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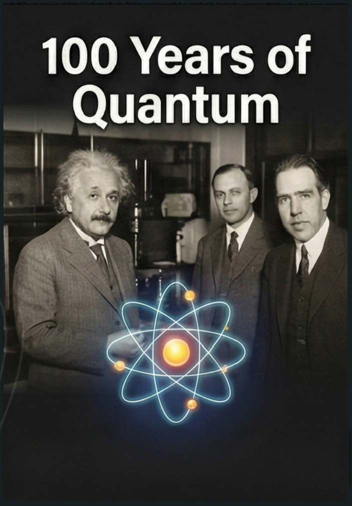
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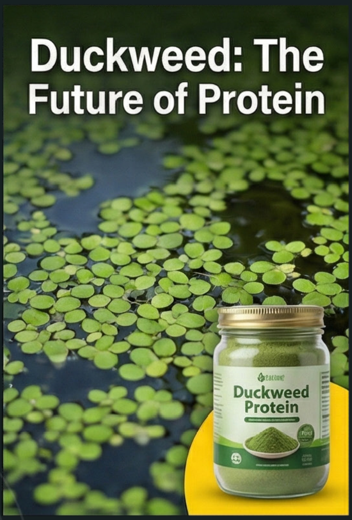
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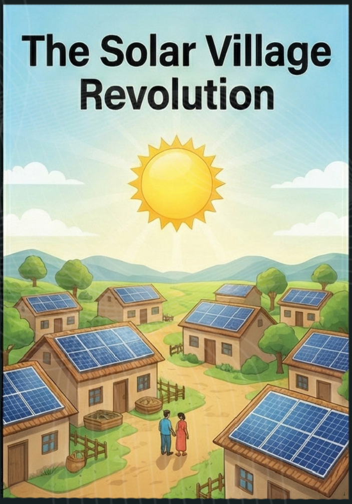
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Hidden Hotspots: How the Environment Fuels the Rise of Antibiotic Resistance

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Antibiotic resistance is often seen as an impending public health crisis connected to hospitals, patients, and medicine misuse. However, this situation is much more complicated than it appears. Resistance arises not only in clinics and intensive care units but also in rivers, soils, wastewater, and even remote places like natural hot springs. These environments support diverse microbial communities that tolerate antibiotics and develop resistance. Following these transformations, nature becomes a potent source of resistance genes. Recently, scientists have identified different trends indicating that environmental bacteria increasingly acquire and exchange resistance traits faster than ever before. Research studies across Europe and Asia have found high levels of resistance genes such as sul1, ermB, and intI1 in soils contaminated by wastewater effluents, even in regions with limited antibiotic use. In aquatic ecosystems, bacteria often resist common antibiotics like sulfamethoxazole and ciprofloxacin(Franklin et al., 2024). These events tend to highlight how human activities, including agriculture and pharmaceutical wastes, could accelerate this evolutionary change.

KINNIYA & WAHAWA HOTSPRINGS:
UNCOVERING THE HIDDEN RESISTANCE

One bacterial group, Pseudomonas, has emerged as a key player in this story. Pseudomonas is one of the first microorganisms to respond in polluted ecosystems. It is known for its capacity to adapt to harsh conditions. Pseudomonas is a frequent carrier of multiple antibiotic resistance genes. For example, a 2024 study from Bangladesh found that Pseudomonas aeruginosa isolated from the Buriganga River demonstrated widespread resistance to tetracyclines and cefotaximes. It also indicates growing resistance to carbapenems, the antibiotics once considered the last line of defence (Sharif et al., 2024).

Our recent studies at NIFS provide new insights into how environmental factors might influence resistance profiles, even in untouched natural areas. We investigated Pseudomonas isolates from two geothermal sites in Sri Lanka: the Kinniya and Wahawa hot springs, and the results were striking. According to our findings, both sites harboured Pseudomonas strains resistant to two antibiotic classes, namely aminoglycosides and fluoroquinolones, which are widely used in clinical medicine. As a noteworthy feature, the resistance levels and diversity varied significantly between the two sites, suggesting that environmental factors play a crucial role in shaping resistance patterns (Gunathilaka et al., 2024).

The Kinniya hot spring is a well-known tourist destination often visited by locals and foreign travellers. Tourists and residents of the area regularly use the Kinniya hot spring for spiritual bathing. It exhibited a significantly higher level of antibiotic resistance. Isolates from Kinniya hot spring showed stronger resistance patterns for fluoroquinolones like ciprofloxacin and aminoglycosides such as gentamycin and amikacin, with some even showing intermediate resistance to these antibiotics. The increased resistance could be due to those reasons that can introduce antibiotic residues and resistant bacteria into the environment via wastewater and runoff.

On the other hand, the Wahawa site is a tube well system in a relatively undisturbed area. It exhibited lower antibiotic resistance levels than the Kinniya hot spring. Although Pseudomonas strains from Wahawa continued to resist aminoglycosides and fluoroquinolones, the overall resistance level decreased. They were susceptible to several β-lactam antibiotics. This difference highlights how human presence and pollution can speed up the evolution of resistance among environmental microbial communities.

These findings are highly consistent with what we see in other parts of the world, particularly that human activities play a significant role in driving environmental antibiotic resistance. Natural microbial communities have the potential to spread the developed resistance genes within themselves to other bacteria through horizontal gene transfer activities. This indicates that the environments such as hot springs, rivers, and groundwater are not isolated ecosystems; they are linked to human health through water use, recreation, agriculture, and the food chain.

Fighting antibiotic resistance is not only a clinical or pharmaceutical issue but also an environmental concern. Monitoring environmental resistomes, expanding genomic surveillance, and integrating molecular tools such as metagenomics could help trace how resistance evolves and spreads. A key part of these efforts is reducing the flow of antibiotics and resistant microbes into the natural environment. Improving wastewater treatment, regulating antibiotics used in agriculture, and ensuring safer disposal of pharmaceuticals, like more innovative prevention strategies, are vital steps to decrease the entry of antibiotics into the ecosystem.

The emergence of antibiotic resistance in Pseudomonas species in Kinniya and Wahawa hot springs is a powerful reminder that resistance is never an isolated process. Antibiotic resistance in natural microbiota is interconnected with several other factors, such as human activities, infrastructure, and environmental interactions. We can intensify our efforts to reduce the spread of resistance by pinpointing and managing these underlying causes. Thus, it might help mitigate the overuse of antibiotics and protect ecosystems that sustain life.