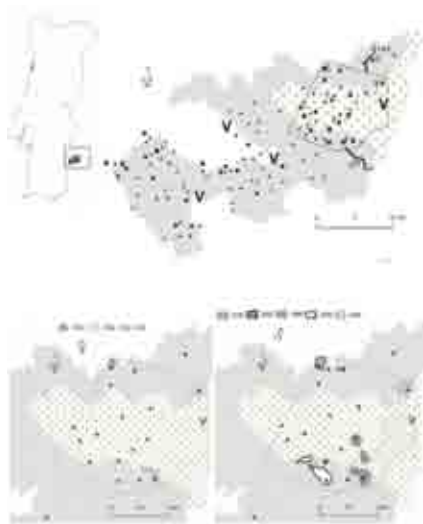


spatial spread and avoid any access to human refuse. The movements of domestic cats would be limited in areas with large patches of natural vegetation providing good conditions for other carnivore mammals such as red foxes.

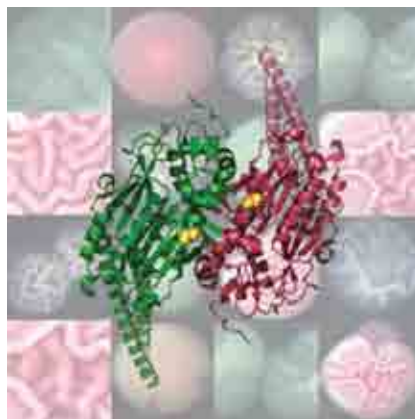


## unveiling the structural basis for translational ambiguity tolerance in a human fungal pathogen

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The genetic code defines the rules that organisms use to synthesize their proteins from the information contained in their genes. The genes are translated into segments of three letters (triplets), meaning that DNA bases (A, C, T and G) are read three at a time during the proteins synthesis process. This translation



is done with high precision assuring that one gene corresponds to one protein only. However, in rare situations, the triplets are read ambiguously originating more than one protein from a single gene, being the alternative proteins in general toxic to cells and promote their death.

Genetic code alterations discovered during the last 40 years in bacteria, fungi, algae and ciliate organisms do not obey to the strict rules of the standard genetic code, thus posing the fascinating question of how these organisms deal with such flexibility. CESAM researchers have now demonstrated how fungi of the genus *Candida* can cope with such flexibility at the protein level.

*Candida albicans* is an opportunistic fungus that causes human infections (mainly oral and genital) known as candidiasis, which are common in immunosuppressed patients,



as the HIV and cancer patients, and elderly people. Beyond the theoretical interest of the discovery, the work reveals new facets of the biology of these fungi that could help scientists better understand the biology of infection of fungi of the genus *Candida*.

The study explains how these fungi can insert different amino acids at single protein sites without disruption of protein structure. Since the environment has direct impact on genetic code fidelity this study provides deep insight on how environmental factors affect protein synthesis and on how protein structure buffers negative effects of environmental variation.

Therefore, this study reveals an unexpected flexibility of gene evolutionary mechanisms and shows how organisms survive and adapt to genetic chaos generated through genetic code ambiguity.

## mineral composition of atmospheric dust in santiago island, republic of cape verde

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Aerosol sampling is being performed at Praia airport during one year (within CVDUST Project) and mineralogical composition is being studied by X-ray diffraction, TEM and Scanning electron microscopy. Structural (crystallochemical) formulas will be computed from XRD and SEM – EDAX analytical data. The identification of the main sources and origins of the particles sampled in the archipelago has been carried out in order to elucidate the role Saharan dust may play in the degradation of Cape Verde air quality.