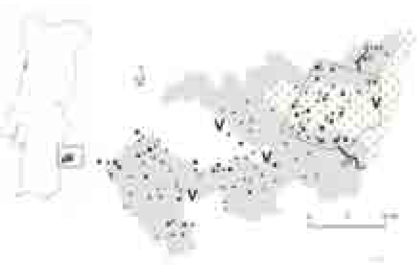
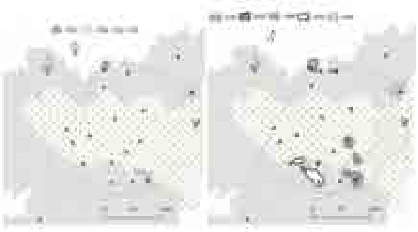
spatial spread and avoid any access to human refuse. The movements of domestic cats would be limited in areas with large patches of natural vegetation providing good conditions for other carnivore mammals such as red foxes.





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

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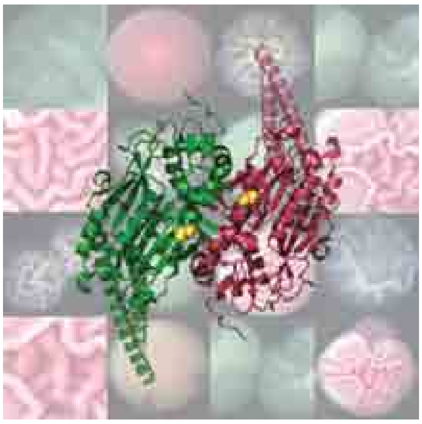

The genetic code defines the rules that organisms use to synthesize their proteins from the information contained in their genes. The genes are translated into segments of three letters (triplets), meaning that DNA bases (A, C, T and G) are read three at a time during the proteins synthesis process.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

Cape Verde is located in an area of massive dust transport from land to ocean, and is thus ideal to set up sampling devices that will enable the characterization and the quantification of the dust transported from Africa. Mineral dust produced from windblown soils and deserts is one of the largest contributors to the global aerosol loading and has strong impacts on regional and global climates, long-term climate trends as well as marine and terrestrial ecosystems.

Mineralogical phases identified include various silicates and aluminosilicates, carbonates, sulphates, phosphates, oxides and hydroxides. Iron hydroxides, such as lepidocrocite and goethite, and carbonates, such as calcite and siderite, are the most discriminating phases, allowing to differentiate 3 subsets. On the contrary, silicates, such as quartz, feldspars and phyllosilicates, do not show any particular tendency, being ubiquitous and generally on small amounts.

The identification of the main sources and origins of the particles sampled in the archipelago is been carried out by integrating complementary tools such as Principal Component Analysis, Positive Matrix Factorization, Chemical Mass Balance, Multilinear Regression Analysis, Air Mass Back trajectories analyses, meteorological data and particle size segregate analysis.

characterization and prediction of biomass pyrolysis products

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Environmental and social concerns, energy security and fossil fuel prices are driving increased R&D and technological interest on the utilization of renewable energy. In particular, the thermochemical conversion of biomass has been actively discussed over the past few decades as a route for producing heat, electricity and synthetic fuels in a sustainable way.

Aiming to accelerate the transition from fossil fuels to renewables, a number of pilot and industrial plants were demonstrated around the world to convert biomass via pyrolysis, gasification or combustion processes.

Biomass is an organic, carbon-based solid fuel with high volatile matter content. The fuel undergoes rapid decomposition when exposed to temperatures above 250ºC, forming a huge set of gas species and a non-volatile residue, called char or charcoal. Such a thermal degradation is called pyrolysis (or devolatilization) and is an important stage of fuel conversion in thermochemical processes. The characterization of this stage is of major importance in the case of biomass fuels in result of their high volatile matter content. The pyrolysis mechanism involves a great deal of physical and chemical transformations (e.g. dehydration, depolymerization) and hence the detailed description of the process is challenging. However, for engineering applications it is often sufficient to describe the ultimate yields and the properties of the pyrolytic products.

In this work, literature data on these issues has been screened and structured, constituting a guide on the general behaviour of biomass pyrolysis. The collected data covers a range of conditions with practical interest for thermochemical applications. Moreover, an empirical model to predict the distribution of pyrolytic products was proposed. The model is suitable to be integrated in comprehensive reactor models simulating pyrolysis, gasification or combustion processes, being an important tool to further develop the biomass conversion technologies.