

# Comparative study of *Plasmodiophora brassicae* field isolates based on pathotyping with an updated differential set

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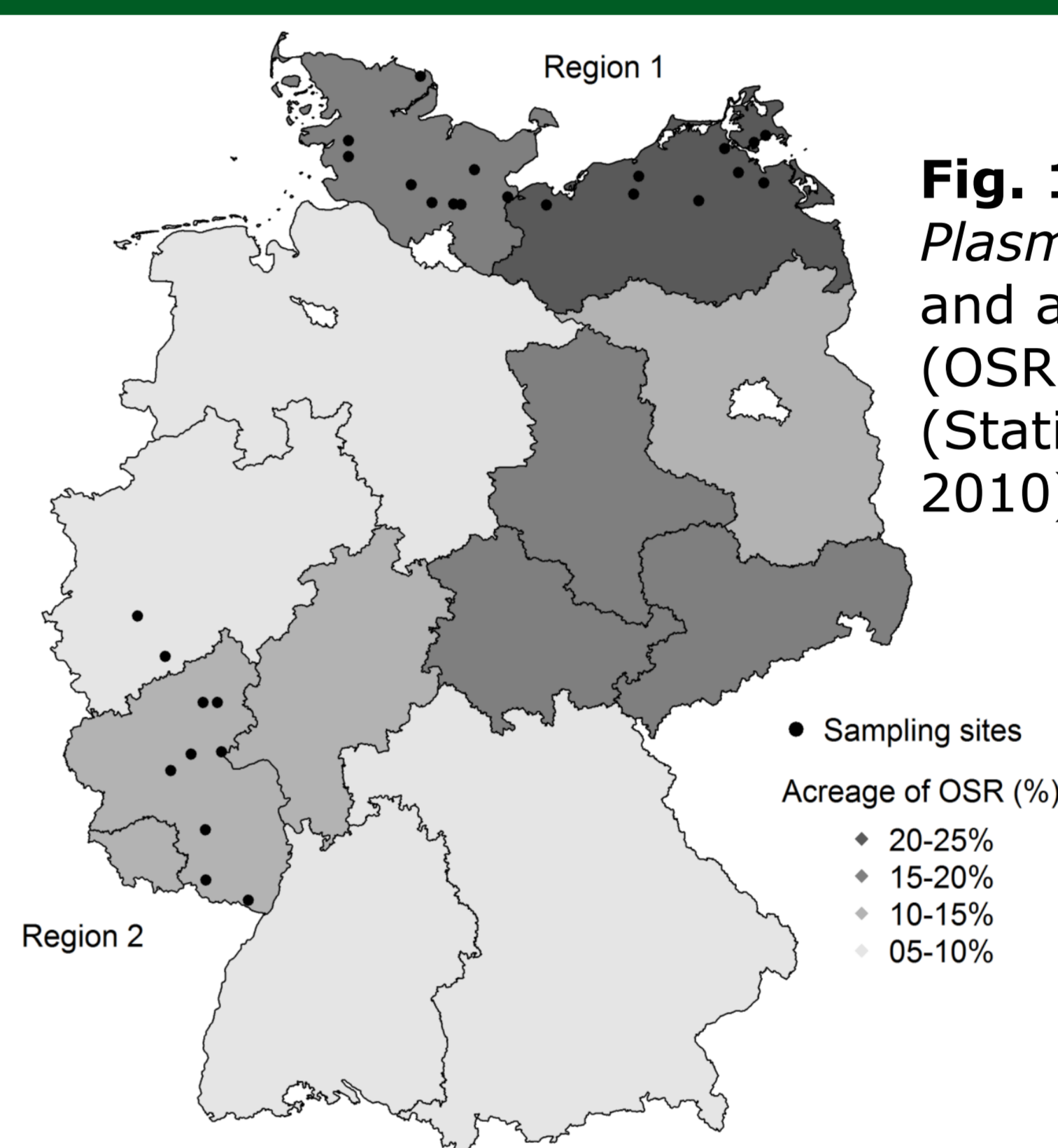
## Introduction & Objectives

- Clubroot is a serious disease of *Brassica* crops caused by the soil-borne pathogen *Plasmodiophora brassicae* and resistance breeding is a powerful tool to control the disease.
- Increasing incidence for resistance breaks were determined. Therefore, monitoring of clubroot occurrence becomes more and more important.
- The number of virulence phenotypes that can be detected is determined by number and diverseness of differential hosts which are used to describe the virulence of pathogen isolates.
- The aim of our work is to characterize selected *P. brassicae* isolates, to compare the two regions of origin and to test the efficacy of the specific combination of *Brassica* genotypes to differentiate between German isolates.

## Materials & Methods

### Soil sample collection , bioassay & data analyses

- In total, 28 *P. brassicae* isolates of two regions (Fig. 1) in Germany were tested for virulence on Brassica hosts of ECD set genotypes ECD01/04/10/11/15, on clubroot-resistant *B. napus* cv. Mendelson and on *B. napus* lines 55 and 102. *B. rapa* cv. Granaat (ECD05) served as universal susceptible control.
- Greenhouse tests were carried out according to standard protocols.
- Plants were harvested after 6 weeks and disease severity was assessed using a scale with 4 classes. Disease ratings were weighted and combined as disease severity (DS) according to Diederichsen & Sacristan (1996, Plant Breeding 115: 5-10).
- The experiment was repeated once.
- Statistical analyses were performed using software R.



**Fig. 1:** Sampling sites of *Plasmodiophora* field isolates and acreage of oilseed rape (OSR) in Germany in 2010 (Statistisches Bundesamt, 2010).

## Results & Outlook

- All isolates were highly aggressive to the susceptible control ECD05 (DS > 80, data not shown). *B. rapa* hosts ECD01 and ECD04 were resistant to all isolates tested (DS ≤ 40).
- Seven *Brassica* hosts reacted differentially to the isolates and 14 different pathotypes out of 49 possible pathotypes were identified according to virulent or avirulent infection patterns. Field isolates of region 1 displayed higher pathogenic variation than isolates of region 2 (Table 1).
- Pairwise comparisons (Mann-Whitney test) of the host/pathogen interactions reveal differences between the host plants according to their interactions with field isolates. In addition, the test displays that some plants react very similarly with regards to their interaction with the pathogen isolates, e.g. Mendelson and *B. napus* 102 or ECD15 and *B. napus* 55 (Table 2).
- An adapted set of differentiating genotypes allows us to better identify the virulence of the occurring *P. brassicae* isolates.

**Table 2:** Correlation between pairs of virulence induced by *Plasmodiophora brassicae* field isolates from Germany on clubroot resistant oilseed rape cultivar 'Mendelson', differential host lines (55,102) and ECD hosts (01,10,11,15). Values in the upper triangle are *p*-values and in the lower triangle correlation coefficients.

	Mendelson	ECD10	55	102	ECD01	ECD11	ECD15
Mendelson		0.007	0.23	<0.001	<0.001	0.66	0.19
ECD10	<b>0.49**</b>		0.26	0.07	0.12	0.32	0.52
55	-0.23	-0.22		0.41	0.90	0.001	<0.001
102	<b>0.79***</b>	0.35	-0.16		<0.001	0.11	0.53
ECD01	<b>0.77***</b>	0.30	-0.02	<b>0.76***</b>		0.09	0.96
ECD11	0.09	0.19	<b>0.59***</b>	0.31	0.32		<0.001
ECD15	-0.26	-0.13	<b>0.85***</b>	-0.12	-0.01	<b>0.71***</b>	

**Table 1:** Disease severity, infection types and pathotype grouping induced by *Plasmodiophora brassicae* field isolates from two regions in Germany (R1/R2) on differential hosts. <sup>1</sup>Pathotype classification based on virulent and avirulent infection type on *Brassica* hosts (DS >/≤ 40). <sup>2</sup>Significant grouping of field isolates according to cluster analysis.

Region/ Isolate	<i>Brassica napus</i> cvs./lines			<i>B. oleracea</i> cvs.		<i>B. rapa</i>	Patho- type Class. <sup>1</sup>	Group <sup>2</sup>
	Mendelson	B.napus55	B.napus102	ECD10	ECD11	ECD15		
R2/01	9	51	0	32	80	65	14	1
R2/02	12	56	1	30	72	53	13	1
R2/03	6	54	4	26	65	56	14	1
R2/04	10	28	0	20	5	4	3	1
R2/05	16	49	0	16	54	65	10	1
R2/06	49	26	93	31	88	13	37	2
R2/07	26	33	1	59	21	9	23	1
R2/08	8	49	0	24	70	81	9	1
R2/09	4	65	0	2	69	52	0	1
R2/10	5	27	3	0	14	23	0	1
R1/01	19	21	0	67	29	7	7	1
R1/02	43	20	46	98	30	12	12	1
R1/03	58	33	99	92	70	40	37	2
R1/04	7	6	0	76	12	4	5	1
R1/05	11	21	3	100	93	21	8	1
R1/06	22	62	0	95	96	82	13	1
R1/07	56	8	30	91	42	3	24	1
R1/08	44	31	8	78	25	3	16	1
R1/09	35	4	16	77	18	1	8	1
R1/10	18	33	47	99	100	45	6	1
R1/11	21	18	0	22	45	6	11	1
R1/12	9	59	0	100	97	74	12	1
R1/13	15	43	1	95	42	27	2	1
R1/14	14	22	1	20	41	28	4	1
R1/15	2	25	0	57	26	1	1	1
R1/16	81	46	58	95	71	35	25	2
R1/17	23	25	0	92	39	30	16	1
R1/18	66	30	77	100	69	26	25	2

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