# Spread model of bacterial canker of kiwifruit in Europe

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Modelling in Plant Health,
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*Pseudomonas syringae* pv. *actinidiae*


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# Psa

- Hosts: *Actinidia* species: *A. deliciosa*, *A. chinensis*, *A. arguta*, *A. kolomikta*
- Damage: discolouration of buds, leaf spots, exudating canker on twigs and trunks, fruit collapse, wilting, sometimes plant death
- First description and economic losses in the 1980s in Japan, Korea → most serious limiting factor for kiwifruit cultivation
- Present in the EU since 1992 (sporadic, low incidence)
- First economic losses occured 2007/2008 in Central Italy
- Genetic characterization: highly aggressive *Psa* **biovar 3** → rapid spread into kiwifruit growing countries in Europe

Picture: Plant Protection Service of Emilia-Romagna (IT), Source: www.eppo.int

# Generic spread models (Robinet *et al.* 2012)

- developed in former EU project PRATIQUE; running in R

A. Logistic Growth model: number of invaded grid cells over time
B. Radial range expansion model: radial spread
C. Simple Logistic Growth model: spread within cells

**D. Dispersal kernel model (dspk)**: local population growth and dispersal parameter determine spread over time

- considers population density in space and time
- Dispersal modelling on large scale spread
- reflect smaller or larger dispersal distances (natural spread)
- reflect frequency of long-distance dispersal (trade or other human assistance)
- **approved for insect pests → applicable for Bacteria?**

DROPSA

# Dispersal kernel model (dspk)

Input-files

- presencefile: hypothetical introduction point(s)
  → Entry point in Italy Lazio region
- habitat file with the occurence of host plant or suitable soil: not used
- CLIMEX output for climatic suitability
  - EI=Ecoclimatic Index
  - GI=Growth Index

# CLIMEX

-CLIMEX 3 (Sutherst *et al.* 2007)
-Template: Mediterranean
- main parameter from Narouei Khandan *et al.* (2013) for the prediction of global distribution (fitted that the majority of known occurences resulted in suitable and very suitable cells)
- Modifications:
a) lower optimum temperature DV1=15°C: severity of the disease decreases gradually below this temperature (Young 2012)
b) upper temperature treshhold DV3=25°C: inhibition of bacterial growth by wound healing tissue (Young 2012)
c) Cold stress parameter (climatic prediction for Europe by EPPO 2012) TTCSA=2; THCSA=0.01

-CLIMEX run with and without irrigation scenario; irrigation from March to September 5.6mm/day total water amount including rainfall

# Parameter setting (dspk)

- Carrying capacity **K** (maximum number of individuals in a cell):
  unknown number of bacterial cells per host
  → number of hosts per grid cell = number of potential infestations = K

K= 0.0807 * 620 hosts/ha *100ha * 1579km$^2$ = 7900369 hosts/grid cell

# Parameter setting (dspk)

- Carrying capacity **K**:
  unknown number of bacterial cells per host
  → number of hosts per grid cell = number of potential infestations = K

0.0807 % of Italian state territory harvested 2012; highest density of hosts in Europe

Transformation from ha to $km^2$

K= 0.0807 * 620 hosts/ha *100ha * 1579$km^2$ = 7900369 hosts/grid cell

500 plants/ha in pergola systems, 740 plants/ha in T-bar orchards: mean = 620 plants/ha

Area of one grid cell

# Parameter setting (dspk)

- Initial population $\mathbf{N_0}$ = 100 * $P_0$ /K
  $P_0$ = 1 → one introduced infected host sufficient for population growth and spread (at t=0); $N_0 = 1.27*10^{-5}$

- Scale parameter **u**: natural spread distance via wind, rain and vectors
  5km/year; u=5

- Multiplication factor $\boldsymbol{\lambda_{max}}$: maximum year to year multiplication of the population under optimal conditions; not limited by the reproduction ability
  → number of potentially host infections within a year
  $\lambda_{max}$ = number of available hosts within a radius of 5km * 0.8 (maximal infection rate 80% in European fields)
  = 314374 infested hosts/year

# Parameter setting (dspk)

- Shape parameter **p**:

  A Small p-value indicates a high frequency of occasional long-distance spread events (trade), over much longer distances than by natural spread mechanisms

  -Long distance between kiwifruit growing regions in Europe

  -Human assisted spread via infected plant material (grafting material, nursery plants and pollen)

→ minor regional spread, high frequency of long-distance dispersal; p = 5

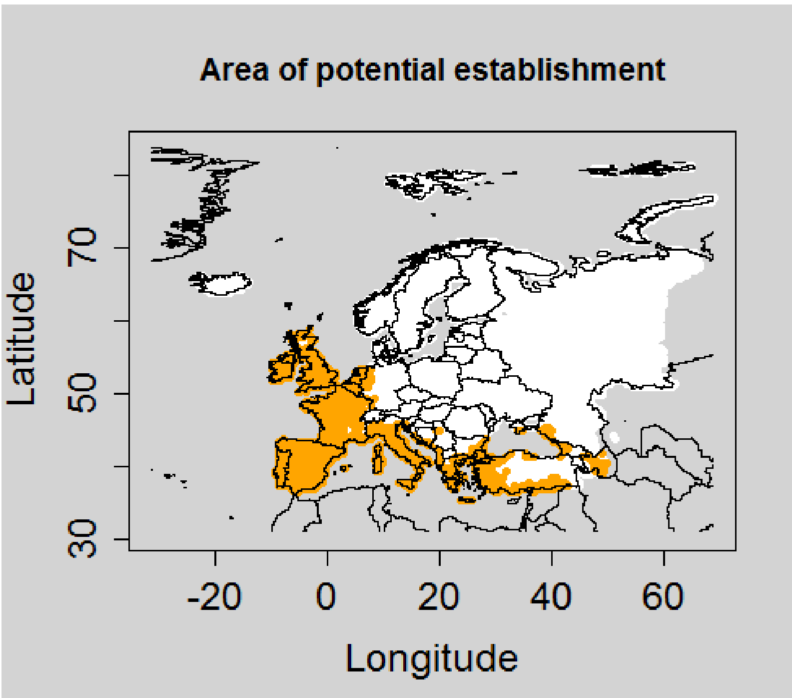
- Time period t: number of years after entry

  $t_0$ = 2007

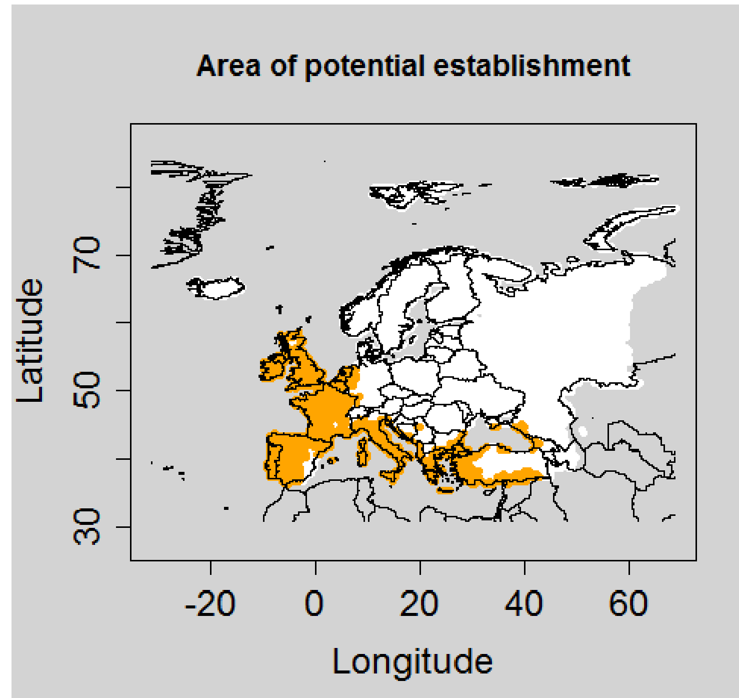
  $t_9$ = 2016

  $t_{13}$ = 2020

# Results: Climatic suitability



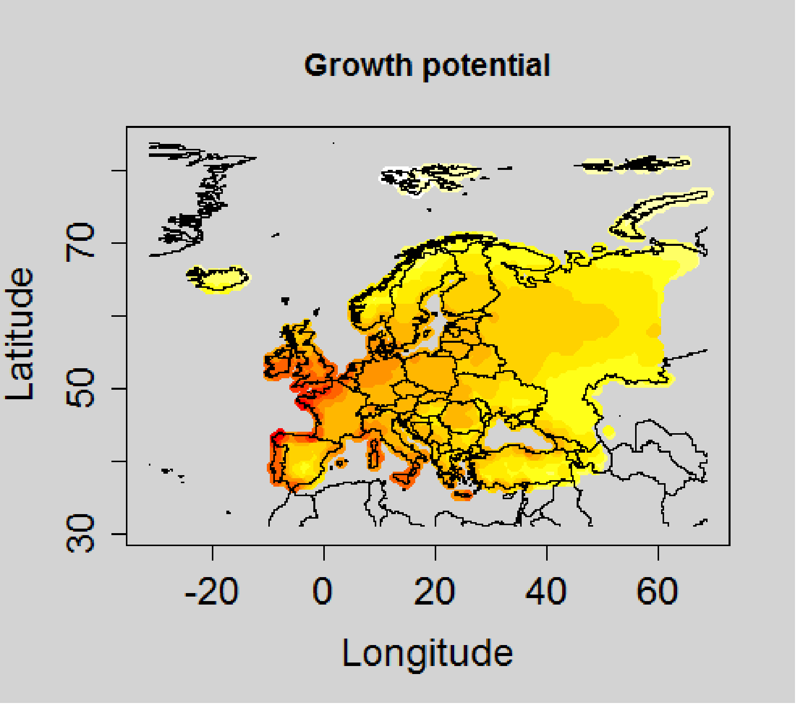

irrigated



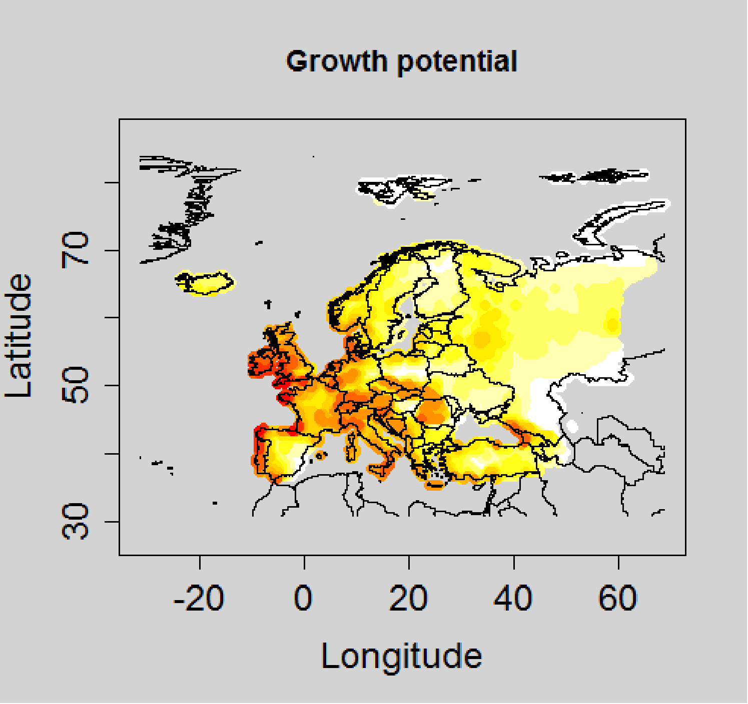

not irrigated

Area of potential establishment (orange: EI>0, white: EI=0) of Psa in Europe

# Results: Climatic suitability



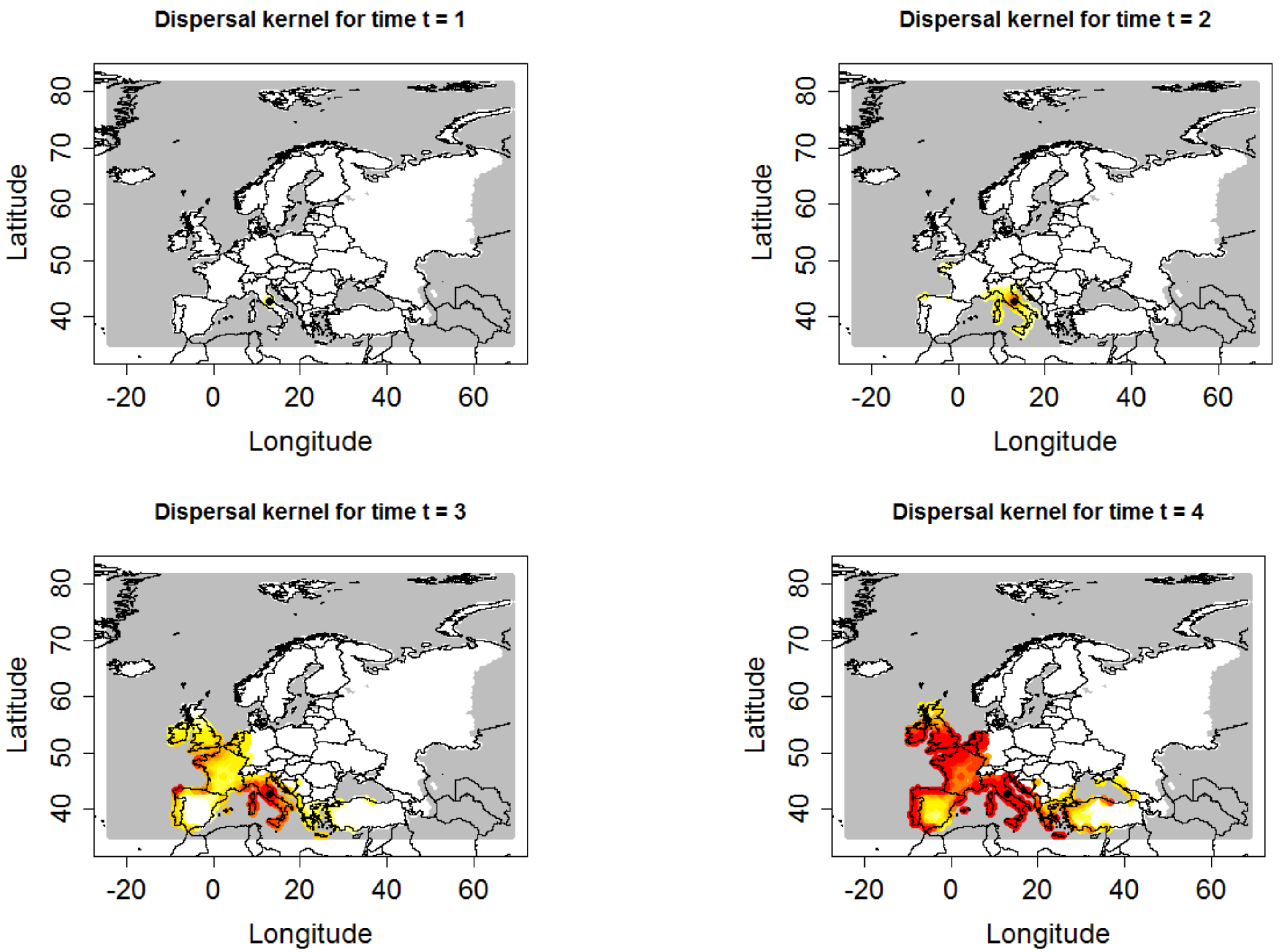

irrigated



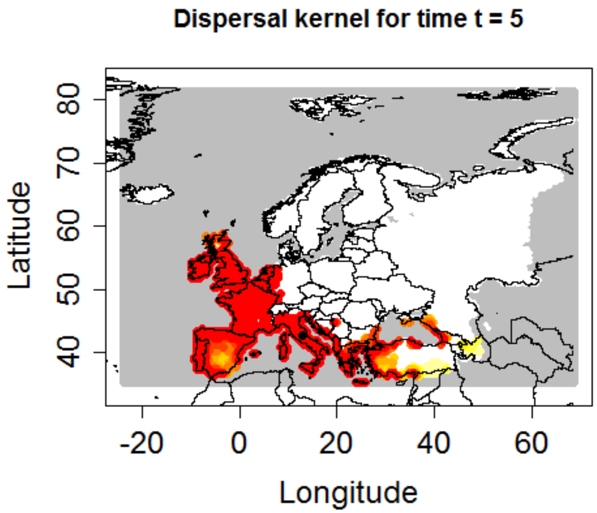

not irrigated

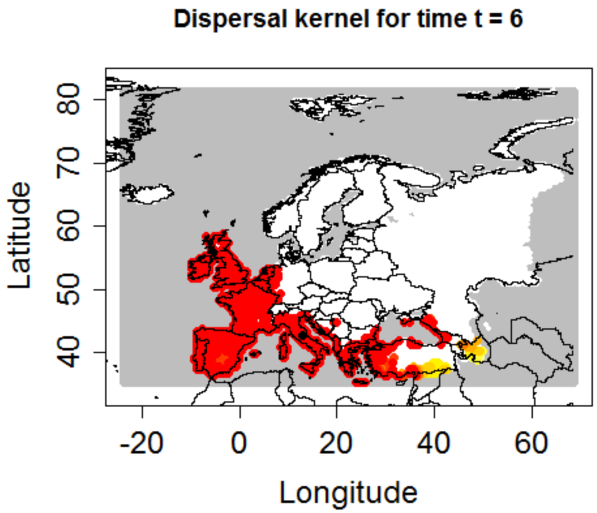
Growth index (right, graduated colors from white [GI=0] to red [GI=100]) of *Psa* in Europe

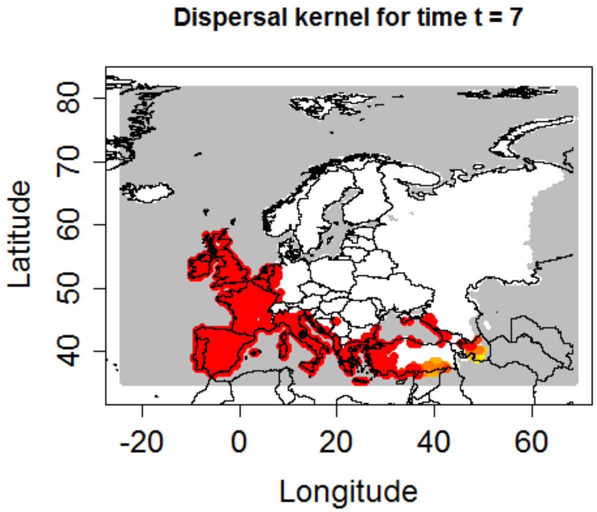
# Results: Spread model

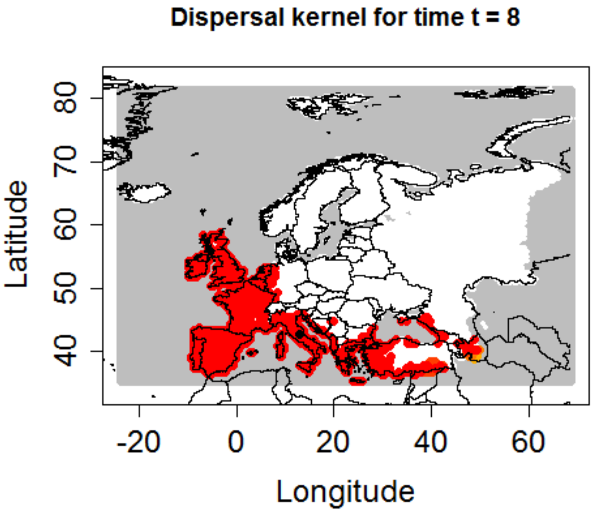


# Results: Spread model

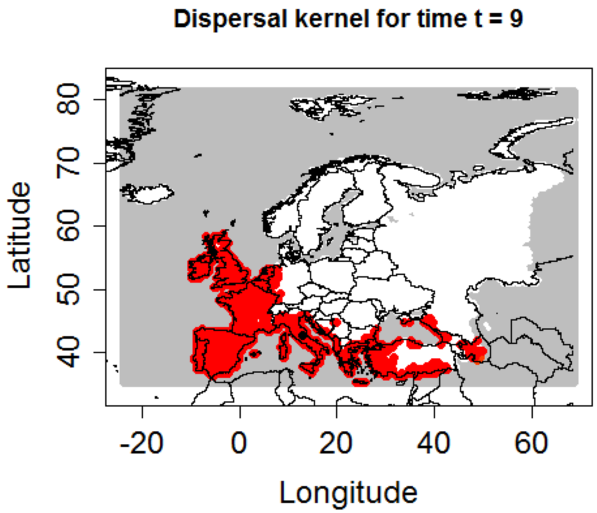


# Results: Spread model




• Spread within 4 years over the whole area of potential establishment

• Saturation (every available vulnerable host infected) of the system 2016 without control and eradication measures

# Conclusion

- Real Spread history

  *Psa* spread within 7 years into all kiwi-growing countries except Bulgaria, despite control and eradication measures.

- rapid saturation of the model reflects high climatic suitability and therefore high damaging potential

# Conclusion

The Dispersal kernel model seems to provide a suitable tool for modelling bacterial spread, if there are sufficient data are available on…

- Pest Biology (in vivo),
- Host Abundance, Management practices (irrigation, annual vs. perennial systems)
- Natural distribution and/ or origin of the bacterium combined with a defined identity (pathovar, strain, species, haplotype)
- Incidence / occurrence in the fields
- Spread mechanisms and natural spread distance.

# Uncertainties and Limitations

But:

- CLIMEX runs with a climate data set from 1961-1990, the last 25 years deviate to some extent noticeable from those `average`years → possibly severe infestations in `non-suitable`areas for establishment

- There is no satisfactory way to include RH (only soil moisture) in CLIMEX, a crucial parameter for many bacteria

- Bacterial characteristics (exponential reproduction, high number of individuals per host) limit the ability to rate population density, carrying capacity and initial population

- distribution data for bacterial pests usually insufficient to deduce stress indices and optimal climatic conditions

# Thank you!

# Annex: CLIMEX Parameter settings

-Template: Mediterranean
-Moisture index: SM0=0.5, SM1=0.8, SM2=2, SM3=3
-Temperature index: DV0=5, DV1=15, DV2=20, DV3=25
-Light index and Diapause index: not used
-Cold stress: *TTCSA=2, *THCSA=0.01
-Heat stress: TTHS=30, THHS=0.0005, DTHS=0, DHHS=0
-Dry stress: SMDS=0.2, HDS=-0.005
-Wet stress: SMWS=3, HWS=0.001
-Cold-dry stress, Cold-wet stress, Hot-dry stress, Hot-wet stress: not used
-Day-degree accumulation above DV0: DV0=5, DV3= 25, MTS= 7
-Day-degree accumulation above DVCS: DVCS=5, *DV4=100, MTS=7
-Day-degree accumulation above DVHS: DVHS=25, *DV4=100, MTS=7
-Degree-days per generation (low optional value, not a limiting factor for *Psa*): PDD=100

# Annex: Literature

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