

Population structure and diversity of *Puccinia striiformis* in the past

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The past worldwide population structure and diversity of the yellow rust causing fungus *Puccinia striiformis* have not been investigated previously at the molecular level. Knowledge on this would shed light on the evolution and temporal dynamics of the pathogen on a global scale, which was the aim of our study. An initial recovery and race identity study was conducted beforehand using old spore samples from the historic “Stubbs collection”, founded in 1956 by the late Dutch plant pathologist R.W. Stubbs and maintained by the Global Rust Reference Center (GRRC), Denmark, since 2010. A new method for recovery using an airbrush sprayer and Novec™ 7100 was highly successful shown by a 96% recovery of 231 isolates that had been stored for up to 45 years in liquid nitrogen (collected between 1958 and 1991) representing 34 countries. The past population structure was investigated with 212 of the pure isolates that represented six geographically spaced populations: NW Europe, the Mediterranean, East Africa, the Middle East, South Asia (Afghanistan, Pakistan and Nepal) and China. DNA was extracted from spore samples with a CTAB method, and 19 multilocus microsatellites (Simple Sequence Repeats) were used for genotyping. DAPC analysis showed that the global *P. striiformis* population consisted of seven (K=7) distinct genetic populations. Recombinant populations were found in China and South Asia whereas clonal populations were found in NW Europe, East Africa and the Mediterranean. Overall, 89 multilocus genotypes were present in the past where the highest genotypic diversity was found in the Chinese population and the lowest genotypic diversity was seen in the NW Europe population. Long distance migration in the past was detected with the resampling of the most frequent multilocus genotypes observed, and additional information was gained when these were combined with the virulence phenotypes. Analysis of the temporal dynamics of the *P. striiformis* in the past populations compared to the contemporary population from a recent study revealed divergence in all geographical population except for the NW European population, which had remained stable for more than five decades. In conclusion, an overall consistent population structure on a global scale exists for the wheat yellow rust pathogen. Our results further facilitate the understanding of the overall pathogen migration worldwide and elucidate the previous finding of the Himalayas and near-Himalayan region as a putative centre of diversity of *P. striiformis*.