



**Fig 7. Factorial Correspondence Analysis individual factor map.** (Protected Designation of Origin/Protected Geographical Indication cheeses & populations as obtained by STRUCTURE). Red numbers (1, 2 & 3) refer to the corresponding populations as defined on Fig 4.

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three populations. As in this previous study [16], we found that one cluster included almost all non-blue-cheese isolates.

Importantly, we revealed in this study that the clustering of cheese isolates mainly corresponded to different cheese types. This might suggest that the different cheese-making processes domesticated their own *P. roqueforti* population from a common pool, leading to their genetic differentiation. Noteworthy, a phenotypic differentiation could also be observed. In particular, population 3, which included mainly isolates from Gorgonzola-type cheeses, displayed colony morphologies which were absent from other populations and grew much slower. A strong selection for some desired phenotypic traits may indeed differentiate populations through selective sweeps [78,79], especially in organisms like fungi with infrequent sex events compared to cycles of asexual reproduction.

However, this interpretation seems difficult to reconcile with the high diversity within clusters and the strong divergence between populations, given the human time-scale for