(Kersters and De Ley, 1975). The following groups of bacteria can clearly be distinguished:

1) *Alc. faecalis* – *Alc. odorans* (56–60% GC): the electrophoregrams of 70 strains are very similar; no differentiation is possible between *Alc. faecalis* and *Alc. odorans*.

2) *Alc. denitrificans* – *Achr. xylosoxidans* (65–70% GC): 50 strains form a fairly homogeneous group, clearly different from the *Alc. faecalis* – *Alc. odorans* group and from the marine *Alcaligenes*. An overall phenotypic similarity between *Achr. xylosoxidans* and *Alc. denitrificans* has been reported by Yabuuchi et al. (1974).

3) *Bordetella bronchiseptica* (67–69% GC): 15 strains display almost identical electrophoregrams and form a tight cluster at the border of the *Alc. denitrificans* – *Achr. xylosoxidans* group. In a numerical analysis Johnson and Sneath (1973) emphasized already the phenotypic relationship between *Alcaligenes* and *B. bronchiseptica*.

4) The protein patterns of the marine *Alcaligenes* strains (*Alc. aquamarinus*, *Alc. aestus*, *Alc. cupidus*, *Alc. pacificus*, *Alc. venustus*) form a heterogeneous cluster completely different from all the other investigated strains.

5) The electrophoregrams of approximately 50 motile so-called *Alcaligenes* and *Achromobacter* strains are different from each other and different from the protein patterns of the strains from groups 1–4. It is very likely that these strains belong to other genera.

The combined data of the electrophoregrams, DNA:rRNA hybridizations (De Ley, J. and Segers, P., unpublished results), DNA base composition and the occurrence of the Entner-Doudoroff pathway (De Ley et al., 1970) will lead towards a thorough revision of the taxonomy of the genera *Alcaligenes* and *Achromobacter*.

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Intra- and intergeneric similarities of the rRNA cistrons of *Acetobacter* and *Gluconobacter*

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The similarities between ribosomal ribonucleic acid cistrons from different bacteria are a rough measure of their phenotypic and phylogenetic relationship (De Ley and De Smedt, 1975; De Smedt and De Ley, 1977). Hybrids were formed between ^{14}C-rRNA from suggested neotypes of *Gluconobacter* and *Acetobacter*, and DNA from other strains of both genera and from organisms which are probably related with these genera on the basis of previous hybridization data (De Smedt and De Ley, 1977; De Ley et al., unpublished). Each hybrid was described by its $T_{m(e)}$ and percentage of rRNA binding; both parameters were plotted on rRNA similarity maps.

Parameters of hybrids formed with rRNA from *Gluconobacter oxydans* subsp. *oxydans* NCIB 9013 showed that the acetic acid bacteria consist of two separate but closely related groups corresponding with both genera *Acetobacter* and *Gluconobacter*. When compared with rRNA from *Acetobacter aceti* subsp. *aceti* NCIB 8621, both genera are indistinguishable, showing that the strains of *Acetobacter* are as varied among themselves as they are versus strains of *Gluconobacter*.

The good correlation between the $T_{m(e)}$ and % rRNA binding of the heterologous hybrids and the numerous phenotypic similarities between both genera show that the sacrosanctity of the type of flagellation as primary criterion to separate genera into different families, does not hold for the acetic acid bacteria.

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Influence of restriction on the transfer of resistance against antibiotics in *Staphylococcus aureus*

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By phage typing *Staphylococcus aureus* can be divided into a number of restriction groups (I–III). Group II strains contain a S-adenosylmethionine-independent restriction enzyme (Sussenbach et al., 1976; Stobberingh, Schiphof and Sussenbach, 1977). A number of restriction-deficient mutants from non-lysogenic strains in group I and II have been isolated (Stobberingh and Winkler, 1977).

The transfer of resistance in *S. aureus* occurs probably by transduction. General transduction with homologous or selected acceptor strains in vitro has been studied by various authors. In vivo and in vitro some kind of high frequency of transduction has been described. With acceptor strains from other restriction groups the frequency of transfer is low.

In this paper the influence of restriction on the frequency of transduction (FOT) of resistance was studied with the help of restriction-deficient mutants. It was shown previously that the FOT varies for different markers (plasmid size), for different transducing phages and for different acceptor strains.

The resistance markers were derived from a series of multiple resistant strains (MR) isolated in the University hospital. They were generally present on plasmids. To study the influence of restriction separately, the markers (resistance against tetracycline, chloramphenicol and penicillin) were first transferred with a suitable phage from each MR strain to the non-lysogenic strain 57. They then all carry the same modification. With such a series of 57 (tet^+) strains as donors and with the same transducing phage (80) the FOT into a series of acceptor strains from different restriction groups and including the restriction-deficient mutants could be studied. The eight (tet^+) markers were easily transferable from strain 57 (group I modification) into group I strains. The FOT into group II strains was very much lower, but the restriction-deficient mutants from group II were good acceptors. The FOT varied from strain to strain quite parallel with the titre of the transducing phage suggesting that the transferred plasmids are just as sensitive to restriction as phage.