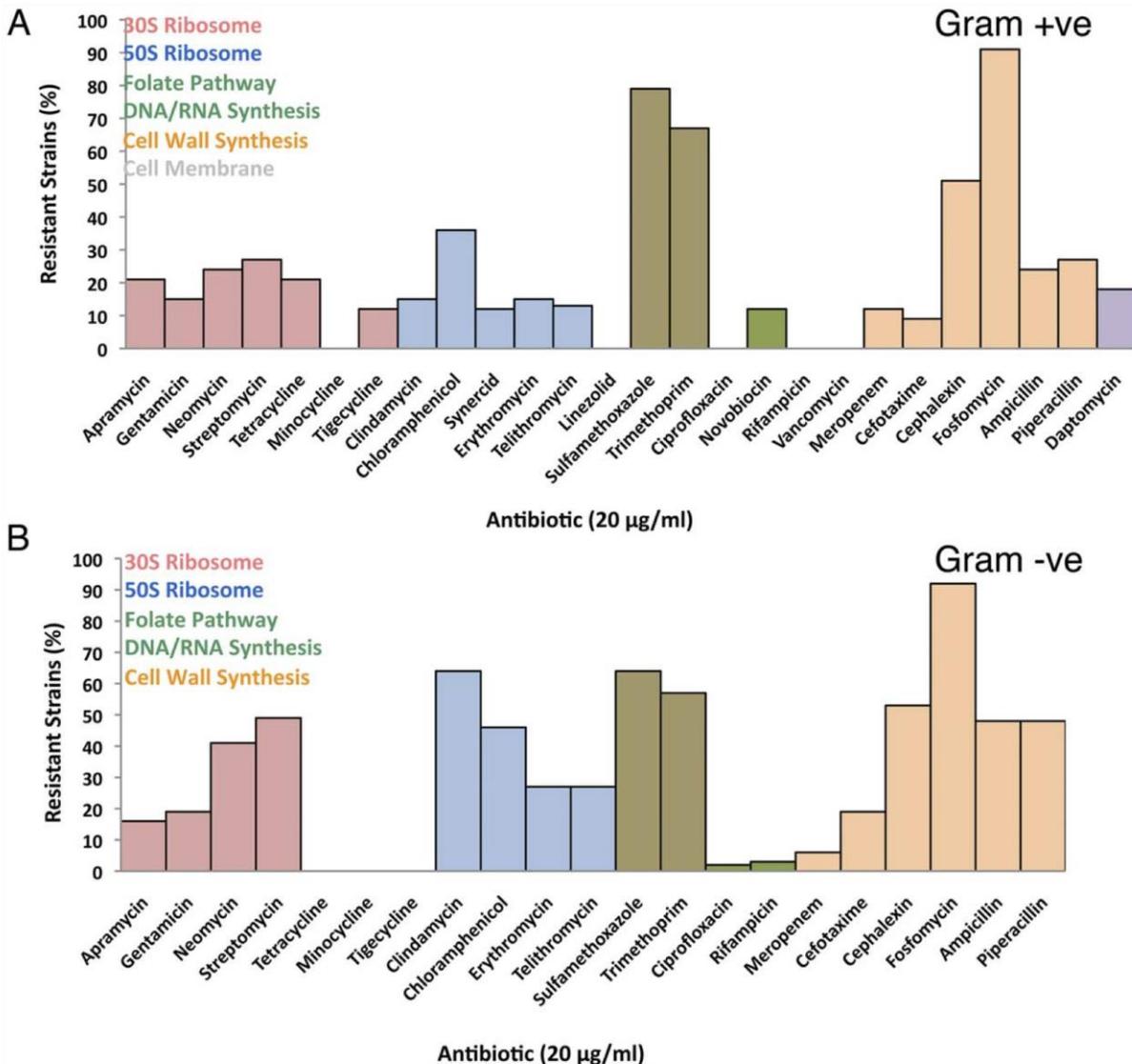




Origins of Antibiotic Resistance



Caption: Different strains of bacteria found in Lechuguilla Cave in New Mexico were tested for resistance to a variety of antibiotics. The antibiotics are grouped by color to show the similar mode of action/target they employ to kill bacteria. (A) Resistance in Gram-positive strains of bacteria; (B) Resistance in Gram-negative strains of bacteria.

BACKGROUND INFORMATION

Since the discovery of the first antibiotic, penicillin, in 1928, antibiotics have revolutionized the fight against bacterial infections. Antibiotics are chemicals that specifically target and kill bacteria. Unfortunately, they are often prescribed unnecessarily and frequently misused by patients. Research has shown that these trends have contributed to the recent evolution of bacteria that are resistant to antibiotics. What is less clear is whether the bacterial genes that confer antibiotic resistance (collectively called the “resistome”) are all newly evolved since the introduction of antibiotics or have evolved independently.

Origins of Antibiotic Resistance

To answer this question, scientists collected bacteria from locations that had never been exposed to humans or modern antibiotics. Their study site, a remote cave located within Carlsbad Caverns National Park in New Mexico, called Lechuguilla Cave, was estimated to have been isolated from human contact and surface contamination (such as rainwater) for at least 4 million years, with extremely restricted access since its discovery in the 1980s. The scientists collected over 500 unique bacterial strains from three locations in the cave. Of these, 93 culturable strains were randomly selected to be screened for resistance to modern-day antibiotics.

About 60% of the bacteria were Gram-negative, which means that they have a protective outer membrane and are resistant to many antibiotics. The remaining bacteria were classified as Gram-positive, meaning they lack this outer membrane. The bacteria were tested for survival against 26 different antibiotics, each falling into one of six categories based on the protein or pathway it targeted within bacterial cells: 30S ribosome, 50S ribosome, folate pathway, DNA/RNA synthesis, cell wall synthesis, or the cell membrane. Each strain of bacteria was tested by placing it on growth medium (food) that contained a high concentration of an antibiotic. If the bacterial strain could reach a cell density (a measure of bacterial growth) of at least half that achieved by the same strain growing without antibiotic, it was considered resistant to the antibiotic.