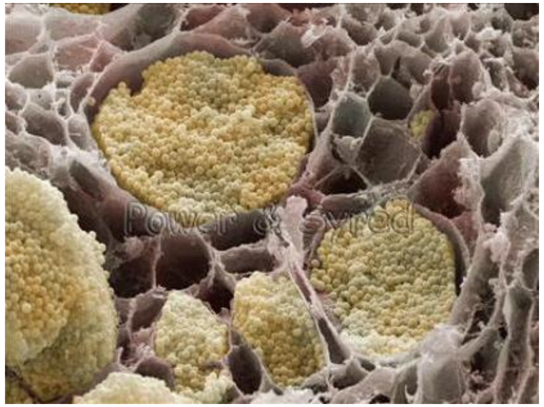
Bundesministerium
für Ernährung
und Landwirtschaft

GFPi

Freie Universität Berlin

Clubroot situation in Germany

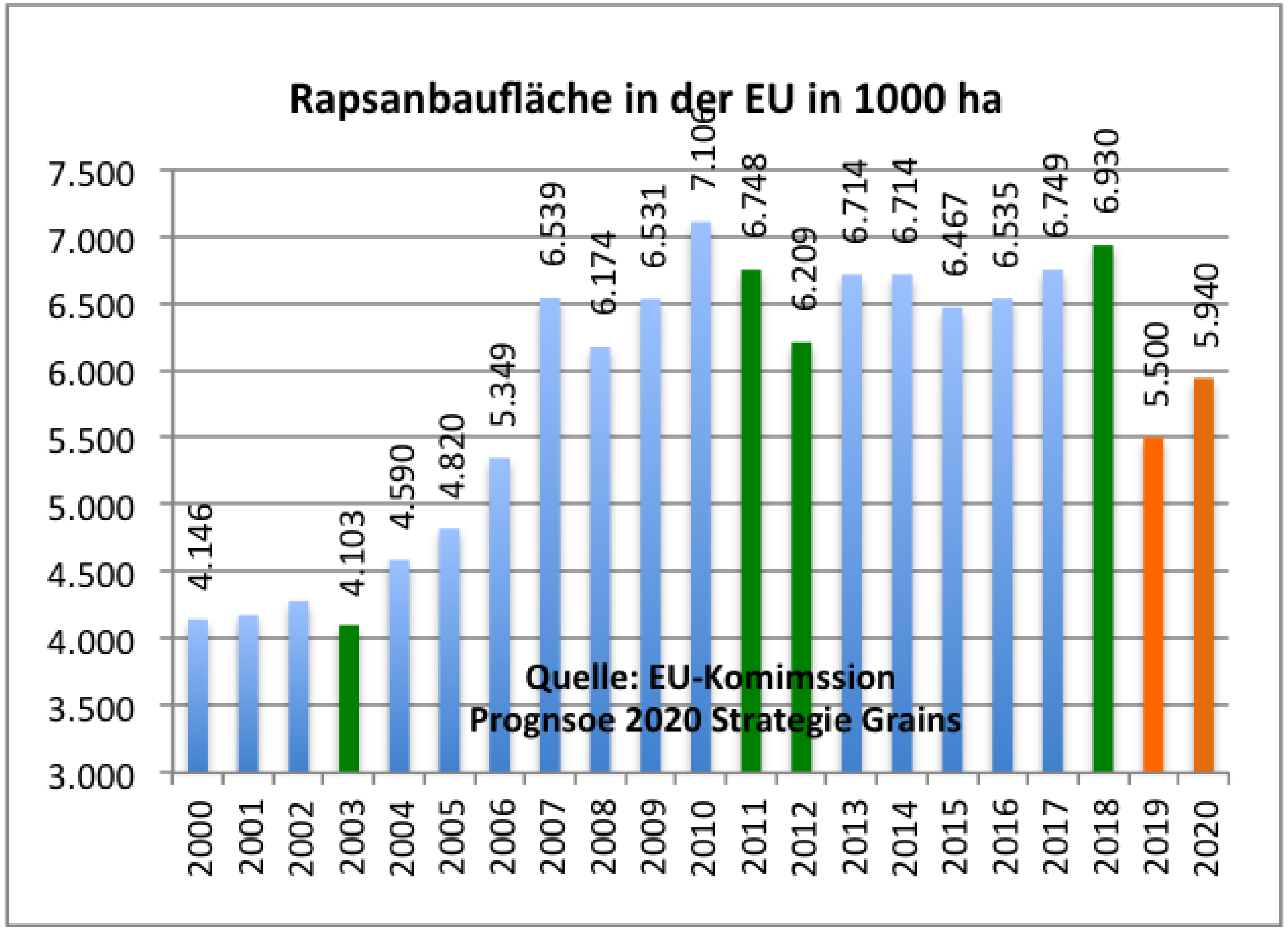


Clubroot Steering Committee Video Meeting

2020, Apr 30th

Elke Diederichsen

Acreage of oilseed rape in the EU



Quelle: EU-Komimssion
Prognsoe 2020 Strategie Grains

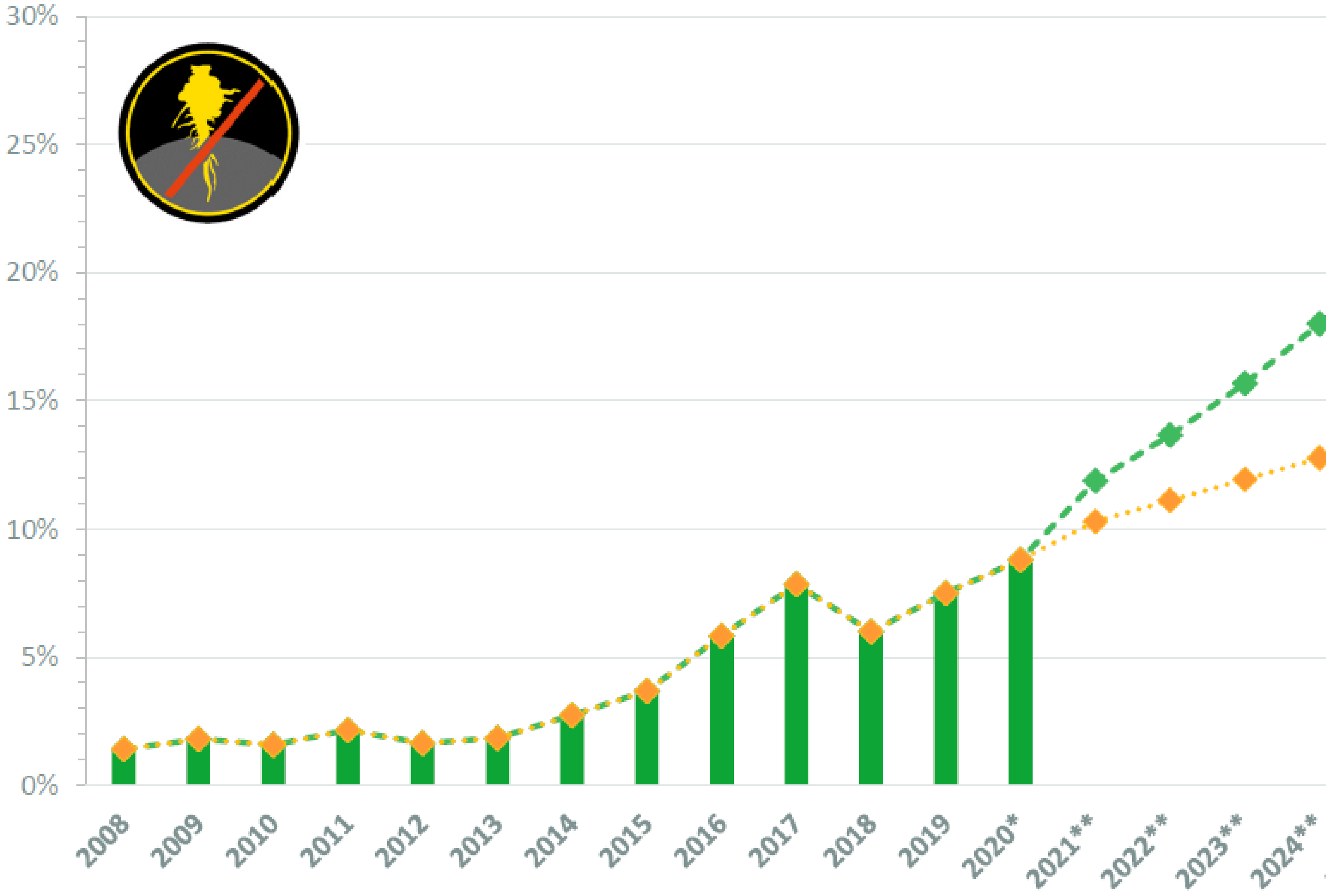
Acreage of winter oilseed rape in **Germany** (2019/2020):

Ca. 900 000 ha, less than before

Decline due to ban of neonictinoids and drought

8 – 10% of oilseed rape crops are infested with clubroot, major cropping areas have a higher proportion

Relative proportion of clubroot infested area and future projections

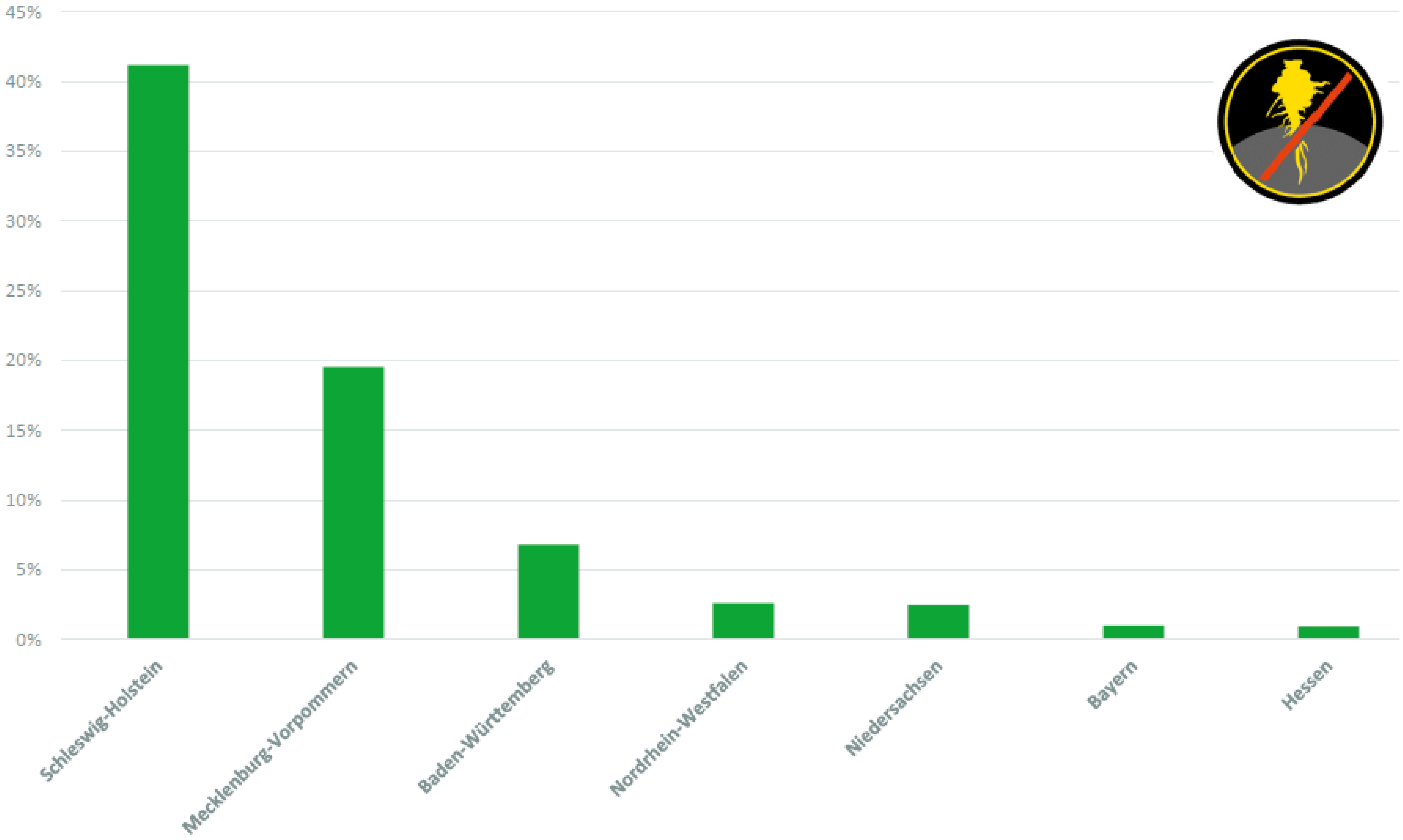


Estimation from Rapool, NPZ and data from Kleffmann group

Future expectations based on exponential (green) or linear (orange) increase

Drought in 2018 and 2019 reduced clubroot incidences slightly

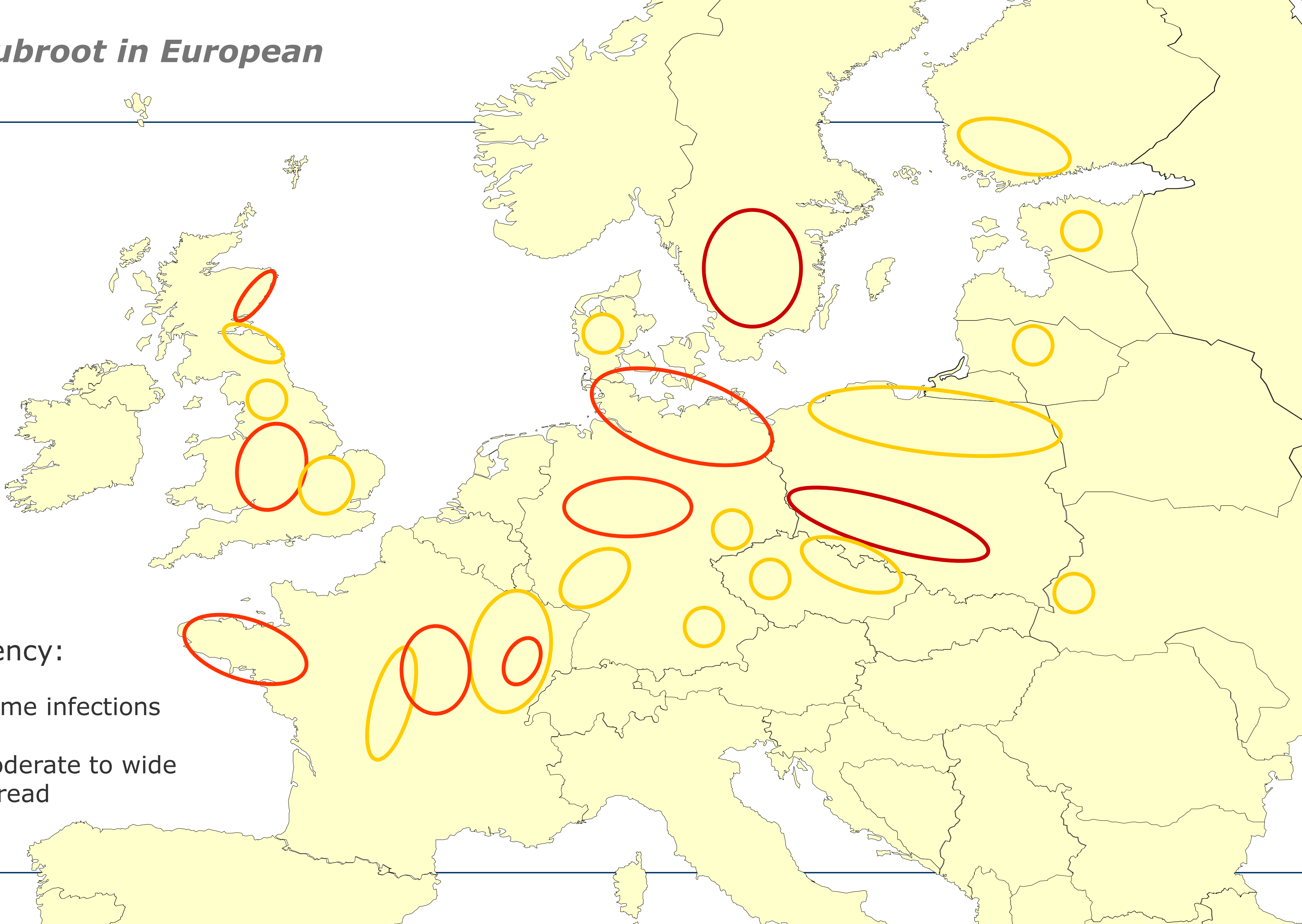
Market share of CR cultivars in different federal states of Germany



Estimation from Rapool, NPZ and data from Kleffmann group

(at harvest 2019)

Presence of Clubroot in European Oilseed Rape



Frequency:

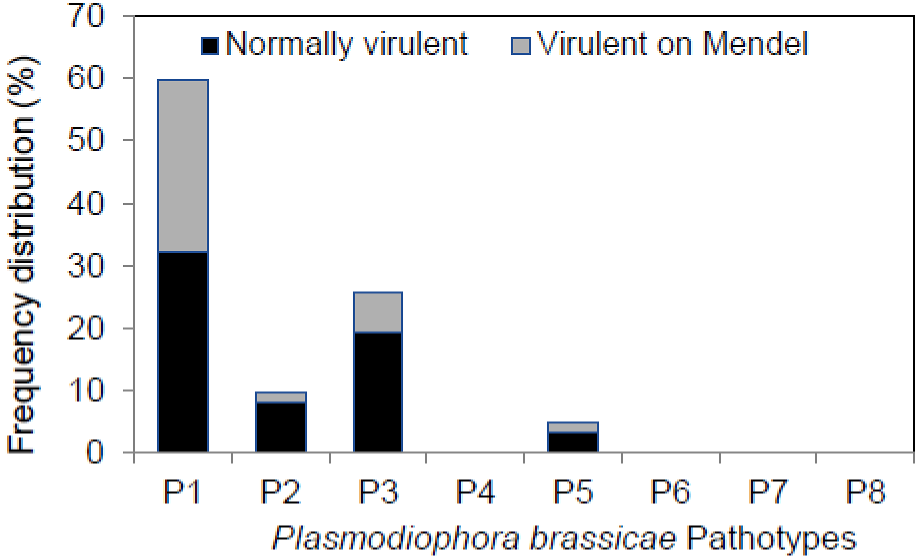
○ Some infections

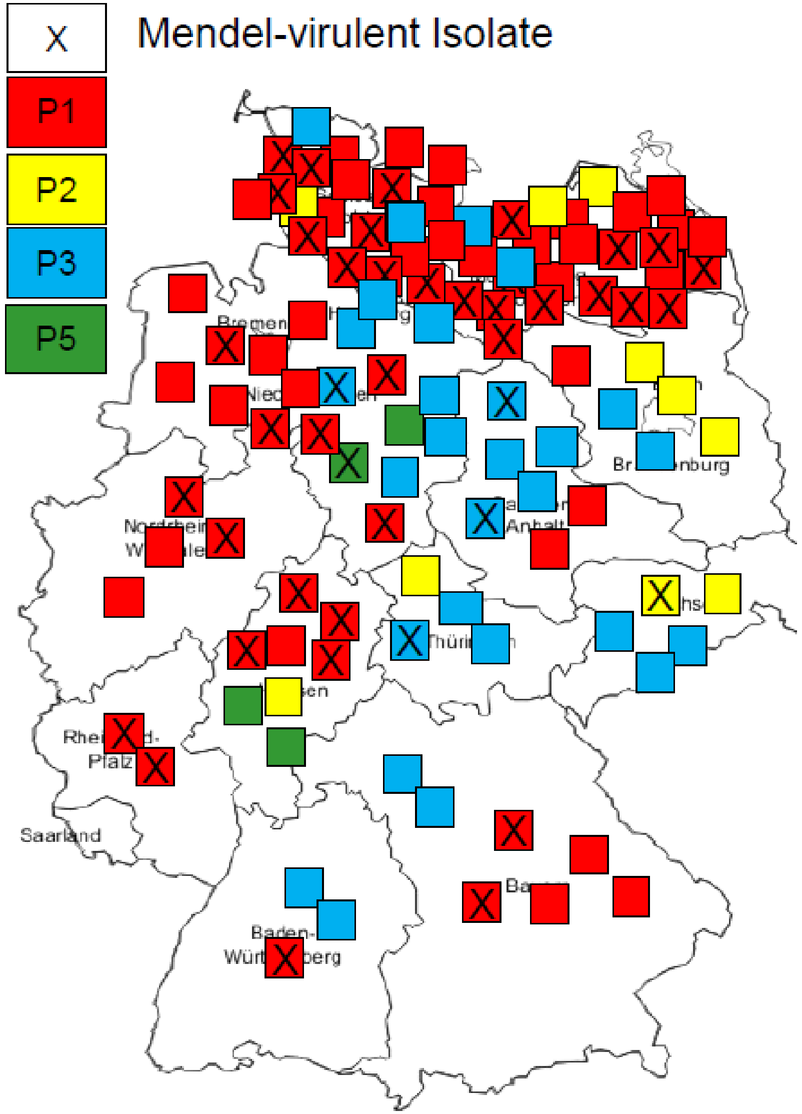
○ Moderate to wide spread

Sources:
S. Goerz, NPZ
CETIOM
B. Strehlow, U of Rostock

Plasmodiophora pathotypes in German oilseed rape crops

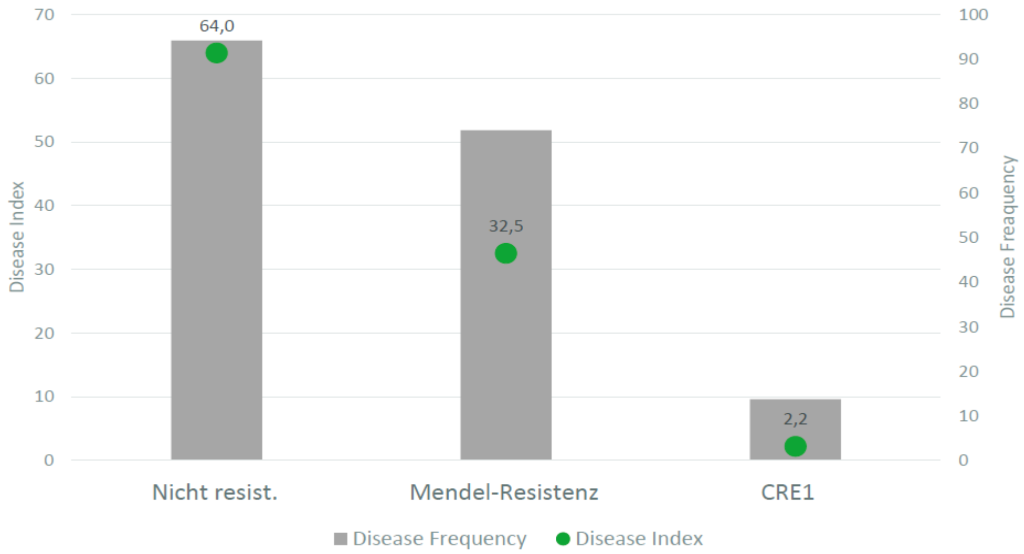
Mendel-resistance is in use since 2001. Virulent isolates are present all over cropping area (39% of all tested isolates), but frequency not as high as expected. 12% of isolates showed some virulence on B. rapa ECD-hosts.



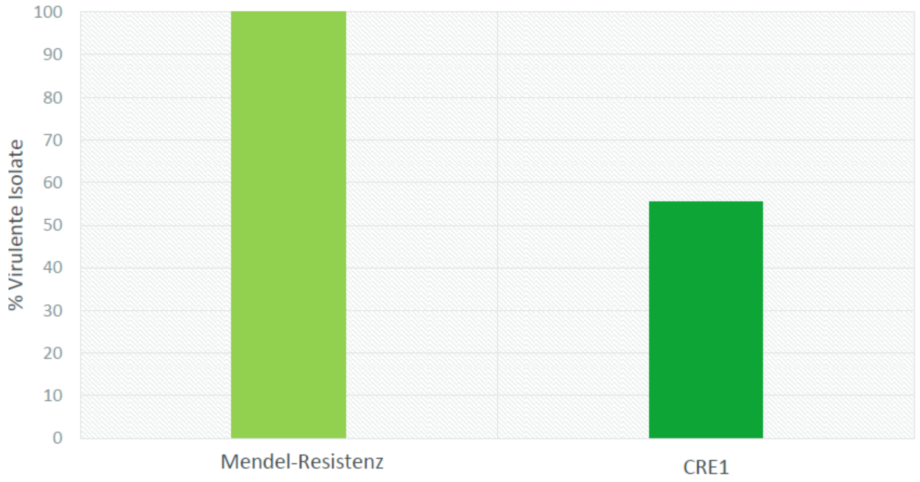


Source: **Nazanin Zamani-Noor, JKI**

CR in new breeding material – CRE1 (NPZ)



Top: Field results from site with Mendel-virulent isolate, data from NPZ



Bottom: Summary of greenhouse data with 20 isolates showing Mendel-virulence

No complete resistance, but significant improvement

Update on nomenclature initiative for CR genes

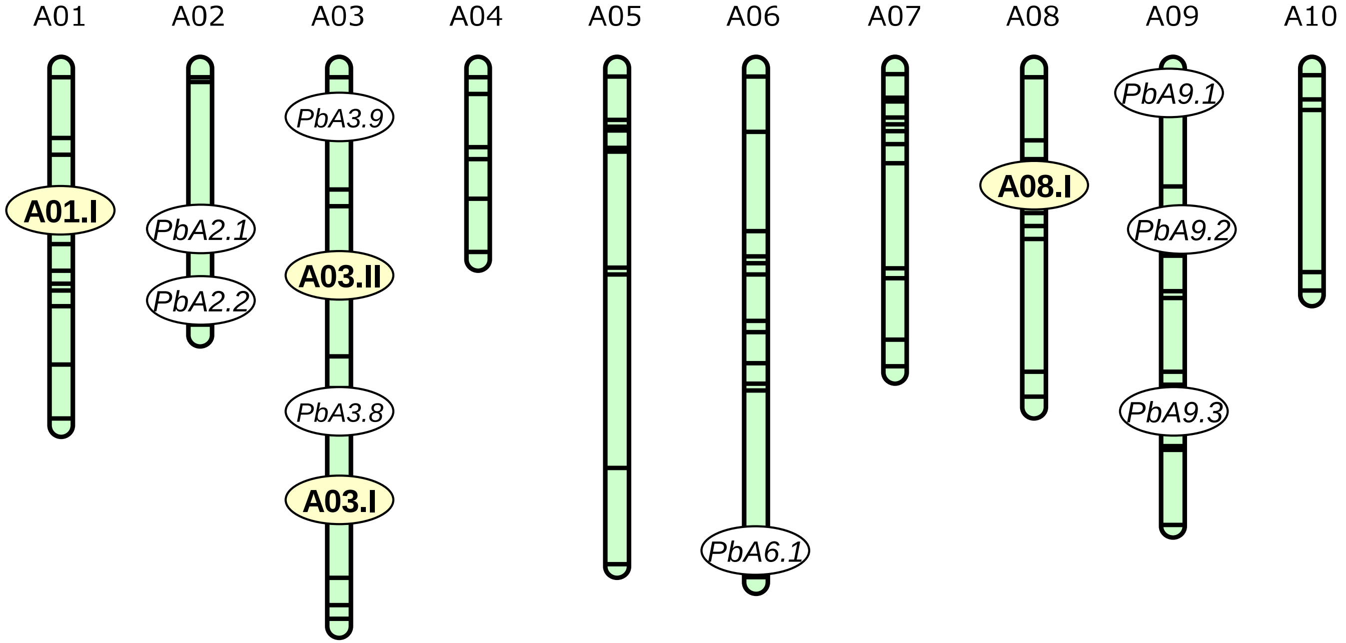
- Gene nomenclature rules help to communicate and to distinguish CR genes

- For gene pyramiding or resistance management, we need to know whether genes are really different

- Make sure to find **novel** CR sources

- Composition of differential sets based on known resistance genotypes

CR loci in A-genome using new QTL names and clusters



- Cluster composition:

A01.I = PbA1.1 + PbA1.2 (old: Crr2 + PbA1.1)
A03.I = PbA3.1 + PbA3.2 + PbA3.5 + PbA3.10 + PbA3.11 (old: CRa + CRb + PbBn-k2/-0107/-1 + Rcr1 + Mendel-Locus)
A03.II = PbA3.3 + PbA3.4 + PbA3.7 + PbA3.12 (+ PbA3.6?) (old: Crr3 + CRk + PbBa3.2 + CRd (+ PbBn-0160)
A08.I = PbA8.1 + PbA8.2 + PbA8.4 + PbA8.5 (+ PbA8.3?) (old: Crr1 + PbBn-0107/-1 + PbBa8.1 + A8-locus (+ PbBn-a?)

Nomenclature of CR loci - Diederichsen et al. - IRC 2019

Status CR gene nomenclature

- 95% of contacted authors have added their data
- Manuscript in preparation
- Invitation to publish as open access mini review in Eur J Plant Pathol

Acknowledgements

Freie Universität Berlin

Nadine Gollinge

Colleagues who provided info, data and graphs:

Christian Flachenecker, Jan Niklas Glameyer, (Norddeutsche Pflanzenzucht NPZ)

Nazanin Zamani-Noor (Julius-Kühn-Institut Braunschweig)

And your attention ☺!

GFPi

Bundesministerium
für Ernährung
und Landwirtschaft