

Worldwide spread of wheat yellow rust from the centre of diversity in Himalayas

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The worldwide population structure, migration patterns and the centre of diversity of wheat yellow rust pathogen *P. striiformis* was inferred based on the microsatellite genotyping of worldwide representative isolates. The population genetic analyses revealed the presence of at least six genetic clusters associated with their likely geographical origin. A high genetic and genotypic diversity and recombinant population structure was identified in the Himalayan and near-Himalayan regions (Nepal, Pakistan and China), while a predominant clonality and low diversity in other parts of the world. Together, the high diversity, recombinant population structure, high sexual reproduction capacity and the abundance of alternate hosts (*Berberis* spp.) suggested the Himalayan and near Himalayan region as the plausible centre of origin of *P. striiformis*. The clustering methods and approximate Bayesian computation (ABC) analyses were used to infer on the worldwide spread of *P. striiformis* from this plausible centre of origin and identify the sources of recent invasive strains/populations. The Himalayan and near Himalayan populations were identified as the most ancestral populations, while analyzing the ancestral relationship among worldwide populations. Among the recent invasive strains/populations, the Middle East-East Africa was identified the source of *PstS1/PstS2*; Europe as the source of South American, North American and Australian populations; and Mediterranean-Central Asian populations as the origin of South African populations. The most recent invasive race groups of Europe, “Warrior” and “Kranich”, were identified to be originated in the pathogen’s centre of diversity in the Himalayan and near Himalayan region. The worldwide spread of *P. striiformis* from its plausible centre of origin reveals the role of both human activities and air dispersal to its long distance dispersal.