

EFFECTS OF VIOMYCIN AND POLYMYXIN B ON PROTEIN SYNTHESIS *IN VITRO*

Sir :

Of aminoglycosidic antibiotics, streptomycin, kanamycin, neomycin, paromomycin, gentamicin and hygromycin cause codon misreading in the bacterial ribosomal system^{1,2)}, but kasugamycin^{3,4)} and spectinomycin⁵⁾ do not.

For the purpose of elucidating the structural basis of miscoding activity of aminoglycosides, the degradation products of aminoglycosidic antibiotics were investigated. Paromamine, neamine, deoxystreptamine, streptamine and N-methyl-deoxystreptamine exhibited miscoding activity, although the grade of miscoding was less than that caused by kanamycin. But actinamine, 3-amino-3-deoxyglucose, and 6-amino-6-deoxyglucose failed to exert miscoding activity by the method employed. It was indicated that the deoxystreptamine or streptamine moiety of aminoglycosidic antibiotics seems to play an important role in the miscoding activity^{6,7)}.

Viomycin, a basic peptide antibiotic, was also reported to cause codon misreading²⁾. It suggests that the basic property of antibiotics might be enough to cause codon

Table 1. Effect of viomycin and polymyxin B on protein synthesis with endogenous mRNA in *E. coli* ribosomal system

| | Relative incorporation of ¹⁴ C-leucine |
|----------------|--|
| Complete | 100 |
| Polymyxin B | |
| 1,000 units/ml | 158 |
| 100 units/ml | 97 |
| 10 units/ml | 105 |
| Viomycin | |
| 100 μg/ml | 16.5 |
| 10 μg/ml | 11.3 |
| 1 μg/ml | 12.3 |

Incorporation of ¹⁴C-leucine (100) = 5.78
μmoles/mg, protein.

The complete reaction mixture contained :
ATP 2 μmoles/ml, 3-phosphoglycerate (3PG) 5
μmoles/ml, ribosome of *E. coli* B 4 mg/ml, S-100
fraction of *E. coli* B 1.5 mg/ml, ¹⁴C-leucine 0.2
μc/ml, KCl 100 μmoles/ml, Tris 50 μmoles/ml
(pH 7.4) and MgCl₂ 10 μmoles/ml.

Incubation : at 37°C for 15 minutes.

misreading, and seems to conflict with our assumption that the deoxystreptamine or streptamine moiety of antibiotics is essential for the miscoding activity.

In order to clarify the discrepancy, the effects of viomycin and polymyxin B, basic peptide antibiotics, on protein synthesis were studied in the ribosomal system obtained from *E. coli* B. The results are presented in this communication.

Viomycin was observed to inhibit protein synthesis with endogenous mRNA, polyphenylalanine synthesis with poly U and polylysine synthesis with poly A, but polymyxin B did not significantly inhibit amino acid incorporation into polypeptide in all the systems examined. By the method employed, both basic peptide antibiotics did not increase significantly the incorporation of lysine, arginine, serine and threonine with poly A and that of phenylalanine, leucine, serine and threonine with poly U. The results are summarized in Tables 1 and 2. Polymyxin B was observed to increase the amino acid incorporation at a concentration of 1,000 units/ml (100 mcg/ml). However, the concentration was too high to attribute to it any significance in the mechanism of action of polymyxin B, because the minimal growth-inhibitory concentration for the organism, *E. coli* B, was 0.02 units/ml.

In the present experiment, viomycin inhibited polypeptide synthesis, but failed to cause miscoding. It appeared to be different from the results obtained by DAVIES *et al.*²⁾ However, the miscoding activity of viomycin seemed to be insignificant even in the paper of DAVIES *et al.*²⁾

In summary, viomycin was observed to inhibit protein synthesis, but not to cause miscoding in an *E. coli* ribosomal system. Polymyxin B did not significantly affect protein synthesis in the same system. The results suggested that the basic property of antibiotics alone seems not to be enough to cause miscoding.

Bottomycin A₂, another basic antibiotic, was observed to inhibit protein synthesis but not to cause codon misreading in a bacterial system^{8,9)}. It also seems to support the conclusion presented above.

Table 2. Effect of polymyxin B and viomycin on the amino acid incorporation with poly U or poly A in an *E. coli* ribosomal system

| | Poly U | | | | Poly A | | | |
|----------------------------|--------|------|------|------|--------|------|------|------|
| | Phe | Leu | Ser | Thr | Lys | Agr | Ser | Thr |
| Complete | 100 | 6.0 | 2.0 | 1.5 | 100 | 7.5 | 0.14 | 0.32 |
| -mRNA | 2.7 | 2.4 | 1.9 | 2.2 | 16.4 | 8.6 | 0.12 | 0.35 |
| Polymyxin B 1,000 units/ml | 149 | 15.2 | 4.1 | 6.5 | 138 | 8.4 | 0.18 | 0.40 |
| 100 units/ml | 93 | 7.1 | 2.7 | 2.7 | 105 | 7.5 | 0.14 | 0.36 |
| 10 units/ml | 98 | 6.4 | 2.5 | 2.9 | 122 | 6.8 | 0.12 | 0.34 |
| Viomycin 100 μ g/ml | 4.6 | 2.9 | 0.56 | 0.24 | 7.3 | 0.7 | 0.05 | 0.02 |
| 10 μ g/ml | 9.2 | 2.1 | 0.76 | 0.20 | 24.9 | 2.8 | 0.06 | 0.09 |
| 1 μ g/ml | 17.4 | 2.0 | 1.10 | 0.56 | 32.7 | 4.9 | 0.09 | 0.26 |
| Kanamycin 10 μ g/ml | 24.1 | 8.4 | 3.7 | 2.8 | 156 | 21.3 | 0.68 | 1.68 |

The number represents relative incorporation of ^{14}C -amino acid. Incorporation of phenylalanine (100) = 89 μ moles/mg protein. Incorporation of lysine (100) = 540 μ moles/mg protein.

In the poly U system, the complete reaction mixture contained: ATP 2 μ moles/ml, 3PG 5 μ moles/ml, GTP 0.03 μ moles/ml, S-30 fraction of *E. coli* B 4 mg/ml, sRNA of *E. coli* B 500 μ g/ml, poly U 50 μ g/ml, ^{14}C -amino acid 0.2 μ c/ml, Tris 50 μ moles/ml, NH_4Cl 160 μ moles/ml and MgCl_2 10 μ moles/ml.

In the poly A system, the complete reaction mixture contained: ATP 2 μ moles/ml, 3PG 5 μ moles/ml, GTP 0.03 μ moles/ml, ribosomal fraction of *E. coli* B 1 mg/ml, S-100 fraction of *E. coli* B 0.8 mg/ml, sRNA of *E. coli* B 500 μ g/ml, poly A 50 μ g/ml, ^{14}C -amino acid 0.2 μ c/ml, Tris 50 μ moles/ml, NH_4Cl 160 μ moles/ml and MgCl_2 10 μ moles/ml.

Incubation: at 37°C for 15 minutes.

NOBUO TANAKA
SATOKO IGUSA

Institute of Applied Microbiology,
University of Tokyo,
Tokyo

(Received December 22, 1967)

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