

# Current diversity of *Phytophthora infestans* infecting cultivated potato in the Peruvian Andes

## Introduction

Late blight (LB) caused by the oomycete *Phytophthora infestans* is the most devastating potato disease worldwide. In Peruvian Andes, *P. infestans* population has been reported previously as A1 mating type [1,2,3,4]. US-1 clonal lineage was dominant in the central Andes until the early 90's [1]. In 2001, EC-1 lineage was reported displacing US-1, and PE-3 was reported in less frequency in the south [2] and north [3,4]. LB causes losses in potato fields from sea level to 4200 m.a.s.l. [5]. Disease management is difficult due to new aggressive pathogen population, susceptibility of potato varieties and farmers' unknowledge about epidemiological issues. Our study had the objective to know the current *P. infestans* population through phenotypic and genotypic based on pathogen samples collected during 2016 – 2017.

## Materials and methods

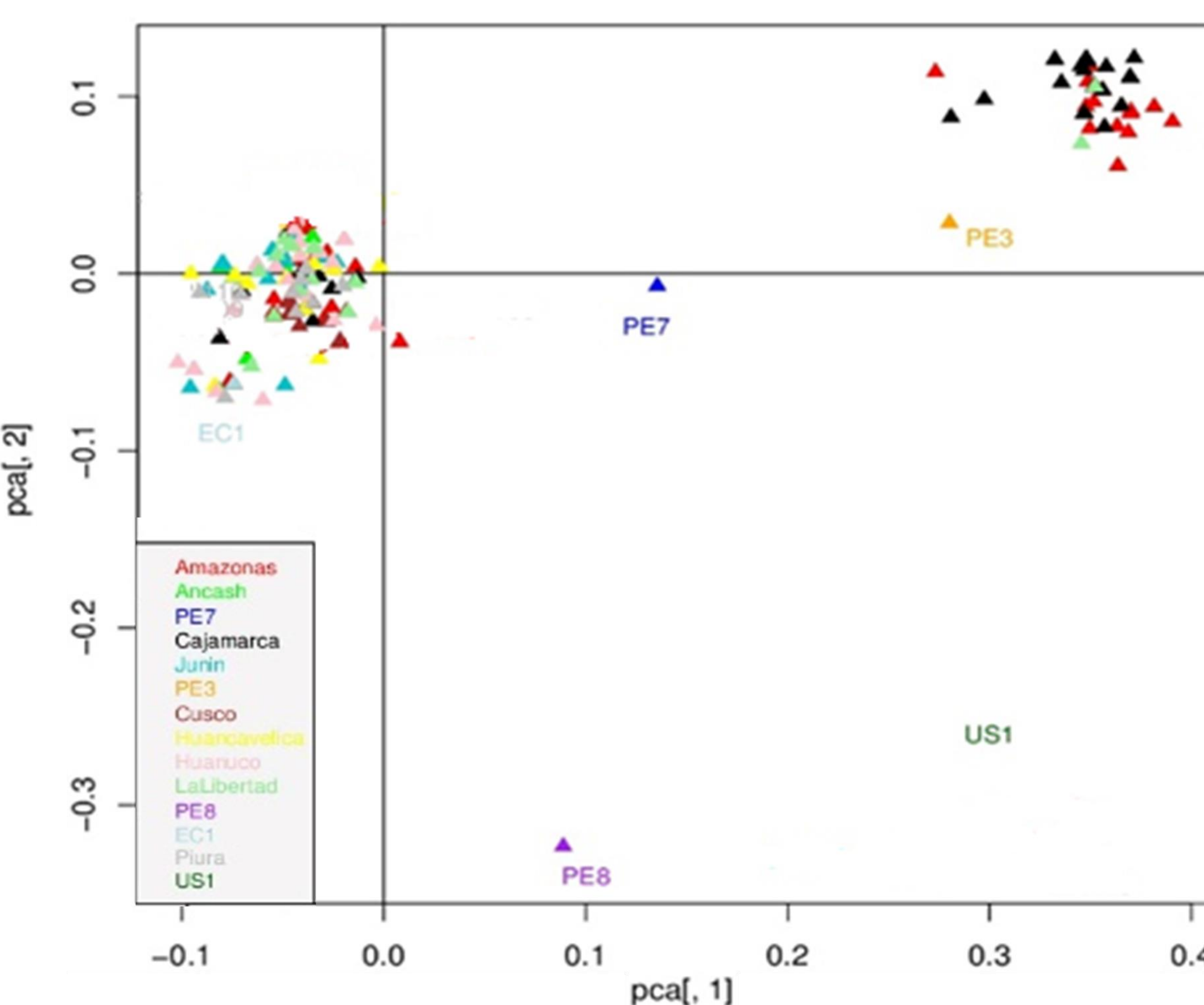
701 single-lesion *P. infestans* samples were collected from nine departments in northern (Piura, Cajamarca, Amazonas, La Libertad), central (Ancash, Huanuco, Junin, Huancavelica) and southern (Cusco) Peruvian Andes located between 1844 and 4078 m.a.s.l. (Fig. 1). A representative set of 213 isolates were phenotypically studied about mating type, metalaxil response and virulence [2]. DNA from 488 remaining samples collected on FTA cards [6] were genotypically by mtDNA haplotype [7] and SSR genotype [8] as well as DNA extracted from isolates mycelia.

## Results

All isolates belongs to A1 mating type. Principal component analysis suggest two well defined groups (Fig 2). SSR phylogenetic analysis enable to identify 131 genotypes and population analysis showed a sub-structuration in two clonal lineages, EC-1 and PE-3, with the mtDNA IIa and Ia, respectively. 94% of the EC-1 isolates were resistant to metalaxyl, whereas the sensitive proportion (47%) in the PE-3 variants was bigger than the resistant (35%) (Fig. 3). In virulence assays, 41 complex physiological races from 142 selected isolates were characterized and the race 1,3,4,7,10,11 was the most frequent in both EC-1 and PE-3.



Fig 1: Geographic sampled area (Provinces are specified in the map, inset table in the left bottom indicates the altitude at which sampling was done and number of samples collected per department) and distribution of clonal lineages found.



## Conclusion

EC-1 clonal lineage continues being dominant while PE-3 is still restricted at north and US-1 seems to be displaced as it was no longer detected infecting cultivated potato (Fig 1).

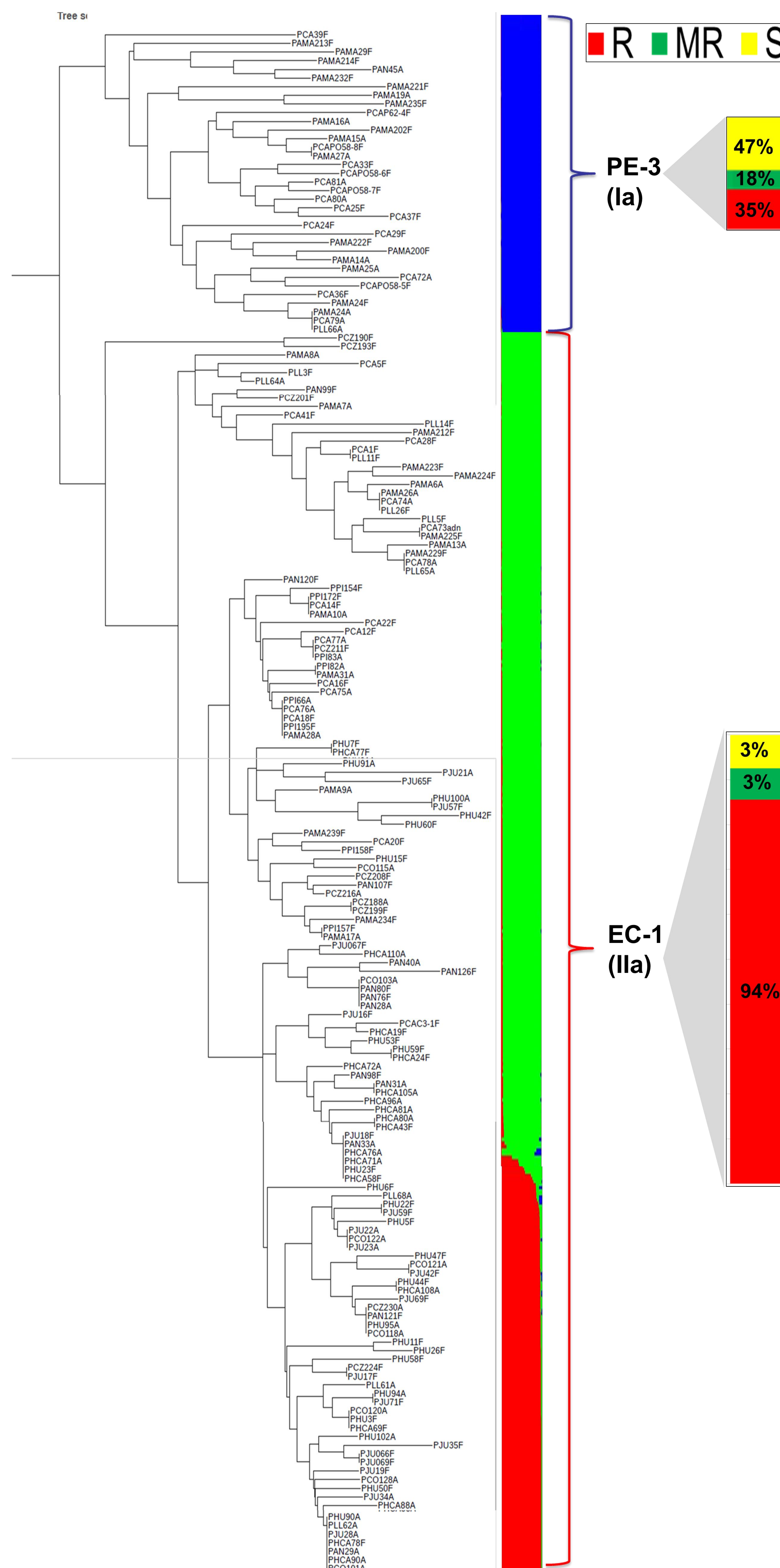


Fig 3: Neighbor Joining dendrogram of the SSR genetic diversity of 701 samples matched with population structure analysis and metalaxil responses per clonal lineages (Resistant (R), moderately resistant (MR) and sensitive (S)).



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