

Abstract: *Phytophthora infestans*, the causal agent of potato late blight which sparked Irish Great Famine in the 1840s, is one of the most important crop pathogens that threaten global food security. Late blight resistance (R) genes were introgressed into cultivated potato (*Solanum tuberosum*). A collection of eleven conventional R potatoes were used to characterize the virulence phenotype of individual *P. infestans* isolates, and as such to monitor the dynamics of *P. infestans* field populations. However, emerging reports suggest that the field strains already breakdown a substantial R genes in different geographic regions, threatening the local potato production. Here we performed genome and transcriptome sequencing analysis on two Chinese field strains. The field strain HB1501 (from north of China) and HN1602 (from south-west of China) overcome all the eleven conventional potato resistance. Our analysis reveals extensive sequence and expression polymorphisms in these strains. In particular polymorphisms at AVR locus enable these strains to overcome conventional R genes. Although field strains have evolved multiple strategies to evade disease resistance, we experimentally verified that the R genes such as *R8/Rpi-Smira2*, *Rpi-vnt1* are still effective against these strains, and are valuable to potato breeding in the future.

Virulence type and phylogeny of two newly emerged Chinese potato late blight strains

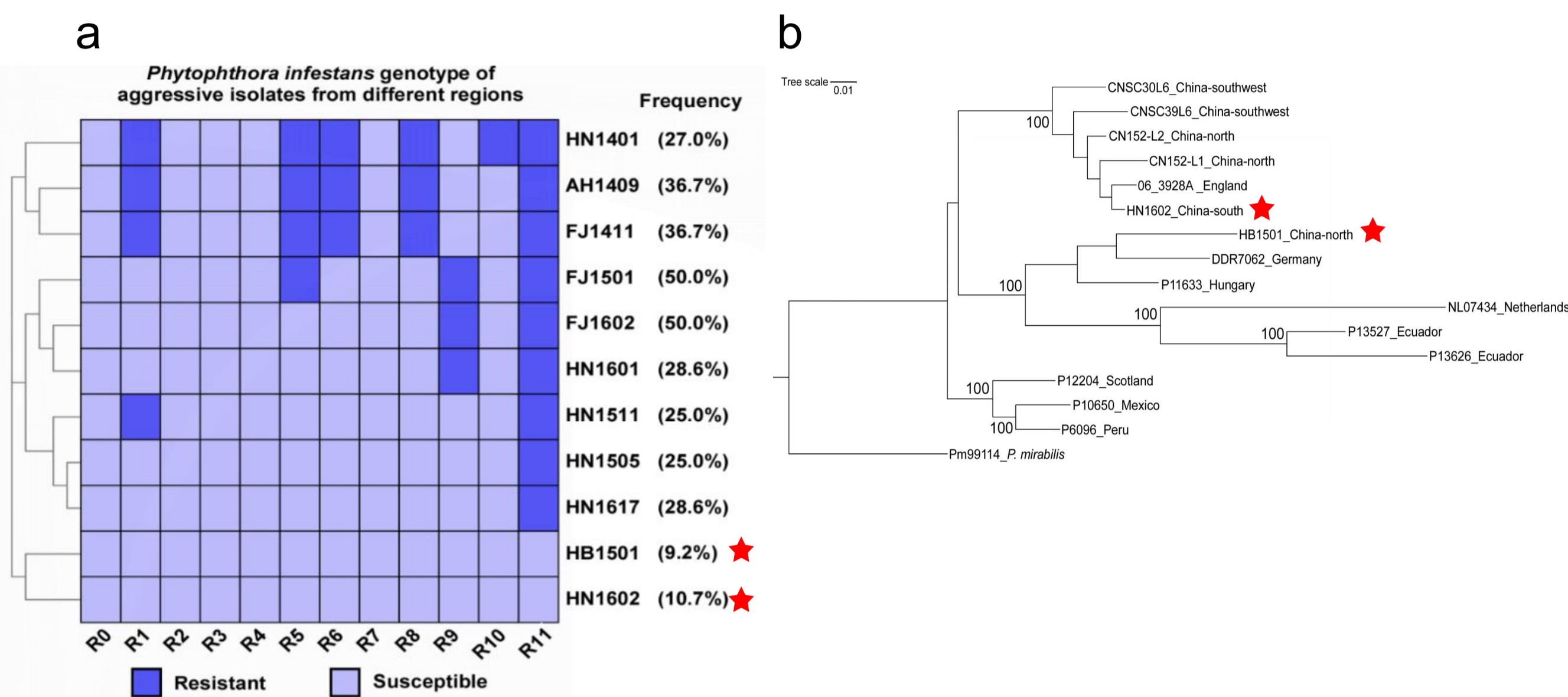


Figure 1 (a) Supervirulent genotype is among the most aggressive *P. infestans* genotypes in the field. Supervirulent isolates HB1501 (northern of China) and HN1602 (southern of China) overcome all of the Stirling potato cultivars. (b) HB1501 and HN1602 are characterized in Chinese strains.

Genome sequence analysis of two Chinese strains

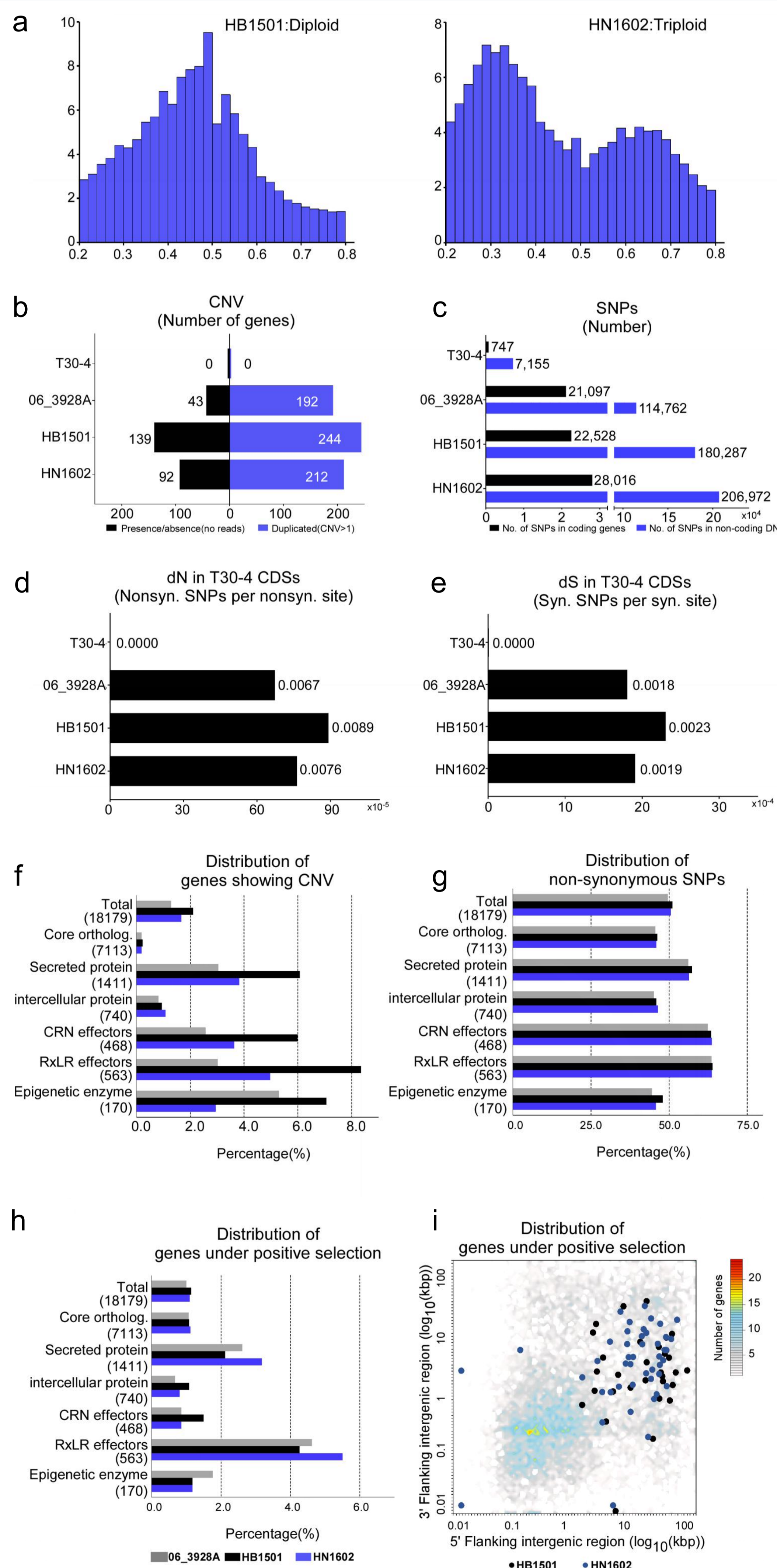


Figure 2 (a) Plidity analysis of HB1501 and HN1602. (b, c) Genomic polymorphisms correlate with copy number variations (CNV) and single nucleotide polymorphisms (SNPs) in HB1501, HN1602 and 06_3928A, which is epidemic blight isolate in England during 2006-2008. (d, e) Comparative analysis of frequency of nonsynonymous substitutions (dN) and synonymous substitutions (dS). (f, i) Distribution of genetic polymorphisms that collectively contribute to the aggressiveness and virulence phenotype of HB1501, HN1602 and 06_3928A.

Reference:

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Raffaello S, Farrer RA, Cano LM, et al. (2010). Science, 330, 6010
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Gene expression polymorphisms in two Chinese strains

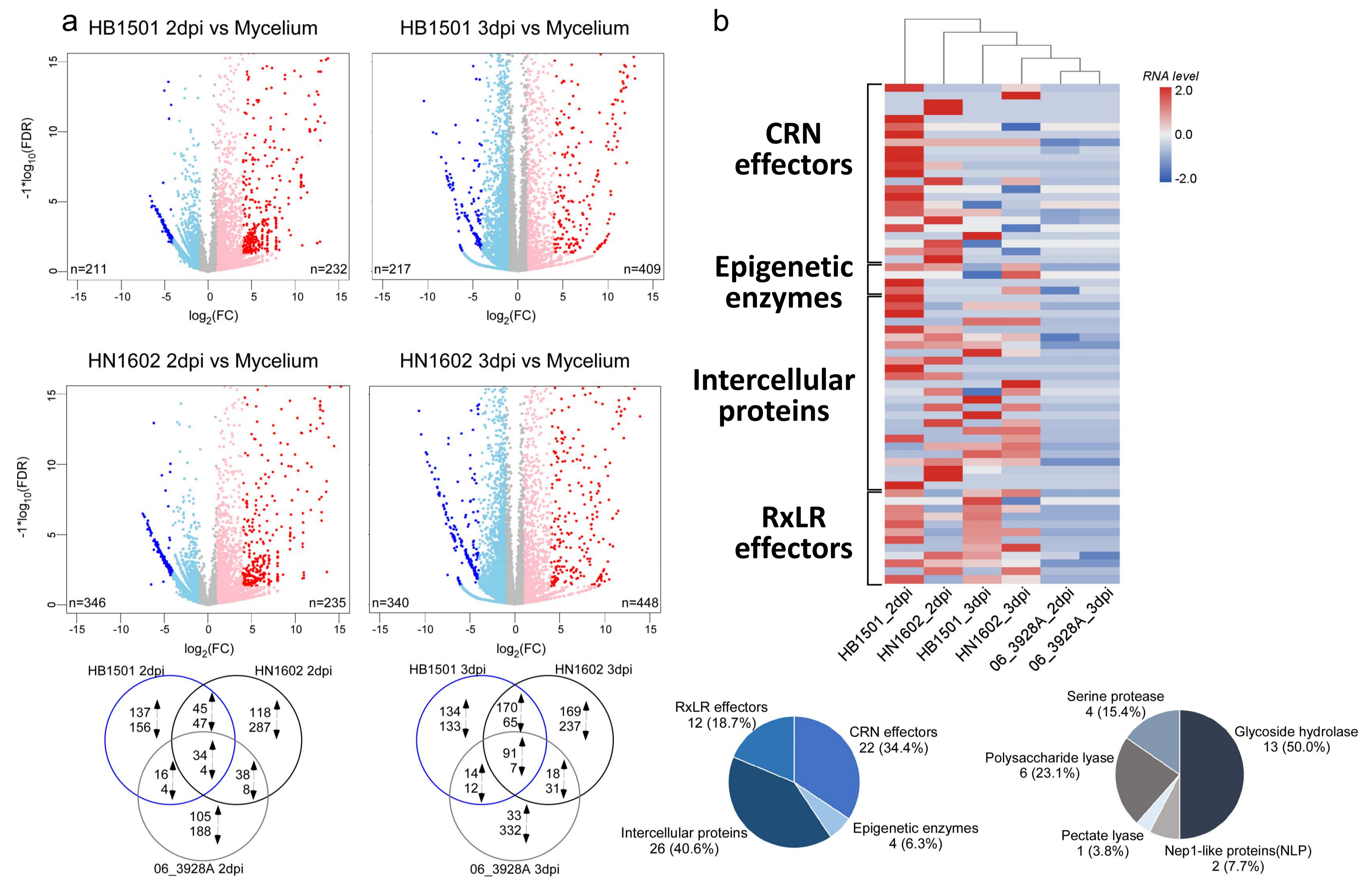


Figure 3 (a). Number of genes that are up-regulated (red) and down-regulated (blue) during potato infection in HB1501 and HN1602 (p value < 0.05 , > 16 fold expression changes). (b). Compared to other reported strains, 64 effector genes only induced in these two Chinese strains that collectively contribute to the aggressiveness and virulence phenotype.

Polymorphism analysis on AVR effector genes underpins pathogen adaptation and pinpoint valuable potato resistance

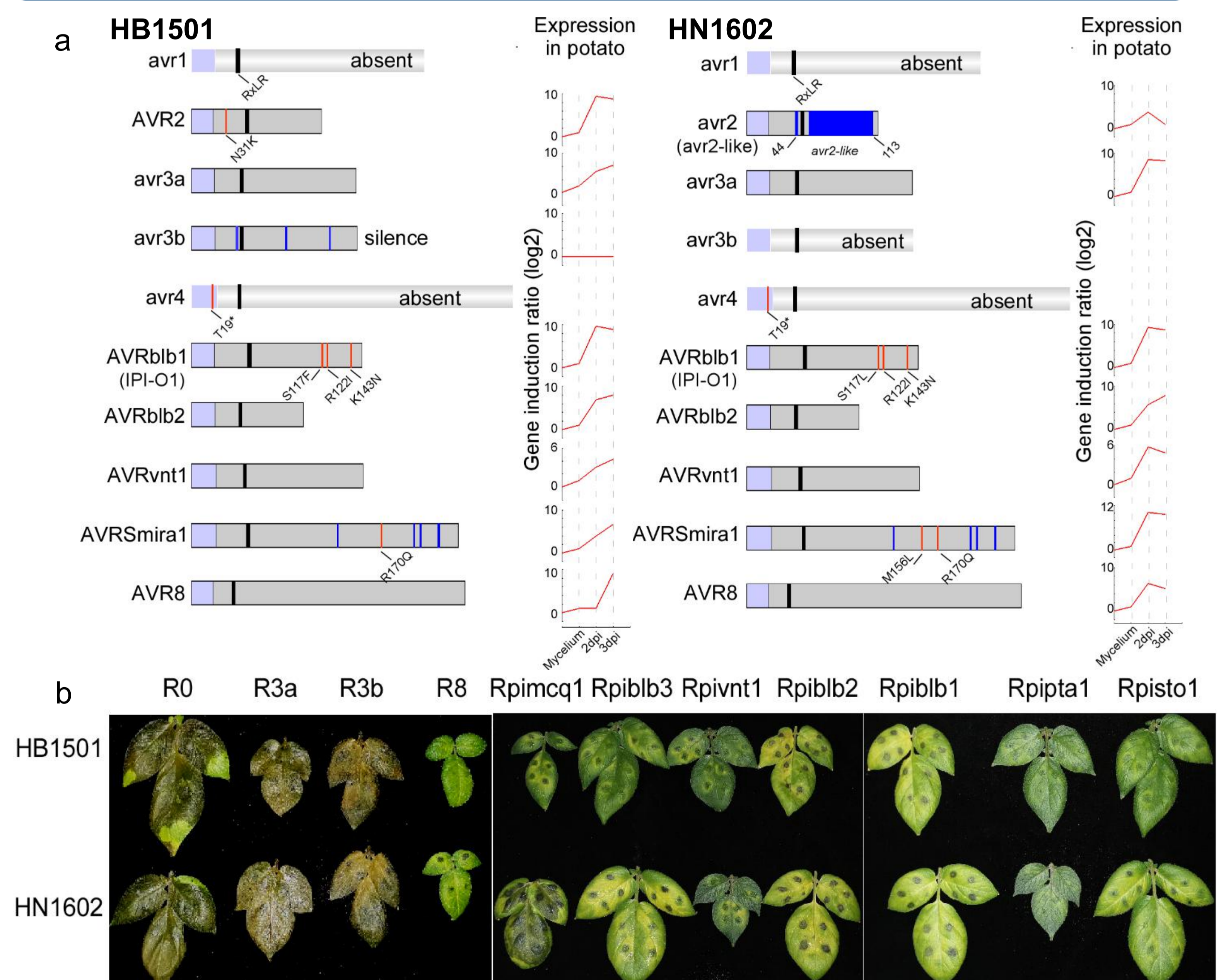


Figure 4 (a) Chinese strains HB1501 and HN1602 contain sequence polymorphisms, gene missing and gene silencing of avirulence (Avr) genes are known to evade recognition in plants carrying the corresponding R1, R2, R3a, R3b and R4. (b) Invariant avirulence genes identify efficient plant resistance genes including *Rpi-b1b1*, *Rpi-b1b2*, *Rpi-vnt1* and *R8*.

Conclusions:

- Two newly emerged strains HB1501 and HN1602 have distinct background and are rich of gene sequence and expression polymorphisms;
- Examination of AVR genes suggest resistance genes such as *Rpib1b1*, *Rpib1b2*, *Rpvnt1* and *R8* may provide valuable resistance to these two strains.

Next works:

- Scale up sequencing input and monitoring pathogen population at genome level;
- How these two strains evolve in Chinese potato field in future.

Acknowledgments:

This work was supported by the Chinese National Science Funds (31972252, 31721004) and Fok Ying-Tong Education Foundation (151025).