jugation, with a preferential transfer of the A-determinant. Following these observations, the physical structure of P111-ACS and of its P111-A segregant has been determined. The plasmids were isolated by CsCl gradient centrifugation in presence of ethidium bromide. After removal of the dye, the contour length of the plasmids was measured by electron microscopy, using SV40 DNA molecules as internal standard. In *E. coli* K12 F⁻, P111-ACS shows both the structures of: 1. a plasmid aggregate formed by 19.2 μm molecules (inferred to be the transfer factor) and 3.2 μm molecules (inferred to be the R-determinants, A, C or S); 2. a plasmid cointegrate of 29.6 μm; occasionally a plasmid cointegrate of 22.8 μm was also observed. In the same host-cell P111-A shows only one structure: a molecule of 22.8 μm in length inferred to be the plasmid cointegrate TF-A. These results are in agreement with a cointegrate state of the R-determinants and the TF during the transfer the A-determinant probably having a preferential attachment to the TF compared to the other replicons.

A New Kanamycin/Neomycin Phosphotransferase Found in Staphylococci

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Aminoglycoside-phosphotransferases I, II and III have been reported to be involved in aminoglycoside resistance of gramnegative bacteria. In two strains of *Staph. aureus* and one strain of *Staph. epidermidis* a phosphorylating enzyme was observed, differing from these enzymes in the substrate profile and in pH optimum. Kanamycin/neomycin phosphotransferase IV rapidly phosphorylated and inactivated kanamycin A, B and C, neomycin B and C, paromomycin, gentamycin A and B, butirosin, lividomycin and ribostamycin. After two hours of incubation amikacin was completely inactivated, but phosphorylation was only slow. This certainly is the reason for the susceptibility of the strains against amikacin. Over the range 25–45 °C, there was significant phosphorylation with optimal activity at 37 °C. A temperature of 55 °C for 15 min inactivated the enzyme completely. Enzymatic activity generally was found over the pH range 5 to 9. For the kanamycins and the ribostamycin group, the optimal pH was 5.5 to 6.0 in citrate phosphate buffer, for the neomycin group 8.0 to 8.5 in *Tris*-maleate buffer. In two strains, resistance to aminoglycosides was found to be plasmid-mediated. The characterization of the resistance plasmids by sucrose gradient centrifugation and electron microscopy revealed molecular sizes of 36.5 (*Staph. aureus* E 142) and 21.5 (*Staph. epidermidis* 147) megadaltons respectively. Preliminary experiments indicate that resistance in *Staph. aureus* 170 might be governed by chromosomally located genes.

Mutual Influence Between λ-Phages and R-Factors

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A few years ago we stated that MS₂-phage-infection of cells carrying R-factors does diminish or even prevent the R-transfer (Path. Microbiol. *40*, 153, 1974, and *41*, 194, 1974). Now we examined the influence of fi⁺ R-factors on λ-lysogeny and vice-versa and obtained the following result: If *E. coli* K12 carrying R192 grown in Columbia broth were infected with phage λ at a multi-plicity of infection of 10 PfU and incubated for 24 h at 37 °C, we could not detect afterwards any lysogenic clones out of one thousand. If *E. coli* K12, which are not carrying an R-factor, were infected and incubated under the same conditions, we found about 70% out of all cells lysogenic after 24 h. After further incubation for 24 h the R-free progeny was 100% lysogenic, the cells carrying an R-factor however only for 30%. If λ-lysogenic and λ-sensitive cells of the same strain were R-infected under equal conditions, both transferred the R-factor in the same frequency. If, however, R-carrying cells were λ-lysogenic, we detected a serious reduction of the frequency of R-transfer. With derepressed fi⁺ R-factors in doing so the ability for building sex-pili was lost. Therefore the interactions between fi⁺ R-factors and λ-phages seems to depend on which of the two genomes is in the cell first. As these investigations were also done with wild-R-factors and wild-strains of *E. coli*, they allow allusions to the influence of the epidemiology of R-factors. The molecular biological explanation of these phenomenona is at work.

Proteus mirabilis Wild-Strains as Donors and Recipients of Wild R-Factors

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At the microbiological examination of urine isolates coli bacteria are isolated beside cells of *Proteus mirabilis*. Thereby most of all the coli bacteria are containing infectious R-factors while the *Proteus* strains are R-negative and do only possess the well-known chromosomal resistance against polymyxin B and tetracycline. This observation shows that – considering the reception of R-factors – *Proteus* does behave differently from the rest of the *Enterobacteriaceae*. Therefore we investigated the chloramphenicol-resistance-transfer of multiple-resistant *Proteus* into antibiotic-susceptible *Proteus* cells, the R-infection of *E. coli* into *Proteus mirabilis* and vice-versa. We obtained the following results: 2 out of 8 multiple-resistant *Proteus* wild-strains did not transfer their resistances on the 39 recipient-strains. The other 6 donor-strains transferred their resistance on the following number of the recipient-strains: 2, 6, 8, 10, 11 and 31. Six of the 39 recipient-strains did not act as recipients with any of the 8 donor strains, 10 strains conjugated with only 1, 10 with only 2 and the rest with 3 to 5 of the donor strains. The frequency of transfer came to 10⁻⁶ and 10⁻⁷. Besides the resistance for chloramphenicol mostly also the other resistances of the donor strains were transferred. From the 39 *Proteus* recipient strains only 12 accepted – with a low frequency – R192 from *E. coli* K12, and out of 8 *Proteus* donor strains only 1 was able to transfer the resistance into restriction-free cells of *E. coli* K12 with the low frequency of 5 × 10⁻⁷. From these results we conclude that *Proteus mirabilis* is a bad donor and recipient for R-factors.

Rifampicin-Resistance in *E. coli*: Comparison of Microbiological and Enzymatic Properties

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The antibiotic rifampicin inhibits the growth of *Escherichia coli* by forming a tight complex with the bacterial RNA polymerase and thus inhibiting the enzyme. Cells