

# Surveillance on potato and tomato late blight populations in India reveal rapid evolution of sub-clonal diversity in the *Phytophthora infestans* 13\_A2 clonal lineage

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## Introduction:

- India is the second largest producer of Potato in the world and biggest limiting factor to its production is the late blight (LB) disease which causes epidemics almost every alternate year resulting in crop losses as well as socio-economic upheaval as much of it is cultivated by small farmers, especially in the east <sup>1</sup>.
- Epidemic disease outbreaks in the recent past 2010-12 and 2013-14 were attributed to 13\_A2 clonal lineages with large sub-clonal variations in case of the latter. The 2010-12 epidemic populations, were less diverse (4 MLGs among 45 isolates), while the 2013-14 LB epidemic populations were highly diverse (24 MLGs among 59 isolates) as well as host adapted <sup>2</sup>.
- With the arrival of the 13\_A2 genotype in India, LB disease incidents have increased and in the last decade, there were at least three severe LB epidemics in different parts of the country <sup>1</sup>.

## Objectives:

Detection of genetic diversity among epidemic causing LB populations of 2019-20 and 2020-21 from the major potato and tomato growing states of India to understand whether this increasing diversity among 13\_A2 populations in India continued in the subsequent epidemic years or were being replaced by other genotypes as in the neighboring countries.

## Materials and Methods:

Blighted leaves and fruits were sampled directly from farmers' field from four states Punjab, Bihar, West Bengal and Sikkim (Figure 1). A total of 142 isolates (78 isolates during 2019-20 and 64 isolates during 2020-21), cultured in axenic form, characterised using standard 12-plexed SSR markers <sup>3</sup> as before <sup>2</sup>. Isolates from previous epidemic years 2010-12 <sup>4</sup> and 2013-14 <sup>2</sup> were also analysed in this study.



Figure 1: Sample collection sites and infected plants

## Key findings :

- **Continuous dominance of 13\_A2 genotype in India** in contrast to trends worldwide.
- Presence and dominance of 13\_A2 genotype has been identified from the border states of **Punjab** (major seed potato producing state of India) and **Sikkim** (organic state, with very high clonal diversity) **for the first time**.
- Inter-state migration of different MLGs have been identified. MLGs were shared between Punjab, Bihar and West Bengal (Figure 2) in 2019-20 and between West Bengal and Sikkim in 2020-21 (Figure 3)
- The 13\_A2 population is rapidly **expanding its sub-clonal diversity in India** with changed phenotypic pathogen characteristics.
- **38 MLGs** (Table 1) **have been identified from the present study of which 37 were newly discovered sub-clonal variants/MLGs** of 13\_A2 genotype identified across both tomato and potato crops. A total of **64 MLGs have been identified from India in the last decade (2010-2021) of which 56 variants were unique**.
- There is the **presence of new sub clones in every epidemic year** in India. **Only one identical MLG** has been found across 2020-21 and 2013-14 epidemic populations. Similarly, one MLG across 2013-14 and 2010-12 populations (Figure 4).
- **No identical MLGs** were identified when Indian LB populations of 2019-20 and 2020-21 were compared with international databases (182 13\_A2 variants/MLGs from different countries of Europe, Asia and Africa).

Pop	N	MLG	eMLG	SE	H	G	Lamba	E.5	Hexp	Ia	rbarD
Punjab	19	5	3.58	0.815	1.193	2.76	0.637	0.764	0.429	-0.0165	-0.0401
S.WB	63	12	4.69	1.126	1.745	3.99	0.749	0.633	0.426	0.2472	0.0788
Bihar	4	2	2.00	0.000	0.693	2.00	0.500	1.000	0.460	0.0000	NA
Sikkim	32	17	7.75	1.086	2.604	10.89	0.908	0.790	0.452	1.0067	0.1924
N.WB	24	8	5.59	0.926	1.849	5.43	0.816	0.828	0.448	1.3665	0.4728
Total	142	38	7.36	1.267	2.949	10.68	0.906	0.535	0.447	0.9520	0.2090

Pop- Population name, N- Number of individual observer, MLG- Multilocus genotype, eMLG- Expected MLG, SE- Standard error, H- Shannon wiener index, G- Stoddart and Taylor's index, Lamba- Simpson index, E.5- Evenness  $E_5$ , Hexp – Nei's unbiased gene diversity, Ia – Index of association, rbarD- Standardised indices of association.

Table 1: Diversity statistics of different *P.infestans* populations, S.WB= Southern West Bengal, N.WB= Northern West Bengal

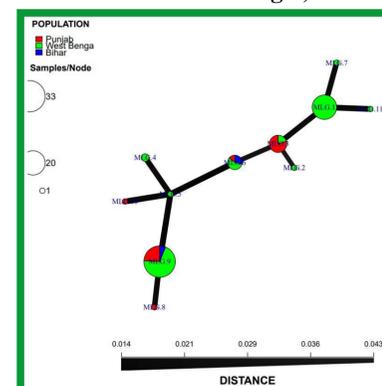


Figure 2: Minimum spanning network (MSN) of multilocus genotypes of *Phytophthora infestans* from 2019-20 growing season.

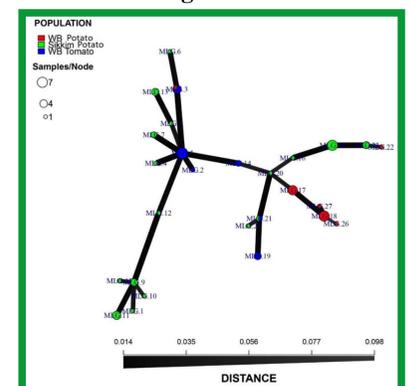


Figure 3: Minimum spanning network (MSN) of multilocus genotypes of *Phytophthora infestans* from 2020-21 growing season.

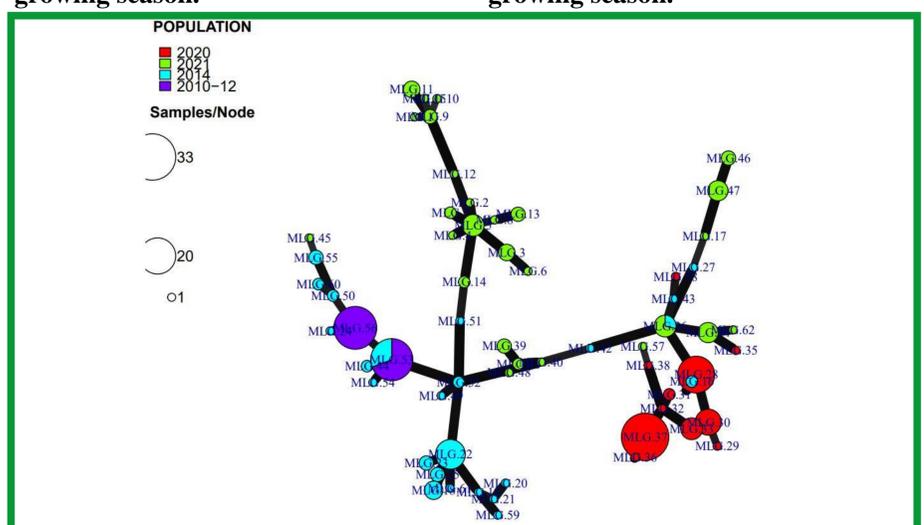


Figure 4: Minimum spanning network (MSN) of multilocus genotypes of *Phytophthora infestans* from populations in India based on epidemic year.

## Impact:

Increase in 13\_A2 sub clonal diversity and increased occurrences of LB epidemics necessitates continued surveillance and characterization for management.

## References :

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