Although Adélie and gentoo penguins are congeneric, interspecific and even intraspecific differences can be substantial. For example, gentoo penguins breeding at Ardley island (South Shetlands), very near to a summer station, can easily be approached to 1 m by a single human. In this respect, they are similar to the birds studied by Nimon *et al.* However, gentoo penguins at the small, undisturbed Hope Bay (Antarctic peninsula) colony will abandon their nests when approached slowly to 20 m by a single human (our unpublished observations). The same is true for sub-Antarctic gentoo penguins[6], a situation which presumably renders ineffective a heart rate measuring system encased in an egg. With such substantial intraspecific differences, it is premature to make interspecific generalizations.

Finally, it is not only penguins near nests that are likely to be disturbed by tourist activities. We observed that a single human approaching to within 20 m of unhandled Adélie penguins commuting between the beach and their colonies in mid-January caused the birds to deviate from their normal tracks. The birds made a 70-m detour for several hours after the human had left the area. We estimated that this single disturbance caused the 12,000 birds commuting on these tracks during the 10 h of observation to cover an extra 840 penguin-km. Observation was by remote-controlled video placed 150 m from the study site[4].

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Oil biodegradation around roots

SIR — Four years after the Gulf War, about 50 km^2 of the Kuwaiti desert still suffers from the intensive oil pollution caused by the Iraqi forces. Although there is experimental evidence for some self-cleaning of this environment through the activity of indigenous microorganisms[1], heavily contaminated areas still fail to support wild plants; however, moderately to weakly contaminated areas with less than about 10% by weight of oil sediments currently support such annuals.

Here we report that roots of such plants and of crop plants grown in polluted sand in pots under field conditions are associated with hundreds of millions of oil-utilizing microorganisms per gram of fresh roots. These microorganisms take up and metabolize various aliphatic and aromatic hydrocarbons rather quickly, thus detoxifying and bioremediating the soil in the immediate vicinity of the roots. This may explain the plant survival mechanism in oil-contaminated soils. Further, this finding paves the way for a bioremediation approach which depends on densely cultivating oil-polluted desert areas with selected crop plants that tolerate oil and whose rhizospheres are rich in oil-degraders. Heavily contaminated areas would first have to be mixed with clean sand to dilute the oil to levels tolerable by the plants.

Individual *Senecio glaucus* plants growing along the polluted border of an oil lake in the Kuwaiti desert. The plant roots and adhering sand particles are white and clean. In contrast, the surface of the transitional zone between the root and shoot is black and polluted.

We initially observed that Kuwaiti desert plants, belonging predominantly to the family Compositae, although growing in black, polluted sand, always possessed white, clean roots. Even the sand adhering to the roots, the rhizosphere, was always clean whereas the sand just apart was black and polluted. We took complete desert plant samples to the laboratory, and also potted three crop plants, corn, tomato and termis, in sand we had previously polluted with 10% by wt crude oil. The pots were kept for 4 weeks in the Botanical Garden, under open conditions.

Whole roots of desert and crop plants, together with the adhering soil particles, were blended for 30 s in sterile water and the suspensions used for plate-counting and isolating oil-utilizing microorganisms using a solid inorganic medium containing 2% crude oil as a sole source of carbon[2]. Representative oil-utilizing strains were isolated, purified and identified, and their potential to take up and oxidize individual alkanes and aromatic hydrocarbons was investigated using GLC analysis of hydrocarbons and cell total fatty acids, as we have described previously[2,3].

Seeds of the three crop plants showed a germination rate of 90–100% in the polluted pots, comparable to seeds in control clean pots. However, 4-week plants in the polluted pots, although quite healthy, grew more weakly than the control plants, reaching 60–75% of their optimum height.

The rhizosphere samples of all plants were rich in oil-utilizing microorganisms. Respective bacterial numbers for corn, tomato and termis were 3.0×10^8, 8.1×10^8 and 5.2×10^8 cells per g fresh roots, and fungal numbers were 4.4×10^5, 1.5×10^5 and 1.4×10^5 propagules per g fresh roots. In all samples, filamentous actinomycetes, probably *Streptomyces*, were present at several thousand propagules per g root. One bacterial genus, *Arthrobacter*, was predominant (>95%) in the rhizosphere of all plants, whereas in the polluted non-rhizospheric soil several other genera, *Rhodococcus*, *Pseudomonas* and *Bacillus*, predominated, with *Arthrobacter* making up <5% of the total. The predominant fungi in the rhizosphere samples belonged to *Penicillium* and *Fusarium*, but in the polluted non-rhizospheric soil *Trichoderma* predominated. In a few cases an oil-utilizing yeast was found as a minor constituent of the rhizospheric microflora.

A total of eight strains of *Arthrobacter*, two of *Penicillium* and two of *Fusarium*, isolated from the rhizosphere of various plants, grew well, utilizing individual even- and odd-chain *n*-alkanes with C_{10} to C_{40} chains and three representative aromatic hydrocarbons, benzene, naphthalene and phenanthrene, as sole sources of carbon and energy. Four representative predominant *Arthrobacter* strains in the rhizospheres of various plants could quickly consume the *n*-alkanes dodecane (C_{12}), hexadecane (C_{16}) and decosane (C_{22}) and the aromatic hydrocarbons naphthalene and phenanthrene from their growth media. GLC analysis of the *n*-alkane-incubated biomass revealed that cells accumulated in their lipids fatty acids equivalent in chain length to the substrate alkanes: that is, the cells could metabolize oil constituents further after their uptake.

In conclusion, the rich oil-utilizing microflora around roots of crop plants obviously clean oil-polluted soil just adjacent to the roots. Our new work consolidates a few earlier reports[4,5] by suggesting densely cultivating suitable plants in polluted Kuwaiti desert areas as a promising approach for their bioremediation. Heavily polluted areas would first have to be mixed with sand from adjacent clean areas to reduce the oil content to 10% by wt or less, the concentrations tolerable by the crops.

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1. Sorkhoh, N. A., Al-Hasan, R. H., Radwan, S. S. & Hoepner, Th. *Nature* **359**, 109 (1992).
2. Sorkhoh, N. A. *et al. Envir. Pollut.* **65**, 1–17 (1990).
3. Sorkhoh, N. A. *et al. J. appl. Bact.* **69**, 850–863 (1990).
4. Lee, E & Banks, M. K. *J. envir. Sci. Hlth* **A28**, 2187–2198 (1993).
5. Thorhaug, A., Marcus, J. & Booker, F. *Mar. Pollut. Bull.* **16**, 355–360 (1985).