visual aids that will support informed decision making and long-term strategic management of late blight, and fungicide and resistance resources.

All infection obviously requires propagules of primary inoculum which, in the case of *P. infestans*, may be asexual or sexual spores carried over from the previous season. Previous work has shown the domination of clonal pathogen lineages within GB potato crops indicating that asexual inoculum carried over on infected tubers is the most prevalent source (Cooke, 2019). Potato seed, volunteer plants in neighbouring fields and plants growing on discard piles are the three main sources of such infection and their management is a key part of blight control strategies (Cooke et al., 2011).

Datasets

The substantial dataset of sampled late blight outbreaks is an excellent resource, but a fundamental challenge in analysing data from crop disease surveillance programs as opposed to experimental data is observation bias. This bias can have several components, including spatial coverage bias (where not all fields are sampled) and detection bias (where some infected fields go undetected). This is often because the survey is focused on objectives other than a complete census of all outbreaks of disease. For example, in the case of the FAB potato late blight outbreak data used in this study, the principal objectives were to report on early outbreaks and sample the pathogen population in order to obtain information about population diversity,

virulence, aggressiveness and fungicide sensitivity. The findings from this data affected management practices and was fed back to the potato industry. Sampling may thus be more intensive at the beginning of the growing season and decrease once blight is very active, or once a scout has already sampled the population in a specific geographic area. The FAB outbreak data could therefore be biased by 'imperfect' detection and it is possible that the resultant ArcGIS and modelling analyses is affected by patterns reflecting the difficulty or manner with which late blight was sampled rather than true patterns in occurrence and abundance. It can be seen, however, that the spatial distribution of reported outbreaks in the FAB data is reasonably uniform across the potato growing areas of GB, with some concentrated regions scattered along the eastern seaboard and throughout Wales and the South West. (e.g., Fig. 12). These areas of higher incidence however, coincide with the areas where potato production is most intense, therefore the distribution of sampled outbreaks broadly matches the distribution of potato and particularly so when normalised to potato density. The number of outbreaks reported in each country also mirrors the scale of potato production, which is greater in England, then Scotland and Wales, although incidence levels are relatively high for Scotland.

Pathogen sampling is also, dependant on suitable weather conditions for disease development and blight incidence varied from season to season and from one location to another. Such variation leads to localised disease epidemics which will have inevitably skewed the sampling intensity. Such marked changes in pathogen population size from one season to the next lead to 'founder effects' or 'genetic bottlenecks' which are known to influence the pathogen population structure over time (Goodwin, 1997). However, the long-term trend in outbreak reporting dates describes a typical epidemic curve for many crop diseases, where the number of new outbreaks increases to a peak then declines with the proportion of uninfected crops and a shift to less favourable climatic conditions. Taken together, our evidence suggests that the quality and level of sampling activity is consistent and sufficient across most of GB and throughout the growing season and thus increases confidence in the outputs of this study. Nevertheless, there remains a potential for observation bias and the present findings should be interpreted with this caveat.

3. Results & Discussion

Objective 1: Occurrence of early outbreaks of late blight

Previous studies have shown that seasons in which late blight infection occurs earlier also result in greater infection pressure throughout the season with more late blight outbreaks sampled (Cooke, 2019). Because early infection increases both risk and the required expenditure on fungicides for blight management there is a clear advantage to the grower of prior knowledge of the regions prone to early infection. Analysis of all the outbreaks in this dataset indicated clearly that there is no single high-risk region from which early infection subsequently spreads (Figs 1-4).

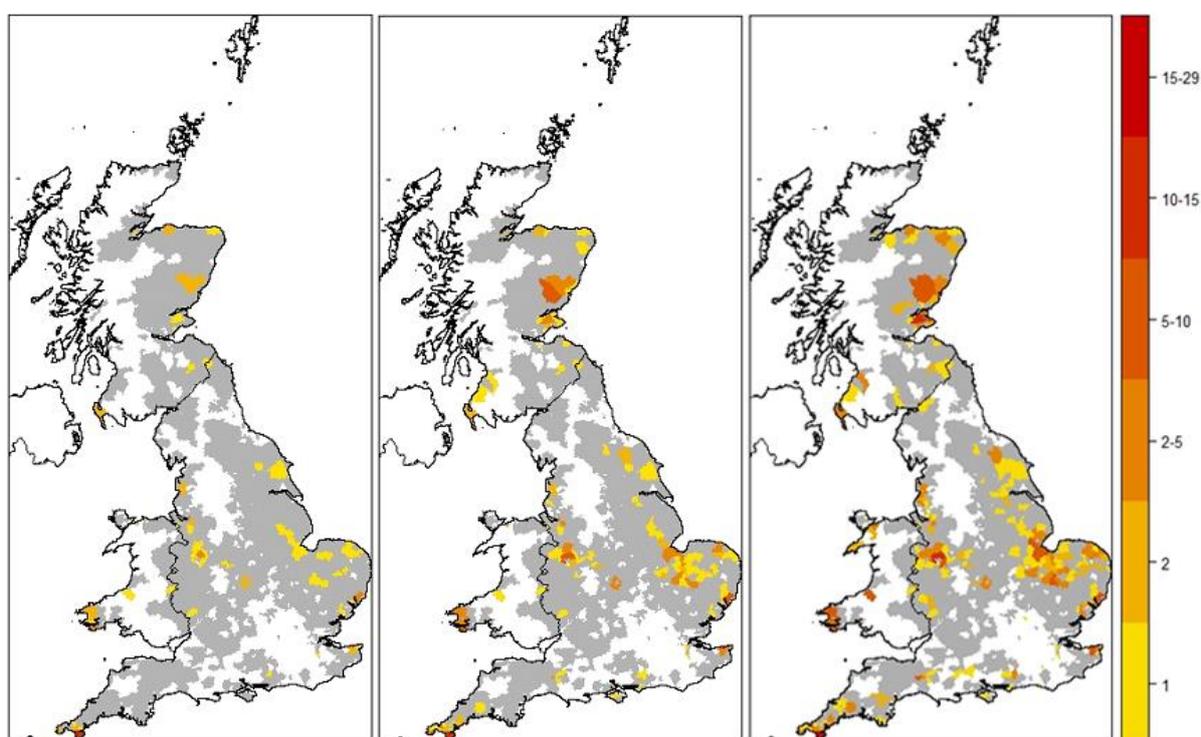


Fig. 1. Choropleth maps of the 5th (left), 10th (middle) and 20th (right) percentiles of the blight outbreak dates of every year from 2005–2018. The colour scale indicates the number of sampled outbreaks per postcode district and grey zones are postcode districts in which >1 ha of potato was grown commercially.

Disease occurred, on average, earlier in crops in the south of Britain than in the north but the main consistent hotspots of the first 10 and 20% of reported outbreaks across all seasons were in the early crops in southwest England, Wales and to a lesser extent in Scotland followed by the English Midlands and the Kent and Essex coast (Figs. 3 & 4). Each season was different but, on average, the earliest 10% of outbreaks occurred in the last two weeks of May and the first week of June (Fig. 2). A more detailed study of the pattern of early disease hotspots over time showed fewer statistically significant hotspots overall and more hotspots that were defined as sporadic (Figs. 5 & 6).

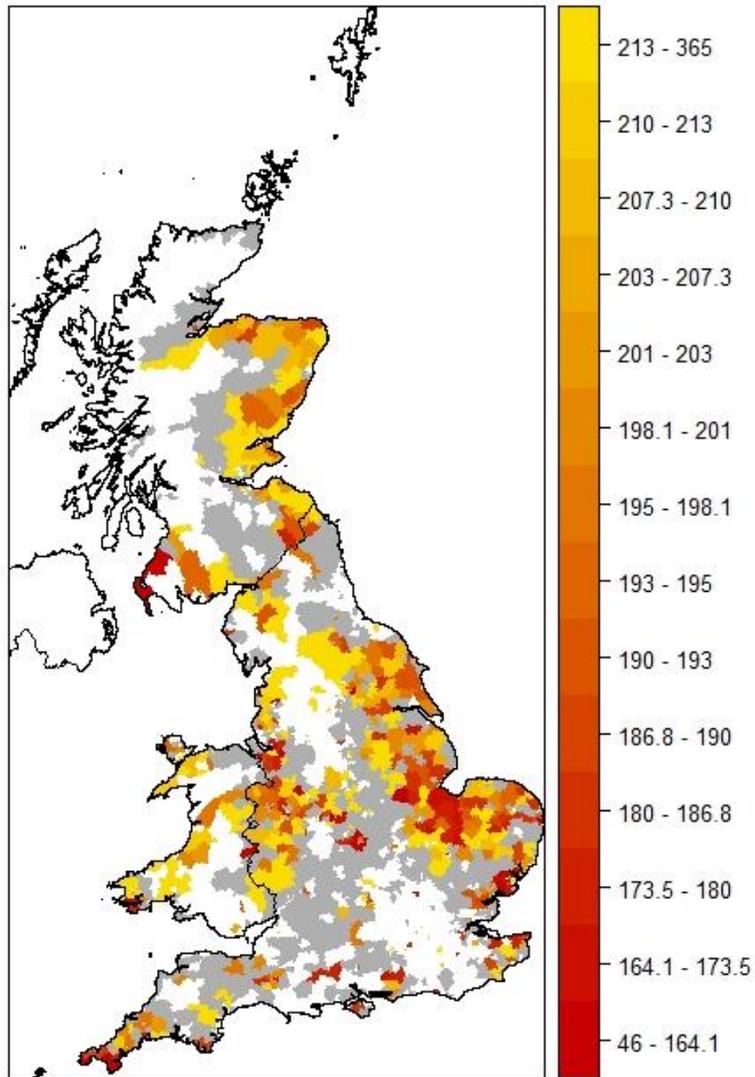


Fig. 2. Median day of year of first late blight outbreak mapped by postcode district. Red indicates areas where outbreaks occur earlier in the year, on average. Yellow indicates areas where outbreaks tend to occur later.

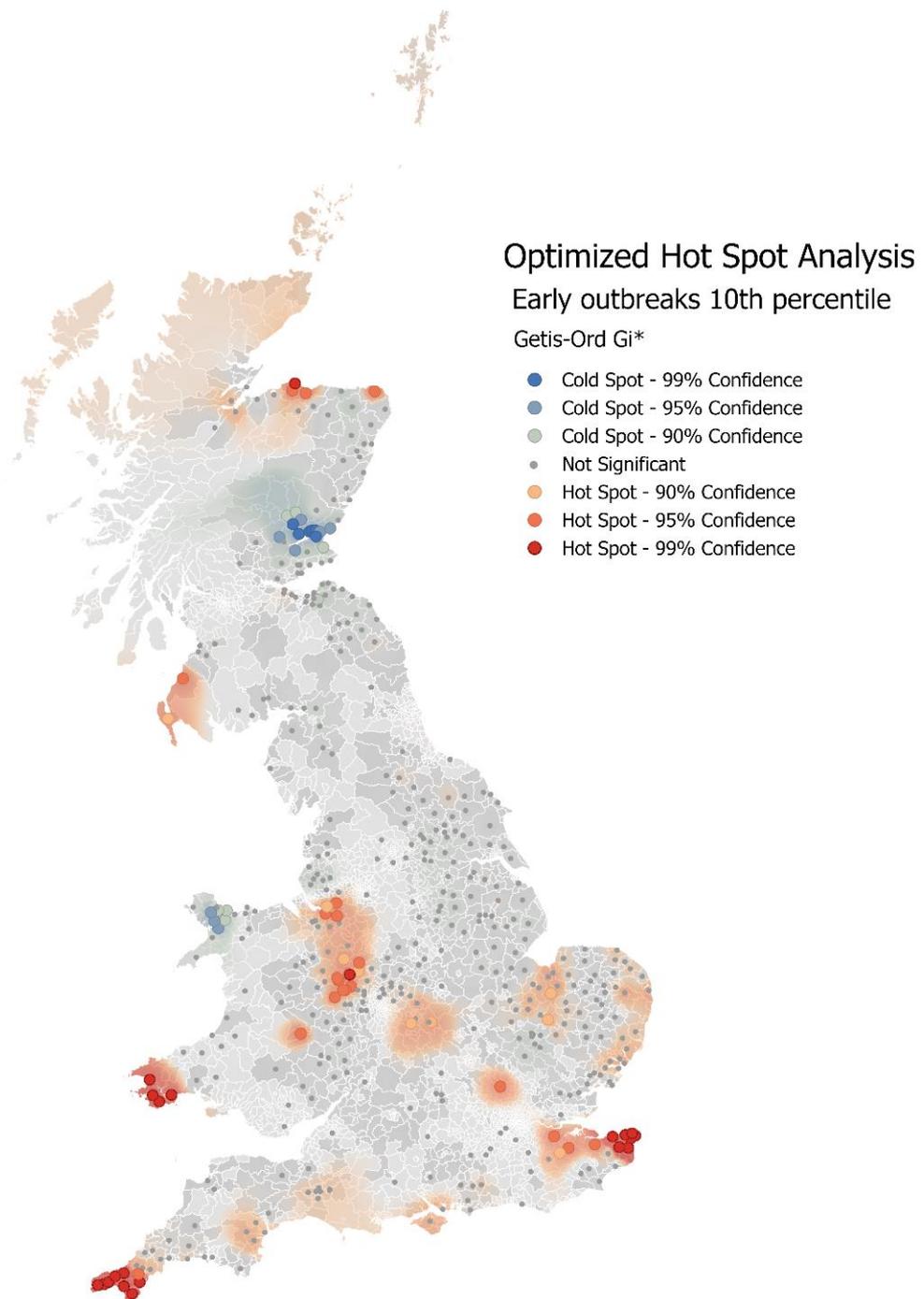


Fig. 3. Statistically significant hot and cold spots derived by OHSAs from the 10th percentile of late blight outbreaks by reporting date, 2003–2018. Inverse distance weighting was used to interpolate a coloured raster surface from the OHSAs points.

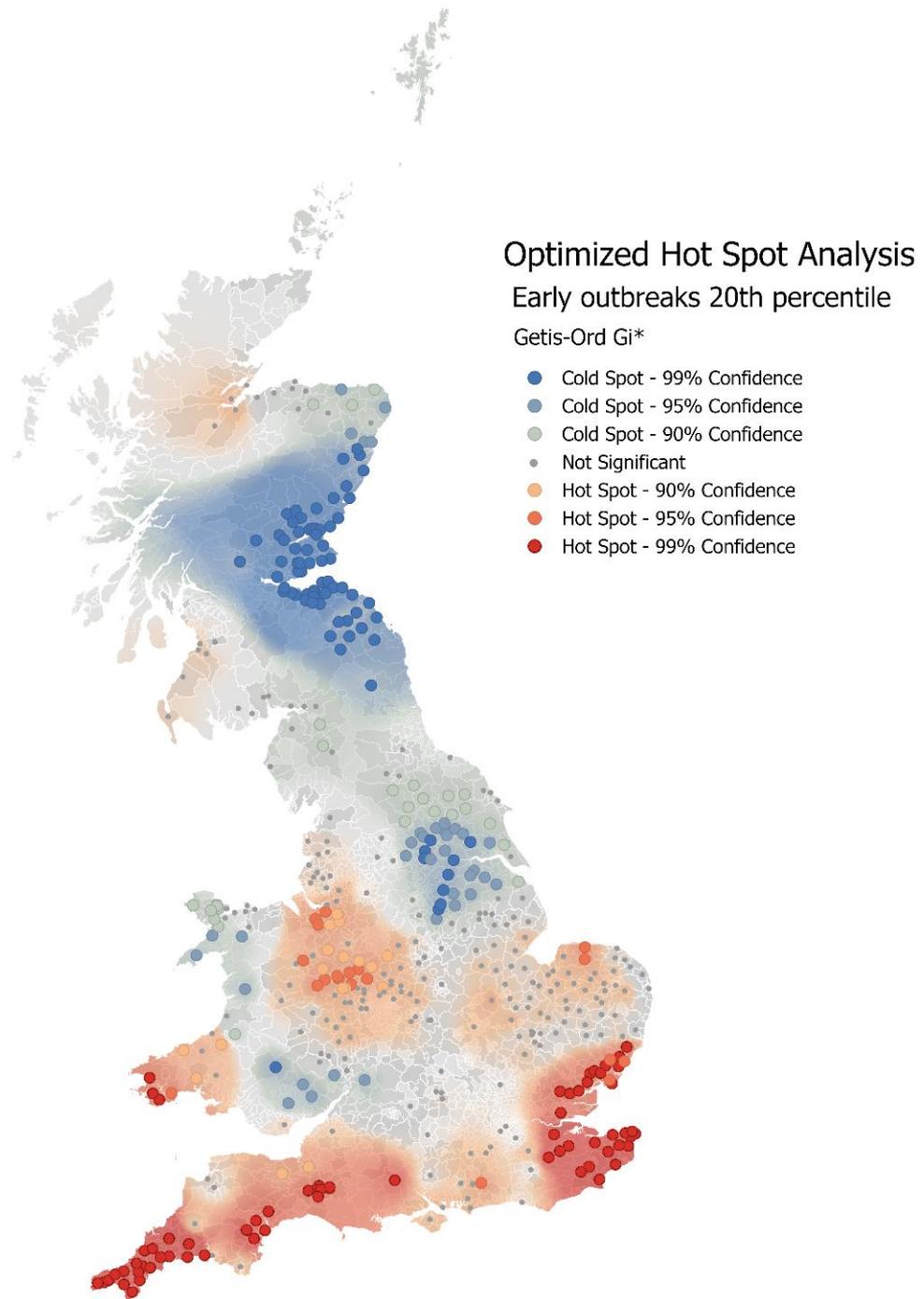


Fig. 4. Statistically significant hot and cold spots derived by OHSa from the 20th percentile of late blight outbreaks by reporting date, 2003–2018. Inverse distance weighting was used to interpolate a coloured raster surface from the OHSa points.

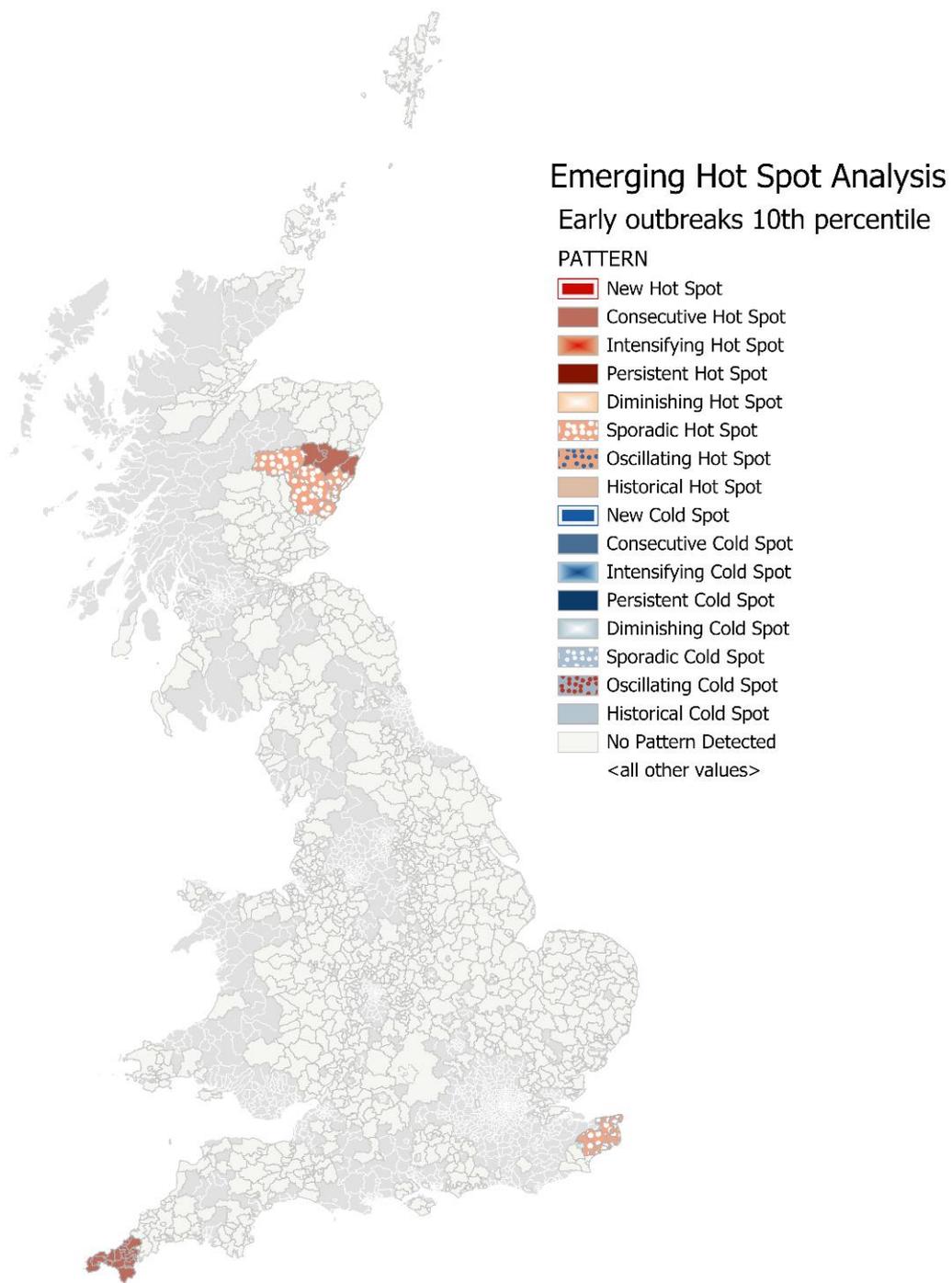


Fig. 5. Space-time patterns of early outbreaks of late blight, derived by EHSA from the 10th percentile of late blight outbreaks (by reporting date), 2003–2018. Postcode districts with no reported commercial potato crops are shaded pale grey and were excluded from the analysis.

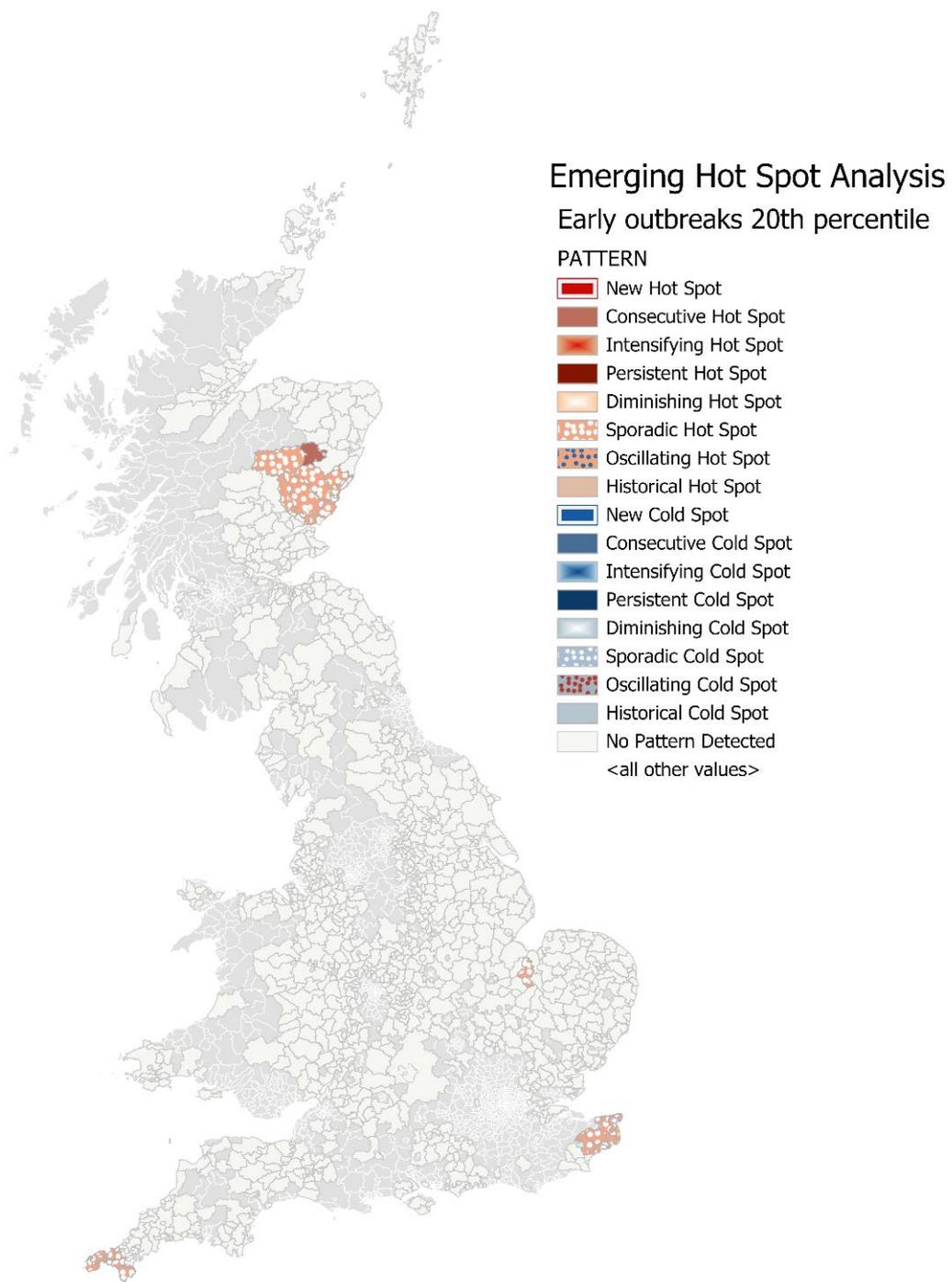


Fig. 6. Space-time patterns of early outbreaks of late blight, derived by EHSA from the 20th percentile of late blight outbreaks (by reporting date), 2003–2018. Postcode districts with no reported commercial potato crops are shaded pale grey and were excluded from the analysis.

Modelling also showed that temperature was the best predictor of early outbreaks (Fig. 7). The onset and spread of late blight remain strongly dependent on the weather and a factor strongly influencing this analysis of early outbreaks was the variation in the disease pressure from season to season both at a national and a local level.

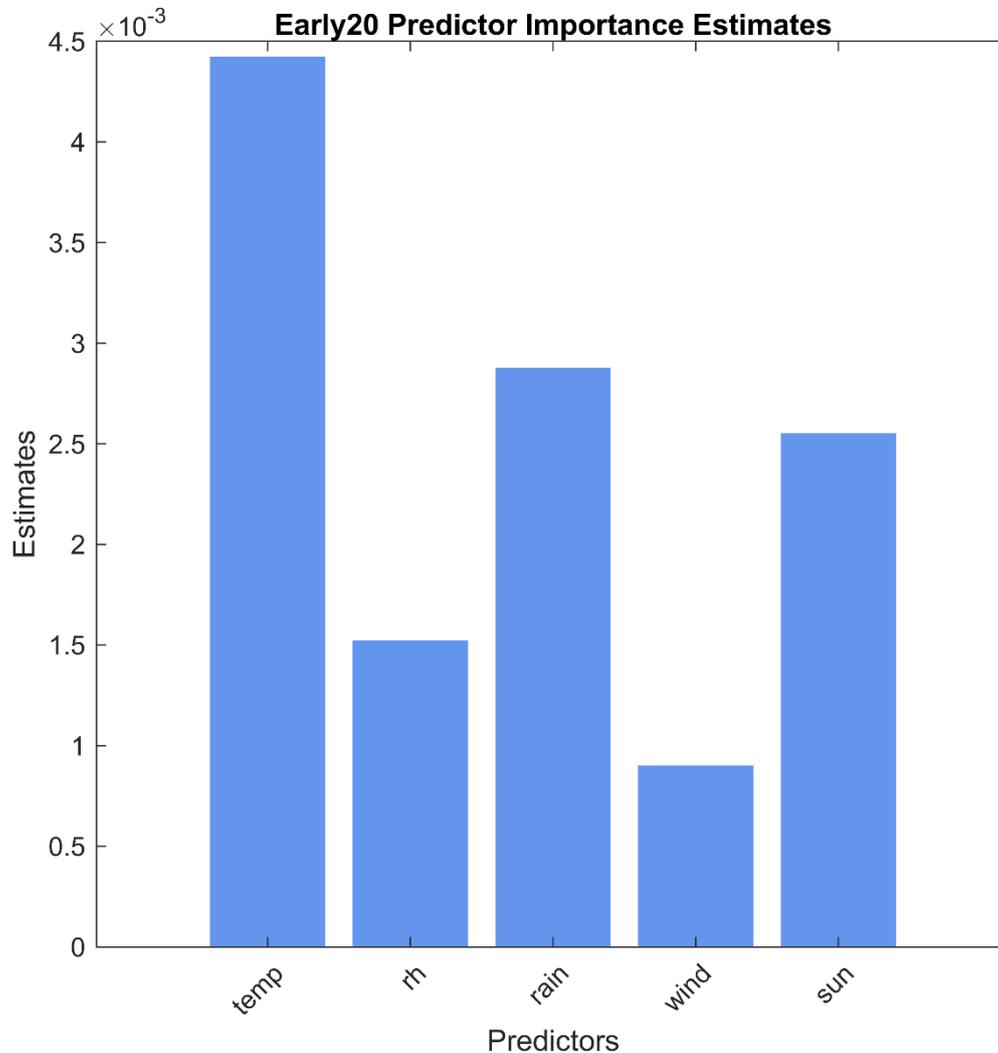


Fig. 7. Importance of climate variables in predicting clusters of early outbreaks of potato late blight.

The total number of sampled outbreaks ranged from 300 in the 2007 season to as few as 58 in 2015. The analysis applied is very sensitive at picking up different patterns of hotspots over time but relatively few passed these carefully defined thresholds. Colour-coded maps were produced to show the overall risk of early outbreaks by postcode district, and the week of the year these were most likely to occur (Appendix 1, Figs. A1 & A2). Using these we made general predictions that the earliest infections occur in regions with the highest density of potato crops and in warmer, low lying mainly coastal regions with earlier crops and more conducive blight weather. Climatic variation made it hard to predict more clearly or find other patterns in early outbreaks. In all potato growing regions, it is important that growers remain aware of primary

infections at the start of the season and manage discard piles and volunteer potato plants (groundkeepers) and ensure high quality blight-free seed is used (Cooke et al., 2011). Such care will reduce early crop infection and aid management practices aimed at preventing rather than controlling disease.

Objective 2: Risk and rate of spread of late blight

An Optimized Outlier Analysis was used to examine all the sampled late blight outbreaks from 2003 to 2018 and identified clustering of disease incidence that provides an indication of future disease risk. The map generated from this analysis (Fig. 8 and Appendix 1, Fig. A3) indicated that the risk of spread of disease among neighbouring postcode districts was highest in the potato growing regions of Tayside, Fife, Lothian, East Anglia and parts of Kent. It was somewhat surprising that other potato growing regions such as the Midlands were not defined as high risk in this analysis, but this may relate to the year to year variation in local disease pressure.

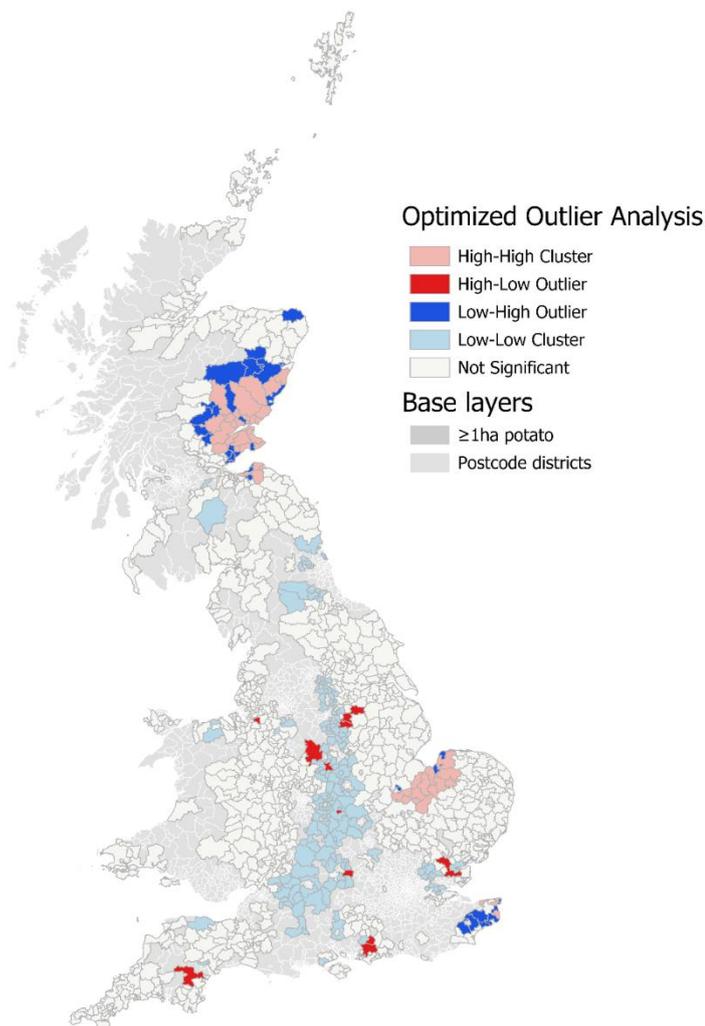


Fig. 8. Output from the Optimised Outlier Analysis tool, showing statistically significant variation between observations and random variation. Postcode districts with no reported commercial potato crops were excluded from the analysis.

The data available in this study allowed us to calculate the rate of spread of a new genotype across potato growing regions of GB. The velocity of spatial spread of newer genotypes 36_A2 and 37_A2 from early foci was calculated as between 3–17 km per week (Figs. 9-11). This highlights that even from a single point of infection the rate of crop to crop spread can have a severe impact on large areas of potato production within even one or two seasons.

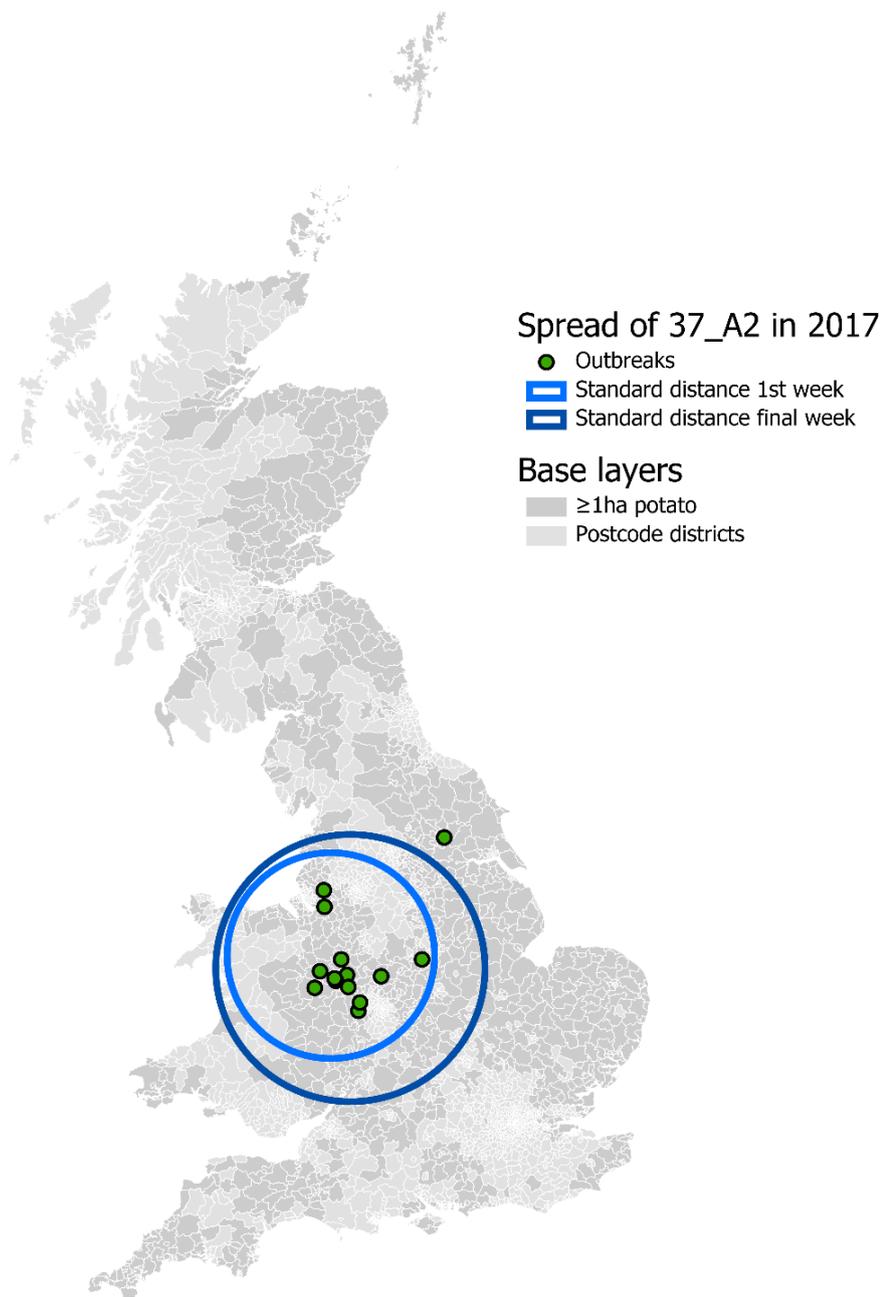


Fig. 9. Standard Distance map representing the spread of genotype 37_A2 in the first and final weeks of the epidemic in 2017.

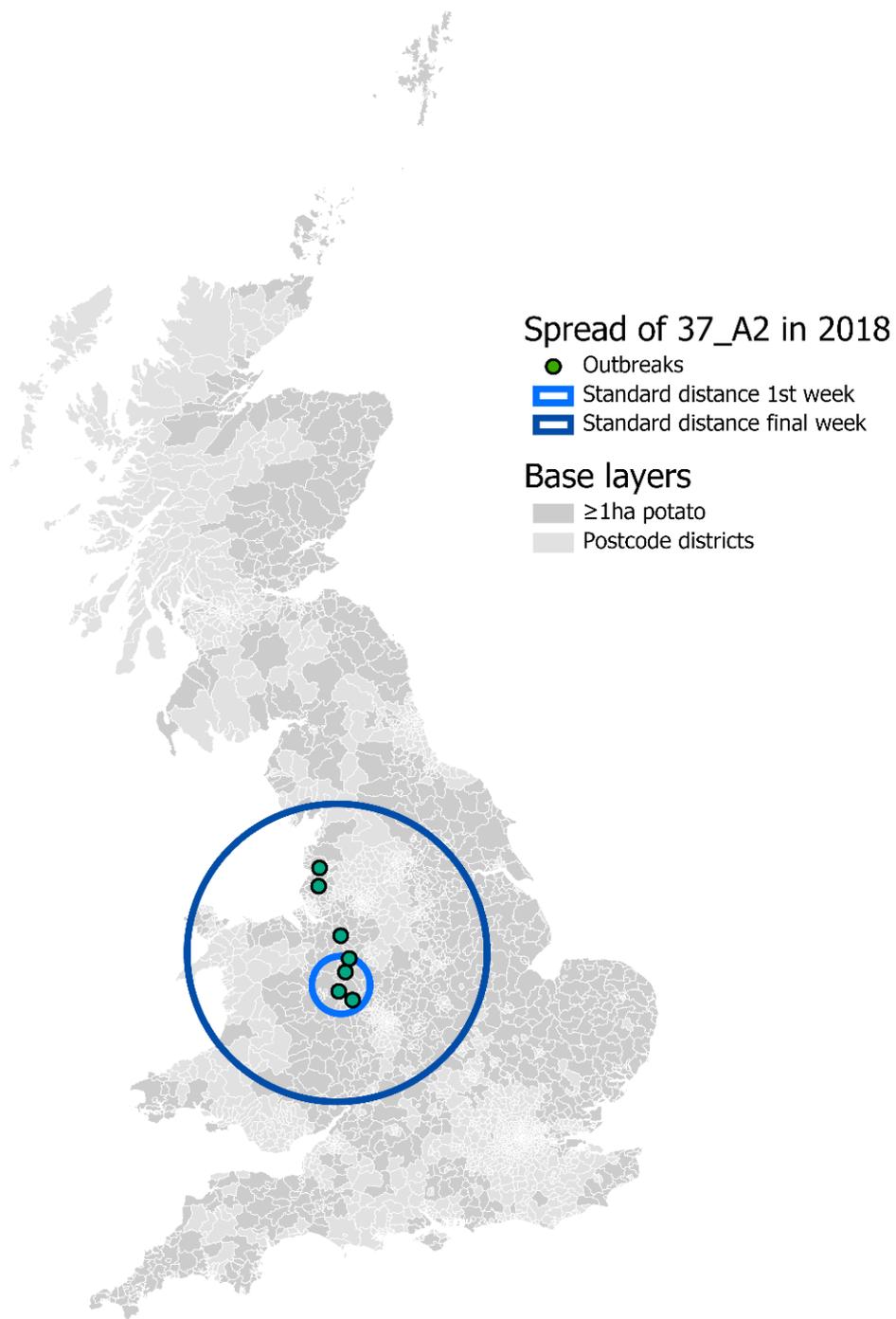


Fig. 10. Standard Distance map representing the spread of genotype 37_A2 in the first and final weeks of the epidemic in 2018.

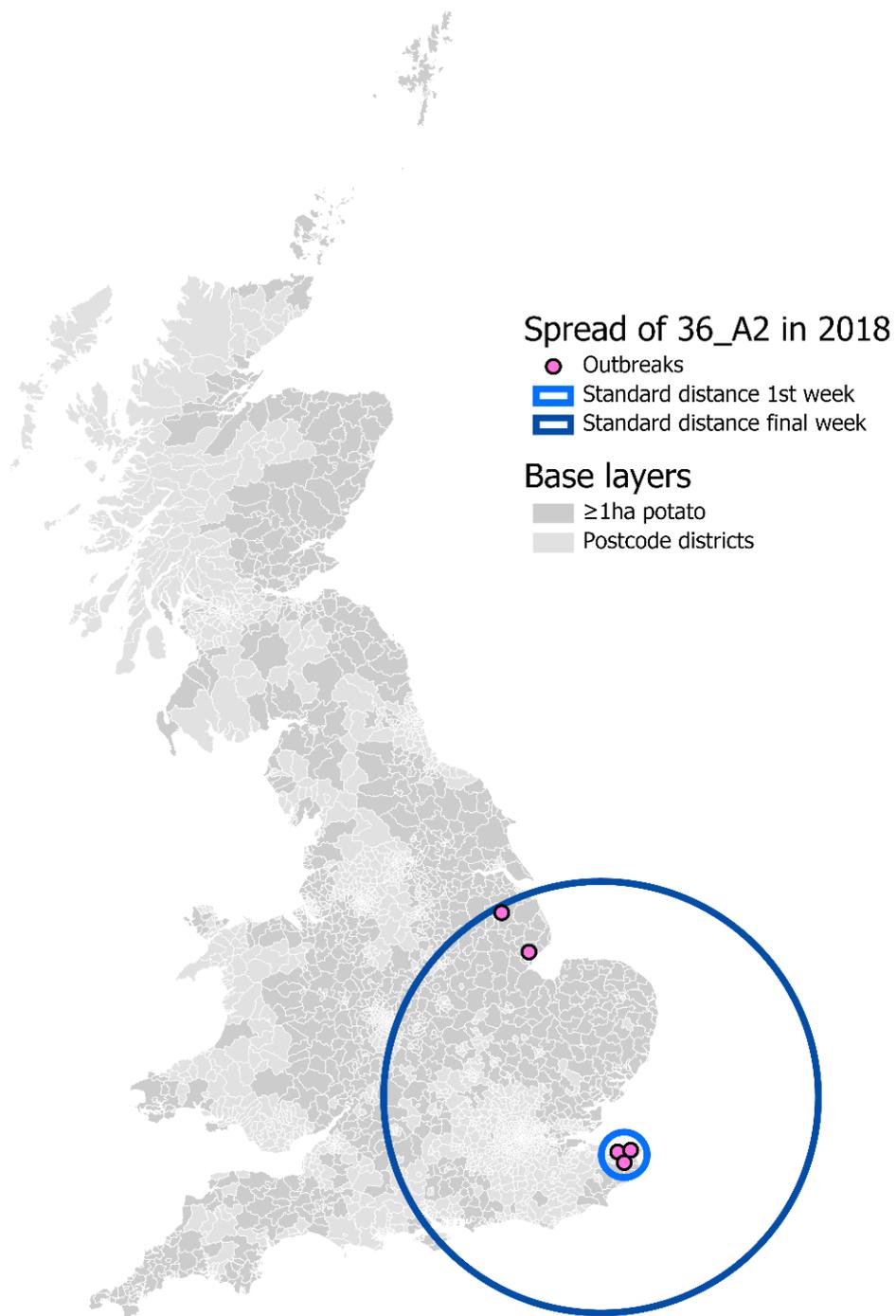


Fig. 11. Standard Distance map representing the spread of genotype 36_A2 in the first and final weeks of the epidemic in 2018.

The 37_A2 lineage was first sampled in the Midlands in late June 2016 and caused tuber blight outbreaks in the same region in addition to being sampled near Doncaster (Cooke, 2019). By the end of the 2017 season it had spread north to North Yorkshire as well as being sampled in eastern England and Kent (Figs. 9 & 10). Its spread appears to be consistent with crop to crop dispersal but new sources of infection via seed cannot be ruled out. This rapid spread had implications for the industry due to its insensitivity to fluazinam (Schepers *et al.*, 2018) leading to weaknesses in some late-season spray programmes and resulting in an increased incidence of tuber blight problems in storage (Cooke, 2019). Genotype 36_A2 was first sampled in mid-April 2018 and despite it being a very low risk year it was also sampled north of The Wash later in the same season (Fig. 11). This lineage is known to be highly aggressive and its rapid spread is also causing management problems for growers.

Objective 3: Risk of late blight over time

An analysis of the accumulated total of sampled outbreaks showed some areas of above average late blight sampling and postcode districts with commercial potato production from which no outbreaks were sampled (Fig. 12).

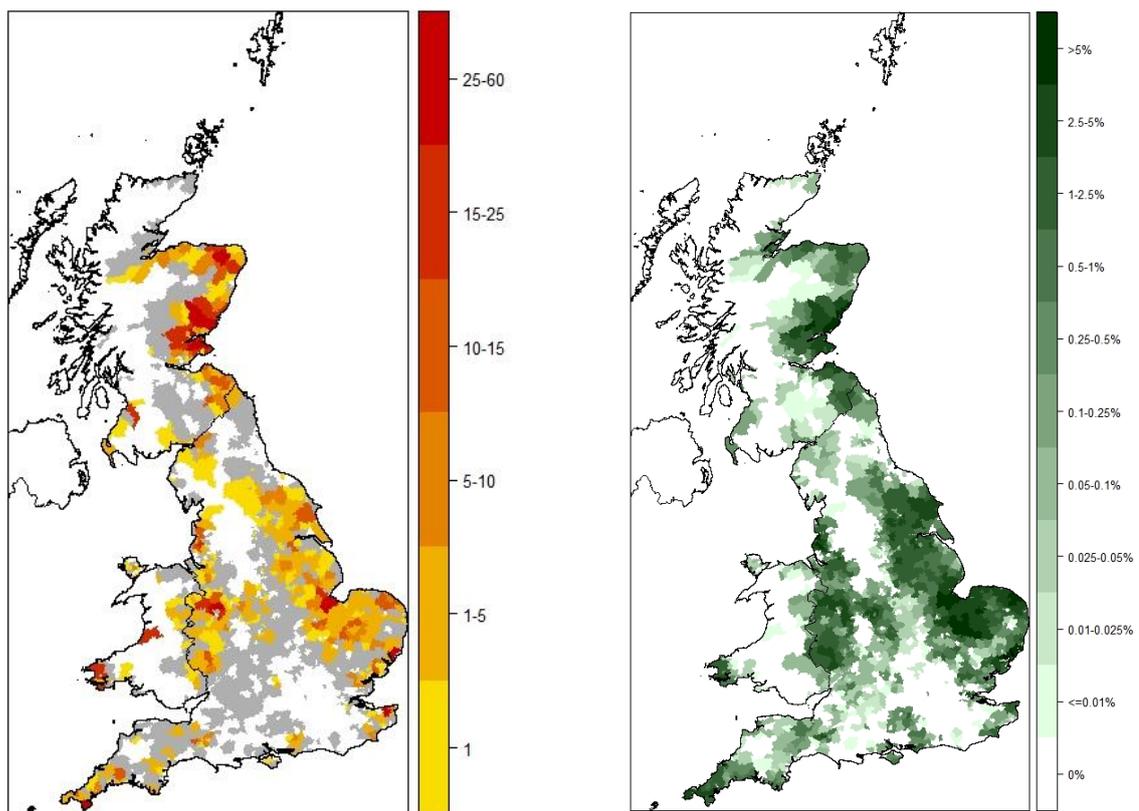


Fig. 12. Left: Total number of sampled late potato blight outbreaks within each postcode district over the time period 2005–2018. Grey areas are postcodes where potatoes are grown, but where blight outbreaks were not reported. Right: Annual average area of potatoes grown

within each postcode district over the time period 2005–2018, normalised by the size of the postcode (potato density).

A comparison with the density of potato cultivation per district however, indicated the low blight sampling corresponded to low potato density and there were no major potato growing areas unsampled. When normalised according to potato cultivation density per postcode the distribution of sampling intensity was shown to be more uniform (Fig. 13).

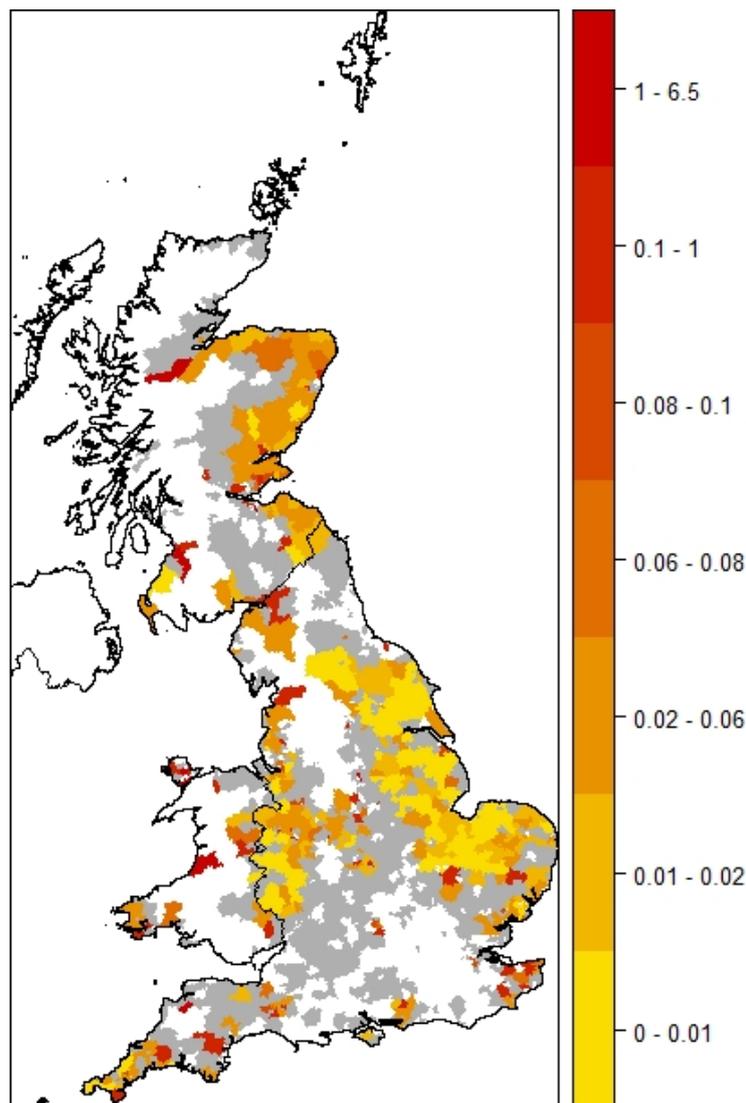


Fig. 13. Total number of late potato blight outbreaks normalised by the annual average area of potatoes grown within each postcode district over the time-period 2005–2018.

Not all potatoes are however, grown commercially and the FAB campaign has encouraged sampling from gardens, allotments, and field trials as they provide another component of the pathogen population. Some of these regions appear as more intensively sampled patches with more samples for the relatively low potato cropping density (Fig. 13). Such samples were however not included in the hotspot data

analysis and most maps thus indicate areas of commercial production in grey (e.g. Fig. 12) or show postcode districts with <1ha commercial potato that are masked out from the analysis. A colour-coded map was produced to show the overall risk of late blight by postcode district (Appendix 1, Fig. A4).

A more detailed statistical analysis of hotspots in ArcGIS showed the most intense outbreak sampling from Kent, an area around The Wash in eastern England and Fife, Tayside and Angus in Scotland. Smaller spots were also recorded in the Midlands and Aberdeenshire (Fig. 14). No cold spots were recorded.

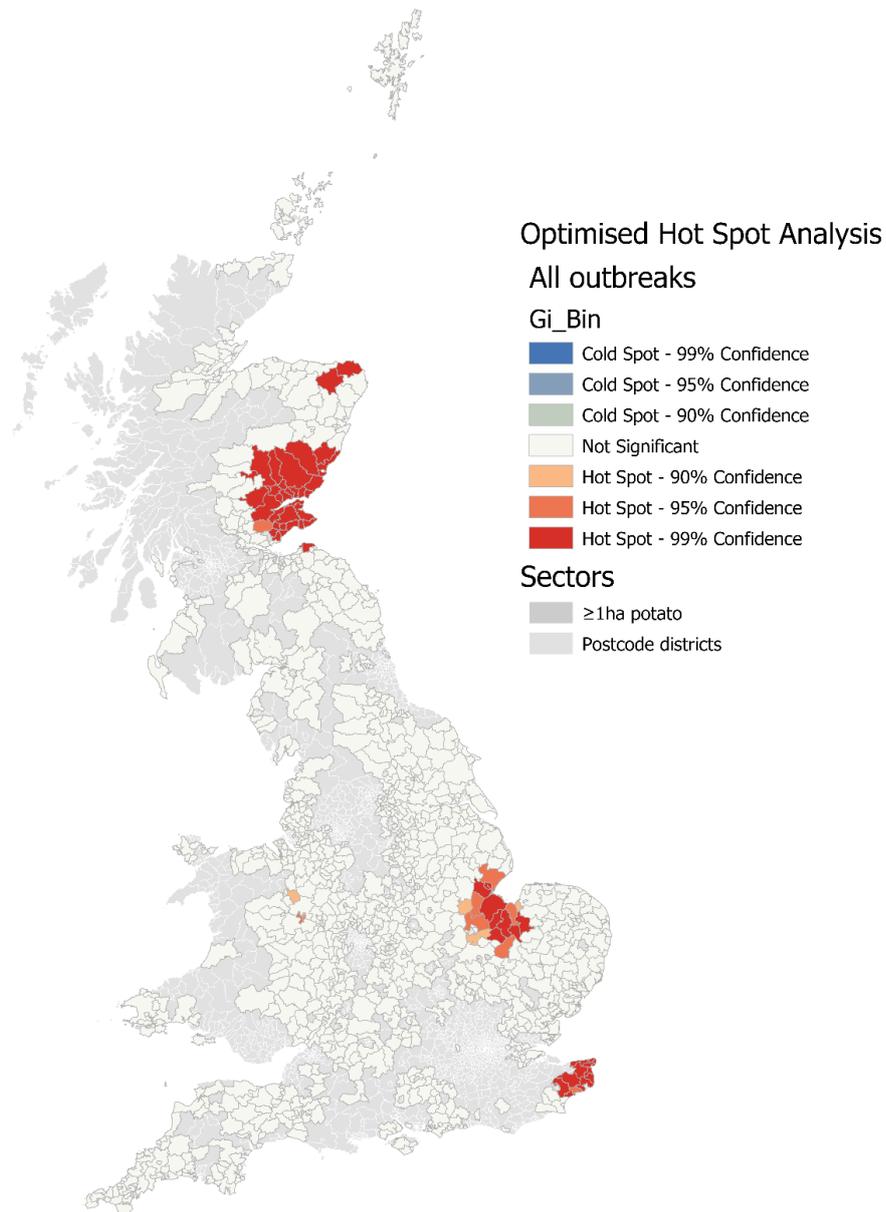


Fig. 14. Statistically significant hot and cold spots derived by OHSA for all reported late blight outbreaks, 2003–2018. Postcode districts with no reported commercial potato crops are shaded pale grey and were excluded from the analysis.

These hot spot regions are areas with the greatest risk of blight over all the years and were also statistically significant hot spots in the space-time analysis (Fig. 15). There were three types of temporal trend identified in the hot spots of incidence: consecutive, sporadic, and new (appearing in the final year) with sporadic hot spot the most common. The prevalence of sporadic and lack of persistent hot spots reflects large inter-annual variation in the distribution of disease. It is perhaps striking that most potato growing districts are not statistically significant hot spots of blight sampling but, as the incidence data shows, this does not indicate an absence of blight but a reduced average risk.

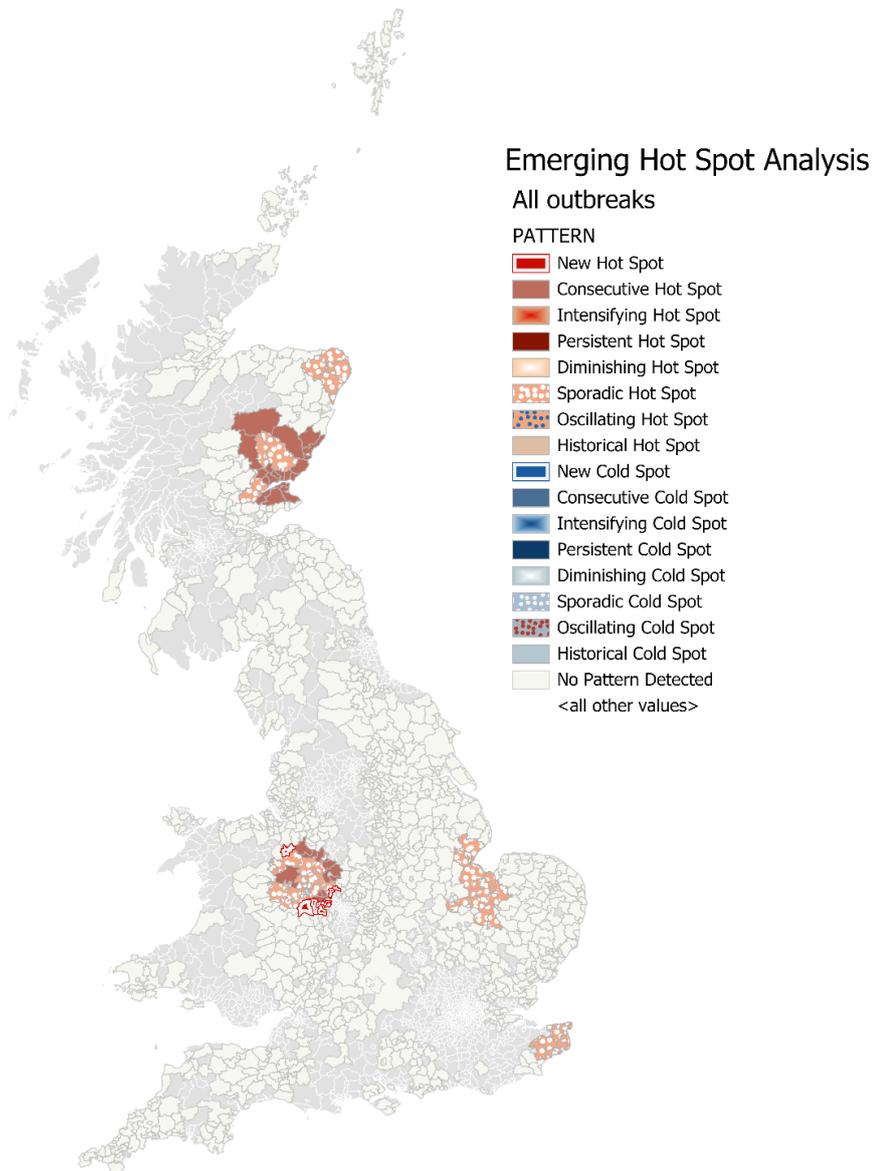


Fig. 15. Space-time patterns of late blight incidence derived by EHSA, 2003–2018. Postcode districts with no reported commercial potato crops are shaded pale grey and were excluded from the analysis.

A neural network model was developed to explore the relationship between outbreak risk and a series of detailed environmental factors. The overall accuracy of the model was high with the best compromise between true positive and false positive rate being of 80 and 15% respectively (Fig. 16).

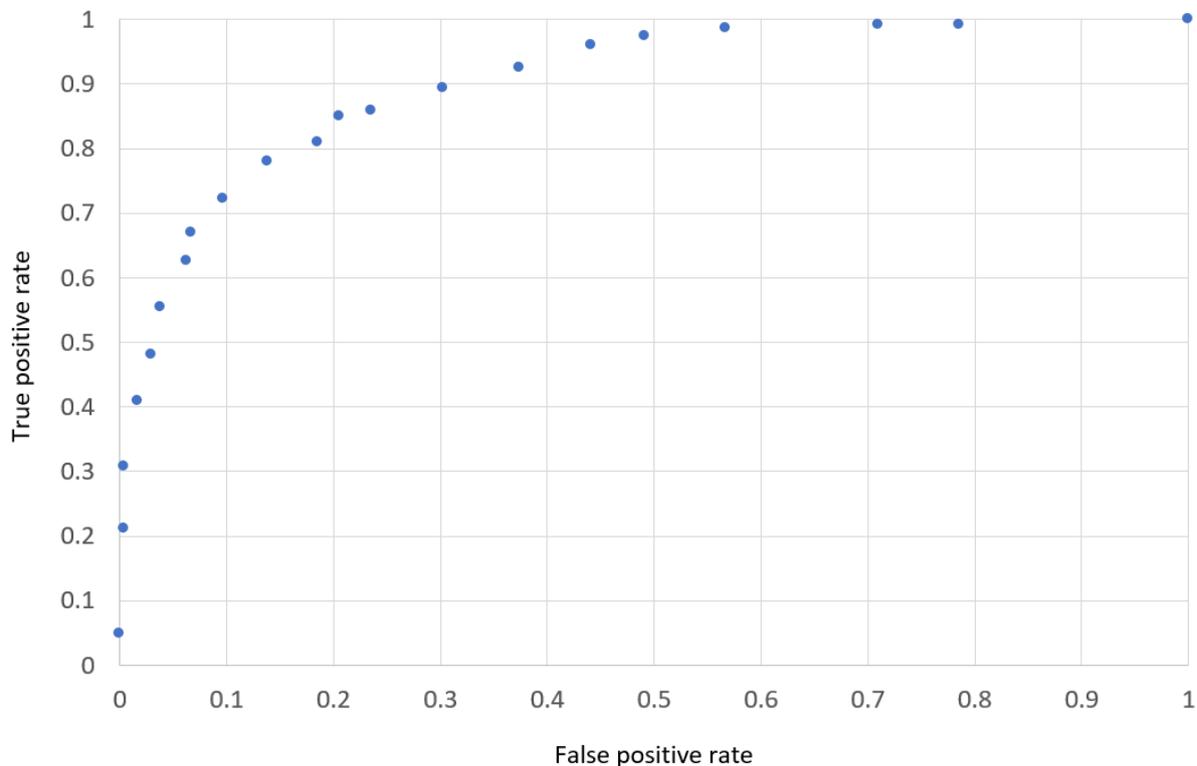


Fig. 16. Receiver Operating Characteristic for model estimating presence/absence of late blight.

A sensitivity analysis to determine the impact of each variable on the model’s ability to predict risk revealed some factors with a clear association but also showed the challenges of this type of analysis. As expected, weather had a strong impact on outbreak risk, particularly temperature, humidity, rainfall and windspeed (Fig. 17). Despite there being no known association between soil class or geological type and risk of late blight in the crop growing on such a substrate there was also evidence of an association with soil conditions and geological type. This analysis picked up above average pH Calcaric and Mollic soils as having a lower blight risk (Fig. 18). A difficulty faced in this analysis is that outbreaks were defined at postcode district level. Such districts vary in size and clearly comprise potato growing land with a range of characteristics (soil, slope, aspect etc). Because of this, topographic factors were averaged across postcodes, instead of individual site conditions being applied to observations in the model. Despite this an association between topography (elevation, slope, aspect) and outbreak risk was also observed (Fig. 19).

At the extremes there are clear differences with flat peaty soils on land at or below sea level in the Fens compared to land of greater elevation and mixed podzol and brown soils in parts of Aberdeenshire. But within regions or postcode districts it is unclear

how representative an average slope or aspect measure is (the resolution is insufficient).

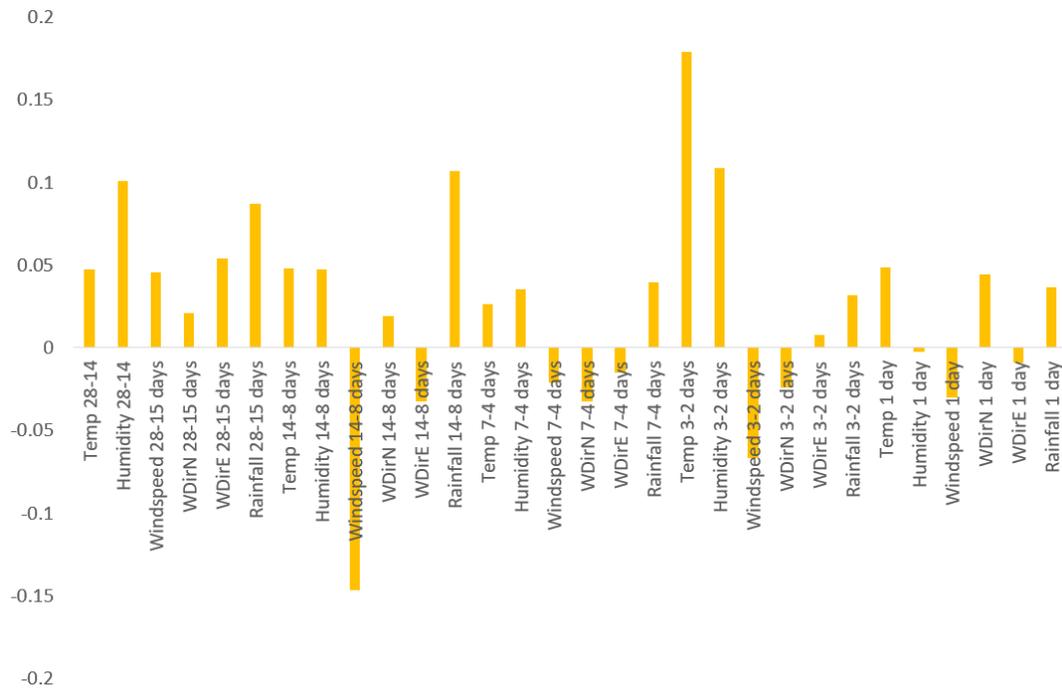


Fig. 17. Sensitivity analysis of model by weather variables. Variables are averaged over the periods given before the field observation.



Fig. 18. Sensitivity analysis of soil diagnostic properties.

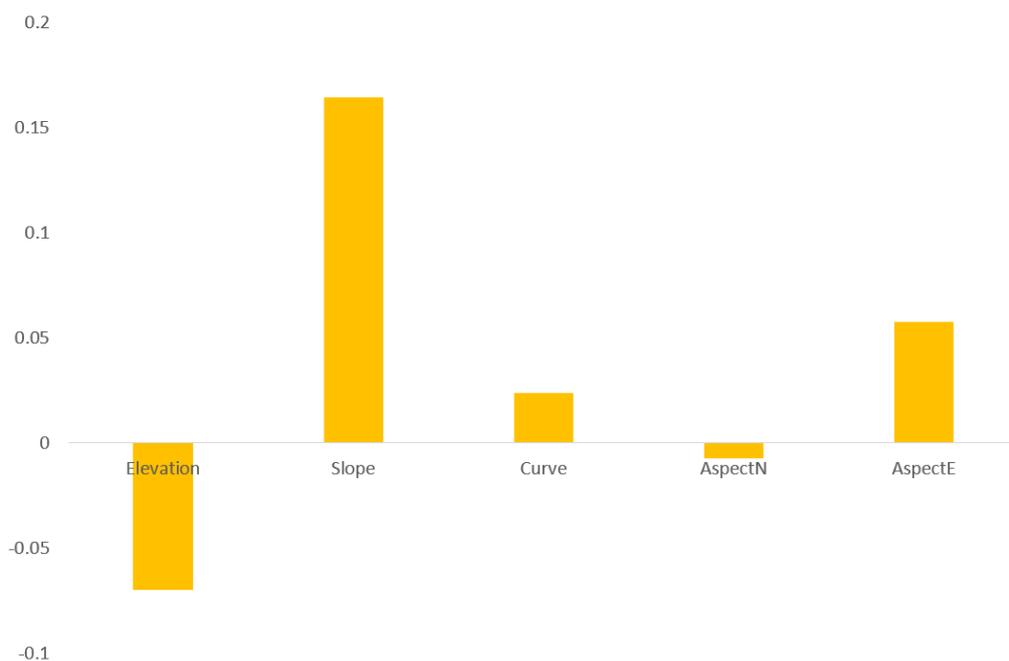


Fig. 19. Sensitivity analysis of model by topography variables. AspectN is slope angle away from North (i.e. increasing towards the South), AspectE is slope angle from East (i.e. increasing towards the West) (it is necessary to have these to avoid a discontinuity in values from 359° degrees to 0°, which would cause issues with the modelling).

All the modelling and sensitivity analysis performed with the neural network model was carried out using the full outbreak data. The original intention was to repeat this work using data from different genotypes and for early outbreaks. However, the number of data points available made it impossible to produce statistically robust models using this approach. For neural network modelling, the number of data points must be greater than the number of input variables, or the model becomes overfitted to the data and effectively meaningless for ‘real’ examples. Using fewer model inputs for individual genotypes would have produced significantly less accurate models. Future work to explore a resolution to this is recommended.

Objective 4: Genetic makeup and spatial distribution of late blight pathogen genotypes

Over the course of this study, the populations of *P. infestans* causing potato late blight on British crops have undergone major changes. New pathogen genotypes may have distinct advantageous traits enabling them to spread preferentially and displace others. This can happen very quickly under optimal conditions as the rate of inoculum production and its ability to spread can develop severe local to regional late blight epidemics. Examples of new traits may be an ability to overcome host resistance (Young et al., 2009, Montarry et al., 2008, Stellingwerf et al., 2018), a different temperature response (Cooke et al., 2012; Mizubuti & Fry 1998), increased aggressiveness (Young et al., 2018) or fungicide resistance (Schepers et al., 2018). Three clones, 8_A1, 13_A2 and 6_A1 have predominated with overall similar mean central tendency locations but with a slight skew to the south for 13_A2 and to the north in the case of 8_A1 (Fig. 20).

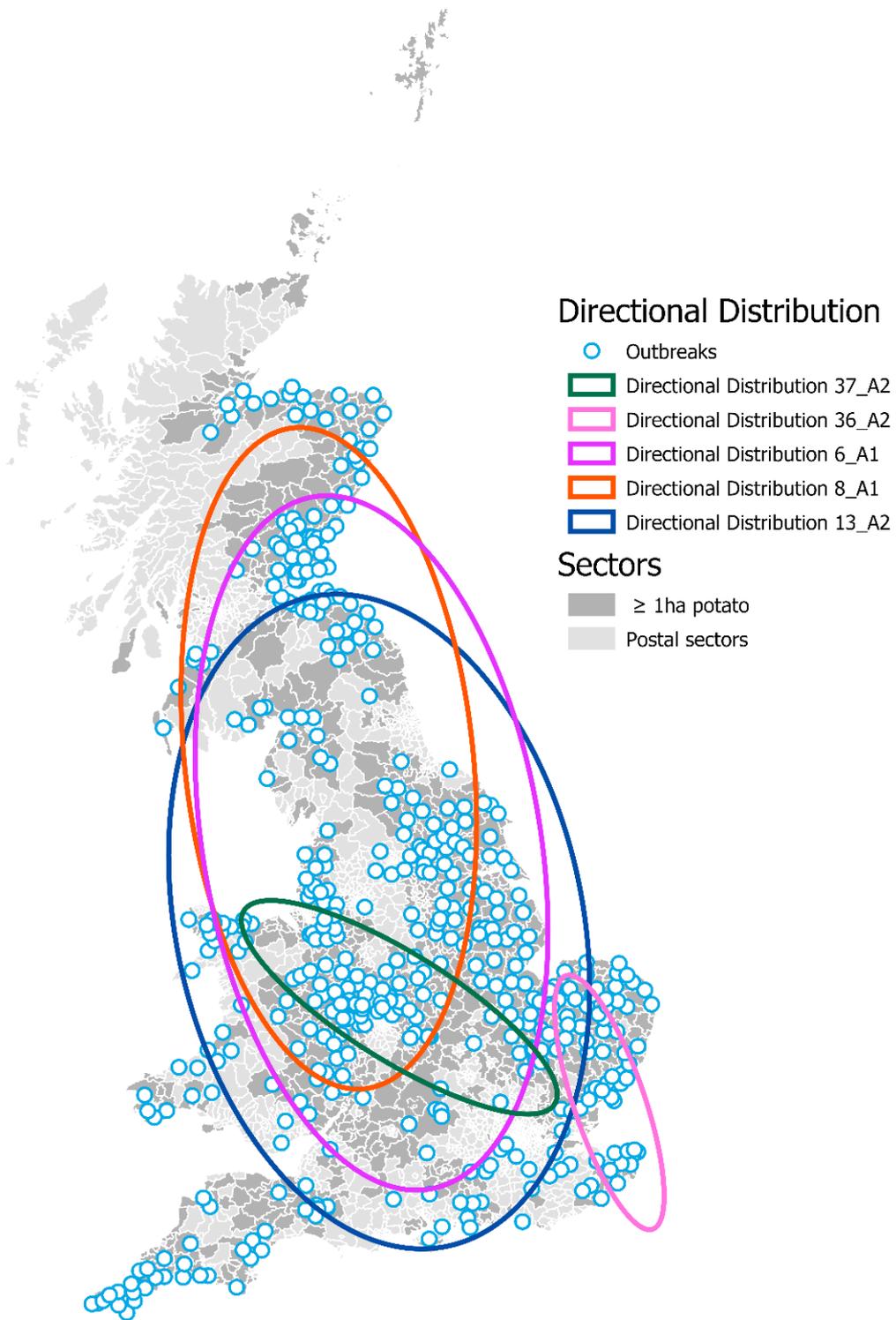


Fig. 20. Spatial characteristics of the different distributions of genotypes: the central tendency, dispersion, and directional trends (2006–2018).

Clone 8_A1 has been present in Europe since at least 1995 when it was reported widely in the UK and the Republic of Ireland (Day et al., 2004). It has been largely displaced by other clones but nonetheless persisted at a low frequency with hotspots in parts of Scotland and Wales (Fig. 21).

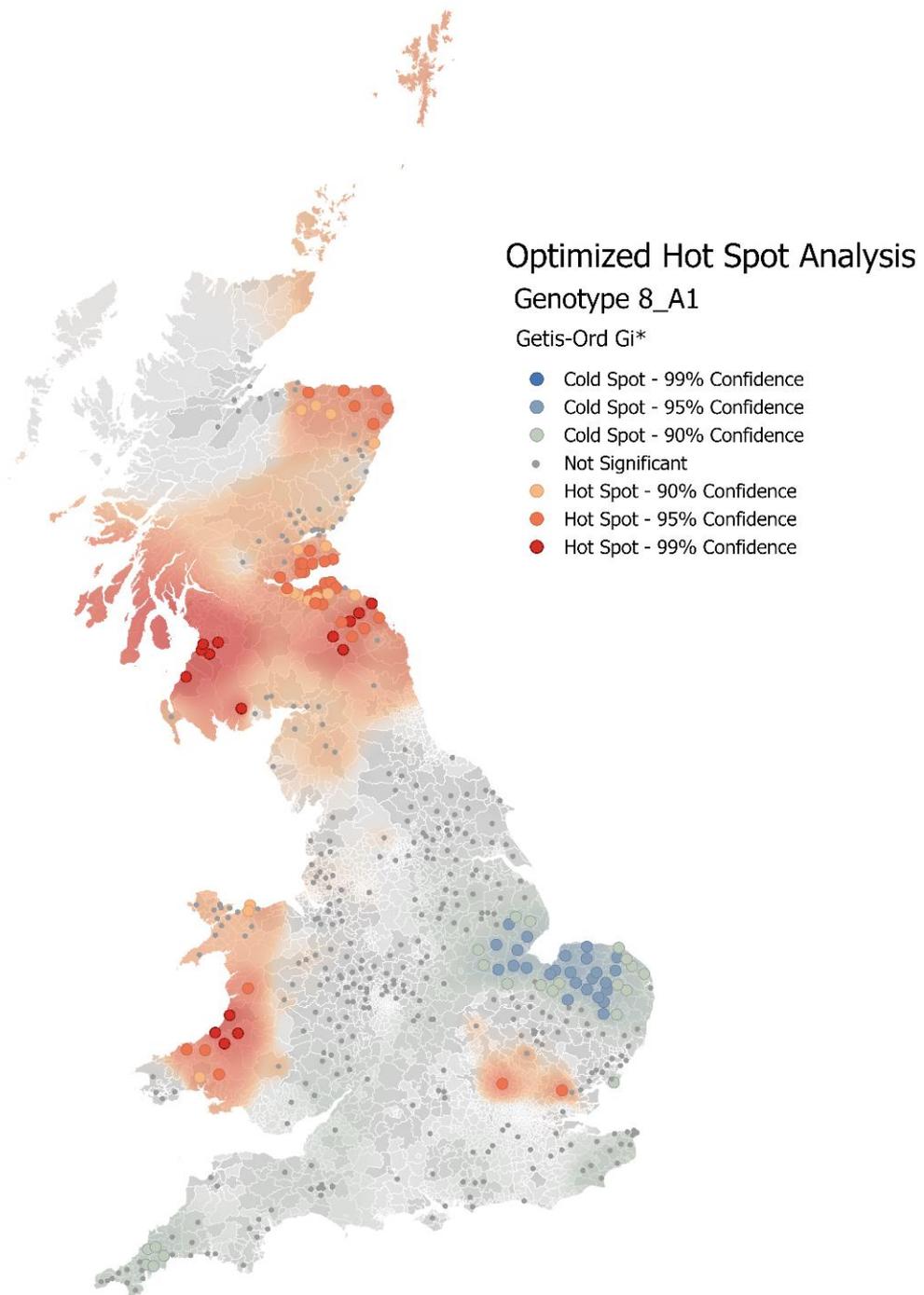


Fig. 21. Statistically significant hot and cold spots derived by OHSA for genotype 8_A1, 2006–2018. Inverse distance weighting was used to interpolate a coloured raster surface from the OHSA points.

Only the Scottish hotspots were statistically significant in the space-time analysis (Fig. 22).

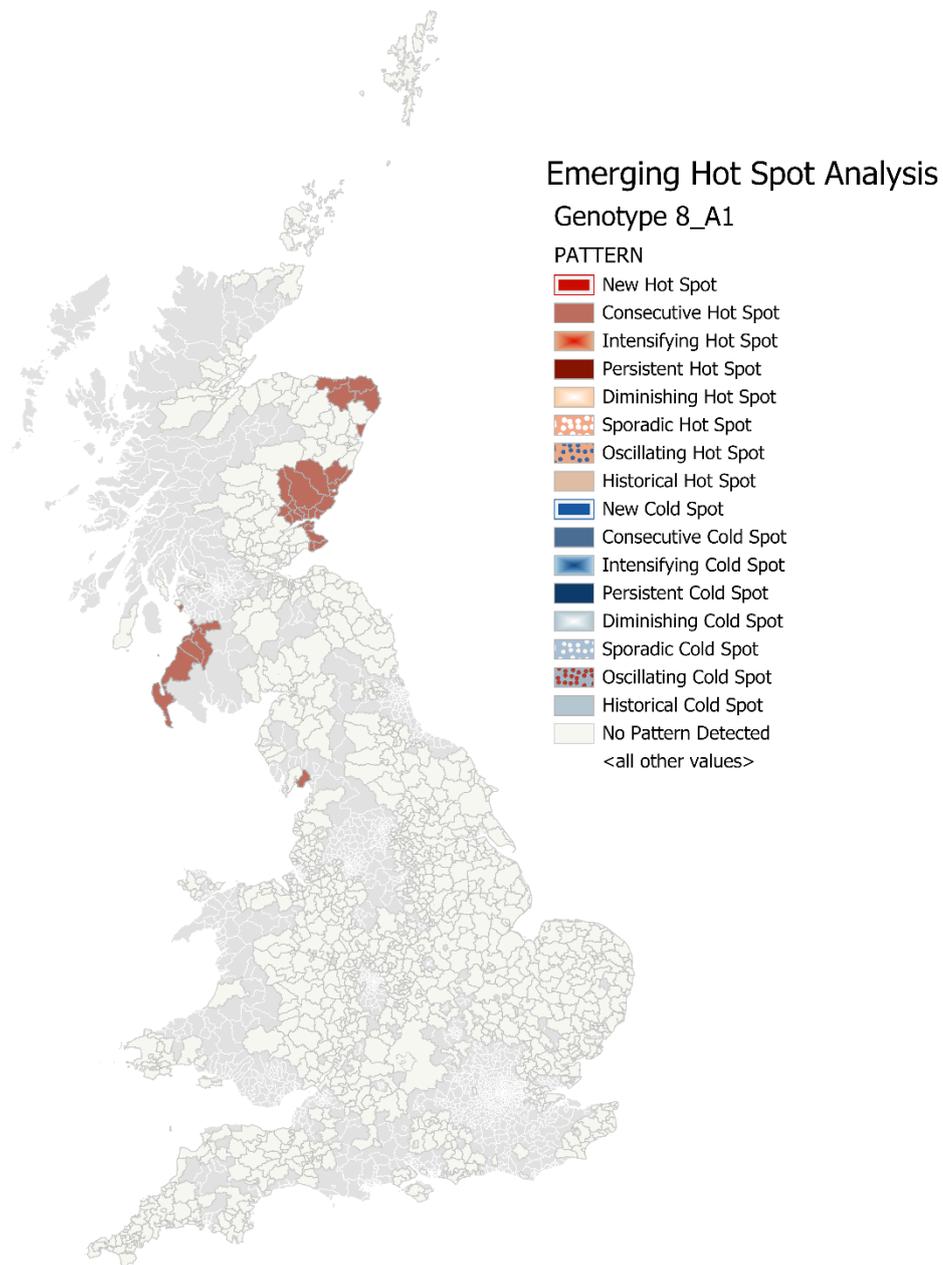


Fig. 22. Space-time patterns of genotype 8_A1 incidence derived by EHSA, 2003–2018. Postcode districts with no reported commercial potato crops are shaded pale grey and were excluded from the analysis.

Genotype 13_A2 had a significant impact on potato late blight management, particularly when it emerged in 2006-8, as it proved aggressive, insensitive to metalaxyl (Cooke et al., 2012) and overcame established sources of blight resistance (Lees et al., 2012). This clone spread rapidly from a serious outbreak on the Essex coast in 2006 to dominate crops across the UK in the following three seasons. Its spread north was also very rapid, found in 80% of Scottish outbreaks by 2007. Despite this initial wide distribution, this long-term analysis indicated that major hotspots of 13_A2 covered most of East Anglia, Lancashire and Wales with northern England and Scotland as cold spots (Fig. 23).

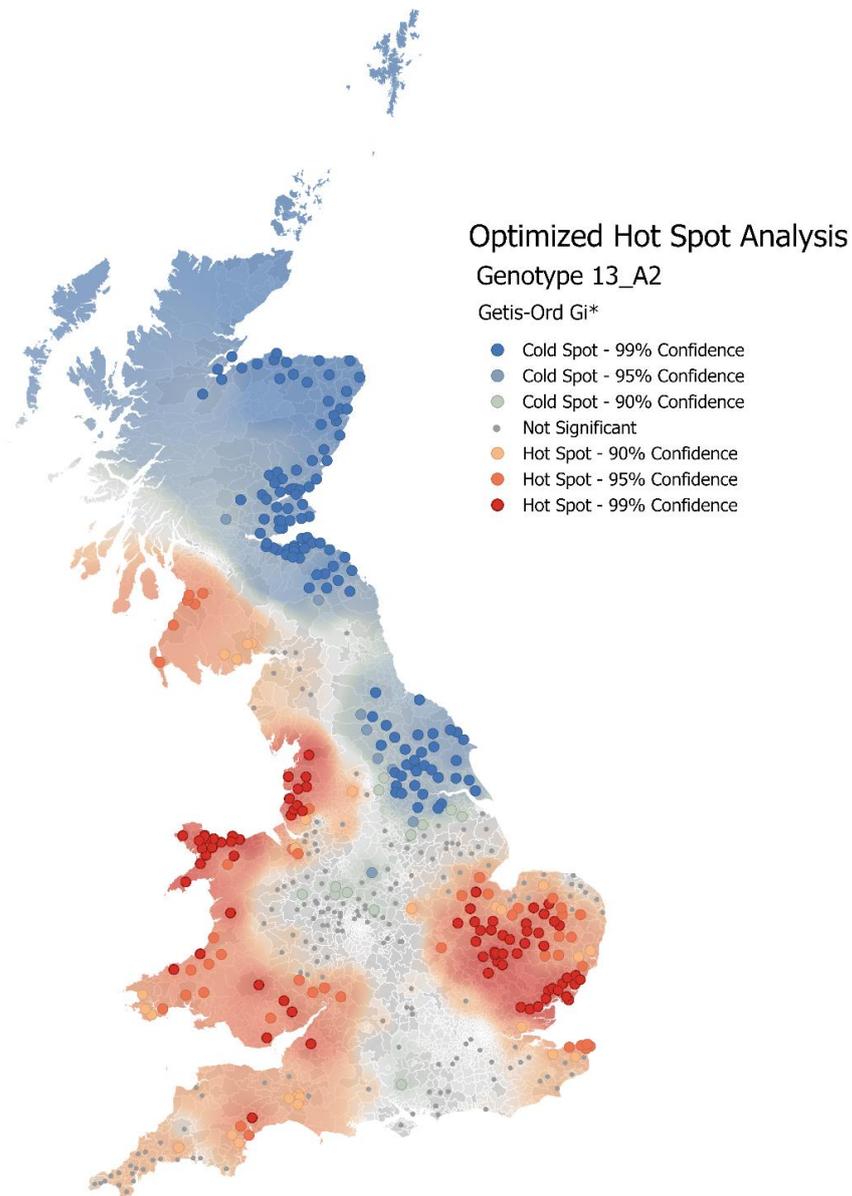


Fig. 23. Statistically significant hot and cold spots derived by OHSAs for genotype 13_A2, 2006–2018. Inverse distance weighting was used to interpolate a coloured raster surface from the OHSAs points.

These cold spots reflect a later distinct transition to a population dominated by 6_A1 in Scotland in 2011 after which the frequency of 13_A2 in Scottish samples remained markedly lower than those from crops in England and Wales low (Appendix 2). This change in genotype explains why the emerging hotspot analysis indicated only sporadic hotspots in the Midlands and Shropshire and persistent hotspots of 13_A2 in Lancashire and East Anglia (Fig. 24).

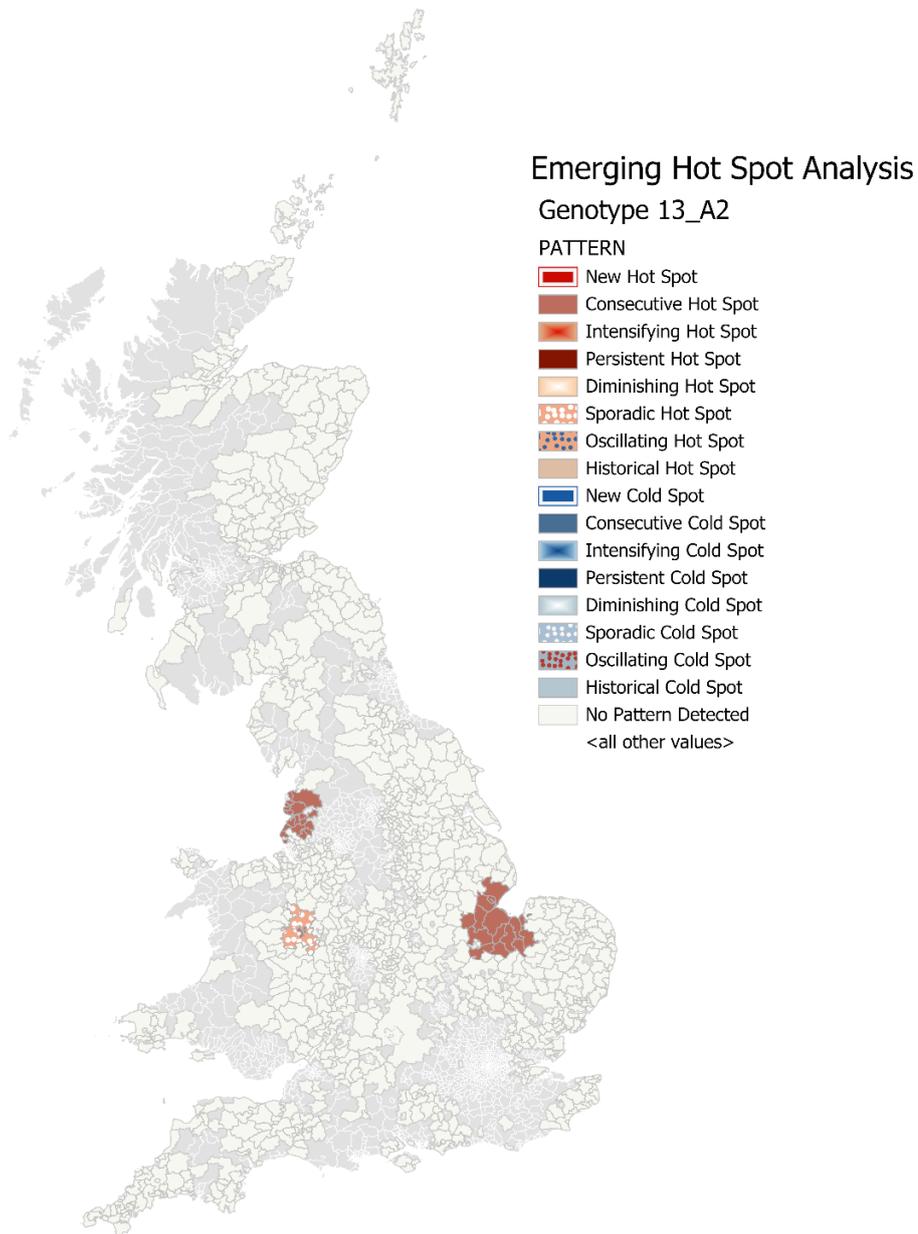


Fig. 24. Space-time patterns of genotype 13_A2 incidence derived by EHSA, 2006–2018. Postcode districts with no reported commercial potato crops are shaded pale grey and were excluded from the analysis.

In contrast, the hotspot analysis of 6_A1 indicated a dominance from the north Midlands to northern England and most of the potato growing area of Scotland (Fig. 25). It has proved persistent with 40-80% of samples being of genotype 6_A1 every year since 2011 across much of Britain (Appendix 2).

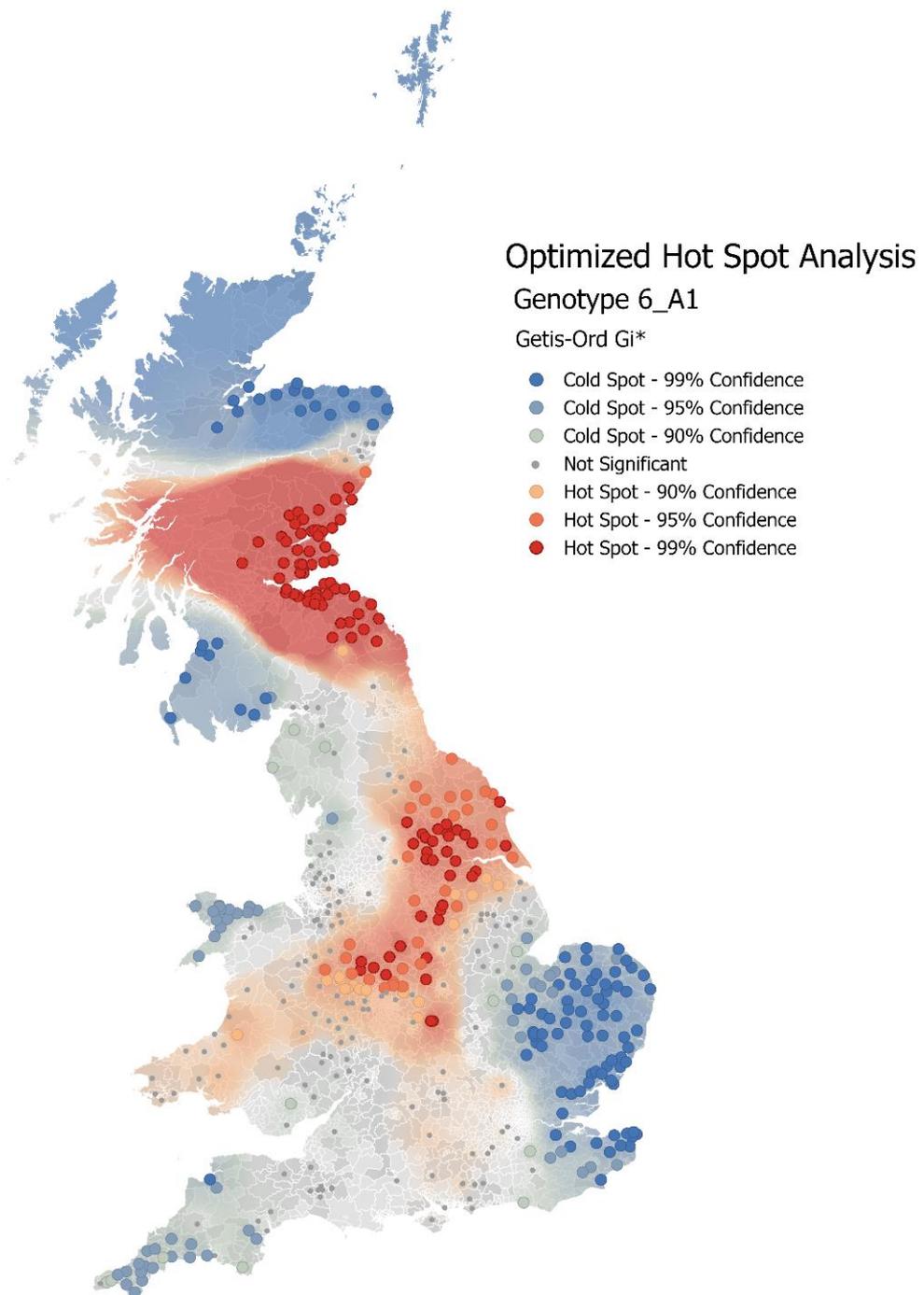


Fig. 25. Statistically significant hot and cold spots derived by OHSA for genotype 6_A1, 2006–2018. Inverse distance weighting was used to interpolate a coloured raster surface from the OHSA points.

The emerging hotspot analysis confirms its long-lasting presence in several regions of Britain as persistent or sporadic hotspots (Fig. 26). Sporadic hotspots are, in general, a sign of the variation in blight conducive conditions with 2010, 2013, 2015 and 2018 being drier warmer years with fewer outbreaks to sample. Genotype 6_A1 has no known insensitivity to any fungicide active ingredient but its persistence suggests an ability to survive well overwinter and that it is fit and aggressive in field epidemics (Cooke et al., 2012).

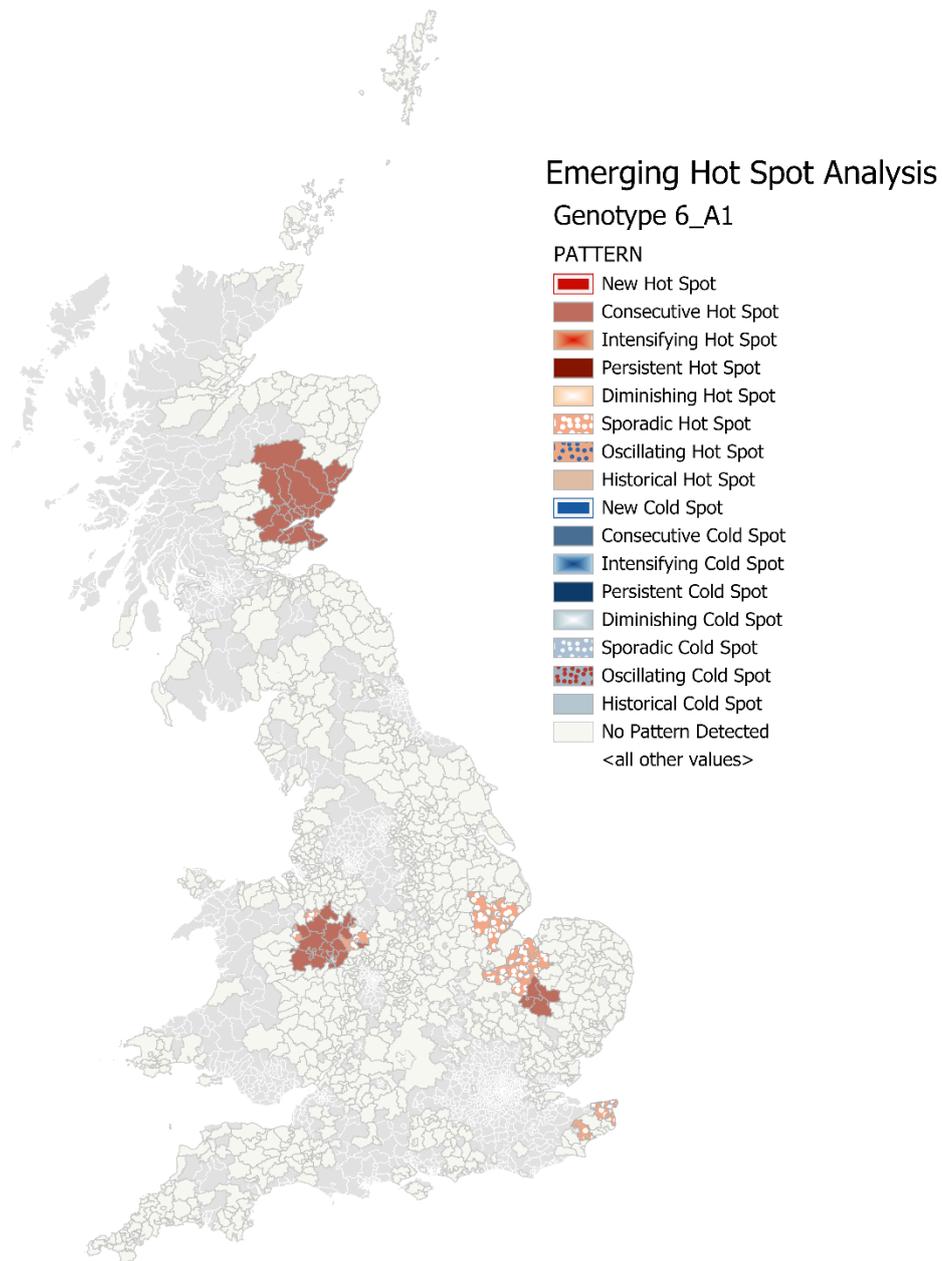


Fig. 26. Space-time patterns of genotype 6_A1 incidence derived by EHSA, 2003–2018. Postcode districts with no reported commercial potato crops are shaded pale grey and were excluded from the analysis.

This analysis presents clear evidence of the recent local emergence and spread of two new threats. As discussed above, genotype 37_A2 emerged first in 2016 and spread rapidly to form a significant and spreading hotspot centred on parts of Shropshire (Fig. 27) and to a lesser extent in Kent.

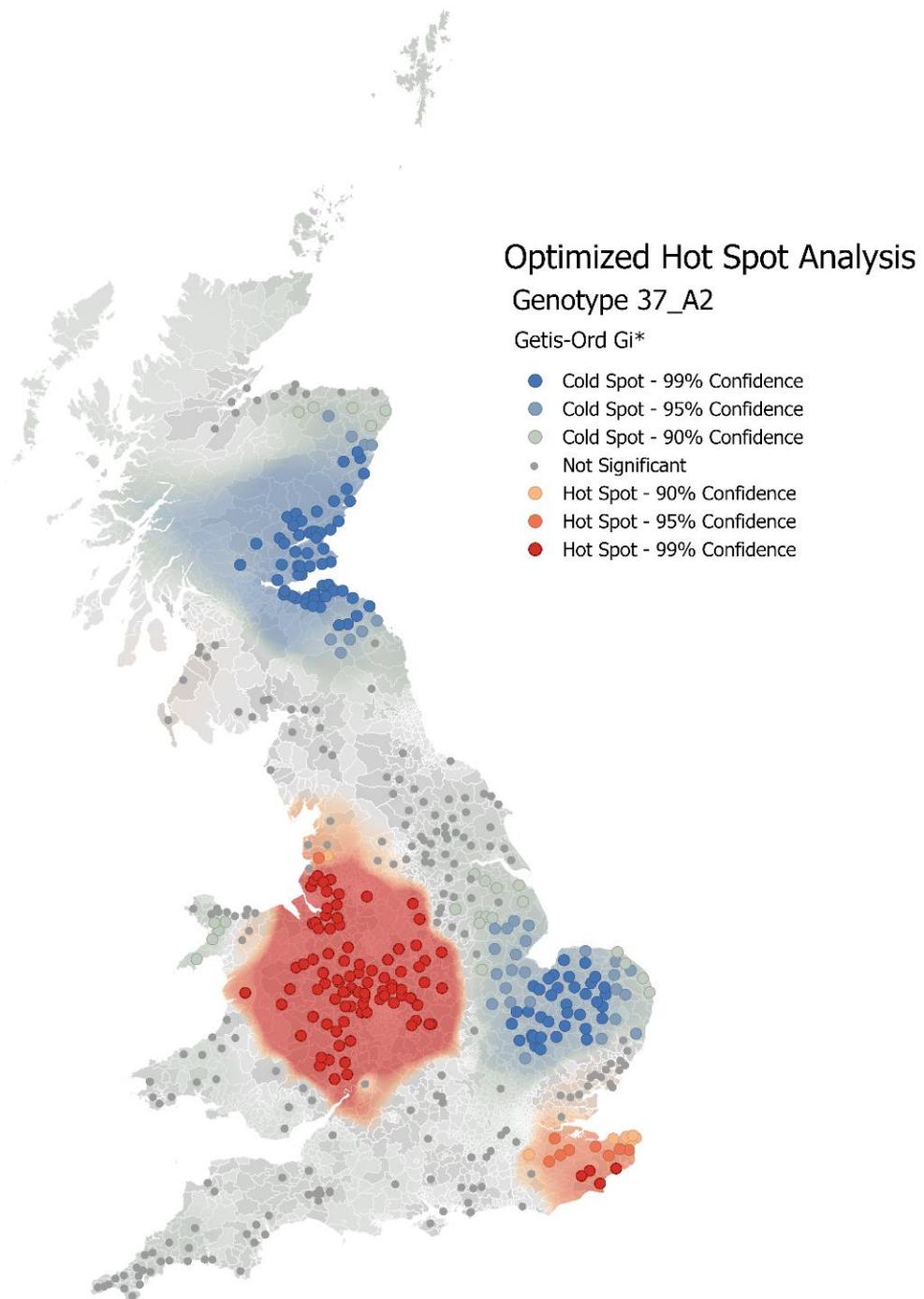


Fig. 27. Statistically significant hot and cold spots derived by OHSA for genotype 37_A2, 2016–2018. Inverse distance weighting was used to interpolate a coloured raster surface from the OHSA points.

These are shown as persistent hot spots in the EHSA (Fig. 28) and probably reflect two distinct introductions. This lineage has subsequently spread to Scotland and Northern Ireland (www.euroblight.net). After widespread reporting of the fluazinam insensitivity of 37_A2 the number of hectares of potato in the UK treated with this product has fallen by over 80% (Garthwaite *et al* 2019). This drop has reduced the selection pressure on the 37_A2 population and the rate of spread and incidence of 37_A2 has subsequently declined to less than 10% of the sampled population in England and has prevented it fully establishing in Scotland (Appendix 2).

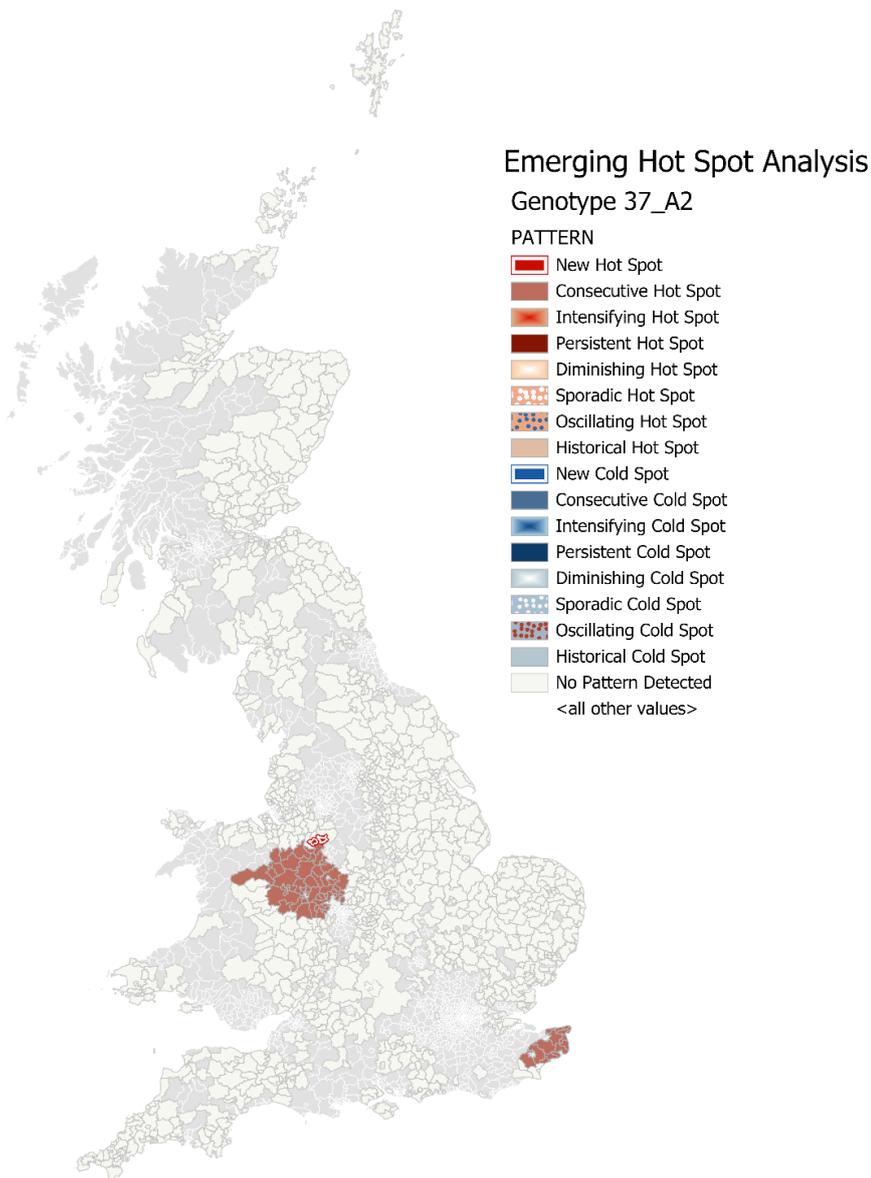


Fig. 28. Space-time patterns of genotype 37_A2 incidence derived by EHSA, 2016–2018. Postcode districts with no reported commercial potato crops are shaded pale grey and were excluded from the analysis.

This is a good example where population monitoring and risk assessment has generated timely new guidance on fluazinam use. Fluazinam producers and the Fungicide Resistance Action Group – UK advice has changed grower behaviour and is protecting this valuable active ingredient for future use. In parts of mainland Europe that are reported to be still relying on fluazinam more heavily, the proportion of 37_A2 remains close to 25% (www.euroblight.net).

Although being first sampled one year later than 37_A2, genotype 36_A2 has formed hot spots in Kent and parts of East Anglia (Figs. 29 & 30) and has spread further in 2019 (Appendix 2). With no reported fungicide insensitivity issues its ability to displace the existing genotypes appears to be related to aggressiveness as it formed larger lesions at low doses of all tested active ingredients to date (Lees et al., 2018).

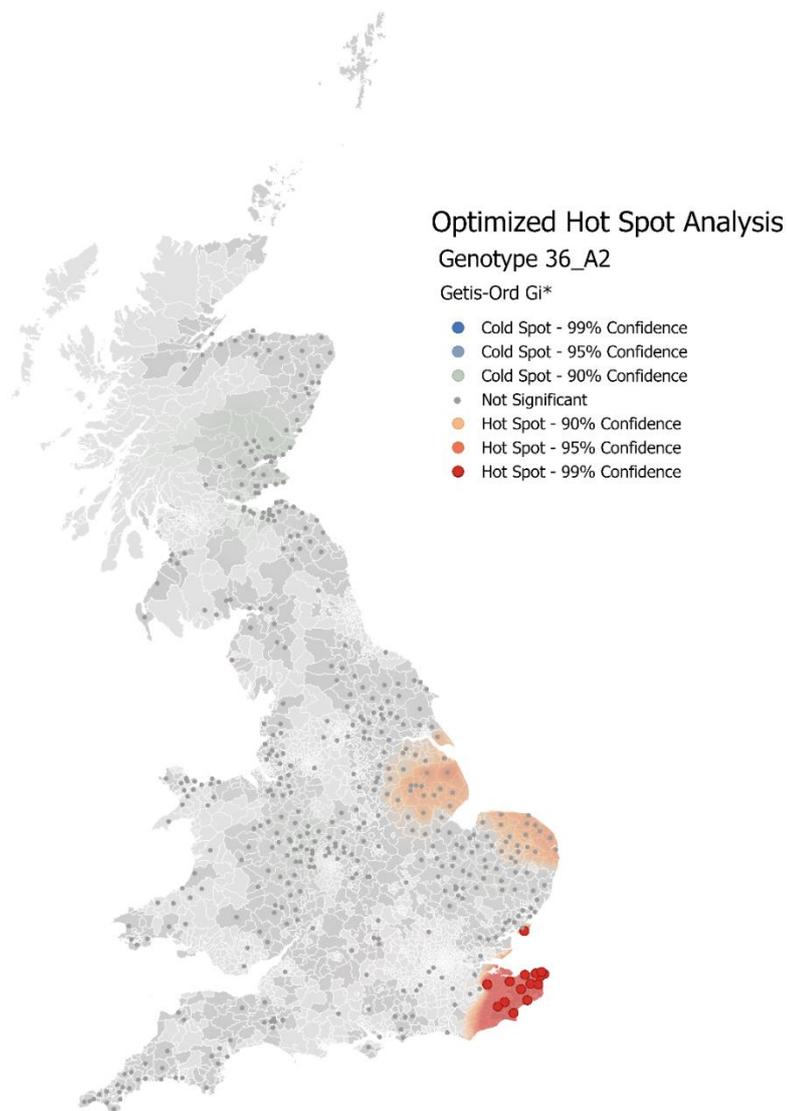


Fig. 29. Statistically significant hot and cold spots derived by OHSa for genotype 36_A2, 2017–2018. Inverse distance weighting was used to interpolate a coloured raster surface from the OHSa points.

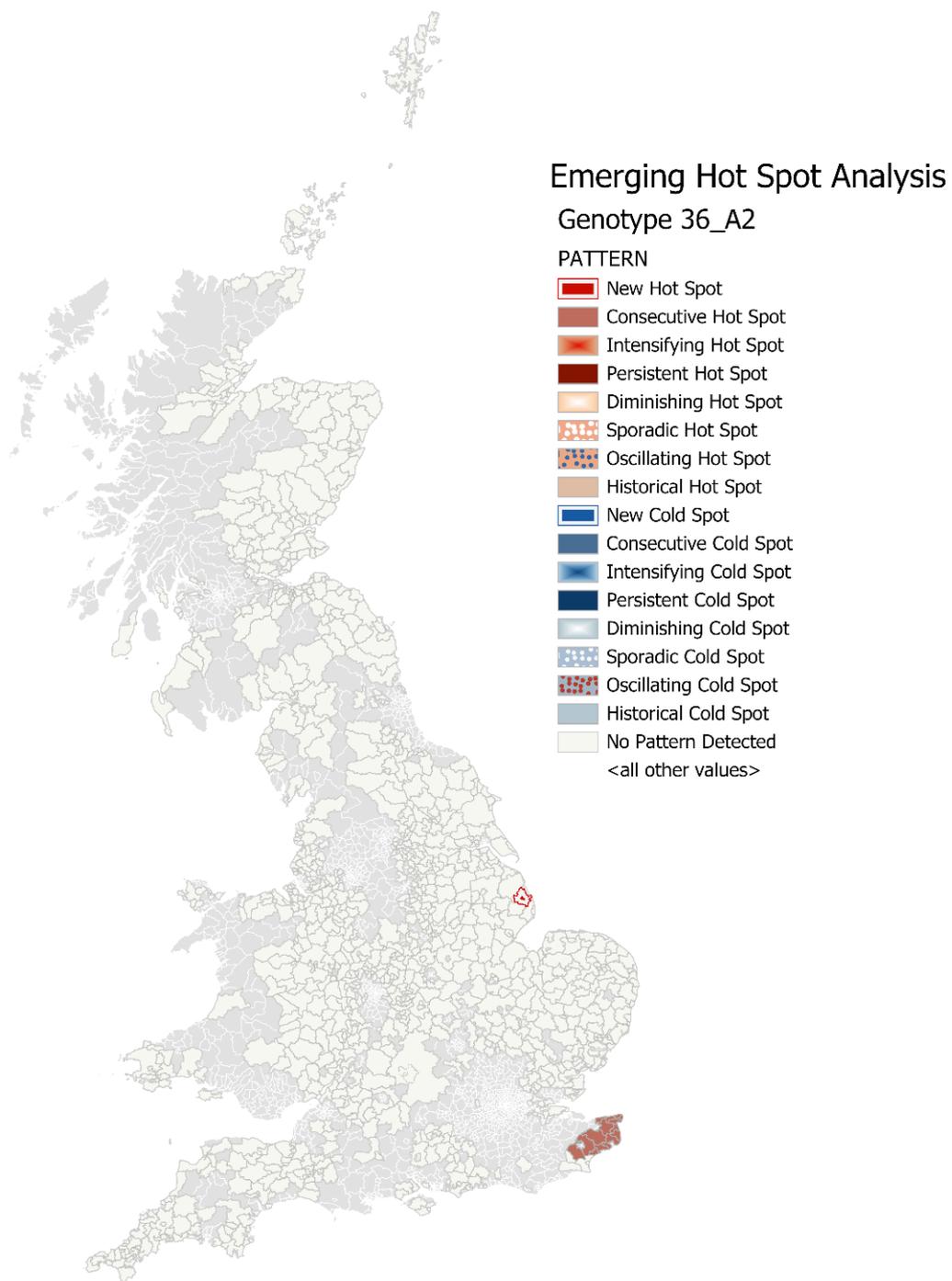


Fig. 30. Space-time patterns of genotype 36_A2 incidence derived by EHSA, 2017–2018. Postcode districts with no reported commercial potato crops are shaded pale grey and were excluded from the analysis.

Machine learning algorithms were used to predict the dominant genotype in each postcode district. The model provided some evidence that precipitation and humidity are the most important predictors, suggesting moisture plays an important role in competition among genotypes (Fig. 31). This analysis was, however, challenging due to fluctuations in the number of outbreaks sampled per year due to between year climatic variation.

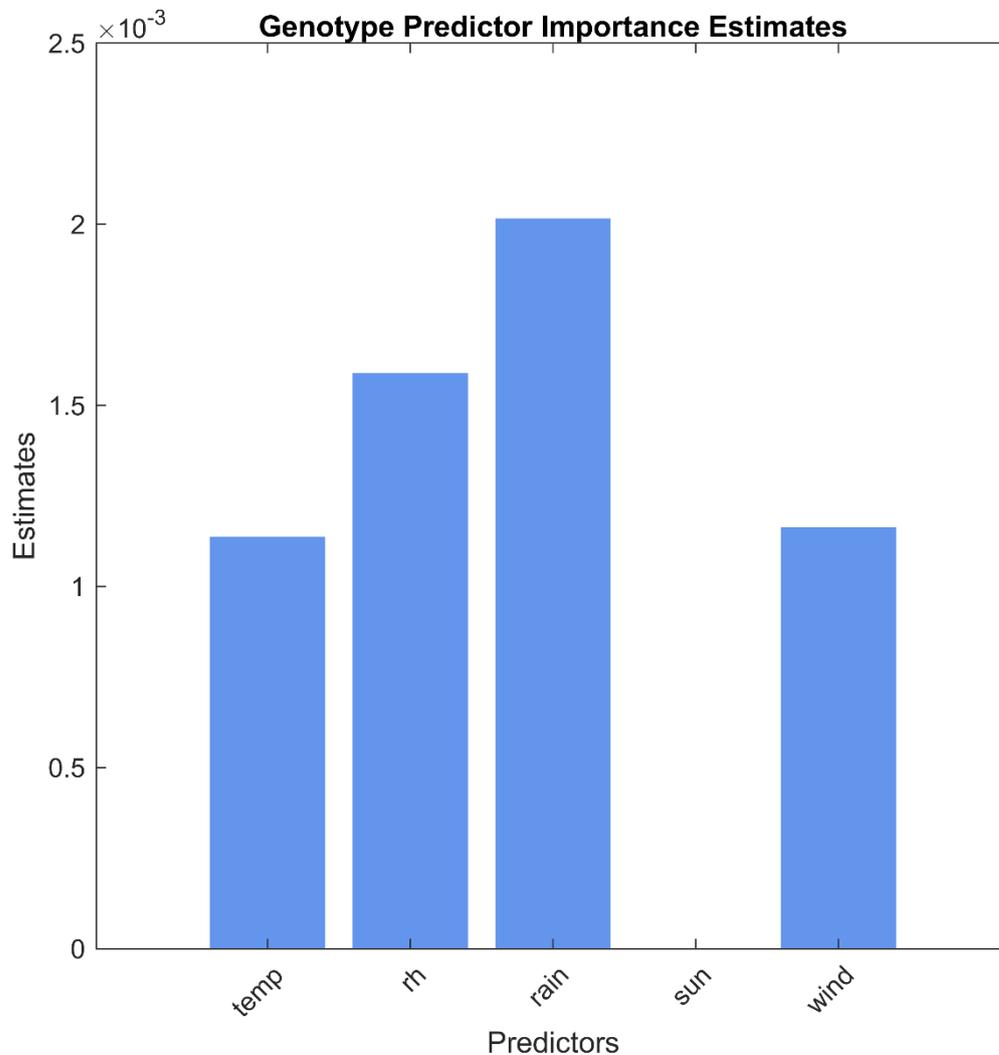


Fig. 31. Importance of climate variables in predicting the dominant late blight genotype in postcode districts.

Finally, a kernel density analysis was used to display the smoothed 13_A2, 6_A1 and 8_A1 genotype distributions each year from 2006–2017 (Figs. 32-35). This supported the hotspot analysis and indicated a clear early spread of the 13_A2 and 6_A1 types over the 2006 and 2007 seasons followed by a patchy distribution in subsequent years. In 2011, a severe epidemic of predominantly 6_A1 late in the season in Scotland resulted in a skewed distribution in subsequent years. Genotype 8_A1 was established almost 10 years before 13_A2 and 6_A1 and its patchy broad distribution

reflects this. A video was also produced to show the changing pattern of genotype distributions each year and is available online with this report or from the authors.

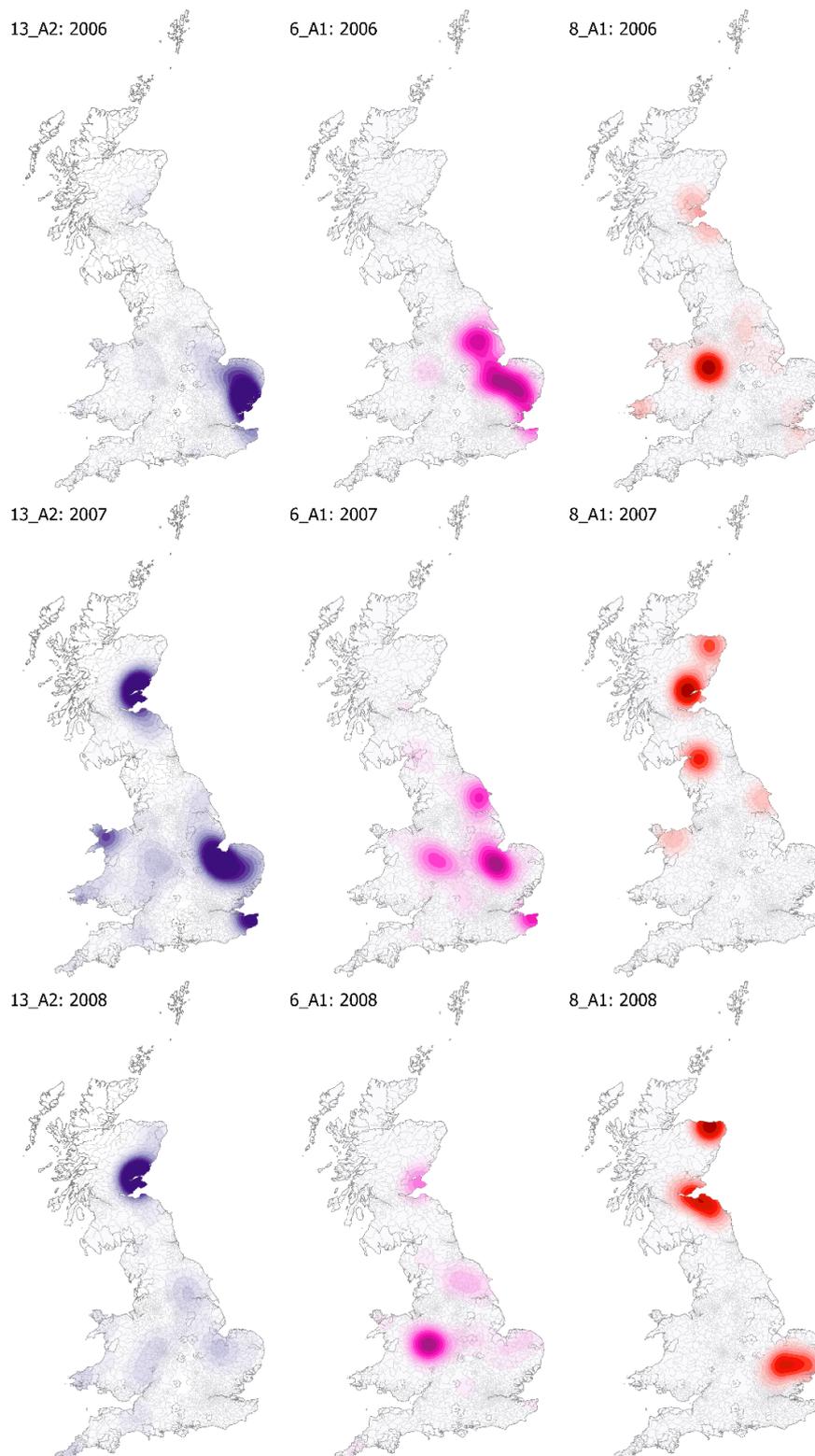


Fig. 32. Kernel density distributions of late blight incidence showing inter-annual variation for genotypes 13_A2, 6_A1, and 8_A1, 2006–2008.

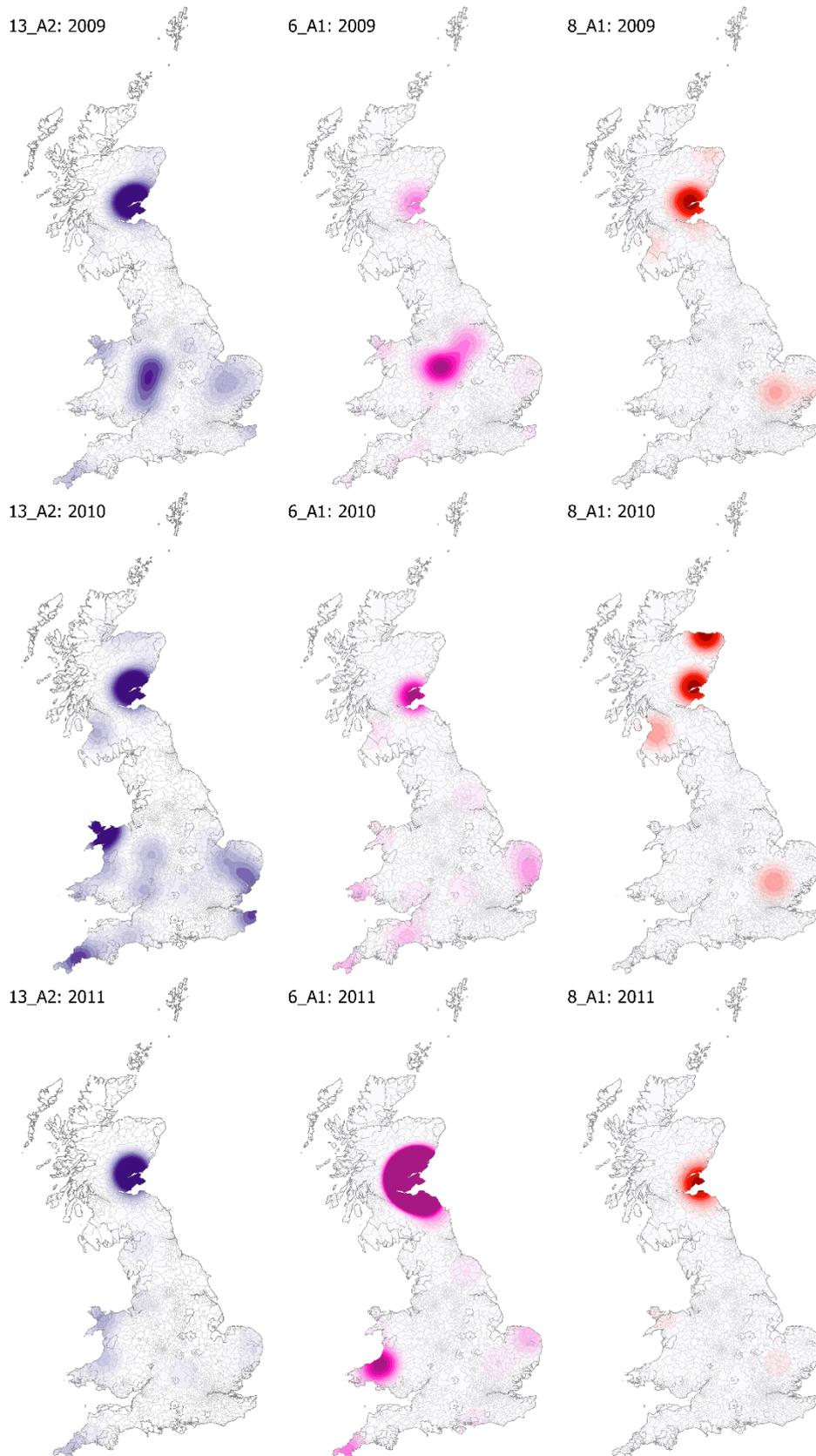


Fig. 33. Kernel density distributions of late blight incidence showing inter-annual variation for genotypes 13_A2, 6_A1, and 8_A1, 2009–2011.

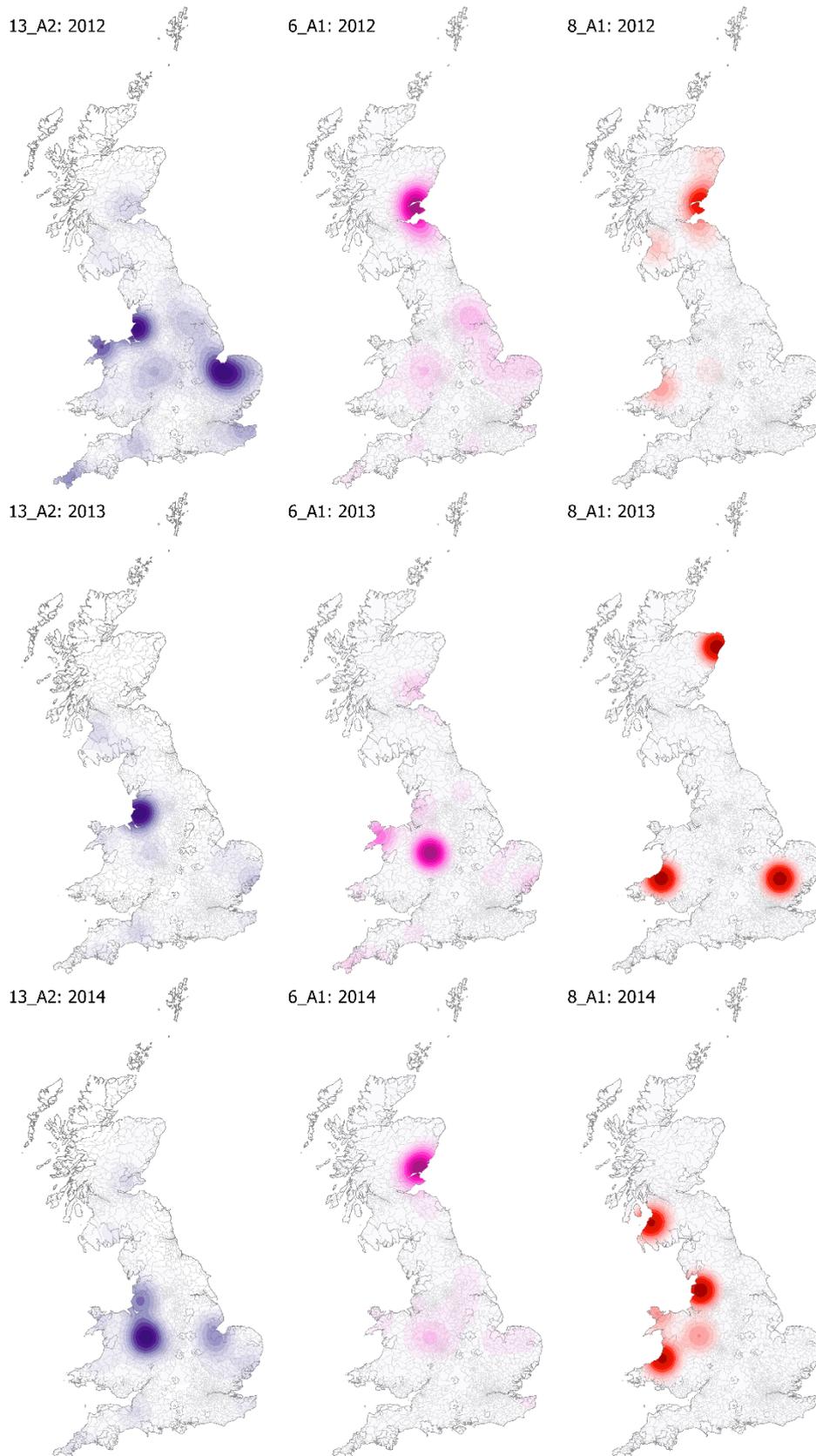


Fig. 34. Kernel density distributions of late blight incidence showing inter-annual variation for genotypes 13_A2, 6_A1, and 8_A1, 2012–2014.

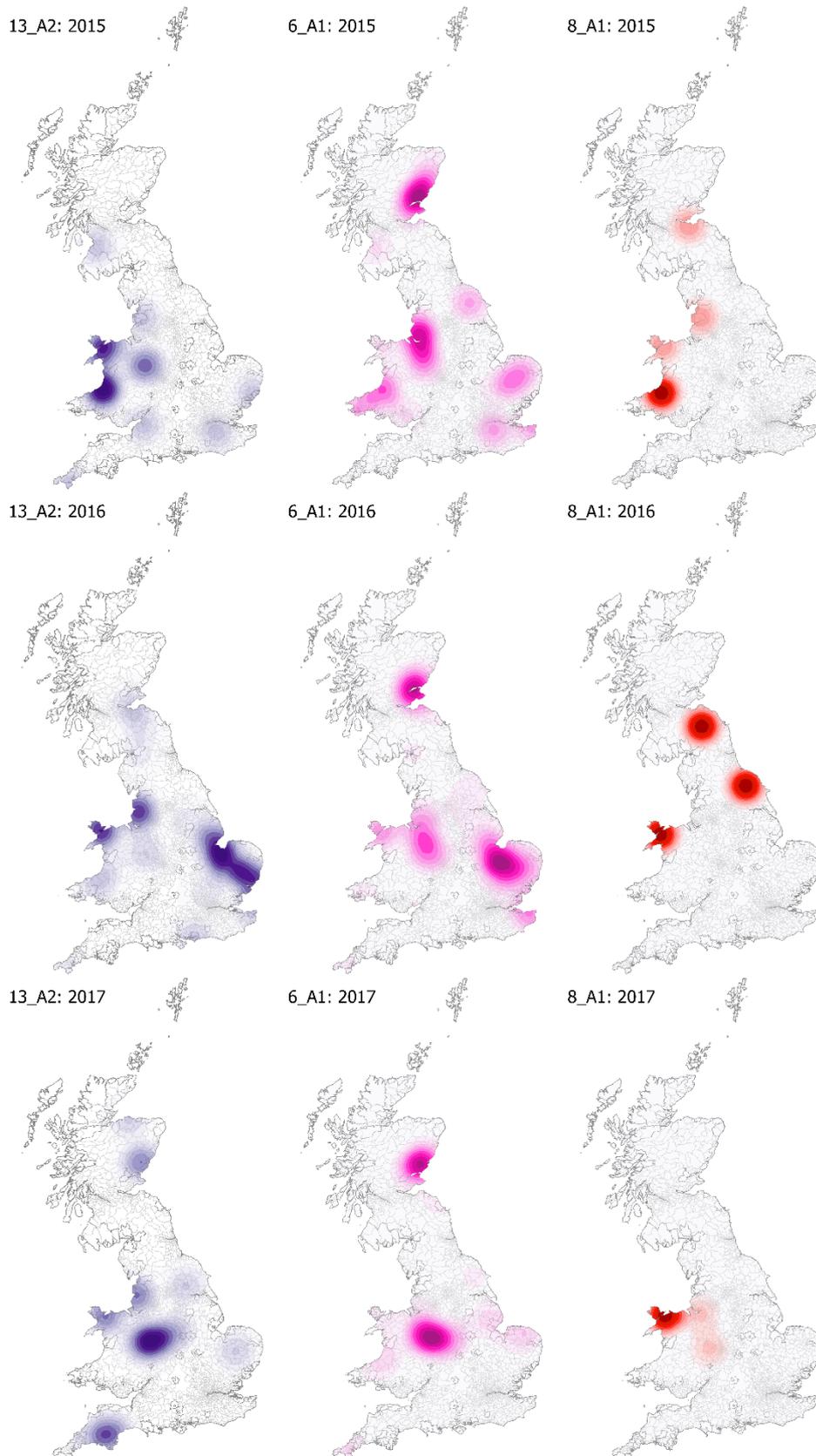


Fig. 35. Kernel density distributions of late blight incidence showing inter-annual variation for genotypes 13_A2, 6_A1, and 8_A1, 2015–2017.

4. Future R&D

Further research is required to identify the principle drivers of change in the spatial distribution of genotypes. This will involve understanding any effects of the environmental variables identified by the modelling work as having an impact on late blight incidence. There is also a need to examine the role of primary inoculum on genotype distributions, i.e. the strength of association between genotype across consecutive growing seasons. There were insufficient data to perform space-time pattern mining or modelling of individual genotypes at a suitably fine temporal resolution. There is a need, therefore, to increase the number of outbreaks sampled each year under the AHDB Potatoes FAB campaign. This is important if we are to develop new tools to predict changes in the distribution of aggressive lineages in order to adapt short-term control strategies in a more timely fashion.

Appendix 1 - Visual aids

We have derived a series of visual aids from this work, and these are presented below arranged by project deliverable.

1. When and where do early outbreaks of late blight occur in different parts of GB?

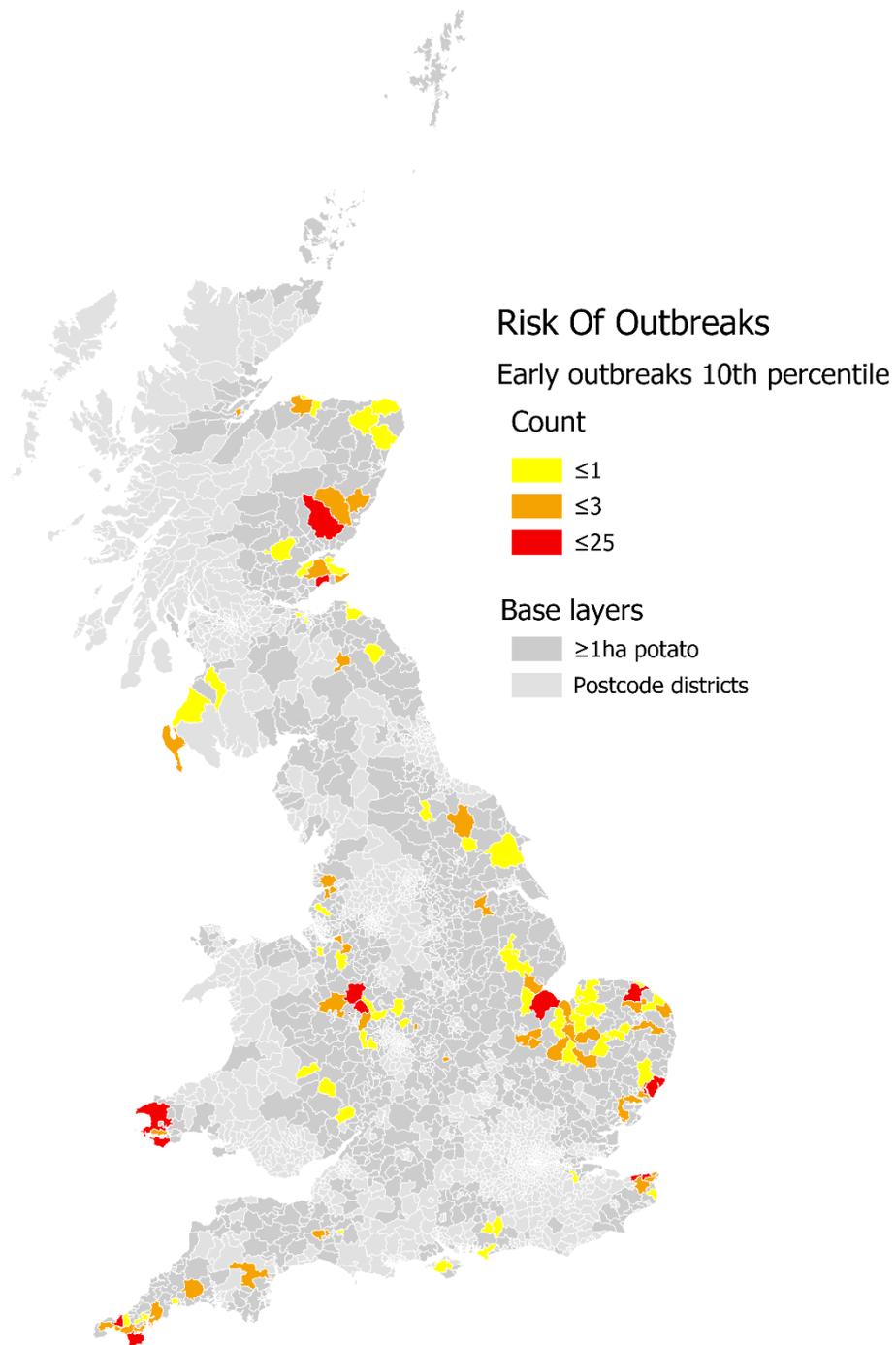


Figure A1. Choropleth map showing a count of the 10th percentile by date of outbreaks within postcode districts containing >1ha potato (grown commercially), 2003-2018.

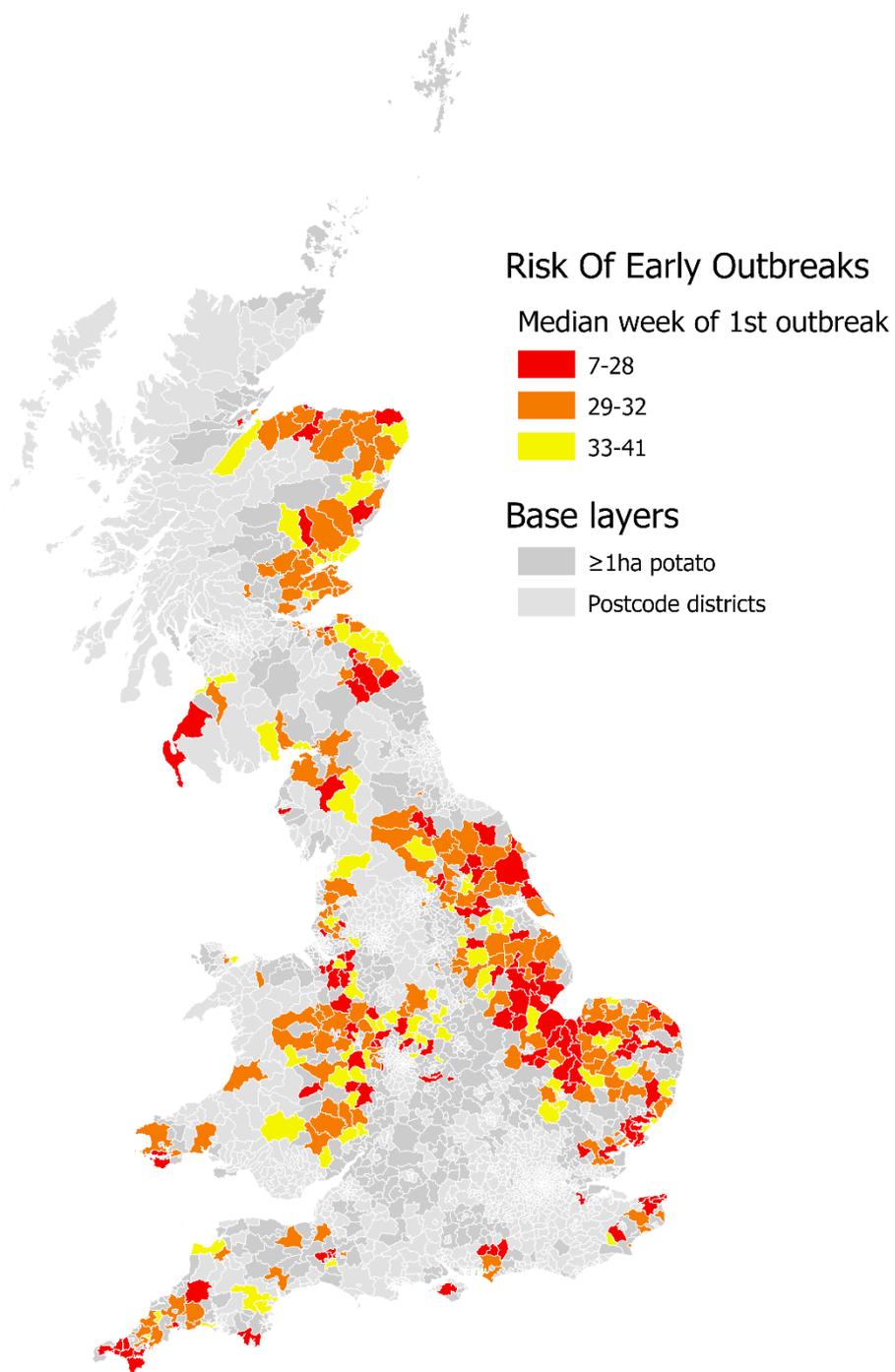


Figure A2. Choropleth map showing the median week of the year for the first late blight outbreaks within postcode districts containing >1ha potato (grown commercially), 2003–2018.

2. What is the risk of spatial spread of late blight in different parts of GB?

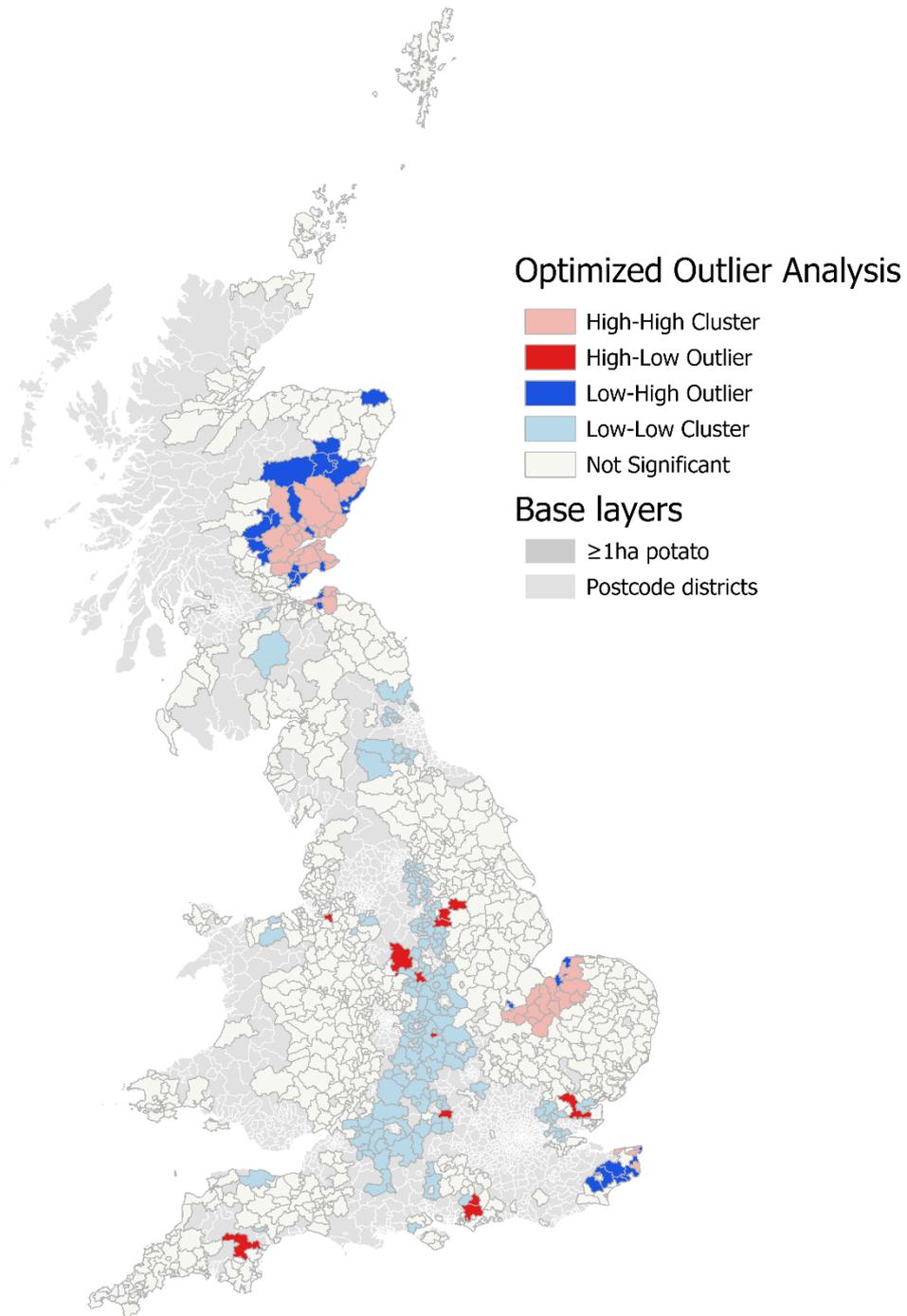


Figure A3. Risk of spread of late blight among postcode districts. Crops in High-High clusters or Low-High outliers are at risk of spread of disease from neighbouring (High) sectors.

3. What is the historical risk of late blight across different parts of GB?

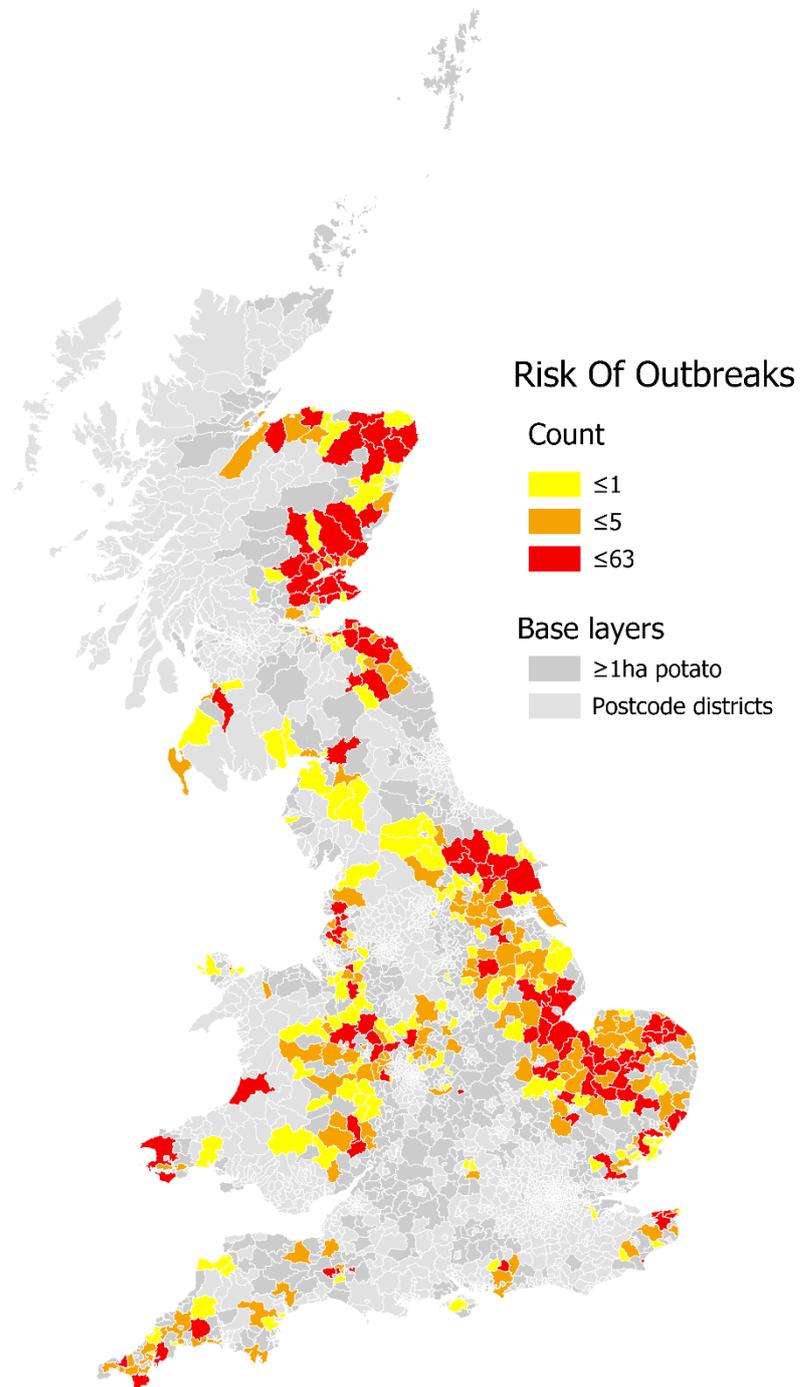


Figure A4. Choropleth map showing a count of all outbreaks within postcode districts containing >1ha potato (grown commercially), 2003-2018.

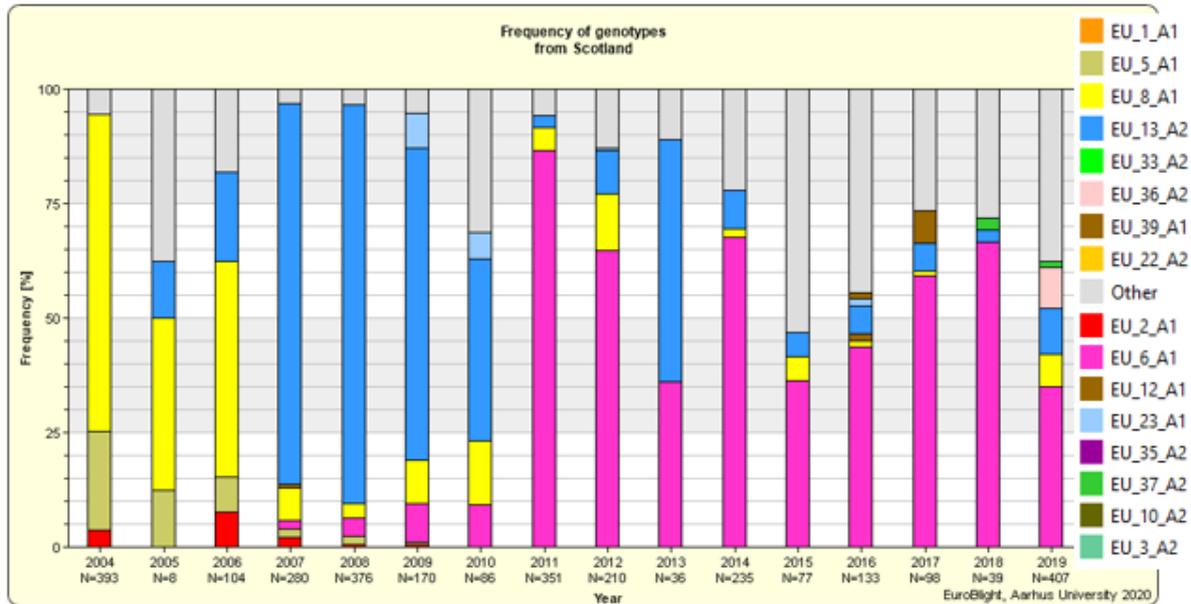
4. How has the genetic makeup and spatial distribution of the late blight pathogen changed over time, and what is driving this change?

In our analysis, we used Emerging Hot spot Analysis and KDE to explore this question. The figures given above show clear changes of genotypes in time and space but do not point to clear and obvious drivers based on the traits in the database. Climatic fluctuations from season to season impact the blight pressure and sampling intensity. The reduced population size and fewer samples over the 4 drier low blight pressure coupled with local high blight pressure in other seasons complicates such long-term analysis. It is easier to identify long-term presence of genotypes than it is to identify changes in distribution over the last 15 years. Eastern Scotland, Wales, the Midlands and Anglia all stand out as persistent areas in this. A visual analysis comparing the EHSA between 13_A2 and 6_A1 does show some spatial variation, but not enough to draw conclusions from. The Bagged Tree model developed to predict the dominant genotype in each postcode district did provide evidence that moisture plays a key role in driving pathogen population change, but the model was not accurate enough to draw any definitive conclusions. A video has been produced from the KDE maps (Figs. 32-35) that animates the changing spatial distribution of pathogen genotypes over time.

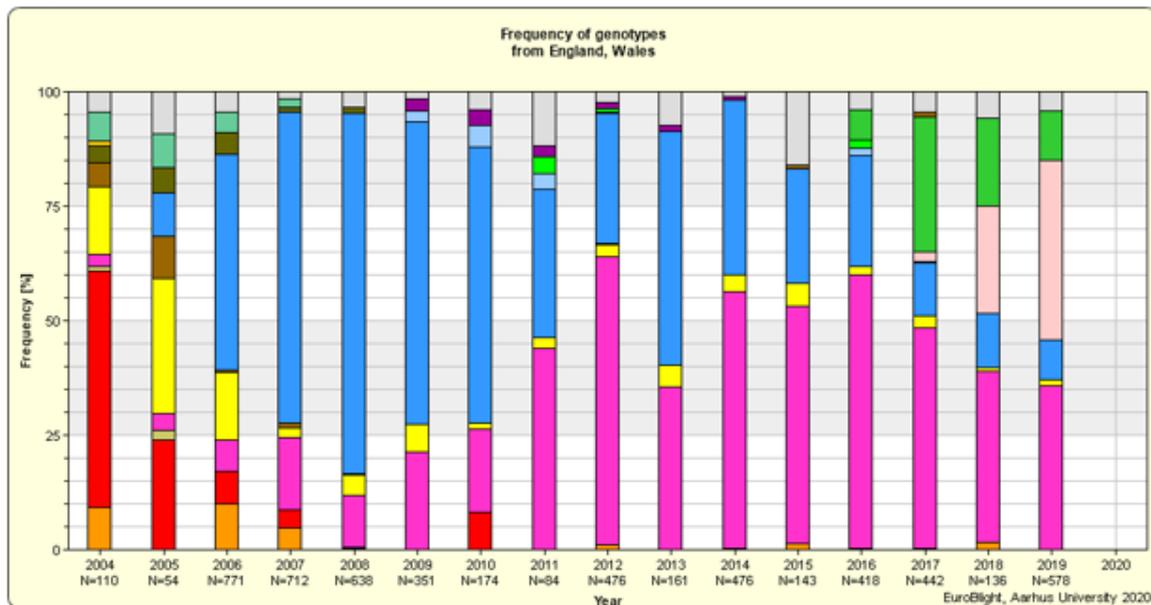
Appendix 2

Proportion of different clonal genotypes of *P. infestans* collected from sampled FAB late blight outbreaks in a) Scotland and b) England and Wales from 2004-2019. Images generated from AHDB data submitted to EuroBlight database and reported via visualisation tool <https://agro.au.dk/forskning/internationale-platforme/euroblight/>

a)

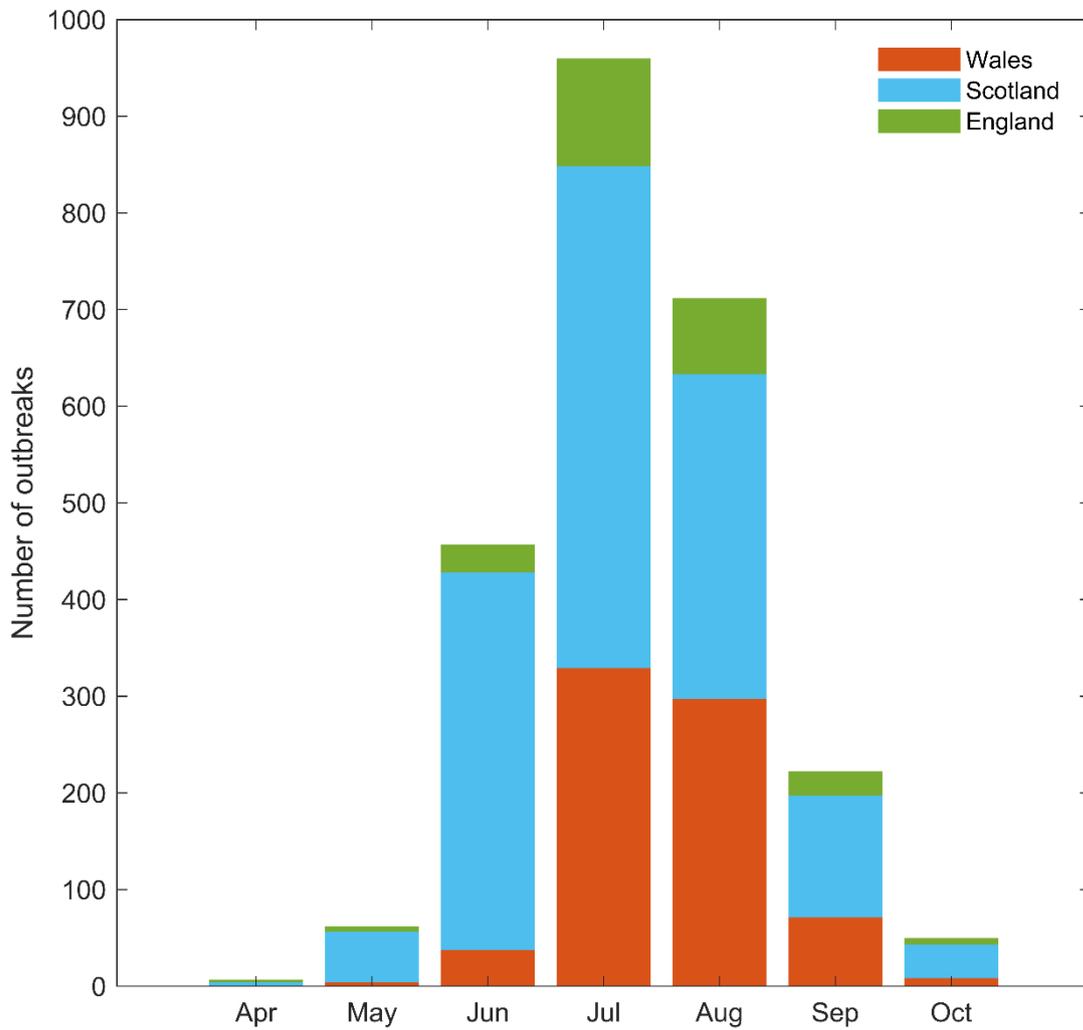


b)



Appendix 3

Cumulative monthly totals of blight outbreaks sampled across England, Scotland and Wales of the period 2003-2018.



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