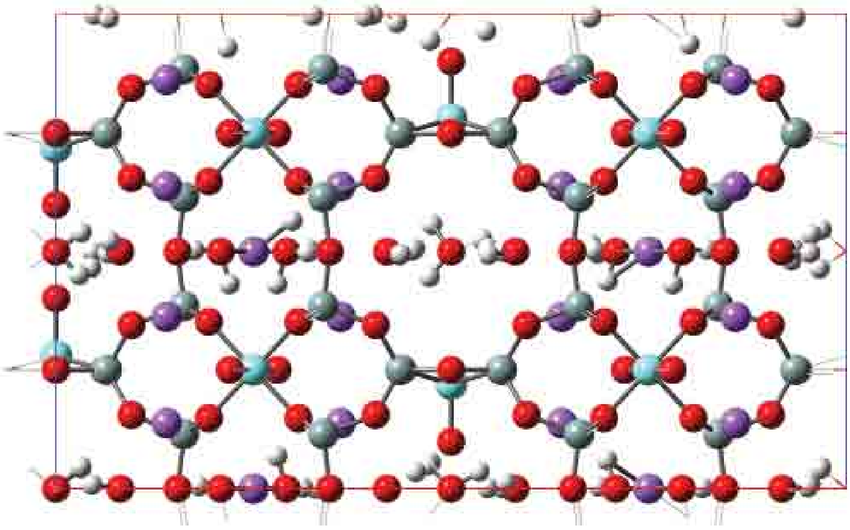
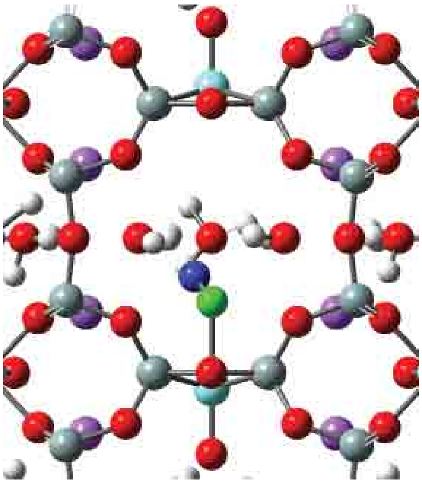
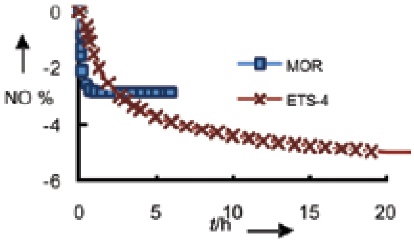




systems sometimes cause undesirable side effects. Besides good NO adsorption capacity, materials must also present an appropriate releasing kinetics, to maintain a given concentration in the surrounding milieu. Often, a slow releasing kinetics is preferred because it allows for easier and safer control of the NO concentration, for longer periods. Clearly, new materials and technologies are needed to store and target-deliver NO in biological amounts.

A novel approach to design nitric oxide storage and releasing microporous agents based on very stable, zeolite-type silicates possessing framework unsaturated (e.g., pentacoordinated Ti^{4+}) transition-metal centers has been proposed (*Journal of the American Chemical Society*, 2011, vol. 133, p. 6396). This idea has been illustrated with ETS-4 [$Na_9Si_{12}Ti_5O_{38}(OH)\cdot xH_2O$], a titanosilicate which displays excellent NO adsorption capacity and a slow releasing kinetics. The performance of these materials has been compared with the performance of titanosilicate ETS-10, [$(Na,K)_2Si_5TiO_{13}\cdot xH_2O$], of benchmark zeolites mordenite and CaA, and of natural and pillared clays. DFT periodic calculations have shown that the presence of water in the pores of ETS-4 promotes the NO adsorption at the unsaturated (pentacoordinated) Ti^{4+} framework ions.

The ability of ETS-4 to release biologically relevant NO amounts was tested using the oxyhemoglobin method, which is based on the principal reaction of oxyhemoglobin with NO to form methemoglobin and nitrate. This reaction also accounts for the inhibitory effect of hemoglobin on the biological effects of endogenous formed or exogenous applied NO.



human-related factors regulate the spatial ecology of domestic cats in sensitive areas for conservation

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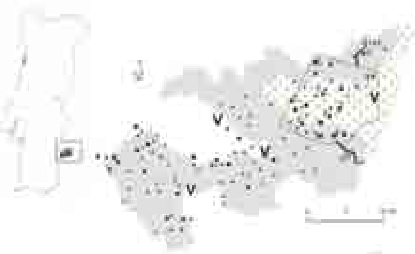
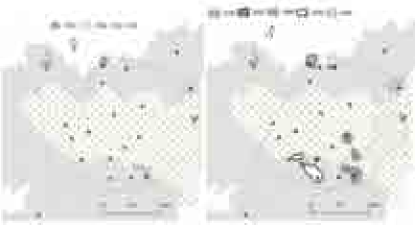
Domestic cats ranging freely in natural areas are a conservation concern due to competition, predation, disease transmission or hybridization with wildcats. In order to improve our ability to design effective control policies, the factors affecting their numbers and space use in natural areas of continental Europe were investigated.

We describe the patterns of cat presence, abundance and space use and analyse the associated environmental and human constraints in a well-preserved Mediterranean natural area with small scattered local farms. We failed in detecting cats in areas away from human settlements (trapping effort above 4000 trap-nights), while we captured 30 individuals near inhabited farms. We identified 130 cats, all of them in farms still in use by people (30% of 128 farms). All cats were free-ranging and very wary of people. The main factor explaining the presence of cats was the presence of people, while the number of cats per farm was mostly affected by the occasional food provisioning with human refuse and the presence of people. The home ranges of eight radio tagged cats were centred at inhabited farms. Males went furthest away from the farms during the mating season (3.8 km on average, maximum 6.3 km), using inhabited farms as stepping-stones in their mating displacements (2.2 km of maximum inter-farm distance moved). In their daily movements, cats notably avoided entering in areas with high fox density. The presence, abundance and space use of cats were heavily dependent on human settlements. Any strategy aiming at reducing their impact in areas of conservation concern should aim at the presence of settlements and their 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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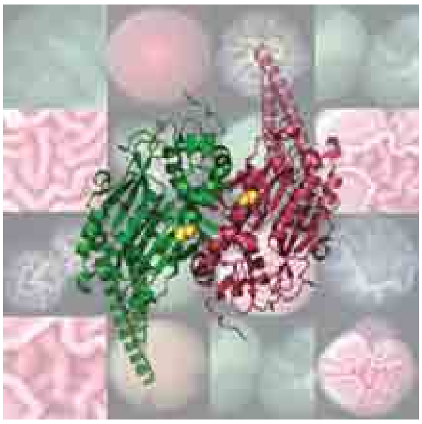
The genetic code defines the rules that organisms use to synthesize their proteins from the information contained in their genes. The genes are translated into segments of three letters (triplets), meaning that DNA bases (A, C, T and G) are read three at a time during the proteins synthesis process. 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.