Seminari Limnologici 2015

Venerdì 30 ottobre, ore 11.00

Consiglio Nazionale delle Ricerche
Istituto per lo Studio degli Ecosistemi
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Worldwide spread of antibiotic resistance

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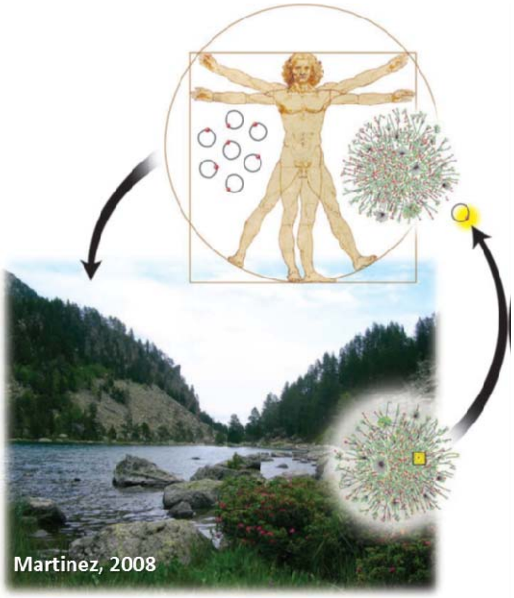
http://www.ise.cnr.it/it/people/researcher/dicesare



Martinez, 2008

The “golden era” of antibiotics in which many new molecules were discovered is over. Antibiotic resistance is spreading worldwide. Many antibiotics are of natural origin, and, thus many antibiotic resistance genes (ARGs) are of natural origin, meaning that the contribution of environmental bacterial communities to the spread of ARGs is crucial. For this reason the environmental and clinical settings are strictly connected. Moreover, antibiotic resistant bacteria from human or animal hosts can reach the environment, in particular waters, by different routes such as industrial and agriculture discharges, hospital wastes, and others. They can come back to the original host through the food chain or through human recreational activity (e.g. swimming). The importance of these different paths for the spread of antibiotic resistance (AR) is only partially known. The exchange of ARGs between environmental and human bacteria by horizontal gene transfer was only recently reported. Moreover, different selective pressures with respect to the human host (e.g. heavy metals) influence the aquatic environment. This suggests the presence of AR selection systems like heavy metal resistance genes that can co-select ARGs, driving the spread of ARGs potentially also to humans. Further studies on the presence and the abundance of ARGs in aquatic environments, and the transfer of ARGs (particularly also in respect to the AR selection systems) to humans are needed.

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Il Direttore
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