THE UNIVERSITY OF MANITOBA

THE NATURE OF ANTIBIOTIC SUBSTANCES FROM STAPHYLOCOCCI

bу

ANDY CHUN-YANG HSU

A THESIS

SUBMITTED TO THE FACULTY OF GRADUATE STUDIES

IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE DEGREE

OF DOCTOR OF PHILOSOPHY

DEPARTMENT OF MEDICAL MICROBIOLOGY

WINNIPEG, MANITOBA

February 1971



TO MY PARENTS AND WEI-JEN

ABSTRACT

THE NATURE OF ANTIBIOTIC SUBSTANCES FROM STAPHYLOCOCCI

Antibiotics from the 29297 and 36534 strains of Staphylococcus epidermidis were purified by acid and Ba(OH)₂, followed by ZnCl₂ which separated the active principles into two fractions. These were designated the zinc-precipitable and zinc-soluble fractions. The use of Dowex and/or Sephadex further increased the specific activity of these antibiotic components. All fractions of both antibiotics were crystallized from aqueous solutions. Recrystallization and methanol precipitation of the antibiotics brought the specific activity to a relatively constant value.

These purified antibiotic fractions contained no carbohydrates, proteins, lipids, nucleic acids or heavy metal ions. All fractions each contained 11 amino acid residues, eight of which they shared in common. Molecular weights were about 1200. No C- or N-terminal amino acid residues were detected. The ratio of L- to D-amino acids for 29297 zinc-soluble and 36534 zinc-precipitable fractions was 7:4, while that for 29297 zinc-precipitable and 36534 zinc-soluble fractions was 5:6. Thus the antibiotics were low molecular weight cyclic peptides of which about half the amino acids were D-isomers.

The peptide sequence of the 29297 zinc-precipitable fraction was tentatively determined. It had the structure:

cyclo-Lys-Ala-Asp-Glu-Ser-Leu-Thr-Gly-Val-Gly-Arg, or cyclo-Lys-Ala-Asp-Glu-Ser-Leu-Thr-Val-Gly-Gly-Arg.

ACKNOWLEDGEMENTS

The author is gratefully indebted to Dr. G. M. Wiseman for his advice, patient guidance and constant encouragement during the years of his study in this University. He also wishes to express his sincere gratitude to Dr. J.C. Wilt, the Head of the Department of Medical Microbiology, for his encouragement and assistance. A special word of thanks is given to all members of the Department of Medical Microbiology for their help throughout these years. He greatly appreciates the financial assistance from the Medical Research Council without which this study would not have been possible. Finally, he would like to thank Miss Marlene Mandal and Mr. J. Mazur for their assistance in preparing this manuscript.

TABLE OF CONTENTS

	PAGE
LIST OF TABLES	iv
LIST OF FIGURES	vii
INTRODUCTION	1
REVIEW OF THE LITERATURE	2
Peptide Antibiotics from Eubacterials I. Bacilysin II. Bacitracins III. Edeine IV. Licheniformin V. Micrococcin and Micrococcin P VI. Mycobacillin VII. Nisins VIII. Polymyxin Group A. Polymyxins A, B, C, D, and E B. Circulins C. Colistins D. Polymyxin M E. Summary IX. Polypeptin X. Serratamolide XI. Subtilins XII. Tyrothricin, Tyrocidines and Gramicidins A. Tyrothricin B. Tyrocidines	2 4 7 23 28 30 34 36 38 51 54 60 62 65 66 68 72 73
C. Gramicidins D. Gramicidin S E. Gramicidin J ₁ and J ₂ XIII. Staphylococcal Antibiotics	78 85 88 91
MATERIALS AND METHODS I. Materials	93 93 93 94 94 94
(3). Concentration of the antibiotic fluids	96 96

	PAGE
(5). Gel filtration	97
field	98 99 101 101
RESULTS	103 103
Production	103 107 107 107
III. Facotrs Influencing Antibiotic Assay	110 110 110 112
PART II. PURIFICATION	115 115 115 115
(2). Precipitation by organic compounds	124 124 127
Soluble Fractions	131 131 131 134
V. Final Purification Schemes for Staphylococcal Antibiotics 29297 and 36534	138 145 145
Effect of 29297 zinc-precipitable fraction on viability of <u>S</u> . <u>aureus</u> 209P	145 147 t
irradiation	147 147 149
(4). Melting points	149 151 151 154
(3). Pronase hydrolysis	154

	PAGE
(4). Oxidation by nitrous acid	157 160
acid oxidases	161 163
DISCUSSION	
SUMMARY	
BIBLIOGRAPHY	
APPENDICES	201

LIST OF TABLES

rable .		PAGE
I.	Ion-Exchange Methods in Bacitracin Purification	11
II.	Amino Acid Composition of Nisin A	39
III.	The Amino Acid Composition of Polymyxins	44
IV.	Summary of the Amino Acid and Fatty Acid Composition of Polymyxins	62
V .	Structure of the Members of the Polymyxin Group of Antibiotics	63
VI.	Amino Acid Composition of Gramicidins Proposed by Ramachandran (1963)	82
VII.	Properties of Staphylococcal Antibiotics	92
VIII.	Effect of Agitation and Supplementation of Dolman-Wilson Medium on Antibiotic Production in Staphylococci	105
IX.	Effect on Antibiotic Production of Proteose Peptone Replacement in Supplemented Dolman-Wilson Medium by Casamino Acids or Corn-Steep Liquor	106
х.	Comparison of Antibiotic Titres of Active Fluids Sterilized by Two Methods	111
XI.	Effect of Assay Medium on the Antibiotic Titres	113
XII.	Relationship Between Antibiotic Titre and Length of Incubation Period of the Indicator Strain	114
XIII.	Effect of Hydrochloric Acid on the Activity of Staphylococcal Antibiotics	116
XIV.	Precipitability of Antibiotic Fluids with Metal Salts at Neutral pH and Solubility of the Resulting Precipitate at Different pH Levels	
XV.	Effect of Barium Hydroxide on the Activity of Staphylococcal Antibiotics	120
XVI.	Composition of the Effects of $MnCl_2$ and $ZnCl_2$ on the Activity of Staphylococcal Antibiotics	

ABLE		PAGE
XVII.	Relationship Between pH of the Antibiotic Fluids, Concentration of Zinc Ions and Recovery of Zinc-Precipitated Antibiotics	123
VIII.	Precipitability of Antibiotic Fluid in the Presence of Some Organic Compounds	125
XIX.	Effect of Methanol on the Activity of Staphylococcal Anti- biotics	126
XX.	Initial Scheme Used for Partial Purification of Staphylo- coccal Antibiotics	128
XXI.	Specific Activity and Percent Recovery of Staphylococcal Antibiotics 29297 and 36534 at Different Purification Stages	130
XXII.	Effect of Dowex 50-X2 Passage on Specific Activity of Zinc-Precipitable and Soluble Fractions of Antibiotics 29297 and 36534	133
XIII.	Efficiency of Sephadex G-15 Gel Filtration in the Further Purification of Antibiotics 29297 and 36534	137
XXIV.	Purification Scheme of Staphylococcal Antibiotic 29297	140
XXV.	Purification Scheme of Staphylococcal Antibiotic 36534	141
XXVI.	Specific Activity and Percent Recovery of Staphylococcal Antibiotic 29297 at Different Stage of Purification	143
XVII.	Specific Activity and Percent Recovery of Staphylococcal Antibiotic 36534 at Different Stage of Purification	144
VIII.	Effect of Antibiotic 29297 Zinc-Precipitable Fraction on Viability of Indicator Strain of Staphylococcus aureus 209P	146
XXIX.	Stability of Partially and Highly Purified Staphylococcal Antibiotics Under Ultraviolet Light Irradiation	148
XXX.	Positive Chemical Tests on Antibiotics 29297 and 36534	152
XXXI.	Negative Chemical Tests on Antibiotics 29297 and 36534	153
XXII.	The Effect of Pronase on Highly Purified Antibiotic Preparations	156

TABLE		PAGE
XXXIII.	Effect of Nitrous Acid Oxidation on the Titre of Highly Purified Antibiotics	158
XXXIV.	Amino Acid Composition of Staphylococcal Antibiotics	159
XXXV.	Oxidative Deamination of Acid Hydrolysates of Purified Antibiotics by L- and D-Amino Acid Oxidases	162
XXXVI.	Amino Acid Content of Peptide Fragments Isolated from Partial Acid Hydrolysates of the 29297 Zinc-Precipitable Fraction	164
XXXVII.	Tentative Peptide Sequences of Fragments Isolated from Partial Acid Hydrolysates of Antibiotic 29297 Zinc-Precipitable Fraction	165

LIST OF FIGURES

FIGURE		PAGE
1.	Effect of Temperature of Incubation on the Antibiotic Production	108
2.	Effect of Length of Incubation on the Antibiotic Production	109
3.	Dowex 50-X2 Elution Patterns of Different Fractions of Antibiotics 29297 and 36534	132
4.	Elution Patterns of Antibiotic 29297 from Sephadex G-15 Columns	135
5.	Elution Patterns of Antibiotic 36534 from Sephadex G-15 Columns	136
6.	Crystal Forms of Staphylococcal Antibiotics	139
7.	The Ultraviolet Light Absorption Spectra of Staphylococcal Antibiotics	150
8.	Tentative Structure of 29297 Zinc-Precipitable Fraction	167

INTRODUCTION

INTRODUCTION

It has been known for many years that the staphylococci produce antibiotics. Most investigations, however, have been mainly concerned with the isolation of these growth-inhibiting strains and the characterization of their inhibitory spectra. Consequently, little was known of their chemical nature.

Hsu and Wiseman (1967) made a study of large numbers of coagulase-positive and negative staphylococci. They found that 4.9% of 1065 coagulase-positive and 8.5% of 387 coagulase-negative strains inhibited growth of the Oxford 209P indicator strain of Staphylococcus. Preliminary work completed on two active strains, 29297 and 36534, showed that the antibiotics were resistant to heat, acid and alkaline conditions, and that they were partially sensitive to trypsin and chymotrypsin. The spectrum of these substances was similar in that growth of Gram-positive but generally not Gram-negative bacteria was inhibited. The available evidence indicated that these substances were not bacteriocins.

This investigation has been continued with a view to the development of satisfactory procedures for the purification of these two antibiotics so that their chemical characterization could be effected. REVIEW OF THE LITERATURE

REVIEW OF THE LITERATURE

PEPTIDE ANTIBIOTICS FROM EUBACTERIALES

The production of antibiotics by microorganisms, which is closely associated with survival of species in nature, is a common phenomenon in the microbial world. The action of these agents is highly selective; each is only active against certain groups of sensitive organisms. Since the discovery of penicillin by Fleming (1929), many such antimicrobial agents have been found and isolated, and some have been utilized for clinical and industrial purposes.

Antibiotics produced by members of <u>Eubacteriales</u> can generally be grouped into three categories according to their chemical nature. They are: (1) protein or lipoprotein polysaccharide complexes, (2) simple pigments, and (3) peptide antibiotics.

Jacob et al. (1953) named the protein or lipoprotein polysaccharide complexes bacteriocins. In contrast to all other antibiotics, bacteriocins act only on strains of the same or closely related species by means of specific receptors, and they are bactericidal. In some ways they closely resemble bacteriophages, except that they can not multiply in the sensitive cells as phages do.

Pigmented antibiotics are simple chemical substances produced by chromogenic species. Their chemical nature is diversified and generally they are highly toxic to higher animals.

Peptide antibiotics differ from normal peptides or proteins not only by their unique biological activity, but by the possession of several other characteristics. Abraham (1957) first stressed that most peptide antibiotics are cyclic and contain both D- and L- amino acid residues. Bodanszky and Perlman (1969) further pointed out the following specific features of peptide antibiotics: (1) Certain amino acids commonly found in proteins, for example, arginine, histidine, and methionine, occur rarely in peptide antibiotics. (2) Not only is the occurrence of D-amino acids quite general, but D- and L-isomers of the same amino acids occur in the same compound, often as next neighbors. (3) Cyclic peptide antibiotics include both heterodetic and homodetic structures. (4) Proline, N-methylated amino acids, and imino acids which probably preclude helix formation, and hence facilitate cyclization, often are found in peptide antibiotics. (5) The formation of small cyclic areas within the macrocyclic structure of the peptide molecule is a common feature. (6) Unusual amino acids and/or non-amino acid moieties are frequently present.

From the survey of known peptide antibiotics from <u>Eubacteriales</u>, one finds that the majority of them are produced by Gram-positive strains. One also discovers that different strains of the same species usually produce different kinds of peptide antibiotics and that strains of completely different species may produce a similar agent. Furthermore, a single strain usually produces a mixture of chemically closely related peptides. Each differs from the other only by one or two residues in the molecule.

Most bacterial peptide antibiotics are stable in heat, resistant to acid hydrolysis, and relatively insensitive to the action of proteolytic enzymes. Their solubilities are highly dependent on the content of hydrophilic and hydrophobic groups in the molecule. Their cyclic nature is shown by failure to detect α -amino and α -carboxyl groups. Unlike the peptide antibiotics isolated from other sources, the non-amino acid moieties so far isolated from peptide antibiotics from <u>Eubacteriales</u> are saturated or unsaturated aliphatic acids and amines. The molecular weight of these peptides varies widely in different cases, from less than 300 for bacilysin to 7000 for nisin.

Some of these peptides, such as the bacitracins, gramicidins, and polymyxins have been used for chemotherapeutic purposes; others, such as nisin and subtilin, have been used in the preservation of food. However most of them have had no practical value because of their high toxicity to animals.

Despite the large numbers of peptide antibiotics that have been shown to be produced by strains of <u>Eubacteriales</u>, only a small proportion of them has been investigated systematically. In this review, only those whose chemical structures are known shall be discussed. Emphasis has been placed on the properties, isolation and structure of the antibiotic.

I. BACILYSIN.

(1). Producing strains and properties of bacilysin:

Abraham <u>et al</u>. (1946) isolated a strain of <u>Bacillus subtilis</u>

(NCTC 7197) from the soil at Oxford which produced a water-soluble antibiotic. Florey <u>et al</u>. (1949) named this antibiotic bacilysin. Newton (1949)

reported another strain, \underline{B} . <u>subtilis</u> A-14 obtained from a contaminated culture of <u>Mycobacterium tuberculosis</u> from Chile which produced bacilysin and several other antibiotics. Gilliver (1949) discovered several other bacilysin-producing strains in the National Collection of Type Cultures and in the collection of Dr. T. Gibson of Edinburgh. They were \underline{B} . <u>subtilis</u> and \underline{B} . pumilus.

Newton (1949) found a bacilysin which contained nitrogen and sulphur and showed that it was insoluble in all dry organic solvents except methanol. An aqueous solution of bacilysin did not form a precipitate with picric, phosphotungstic, or trichloroacetic acids or lead acetate. It gave a positive ninhydrin test and Pauly diazo reaction (Pauly, 1904), and the Molisch test was negative. The bacilysin was active against staphylococci and corynebacteria, but B. anthracis and Streptococcus pyogenes were not affected. Florey et al (1949) showed that bacilysin was easily extracted by phenol from broth. The substance gave a negative biuret test. It was stable in aqueous solution at 100°C for five minutes at pH 7, was largely inactivated under these conditions at pH 2 or pH 9, and was inactivated by trypsin but not by pepsin. Bacilysin caused a rapid lysis of cultures of staphylococci growing in a liquid medium, but a small proportion of the cells survived and soon multiplied to yield a highly resistant strain. Rogers et al (1965a) showed that highly purified bacilysin had no sulphur content and gave a negative result for the diazo reaction.

(2). Isolation:

Newton (1949) isolated bacilysin by acidification of the culture

fluid, adsorption of bacilysin to activated charcoal, and elution with a mixture of ethanol and potassium phosphate solution. The eluate was percolated rapidly through a column of alumina, and was concentrated and lyophilized.

Rogers et al. (1965a) obtained crude bacilysin by acidification of the whole culture with acetic acid and removal of bacterial cells. The fluid was neutralized and passed through a Zeo-Karb (SRC-5, H⁺ form) ion exchange resin column. Bacilysin was eluted from the resin with an aqueous pyridine solution and concentrated. Further purification was achieved by chromatography in pyridine-acetate buffers on columns of Dowex 50-X2 and Dowex 50-X8, respectively, and by gel filtration in aqueous propanol on Sephadex G-25. The purified bacilysin behaved as a single ninhydrin-positive substance when it was subjected to paper chromatography and to paper electrophoresis.

(3). Structural studies:

Newton (1949) found alanine, tyrosine, leucine and phenylalanine residues in the acid hydrolysates of bacilysin. Rogers et al. (1965b) noted that bacilysin contained C, H and N but no Cl or S. A possible empirical formula was C12H18N2O5 with a molecular weight of 270. Acid hydrolysates of bacilysin contained two ninhydrin-positive compounds which behaved like alanine and tyrosine respectively on paper chromatography and electrophoresis. Quantitative analysis indicated that both compounds had an equal molar ratio. Enzymatic studies showed that each had the L-configuration. However, the ultraviolet spectrum of bacilysin showed that no

tyrosine residue was present in the molecule and a nuclear-magnetic-resonance analysis indicated that olefinic and aromatic protons were absent. Hydrolyzed by leucine aminopeptidase and by pronase, bacilysin gave alanine and an uncharacterized amino acid. This substance might be a cyclohexanone with a 2,3-epoxy-1-oxo group. Since the results of electrometric titration showed that bacilysin was a peptide containing one free α -amino group and one free carboxyl group, and since the dinitrophenyl (DNP) derivative of bacilysin yielded DNP-alanine on acid hydrolysis, the tentative structure as shown below (1) was suggested by Rogers et al. (1965b).

II. BACITRACINS.

(1). Producing strains:

Johnson et al. (1945) isolated a <u>Bacillus</u> strain with strong antibiotic activity from a patient called Tracy. The culture was first identified as <u>B</u>. <u>subtilis</u> and called "Tracy I strain", the active principle being named "bacitracin". Burden (cited by Meleney and Johnson, 1949)

reclassified it as \underline{B} . <u>licheniformis</u>. This classification was confirmed by Smith (cited by Welch and Lewis, 1951) and was also supported by the seventh edition of Bergey's Manual of Determinative Bacteriology (1957). This strain has lately been designated ATCC 10716.

Magarao et al. (1944) found a <u>Bacillus</u> which lysed <u>Mycobacterium</u> tuberculosis. This strain was later separated into two species, <u>B. subtilis</u>, and <u>B. licheniformis</u>. Antibiotics produced by the <u>B. subtilis</u> strain were described by Newton (1949) (see page 4). The <u>B. licheniformis</u> strain was known as "A-5" and the antibiotic produced was called "ayfivin" (Arriagada et al., 1949). Ayfivin was found to be identical with bacitracin by Newton and Abraham (1950) who used counter-current distribution. Consequently the name "ayfivin" was abandoned.

(2). Properties of bacitracin:

Anker et al. (1948) reported that bacitracin was stable at acid or neutral pH but was rapidly inactivated above pH 9. Hydrogen peroxide destroyed its activity rapidly. It was soluble in water and polar organic solvents but insoluble in non-polar solvents. In aqueous solution, its activity passed through a nitrocellulose membrane which held back particles of molecular weight 2000 or more. The antibiotic was precipitated by salts of heavy metals. The precipitate was inactivated if heavy metal ions low in the electromotive series were used. On the other hand, heavy metal ions high in the electromotive series such as zinc, did not result in inactivation, but precipitation of the active material was incomplete. Besides the heavy metals, bacitracin was precipitated from aqueous solution by organic acids

and other protein precipitants.

Arriagada et al. (1949) noted that bacitracin behaved as a weak base. It gave positive results with the ninhydrin test and with Knoop's test for histidine (Knoop and Windaus, 1905, Windaus and Knoop, 1906). It was stable for 10 min at 100° C in aqueous solutions at pH 2, 7 and 10. Bacitracin was not affected by trypsin and pepsin but traces of Cu⁺⁺ ions diminished its biological activity. The agent acted mainly against Grampositive strains including mycobacteria and Gram-negative species were relatively insensitive.

Craig et al. (1952a) found that bacitracins A, B, D, and E all exhibited low intensity ultraviolet absorption maxima at 253 $\text{nm}^{(1)}$, whereas bacitracin C absorbed more strongly at 258 nm with a shoulder at 253 nm.

(3). Isolation:

(a). By extraction and precipitation methods:

Johnson et al. (1945) extracted bacitracin from crude fluid with n-butanol and concentrated the resulting extract in vacuo. Anker et al. (1948) effected further purification by mixing the concentrated extract with an ether-butanol mixture and then acidified this with HCl. After separation of two phases, the aqueous layer was extracted with the nutanol-ether mixture and then ether alone. The final aqueous solution was distilled, neutralized, and lyophilized. For commercial purposes, Anker et al. (1948) suggested further purification of the butanol extract with MgO to remove pigments at neutral pH and in the cold or by precipitating bacitracin with salicylate.

⁽¹⁾ nanometer: One nanometer equals 10^{-9} meter.

Sharp et al. (1949) adsorbed bacitracin to charcoal and eluted it with acidified n-butanol. Bacitracin was precipitated from butanol as the picrate which was dried and redissolved in acidified ethanol. The resulting bacitracin hydrochloride was precipitated with dry ether and dissolved in water before lyophilization.

Johnson and Meleney (1950) used ammonium molybdate in the isolation of bacitracin. Bacitracin was precipitated as the molybdate from broth. This was extracted with water at neutral pH and the extract was then repeatedly treated with n-butanol.

Regna and Solomons (1951) precipitated bacitracin from broth by the monosodium salt of Polar Yellow 5G. Methylene disalicylic acid (Baron, 1956) and lignins (Ziffer and Cairney, 1962) were also used as precipitants of bacitracin for commercial use.

(b). By ion-exchange chromatography:

Many attempts have been made to use ion-exchange resins as a means of isolating bacitracin. Usually, the use of ion-exchange chromatography alone failed to achieve the goal of high purity. Other processes, such as extraction and precipitation, are required for prior concentration or for further purification. Important work concerning the use of ion-exchangers for bacitracin purification is summarized in Table I.

TABLE I

ION-EXCHANGE METHODS IN BACITRACIN PURIFICATION

investigators	starting material	type of resin used	eluting fluid	note
Shortridge (1957)	culture fluid, pH 5.0	Amberlite IRC-50 (ammonium form)	2% NH ₄ OH	eluting fluid active
Hodds (1958)	culture fluid, pH 4.5	Amberlite IRC-50 (acid form)	2N NaOH	11 11
Zinn and Chornock (1958)	Zn-bacitracin, pH 4.0	Amberlite MB-4		effluent active
Chaiet and Cochrane (1959)	(1) culture fluid, pH 4.0	acid form of Duolite C-10, Duolite C-25, Amberlite IRC-50, Amberlite XE-89, or Dowex 50 X1	dilute NH4OH	eluting fluid active
	(2) concentrated eluate from (1)	Duolite A-7 (acetate form)		effluent active
Konigsberg and Craig (1959)	commercially purified sample, pH 4.5 or further purified by countercurrent distribution at pH 4.5	carboxymethyl cellulose	(1) 0.05M sodium acetate buffer, pH 4.5(2) pyridine-acetate buffer, pH 4.9	eluting fluid active

(c). By countercurrent distribution methods:

Barry et al. (1948) studied commercial bacitracin by counter-current distribution in the system sec-butanol-1.7% acetic acid, and found that bacitracin resolved into a major band (83% of sample) and two smaller bands. Craig et al. (1949a,b) obtained similar results in their distribution studies.

Sharp et al. (1949) studied the purity of bacitracin hydrochloride by the countercurrent distribution technique in the system amyl alcohol-n-butanol-0.1M phosphate buffer at pH 7, and found that bacitracin contained three active constituents. Newton and Abraham (1950) used the same system for bacitracin separation by countercurrent distribution. They also obtained three active components referring to them as bacitracins A, B, and C. After redistribution in the same system, bacitracin A appeared to be homogeneous but the homogeneity of bacitracins B and C was still uncertain after the same treatment.

Craig et al. (1952a) found five active components in commercial bacitracin by countercurrent distribution. Bacitracin A was a major constituent (60% of the total), whereas the other components, B, D, E and F occurred only in small amounts.

Newton and Abraham (1953a) resolved bacitracin into at least 10 active polypeptides using countercurrent distribution. These were called bacitracins E, D, B, A', A, C, G, F_1 , F_2 , and F_3 according to the order of their partition coefficients.

(d). Other methods:

Porath (1952) showed that "pure" bacitracin preparations obtained by countercurrent distribution were still heterogeneous. He proposed the use of charcoal and electrophoresis for further purification. The bacitracin preparations were adsorbed to active charcoal and eluted with acidic hexanol-ethyl acetate. Zone electrophoresis was performed on columns filled with a suspension of cellulose powder in sodium acetate buffer. As the result of this improved purification, Porath (1954) obtained two new bacitracins, H and I.

(4). Structural studies:

(a). Structure of bacitracin A:

Barry et al. (1948) found that the purified major component of bacitracin (bacitracin A) contained nine amino acid residues, one of which was not identified. The known amino acids were phenylalanine, leucine, isoleucine, glutamic acid, aspartic acid, lysine, histidine, and cystine and the unknown substance might be ornithine or hydroxylysine. Ammonia was also present while methionine, valine, threonine, serine, proline and arginine were absent. Sharp et al. (1949) noted the presence of ornithine. They also showed that bacitracin A had three ionized groups which could be detected by titration at pH 2 - 5, pH 5.5, and pH 10 - 12.

Craig et al. (1949b) believed that the major component of bacitracin (bacitracin A) was a polypeptide consisting of L-histidine, L-leucine,
L-cysteine, L-glutamic acid, DL-phenylalanine, DL-aspartic acid, D-isoleucine, L-valine and ornithine whose configuration they were unable to

determine.

Porath (1952) reported that bacitracin A contained two aspartic acid, one glutamic acid, one leucine, one isoleucine, two or three phenylalanine, one cysteine, one histidine, one lysine and one ornithine residue in the molecule with a molecular weight of 1460. Similar molecular weight figures for bacitracin A were also reported by Craig et al (1952b, 1953) and by Newton and Abraham (1953b).

Craig et al (1952b) revealed that acid hydrolysates of bacitracin A contained two DL-aspartic acid, one D-glutamic acid, one L-leucine, two L-isoleucine, one D-phenylalanine, one L-cysteine, one L-histidine, one L-lysine, one D-ornithine, on NH3 and in addition, two unknown ninhydrinpositive residues. The unknown substances behaved as methionine and tryptophan on chromatography but neither of these two amino acids was involved as was shown by their failure in isolation experiments and chemical qualitative determinations. Craig et al (1953) found one of the unknown substances to have the empirical formula $C_5H_8{\rm O}$ whereas the empirical formula of bacitracin A was $C_{65}H_{102}O_{17}N_{16}S$. Bacitracin A was believed to be cyclic since only δ -DNP-ornithine and DNP-histidine were isolated from the hydrolysates of DNP-bacitracin A. A second ring involving the sulphur group was also proposed by Craig et al (1953) because the thiol group could be detected only after hydrolysis with acid. Similar proposals were made by Newton and Abraham (1953b). The ring structure was also supported by Ingram (1953) who examined bacitracin A with the methylation technique.

Based on his own findings, Porath (1953) proposed a possible

arrangement of amino acid residues in the bacitracin A molecule as shown below (2). He believed that the distribution of amino acids in bacitracin

A was highly asymmetrical. The molecule consisted of a lipophilic and a lipophobic part. The uneven distribution of basic and acidic amino acids made the lipophilic part of bacitracin A strongly polar.

Lockhart et al. (1954a) suggested that the sequence shown below (3)

was present in bacitracin A. They also believed that the Ileu side of this sequence was connected to a peptide containing ornithine, phenylalanine and isoleucine residues with ornithine as the N-terminal amino acid residue. The Glu residue on the right hand side was connected to aspartic acid. In this cyclic structure, most of the polar side chain was grouped together on one part of the ring and most of the non-polar side chain on the other.

Porath (1954) found a small amount of DNP-isoleucine in the acid hydrolysates of bacitracin A but thought this was a contaminant. Lockhart $\underline{\text{et}}$ $\underline{\text{al}}$. (1954) also reported the isolation of DNP-isoleucine from the acid

hydrolysate. However, an attempt to degrade bacitracin A by the Edman method yielded only 5% of the theoretical amount of 3-pheny1-2-thiohydantoin expected from an N-terminal isoleucine.

After careful study Piez (1954) suggested that the unknown substance in the position occupied by methionine found by Craig et al. (1952b) might be an alloisoleucine.

Craig et al. (1954) restudied the partial acid hydrolysates of bacitracin A and concluded that bacitracin A contained three isoleucine residues rather than two as reported earlier (Craig et al., 1952). They also confirmed the existence of alloisoleucine and noted that it was the N-terminal residue of bacitracin. Elementary analysis showed: C, 55.2; H, 7.3; N, 15.8; and S, 2.2% Thus the empirical formula was $C_{68}H_{107}O_{18}N_{17}S$ for bacitracin A. The results of partial hydrolysis suggested the following sequence (4).

$$(2)$$

$$\text{Ileu} \rightarrow \text{Cys} \rightarrow \text{Leu} \rightarrow \text{Glu} \rightarrow \text{Ileu} \rightarrow \text{Lys} \rightarrow \text{Orn} \rightarrow \text{Ileu}$$

$$Asp \leftarrow \text{His} \leftarrow \text{Phe}$$

$$Asp$$

$$(4)$$

The thiazoline ring should be as follows (5):

$$C_{4}H_{9} - C - C - C - CH_{2} 0$$
 $N - CH - C - Leu - C$
(5)

⁽²⁾ \longrightarrow means a peptide bond from a carboxyl group to an amino group.

However, this structure failed to account for the occurrence of a peptide fragment of $Cys-SH\longrightarrow Ileu\longrightarrow Phe$ which was found in partial acid hydrolysate. Also the position of an amide group still remained to be determined.

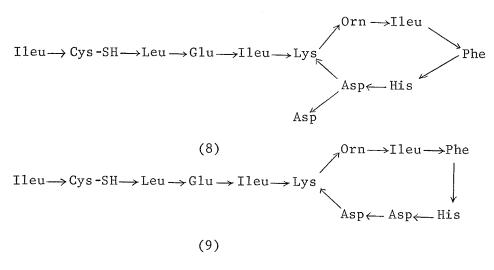
Lockhart and Abraham (1954a,b) also found D-alloisoleucine to be the N-terminal group of bacitracin A. Based on their partial acid hydrolysis studies, they proposed a tentative structure for bacitracin A (see below, 6) in which the α -amino group of lysine appeared to be joined to an isoleucine residue and the ϵ -amino group to an aspartic acid residue. Aspartic acid linked to lysine had the L-configuration and the second aspartic acid residue, the D-configuration.

$$Ileu \rightarrow Cys-SH \rightarrow Leu \rightarrow Glu \rightarrow Ileu \xrightarrow{\bowtie} L-Asp \leftarrow (D-Asp) \leftarrow His$$

$$\uparrow Orn \longrightarrow Ileu \longrightarrow Phe$$
(6)

These authors modified this structure to another (shown below, 7) in which the dotted line represented a tentative unknown linkage. They also believed that the glutamic acid or one of the aspartic acid residues in this structure could be present as glutamine or asparagine respectively. A thiazoline ring which involved the carboxyl group of the isoleucine residue and the adjacent cysteine was also present.

Lockhart et al. (1955) and Hausmann et al. (1955a) reconfirmed the condensation of the N-terminal isoleucine with the cysteine residue to form a thiazoline ring. They also found that there were three of the isoleucine residues in bacitracin A, which supports the work of others. After studying their partial acid hydrolysis data, Hausmann et al. (1955b) reported two possible amino acid sequence formulae for bacitracin A (8 and 9). Structure



(8), which was similar to the one proposed by Lockhart and Abraham (1954b), was preferred because it accounted for all the partial hydrolysis data obtained with the exception of peptide fragments of DNP—Phe \rightarrow Ileu—Leu and Phe \rightarrow Ileu.

Weisiger $\underline{\text{et al}}$. (1955a) rejected structure (2) proposed by Porath on the grounds that a peptide fragment containing Lys, Asp, Orn, and Ileu found in their acid hydrolysate of bacitracin A could not arise from this formula.

Lockhart and Abraham (1956) reconfirmed the correctness of their proposed structure for bacitracin A (7) and pointed out that an isoleucine

residue was joined to the α -amino group of lysine and an aspartic acid residue to the ϵ -amino group. The arrangement around the lysine residue in bacitracin A would appear to be as shown in (10).

$$D-Asp \not\leftarrow L-Asp \xrightarrow{\mathcal{E}} L-Lys \xleftarrow{\alpha} L-Ileu \longleftarrow D-Orn$$

$$(10)$$

Wrinch (1957) proposed a cyclol theory to explain the formation of Phe \longrightarrow Ileu \longrightarrow Cys-SH and Phe \longrightarrow His fragments. According to this theory, the \varpropto -carboxyl carbon atom of phenylalanine was bound to the \varpropto -amino groups of histidine and isoleucine. The structure of bacitracin A would be as shown below (11).

This, however, still remains to be proved.

Craig et al. (1958) summarized all the findings in the literature and concluded that the sequence formula of bacitracin A should be as shown in (12).

$$\begin{array}{c|c} \text{CH}_3 & \text{S---CH}_2 \\ \hline \\ \text{CH}_3\text{--CH}_2\text{--CH--CH--C} & \text{O} \\ \hline \\ \text{NH}_2 & \text{N----CH---C} \rightarrow \text{L--Leu} \\ \hline \\ \text{D--Asp--NH}_2 & \\ \hline \\ \text{D--Phe} \longrightarrow \text{L--His} \longrightarrow \text{L--Asp} \\ \hline \\ \text{L--Ileu} \leftarrow \text{D--Orn} \leftarrow \text{L--Lys} \leftarrow \text{L--Ileu} \\ \hline \end{array}$$

(b). Structural studies on bacitracin B:

Craig et al. (1952a) showed that bacitracin B had the same amino acid composition as bacitracin A with an additional spot whose position on the paper chromatogram corresponded to that of valine. However, they believed that it was not valine. The existence of a valine-like substance in bacitracin B was also reported by Newton and Abraham (1953a) and by Lockhart et al. (1954) as well as by Lockhart and Abraham (1954).

By comparison of the results obtained from hydrolysates of bacitracins A and B, Lockhart and Abraham (1954) thought that the difference between the bacitracin B molecule and bacitracin A molecule was that B contained the sequence Lys \rightarrow Orn \rightarrow Val \rightarrow Phe and A had the sequence Lys \rightarrow Orn \rightarrow Ileu \rightarrow Phe.

(c). Structure of bacitracin F:

Craig et al. (1953) noted that bacitracin A was not stable in neutral or alkaline pH and was slowly transformed to give mainly bacitracin F. Newton and Abraham (1953a,b) found bacitracin F to be a mixture of bacitracins F_1 , F_2 and F_3 , separable by countercurrent distribution methods.

Hausmann $\underline{\text{et}}$ $\underline{\text{al}}$. (1955b) showed that transformation from bacitracin

A to bacitracin F involved the loss of ammonia. Quantitative amino acid analysis revealed all the amino acid residues normally found in bacitracin A to be present in bacitracin F except cysteine and alloisoleucine. Hydrolysis of fully DNP-substituted bacitracin F gave only one DNP-amino acid, $\boldsymbol{\delta}$ -DNP-ornithine. A crystalline acid which had sulphur and nitrogen in a 1:1 ratio, a molecular weight of 207 and the formula $C_9H_{11}O_3NS$, was found in hydrolysates of bacitracin F.

Weisiger et al. (1955b) believed that the acid substance $C_9H_{11}O_3NS$ had structure (13).

With the loss of two moles of ammonia which was thought to be liberated from isoleucine and asparagine residues of bacitracin A, the formula of bacitracin F might be (14).

However, Craig et al (1958) pointed out that bacitracin F behaved as a neutral substance and gave a strong ninhydrin color which would not occur with a substance having merely the free δ -amino group of ornithine. Furthermore, a mole of ammonia was still present and unaccounted for in the amide determination which could not be explained by the proposed formula. Konigsberg and Craig (1962) showed that bacitracin F had the empirical formula $C_{66}H_{99}O_{17}N_{16}S$. Bacitracin A was transformed to bacitracin F actually by the loss of one mole of ammonia, two hydrogens and a gain of one oxygen atom. Amide determination by Conway's procedure (Conway, 1933) indicated that the amide group of bacitracin A still to be present in bacitracin F. Therefore, the correct formula of bacitracin F should be (15):

(d). Structural studies of other bacitracins:

Much less work has been done on the structures of other bacitracins. The only information available is from Newton and Abraham (1953b) who pointed out that all bacitracins contained cystein, orithine, lysine, histidine, aspartic acid, glutamic acid, leucine and/or isoleucine, and phenylalanine residues. Bacitracin D and bacitracin E differed from bacitracin A by having

a substance behaving like valine on a paper chromatogram. Bacitracin C differed from A by having a glycine-like substance. Smaller amounts of the valine-like substance were also obtained from bacitracins C, G, F_1 , F_2 , and F_3 . Furthermore, all bacitracins had a masked thiol group which appeared in mild acid hydrolysis. All bacitracins except bacitracins E and D contained an amide group.

III. EDEINE.

(1). Producing strains and properties of edeine:

Kurylo-Borowska (1959a) isolated a strain of <u>B. brevis</u> Vm 4 from soil which produced an antibiotic that he named "edeine". The yield of edeine from this strain was low. Chmara and Borowski (1966) obtained a highly antibiotic-producing mutant by induction with ultraviolet light. The strain was identified as B. brevis Vm 4-no. 587.

Kurylo-Borowska (1959b) noted that edeine was a strongly basic material which was soluble in water, water-saturated phenol, ethylene glycol, and acid methanol but insoluble in other organic solvents. It gave positive reactions in biuret, ninhydrin, Millon and Sagakuchi tests and formed precipitates when picric and flavianic acids, sodium tungstate or reinecke salt were added to edeine aqueous solutions. The antibiotic was more stable in acid than in alkaline medium. However, heating to 60°C for 30 min. at acid pH caused 75% inactivation. Edeine was affected by the presence of serum or blood and was inactivated slowly by trypsin. It was active against Gram-positive and Gram-negative microorganisms and mycobacteria were also

sensitive. Kurylo-Borowska (1962) further showed that the growth of some fungi and yeasts was inhibited by edeine, and that it also had a high toxicity to mammalian neoplastic cell cultures and to experimental animals.

Roncari et al. (1966) showed that edeine solutions absorbed maximally at 272 nm. Chmara and Borowski (1968) noted that both edeines

A and B exhibited the same inhibitory spectrum but that edeine A was more active than edeine B. Some, but not all, strains of bacteria were resistant to both edeines A and B.

(2). Isolation:

Kurylo-Borowska (1959b) isolated edeine by adsorption to activated charcoal and elution with acidified methanol. Edeine also was isolated by direct extraction from neutralized broth with phenol. The phenol was removed by extraction with ether, and the isolated material was dried <u>in vacuo</u>. Further purification was obtained by partition chromatography on silica gel using isopropanol-methanol-water mixture as a developing fluid.

Roncari et al. (1966) separated edeine from the culture broth by extraction with phenol, and further extraction of the phenolic solution with 5% acetic acid. Further purification after concentration was effected by gel-filtration on Sephadex G-25 and countercurrent distribution. Roncari et al. (1966) found only one active component in edeine preparations.

Borowski and Chmara (1967a,b) adsorbed edeine to a cation exchange resin, Wofatit CP-300 (Na $^+$ form), from diluted culture broth. The edeine was eluted with $\rm H_2SO_4$ solution. Further purification was effected on a carboxymethyl cellulose 70 (Na $^+$ form) column in a NaCl gradient with sub-

sequent desalting on Sephadex G-25. By this method, they found that edeine was a mixture of four biologically active compounds which they named edeine A, B, C and D. Edeines A and B were major components of the complex, while edeine C was present in very small quantities and edeine D in traces. Borowski et al. (1966, 1967) found that these four components could also be separated by paper chromatography.

Hettinger et al. (1968) pointed out that edeine B was very soluble in phenol. With the method of Roncari et al. (1966), edeine B was lost during the step in which edeine was extracted from phenol in aqueous acetic acid. They modified their earlier procedure (Roncari et al., 1966) through adsorption of edeine on Dowex 50-X4 (H⁺ form) resin and elution with NH40H solution. The eluate was neutralized with acetic acid and concentrated. Further purification was achieved on Sephadex G-25 and with countercurrent distribution in the system phenol-ammonium acetate-acetic acid.

(3). Structural studies:

Kurylo-Borowska (1959b) found that acid hydrolysates of edeine showed six ninhydrin-reacting spots on paper chromatograms. Four of these spots had the same R_f values as glycine, arginine, tyrosine and glutamic acid. Roncari et al. (1966) showed that edeine contained glycine, isoserine, α, β -diaminopropionic acid, isotyrosine and spermidine residues as well as an unknown ninhydrin-positive substance (16). Roncari et al. (1966)

$$\mathtt{CH}_3\,\text{-}\mathtt{CH}_2\,\text{-}\mathtt{CH}_2\,\text{-}\mathtt{CH}_2\,\text{-}\mathtt{NH}\,\text{-}\mathtt{CH}_2\,\text{-}\mathtt{CH}_2\,\text{-}\mathtt{CH}_2\,\text{-}\mathtt{NH}_2$$

believed edeine to have a molecular weight of 1500.

Hettinger and Craig (1968) reported that when edeine A acid hydrolysates were subjected to paper chromatography and electrophoresis, seven ninhydrin-positive compounds were present. These were identified as glycine, isoserine, β -tyrosine, α , β -diaminopropionic acid, spermidine, 2,6-diamino-7-hydroxyazelaic acid (DAHA, 17) and 2,6-diamino-7-nonenedioic acid (DAND, 18). Hettinger and Craig (1968) found that DAND was an artifact which arose

under acid hydrolysis conditions by dehydration of DAHA. All the six natural amino acid residues present in edeine A were in an equal molecular ratio.

The molecular weight of the free base of edeine A was 775 and the acetate,

995.

Hettinger et al. (1968) noted that edeine B contained the amino acids, glycine, isoserine, β -tyrosine, α , β -diaminopropionic acid and DAHA as did edeine A but spermidine in edeine A was substituted by N-guanyl-N'-(3-aminopropyl)-1,4-diaminobutane (guanylspermidine, 19) in edeine B. All

$$\begin{array}{c} \text{NH} \\ \parallel \\ \text{NH}_2\text{-C-NH-CH}_2\text{-CH}_2\text{-CH}_2\text{-CH}_2\text{-NH-CH}_2\text{-CH}_2\text{-CH}_2\text{-NH}_2 \\ \end{array}$$

six compounds had also an equal molecular ratio. Acidimetric titration of edeine A indicated that a total of seven groups were titratable between pH 1.5 and 12.0 and with edeine B, only a total of six were detected at the same pH range. In the case of edeine A, five could be accounted for as free amino groups, one as the hydroxyl group of β -tyrosine and one a free carboxyl group. In the case of edeine B, the missing one might be a guanidino group whose pK was greater than pH 12.

Hettinger and Craig (1970) noted that edeine A was a mixture of the antibiotic peptide edeine A_1 and its inactive isomer, edeine A_2 . Likewise, edeine B was a mixture of active edeine B_1 and inactive edeine B_2 . Determined by examination of fragments obtained by partial acid hydrolysis, the amino acid sequence of edeine A_1 was $N-(\beta$ -tyrosyl)-isoseryl- $(\alpha \rightarrow \alpha)$ -2,3-diamino propionyl- $(\alpha \rightarrow \alpha)$ -2,6-diamino-7-hydroxyazelayl- $(\omega \rightarrow \alpha)$ -glycyl- $NH(CH_2)_3NH(CH_2)_4NH_2$ (20). In edeine B_1 , the sequence was identical except that the terminal amino group of the spermidine residue was replaced by a

guanidino group of guanyl spermidine. Edeines A_2 and B_2 had identical sequences with edeines A_1 and B_1 respectively except that the isoseryl-2,3-diaminopropionyl linkage was $\alpha \rightarrow \beta$ instead of $\alpha \rightarrow \alpha$.

IV. LICHENIFORMINS:

(1). Producing strain and properties of licheniformins:

Licheniformin was isolated from a stock strain of \underline{B} . <u>licheniformis</u> by Callow and Hart (1946). It was active against Gram-positive bacteria and the mycobacteria but had little effect on Gram-negative species (Callow and Hart, 1946; and Callow <u>et al</u>., 1947a,b).

These authors (1947b) also noted that licheniformin could be autoclaved at 10 lb. pressure for 10 min. over the pH range 1 - 9. Licheniformin hydrochloride was very soluble in methanol, soluble in water, sparingly soluble in ethanol and insoluble in dry n-butanol, acetone, or non-polar organic solvents. It was charred on heating strongly, and was positive with biuret and Sakaguchi tests but negative with ninhydrin, Molisch and glucosamine tests. The antibiotic activity of licheniformin was not altered by serum, and it was moderately toxic to mice.

(2). Isolation:

Callow and Hart (1946) proposed the following method for licheniformin isolation: The whole culture was first acidified to pH 2 with HCl and then treated with ethanol. The precipitate resulting was extracted with diluted acid and heat. The active principle was then precipitated out

from the solution by mixing with a large volume of ethanol. This method was later modified by Callow et al. (1947a,b). After boiling the whole culture at pH 2, they then removed the solid and the liquid was neutralized to pH 5 with filtration through a bed of active charcoal. Elution was effected by passage through acidified n-butanol saturated with water. The active eluate was concentrated and passed through a column of activated charcoal. The effluent was adjusted to pH 10, clarified, and neutralized, the licheniformin being then precipitated from solution as the picrate. This was converted to hydrochloride with concentrated HCl and the hydrochloride was precipitated by the addition of acetone.

Callow and Work (1952) separated licheniformin into licheniformins A, B, and C by countercurrent distribution.

(3). Structural studies:

Callow and Work (1952) showed that licheniformin A and licheniformin B hydrolysates gave glycine, serine, proline, valine, phenylalanine, lysine, arginine and aspartic acid residues and licheniformin C contained an additional glutamic acid residue. Licheniformin A hydrochloride had C, 44.4; H, 7.0; N, 18.1 and Cl, 11.9%; licheniformin B hydrochloride had C, 44.7; H, 7.2; N, 18.4 and Cl, 10.4% and licheniformin C hydrochloride had C, 44.7; H, 8.1; N, 17.8; and Cl, 11.5% Licheniformins A and B were all composed of seven glycine, six arginine, three serine, two proline, two phenylalanine, two valine, 12 lysine and one aspartic acid residues. Since all licheniformins failed to react with 1-fluoro-2,4-dinitrobenzene (FDNB) reagent, it was believed that they were all cyclic peptides.

Ogston (1952) determined the molecular weights of licheniformins by sedimentation and diffusion methods, and found that licheniformin A was 4400, B, 3800 and C, 4800.

V. MICROCOCCIN AND MICROCOCCIN P.

(1). Producing strains and properties of micrococcins:

Su (1948a) isolated a strain of Micrococcus from sewage which was inhibitory to many Gram-positive microorganisms and mycobacteria but inactive against Gram-negative species. The substance responsible for this effect was designated micrococcin.

Fuller (1955) found a strain of \underline{B} . $\underline{pumilus}$ in soil collected in East Africa which was an active antibiotic-producer. Abraham \underline{et} al. (1956) showed both micrococcin and the antibiotic from \underline{B} . $\underline{pumilus}$ to have very similar biological, chemical and physical properties and believed the antibiotic from \underline{B} . $\underline{pumilus}$ was a substance closely related to micrococcin. Therefore, they proposed the name "micrococcin P" for the antibiotic produced by this strain.

Both micrococcins were only slightly soluble in water, but readily soluble in polar organic solvents and insoluble in non-polar organic solvents. Their aqueous solutions appeared to be neutral in reaction, dextrorotatory, and fluoresced in ultraviolet light. They were freely dialysable. Crystalline preparations of micrococcins melted at 220 - 230°C with decomposition. Both were thermostable, withstanding 115°C for at least 10 min. Their antibacterial activity was not affected by incubation with pepsin, trypsin,

cysteine or serum. However, they were rapidly destroyed by alkali, light and copper ions. Qualitative tests showed that they contained nitrogen and sulphur but no halogens. The ninhydrin reaction was negative with both micrococcins (Su, 1948b; Heatley and Doery, 1951; Fuller, 1955; and Abraham $\underline{\text{et al}}$., 1956).

(2). Isolation:

Su (1948b) brought the whole culture to pH 2 with concentrated HC1 and repeatedly extracted the resulting precipitate with ethanol after which the ethanolic solution was concentrated and extracted with chloroform. The active principle was precipitated from chloroform and the solution was passed through an alumina column with ethanol as an eluting fluid. The same process was used by Heatley and Doery (1951), but they managed to crystallize the micrococcin from its ethanolic solution. The crystalline product was homogeneous as judged by countercurrent distribution.

Fuller (1955) used acidification of the culture with HCl and precipitation with ammonium sulphate in the isolation of micrococcin P. The precipitates were extracted with ethanol and the ethanolic solution was evaporated to dryness. The residue, after being washed with ether and water, was dissolved in ethanol. This ethanolic solution was further purified by passage through an alumina column. The effluent was then dried and the residue was crystallized from a mixture of acetic acid and ethyl acetate.

(3). Structural studies:

Heatley and Doery (1951) showed by elementary analysis that micro-

coccin was C-methyl, 6.9; C, 49.0 - 49.5; H, 4.6; N, 13.9; and S, 15.9% with an empirical formula $C_{25}H_{28}O_6N_6S_3$. Ammonia present in acid hydrolysates amounted to 24.2% of the total nitrogen in micrococcin. The molecular weight of micrococcin appeared to be between 2170 and 2720.

Fuller (1955) noted that micrococcin P was composed of C, 48.9; H, 4.9; N, 13.7; S, 16.0 and O, 16.7% which corresponded to a minimal formula of $C_8H_9N_2O_2S$.

Abraham <u>et al</u>. (1956) showed that on acid hydrolysis, both micrococcins broke down to give a series of compounds which could be separated into soluble and insoluble components in cold diluted hydrolysate mixture. The acid soluble fraction was composed of L-threonine, propionic acid, ammonia, an ether-soluble substance $C_7H_7O_3NS$, a substance with the formula $C_8H_{12}O_2N_2S$, and two unknown ninhydrin-positive compounds. The acid-insoluble fraction contained a substance with the formula $C_24H_23O_5N_5S_4$ and another of composition $C_16H_19O_3N_3S_3$. Brookes <u>et al</u>. (1957), by degradation and synthesis, identified the substance $C_7H_7O_3NS$ as 2-propionyl-thiazole-4-carboxylic acid (PCTA, 21), and the substance $C_8H_{12}O_2N_2S$ as (+)-2-(1-amino-2-methypropyl)-thiazole-4-carboxylic acid (AMPTCA, 22). The molecular weight of micrococcin

P was estimated to be about 2200.

Mijovic and Walker (1960) identified the two unknown ninhydrin-

reacting substances reported by Abraham et al. (1956) as aminoacetone and 2-amino-propan-1-ol respectively. These authors also reported that there were two threonine, four aminopropanol, two propionic acid and two AMPTCA present in one molecule of antibiotic. Aminoacetone was not stable in acid hydrolysis and only 0.51 mole could be isolated from every mole of micrococcin P. Micrococcin P also had four acetylable and two free carbo-xyl groups in the molecule.

Brookes <u>et al</u>. (1960a,b) believed that the substance $C_{24}^{H}_{23}^{O}_{5}^{N}_{5}^{S}_{4}$ found by Abraham <u>et al</u>.(1956) on acid hydrolysis might have a polythiazole structure (23) which arose by cyclisation and dehydrogenation of a polycysteine peptide.

Dean $\underline{\text{et}}$ $\underline{\text{al}}$. (1961) noted that the AMPTCA had the D-configuration in micrococcin P.

The detailed structure for both micrococcins is still unknown.

VI. MYCOBACILLIN.

Majumdar and Bose (1958) isolated a strain of \underline{B} . subtilis in India which produced a highly active antifungal substance which they called "mycobacillin". They noted that mycobacillin was soluble in lower alcohols, acetone, acetic acid, NaOH, HCl, pyridine and water above pH 7, but insoluble in ether and chloroform. It was thermostable but the stability was greater at acid than at alkaline pH. Mycobacillin gave positive reactions to biuret, xanthoproteic and Millon's tests, but was ninhydrin negative. It had no effect on the growth of Gram-positive or Gram-negative bacteria, inhibiting only fungi.

Majumdar and Bose isolated mycobacillin by extraction of the culture with n-butanol and precipitation from the butanolic solution with HCl. The active precipitates were dissolved in NaOH solution and reprecipitated with HCl. These were dissolved in ethanol and reprecipitated by ether. The last step was repeated until ultimately mycobacillin was crystallized from the ethanolic solution.

The authors showed mycobacillin to have a molecular weight of 1775 by their diffusion method (Majumdar and Bose, 1958). Majumdar and Bose (1960) reported that the molecule of mycobacillin contained five aspartic acid, two glutamic acid, two tyrosine, one serine, one alanine, one leucine and one proline residue, as shown below (24).

$$G1u \longrightarrow Asp \longrightarrow A1a \longrightarrow Asp \longrightarrow Pro$$

$$Asp \longleftarrow Ser \longleftarrow Tyr \longleftarrow Asp \longleftarrow Tyr \longleftarrow G1u$$

$$(24)$$

Banerjee and Bose (1963) further found that four out of five aspartic acid and two glutamic acid residues were D-isomers and the rest were L-isomers. However, the position of L-aspartic acid in the mycobacillin molecule still must be decided.

VII. NISINS.

(1). Producing strains and properties of nisin:

Mattick and Hirsch (1944) isolated several strains of group N streptococci which produced an inhibitory substance named nisin from old milk. Nisin was found to be dialysable, and it was active against Grampositive but inactive against Grampositive bacteria. Mattick and Hirsch (1947) identified the nisin-producing strains as Streptococcus lactis and found mycobacteria also to be sensitive to nisin. They also noted that nisin was stable when boiled in acid solutions or stored for months as a dry powder. Berridge (1949) found that although nisin solutions could withstand boiling for 10 min., they were not autoclavable. Nisin was also quickly destroyed under alkaline conditions or in an enzyme-rich medium such as blood. Except for ethanol and formamide, those organic solvents that dissolved nisin usually destroyed its biological activity. Nisin was very soluble in water at low pH.

(2). Isolation:

Mattick and Hirsch (1947) showed that nisin could be isolated by acidification of the culture broth, extraction with a mixture of chloroform

and sec-octanol followed by precipitation with ethanol. Berridge (1949) found that nisin could be further purified by precipitation from phosphate buffer with NaCl and crystallized from acetone.

Hirsch (1951) suggested the nisin-producing strain actually synthesized several antibiotics. Berridge (1952) isolated nisins A and B from a preparation by countercurrent distribution, and Bavin et al. (1952) obtained similar results. Berridge et al. (1952) showed that the crystalline nisin was a mixture of 49% nisin A, 32% B, 12% C, 5% D and possibly 3% of nisin E.

Cheeseman and Berridge (1957) proposed an improved method for nisin isolation which involved salting out, solvent extraction and fractional precipitation with acetone as well as countercurrent distribution. This method was found to give a better percentage recovery and lower amounts of impurities in the final products.

(3). Structural studies:

Berridge (1949) showed that the acid hydrolysates of nisin contained alanine, valine, leucine, isoleucine, cysteine, and aspartic acid residues together with several unidentified substances.

Berridge et al. (1952) noted that the chromatogram of acid hydrolysates of nisins A, B and C were strikingly similar and only slight differences were apparent in that of nisin D. The results showed that all four nisins contained leucine and/or isoleucine, alanine, glycine, proline, aspartic acid, histidine and lysine. Valine and methionine were present in nisins A, B and C but absent from D. There were two other amino acids, lanthionine and a cystathionine-like substance present in all four nisin

molecules. Quantitatively, hydrolysates of mixed nisins consisted of four leucine, two valine, two alanine, two glycine, two proline, one serine, two lysine, two histidine, one aspartic acid, two methionine, one lanthionine, and four cystathionine-like residues. Newton and Abraham (1953c) believed the cystathionine-like substance found by Berridge et al. (1952) actually was one of the β -methyllanthionines, $C_7H_{14}O_4N_2S$ (25) which might be identical to the C_7 amino acid isolated from subtilin (see page 67).

Cheeseman and Berridge (1959) showed that nisin A contained nine leucine and isoleucine, three methionine, three valine, two proline, four alanine, six glycine, one serine, three aspartic acid, three histidine, nine lysine, nine β -methyllanthionine, and three lanthionine residues with a molecular weight of 6826. They also reported that there were no free α -amino or α -carboxyl groups in nisin A and the only free groups found were the α -amino group of lysine and the imino group of histidine. Thus, they believed that nisin A was a cyclopeptide.

Bodanszky and Perlman (1964) believed that the number of amino acid residues and the molecular weight of nisin A reported by Cheeseman and Berridge (1959) were too high. According to their proposal, nisin A

might have only 18 amino acid residues with a molecular weight around 2500 (Table II). This was partially confirmed by Gross and Morell (1967) who found a value of 3290 by amino acid analysis and a value of 3510 by the method of partial substitution for the molecular weight of nisin A.

Gross and Morell (1967) discovered a new amino acid, dehydroalanine, (26) present in the nisin molecule. The biological activity of nisin was believed to be directly related to the presence of dehydroalanine.

$$CH_2 = C - COOH$$
 NH_2
(26)

After studying the migration pattern of nisin with polyacrylamidegel electrophoresis, Ingram et al. (1967) disagreed with the proposal of Bodanszky and Perlman (1964). They believed the molecular weight of nisin A should be 7000. Jarvis et al. (1968) held a similar point of view according to their ultracentrifugation analysis. To summarize, detailed structures of the nisins have yet to be elucidated.

VIII. POLYMYXIN GROUP.

A. POLYMYXINS A, B, C, D, AND E.

(1). Producing strains and nomenclature:

Ainsworth <u>et al</u>. (1947) isolated <u>B</u>. <u>aerosporus</u> (synonymous with <u>B</u>. <u>polymyxa</u>) from the soil and found that it produced an antibiotic which they named "aerosporin". Simultaneously, Stansly <u>et al</u>. (1947) found a

TABLE II

AMINO ACID COMPOSITION OF NISIN A

amino acid	reported by Cheeseman & Berridge (1959)	reported by Bodanszky & Perlman (1964)
Isoleucine and Leucine	9	3
Methionine	3	1
Valine	3	1
Proline	2	1.
Alanine	4	1
Glycine	6	2
Serine	1	-
Aspartic acid	3	1
Histidine	3	1
Lysine	9	3
β- Methyllanthionine	9	3
Lanthionine	3	1
Total	55	18

strain of \underline{B} . polymyxa in soil and called the antibiotic substance it produced, "polymyxin". Benedict and Langlykke (1947) also noted the existence of antibiotic-producing strains of \underline{B} . polymyxa in the soil.

Brownlee and Jones (1948) noted that both aerosporin and polymyxin had an identical inhibitory spectrum and similar chemical composition. They also found that strains of \underline{B} . aerosporus and \underline{B} . polymyxa were identical. For these reasons, they proposed that polymyxin be the generic name for this group of antibiotics and suggested that aerosporin designate polymyxin A and that the original polymyxin designate polymyxin D.

Jones (1948c) reported the isolation of polymyxins B, C, E from different strains of \underline{B} . polymyxa. He also noted that various strains of \underline{B} . polymyxa could produce the same polymyxin but that a given strain produced only the one type of polymyxin.

(2). Properties of polymyxins:

Ainsworth et al. (1947) found that polymyxin A was active against Gram-negative but inactive against Gram-positive bacteria. Stansly et al. (1947) reported a similar activity for polymyxin D. These authors showed that polymyxin D was inactivated by pepsin, trypsin, pancreatin and erepsin with prolonged incubation and that it was dialyzable through cellulose membranes. Jones (1948a) showed that polymyxin A was a basic peptide having pK values of 5.8 and 10.5 and also that it would form salts with mineral acids. Catch and Friedmann (1948) noted that polymyxin A was labile in alkaline but stable in acid conditions, freely soluble in water and methanol and precipitated by many base precipitants and acid azo-dyes. It had no

characteristic absorption or fluorescence in the ultraviolet region of the spectrum. Similar properties were also reported for polymyxin D.

Although there is no information available regarding the properties of polymyxins B, C and E, it is generally believed that they are similar to polymyxins A and D.

(3). Isolation:

Ainsworth et al. (1947) isolated polymyxin A by adsorption from broth with activated charcoal and elution with aqueous acetone. The polymyxin was precipitated by the addition of dry acetone. A similar method was used by Stansley et al. (1947) to obtain polymyxin D. However, they further purified polymyxin D to the hydrochloride salt from the water-insoluble picrate. Catch and Friedmann (1948) further purified the acetone precipitates of polymyxin A by fractional precipitation as the helianthate and then converted the helianthate salt to hydrochloride or sulfate salts by treatment of methanolic suspensions of polymyxin A helianthate with the appropriate mineral acid. The hydrochloride was then repeatedly precipitated by acetone.

Porter et al. (1949) proposed the use of isopropanol extraction under acid conditions to separate polymyxin from the culture broth. The extract was concentrated and the concentrate was adsorbed on acid-washed aluminum oxide columns. Elution was accomplished by water and NaOH solution. After the eluate was neutralized, the active principle was precipitated as picrate which was subsequently converted to hydrochloride with the addition of HCl to the acetone solution of polymyxin picrate. The

polymyxin hydrochloride was crystallized from aqueous solution with the aid of ammonia.

Regna et al. (1949) purified crude polymyxin B by chromatography on cotton sodium succinate followed by precipitation as the salt of the dye, Polar Yellow, and crystallization as the salt of naphthalene- β -sulfonate. Wilkinson (1949) also crystallized polymyxins B and E as naphthalene- β -sulfonates.

(4). Structural studies:

Catch and Friedmann (1948) found polymyxin A hydrochloride to have the analysis: C, 45.5; H, 7.7; N, 15.8; and C1, 14.0%. Sulphur and phosphorus were absent. Jones (1948a) found that acid hydrolysates of polymyxin A contained leucine and threonine with a molar ratio of 1:3 and an unknown acid residue. This unknown basic amino acid was identified by Catch and Jones (1948) as d, r-diaminobutyric acid (DAB). Jones (1948b) showed that leucine in the polymyxin A molecule had a D-configuration, and that threonine was an L-isomer but was not able to determine the configuration of DAB. Brownlee and Jones (1948) reported the existence of an unknown, optically active fatty acid with a formula of C9H1802 and determined that the DAB in polymyxin A was an L-isomer. Catch et al. (1948) confirmed the presence of D-leucine, L-threonine and L-DAB by isolation. They also noted that DAB was a mixture of L-DAB and D-DAB in a proportion of 3:1 but believed that the D-DAB was an artifact. They found the same unknown fatty acid also to be present in polymyxin B.

Jones (1948b) noted that all polymyxins appeared to have in the

molecule threonine, DAB and a saturated optically active fatty acid, but they differed from each other qualitatively in composition of other amino acids (Table III).

Short (1948) showed that polymyxin B contained two molecules of phenyl-alanine and three of threonine in the peptide component and had a minimum molecular weight of 2500. She also found that polymyxin E had a threonine content of 14.36% and the molecular weight corresponding to this figure would be of the order of $(835)_n$.

Catch <u>et al</u>. (1949) found that the unknown fatty acid was similar to pelargonic acid and was present as an N-acyl grouping. Also, they noted that the fatty acids found in polymyxins A, B and D were identical.

Gore and Peterson (1949) examined polymyxins A and D with infrared spectrophotometric methods and noted that polymyxins A and D were different antibiotics. The unknown fatty acid constituent was similar to but not identical with pelargonic acid. The unknown fatty acid constituent had more methyl groups than the natural pelargonic acid. This led to the identification of the unknown acid as D-6-methyl-octan-l-oic acid (MOA) by Wilkinson (1949).

Bell et al. (1949) noted that polymyxin D hydrochloride consisted of: C, 43.5; H, 7.8; N, 15.2; O, 23.2; and Cl, 10.3% with a molecular weight of 1144 and an empirical formula $C_{50}H_{97}N_{15}O_{15}Cl_4$. It had one D-leucine, three L-threonine, one D-serine, and five L-DAB. After reaction of the polymyxin D with FDNB reagent, four r-DNP- α -amino-butyric acid and a free DAB were isolated. This indicated that the molecule had only four free r-amino groups present.

TABLE III

THE AMINO ACID COMPOSITION OF POLYMYXINS (Jones, 1948b)

Polymyxin	Leucine	Phenylalanine	Threonine	Serine	DAB
A	+	-	+	***	+
В	+	+	+	-	+
C	-	+	+	-	+
D	+	-	+	+	-
E	+	-	+	-	+

From pressure-area measurements, Few and Schulman (1953) concluded that there was no significant difference in the molecular weights of polymy-xins A, B, D and E. The molecular weight of the polymyxins had a mean value of 1250.

(i). Structures of polymyxin B:

Hausmann and Craig (1954) revealed the presence of more than one peptide in the crystalline polymyxin B preparation purified by Regna $\underline{\text{et}}$ al. (1949) by countercurrent distribution. The major component was designated polymyxin B_1 and the minor, polymyxin B_2 . Polymyxin B_1 contained a fatty acid identical to MOA but the B_2 had an unknown C_8 fatty acid which was not optically active. Polymyxin B_1 consisted of five L-DAB, two L-threonine, one L-leucine, one D-phenylalanine, one D-DAB, and one (+)-MOA, with an empirical formula $C_{56}H_{99}O_{14}N_{16}$ and a molecular weight of 1220.

After carefully studying the results of partial acid hydrolysis, Hausmann (1956) proposed two tentative structures (27a and 27b). He believed either of these two structures fulfilled all the requirements of the data.

$$\begin{array}{c|c} & \text{rNH}_2 \\ & \text{rNH}_2 \text{-DAB} \longrightarrow \text{DAB} \longrightarrow \text{Thr -OH} \\ & \uparrow & \downarrow \\ & \text{Leu} & \text{DAB -rNH}_2 \\ & \uparrow & \downarrow & \\ & \text{Phe} \longleftarrow \text{DAB} \longleftarrow \text{DAB} \longleftarrow \text{Thr} \longleftarrow \text{DAB} \longleftarrow \text{MOA} \\ & \downarrow & \downarrow & \downarrow \\ & \text{rNH}_2 & \text{OH} & \text{rNH}_2 \\ & & & & & & & & \\ & & & & & & \\ & & & & & & & \\ & & & & & & & \\ & & & & & & & \\ & & & & & \\ & & & & & & \\ & & & & & \\ & & & & & & \\ & & & & \\ & & & & & \\ & &$$

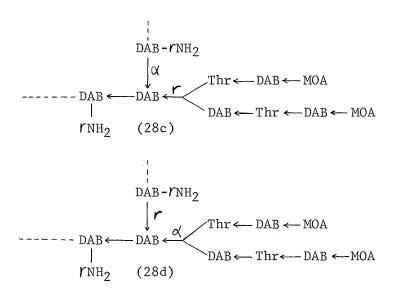
$$\begin{array}{c} \text{rNH}_2 \\ \\ \text{rNH-DAB} \longrightarrow \text{DAB} \longrightarrow \text{Thr-OH} \\ \\ \downarrow \\ \text{Leu} \\ \uparrow \\ \text{Phe} \longleftarrow \text{DAB} \longleftarrow \text{DAB} \longleftarrow \text{DAB} \longleftarrow \text{Thr} \longleftarrow \text{DAB} \longleftarrow \text{MOA} \\ \downarrow \\ \downarrow \\ \text{rNH}_2 \\ \text{rNH}_2 \\ \text{OH} \\ \text{rNH}_2 \\ \end{array}$$

Independently, Biserte and Dautrevaux (1957a) also came to the same conclusion from their structural studies of polymyxin B. They believed that polymyxin B_1 could have either an octacyclopeptide (28a) or heptacyclopeptide structure (28b) with a side chain formed of two or three amino acids attached to a DAB residue. The α -amino group of DAB terminating this side chain was the D-isomer and was joined to the carboxyl group of MOA.

$$\begin{array}{c} \text{rNH}_2 \\ \text{rNH}_2\text{-L-DAB} \longrightarrow \text{L-DAB} \longrightarrow \text{L-Thr-OH} \\ \downarrow \\ \text{L-Leu} \qquad \qquad \downarrow \\ \text{D-Phe} \longleftarrow \text{L-DAB} \longleftarrow \text{L-DAB} \longleftarrow \text{L-Thr} \longleftarrow \text{D-DAB} \longleftarrow \text{MOA} \\ \downarrow \\ \text{rNH}_2 \qquad \qquad \text{OH} \qquad \text{rNH}_2 \\ \end{array}$$

$$\begin{array}{c} \text{rNH}_2 \\ \text{rNH}_2\text{-L-DAB} \longrightarrow \text{L-DAB} \longrightarrow \text{L-Thr-OH} \\ \downarrow \\ \text{L-Leu} & \downarrow \\ \text{D-Phe} \longleftarrow \text{L-DAB} \longleftarrow \text{L-DAB} \longleftarrow \text{L-DAB} \longleftarrow \text{L-Thr} \longleftarrow \text{D-DAB} \longleftarrow \text{MOA} \\ \downarrow & \downarrow \\ \text{rNH}_2 & \text{rNH}_2 & \text{OH} & \text{rNH}_2 \\ \end{array}$$

Furthermore, the carboxyl group of threonine in the octacyclopeptide ring could join with either an α -amino (to be called 8α) (28c) or α -amino group (to be called 8α) (28d) of the DAB. In the heptacyclopeptide ring, the carboxyl group of DAB could attach to either α -amino (7 α) or α -amino groups (7 α) of the DAB in the ring (28c,d).



Thus one of the four possible alternatives, 70, 7r, 80 or 8r might be the structure of polymyxin B_1 . These four cyclic peptides were synthesized by Vogler et al. (1959, 1960, 1961) and by Studer et al. (1961, 1963). Vogler et al. (1963) reported that both synthetic 80 and 8r were not identical with the natural product in view of their low in vitro antibacterial activity against Brucella bronchiseptica. Both cyclic variants 70 and 7r were highly active. However, on the basis of microbiological experiments, 7r was more favored than 70, although other properties of 70 more closely resembled the natural polymyxin 8r. The difference between the natural

product and synthetic 76 was that the latter had optical activity. Therefore, it was concluded that none of the four synthesized substances was identical with natural polymyxin B_1 .

Suzuki et al. (1963d), by means of enzymatic hydrolysis studies, pointed out that D-DAB was not present in the polymyxin B_1 molecule and the DAB next to the fatty acid was an L-isomer. Furthermore, the side chain of polymyxin B_1 was linked to the α -amino group of DAB in the cyclic portion and the γ -amino group was involved in the ring formation (7%). Wilkinson and Lowe (1964a) also believed that polymyxin B_1 had no D-DAB residue present and the structure of polymyxin B_1 might be either 7% or 8 γ .

Suzuki et al. (1964) further proved that the polymyxin B_1 had a 70 structure with all L-DAB. This was confirmed by Vogler et al. (1965) by synthesis.

For polymyxin B₂, Wilkinson and Lowe (1963) noted that it had the same amino acid residues as polymyxin B₁ but with an unknown optically inactive fatty acid, $C_8H_{16}O_2$, rather than an optically active methyloctanoic acid. This unknown acid was identified as isooctanoic (3)(6-methylheptanoic) acid by Wilkinson and Lowe (1963). Wilkinson and Lowe (1964b) showed that polymyxin B₂ had a similar structure to B₁ except the (+)-MOA was substituted by IOA. Wilkinson and Lowe (1964c) finally decided that polymyxin B₂ should have a 70 structure similar to other polymyxins.

(ii). Structure of polymyxin E:

Suzuki et al. (1965) fractionated polymyxin E into polymyxin E_1 and polymyxin E_2 by countercurrent distribution. Amino acid composition of polymyxins E_1 and E_2 was the same as those of unfractionated polymyxin (3) Isooctanoic acid is also known as IOA.

E, namely, six L-DAB, two L-threonine, one L-leucine and one D-leucine. The fatty acids obtained from the acid hydrolysates of polymyxins E_1 and E_2 were identified as MOA and TOA respectively. Partial hydrolysis studies revealed that both antibiotics had the 7d structure similar to polymyxin B except the position of D-phenyl-alanine in the ring of polymyxin B was substituted by D-leucine in polymyxin E (29).

$$\begin{array}{c} \text{rNH}_2 \\ \text{rNH}_2\text{-L-DAB} \longrightarrow \text{L-DAB} \longrightarrow \text{L-Thr-OH} \\ \downarrow \\ \text{L-Leu} \\ \uparrow \\ \text{D-Leu} \longleftarrow \text{L-DAB} \longleftarrow \text{L-DAB} \longleftarrow \text{L-DAB} \longleftarrow \text{L-Thr} \longleftarrow \text{L-DAB} \longleftarrow \\ \downarrow \\ \downarrow \\ \text{rNH}_2 \\ \text{rNH}_2 \\ \text{OH} \\ \text{rNH}_2 \\ \end{array}$$

(iii). Structure of polymyxin D:

Hayashi et al. (1966) found that polymyxin D also was a mixture of two components separable by the countercurrent distribution method. Both polymyxins D_1 and D_2 had the same amino acid compositions, five L-DAB, three L-threonine, one D-leucine and one D-serine. The fatty acid found in polymyxin D_1 was identified as MOA and in polymyxin D_2 , TOA. Based on partial acid and enzymatic hydrolyses, the structure of polymyxins D were identified as the 7α -type like other polymyxins (30).

(iv). Structures of polymyxin A:

Wilkinson and Lowe (1966) reported that polymyxin A could be separated into two components, polymyxins A_1 and A_2 by countercurrent distribution. Both polymyxins A had five L-DAB, three L-threonine, one D-leucine,

and one D-DAB. Just like other polymyxins, polymyxin A_1 contained MOA, and polymyxin A_2 , IOA. Both A_1 and A_2 were found to be of the 7d-type (31).

$$\begin{array}{c} \text{rNH} \\ \text{PNH}_2 \\ \text{rNH}_2 - \text{L} - \text{DAB} \longrightarrow \text{L} - \text{DAB} \longrightarrow \text{L} - \text{Thr} - \text{OH} \\ \text{HO} - \text{L} - \text{Thr} \\ \text{D} - \text{Leu} \longleftarrow \text{L} - \text{DAB} \longleftarrow \text{L} - \text{DAB} \longleftarrow \text{D} - \text{DAB} \longleftarrow \text{L} - \text{Thr} \longleftarrow \text{L} - \text{DAB} \longleftarrow \\ \text{D} - \text{Leu} \longleftarrow \text{L} - \text{DAB} \longleftarrow \text{L} - \text{DAB} \longleftarrow \text{D} - \text{DAB} \longleftarrow \text{L} - \text{Thr} \longleftarrow \text{L} - \text{DAB} \longleftarrow \\ \text{IOA} \\ \text{rNH}_2 \\ \text{(31)} \end{array}$$

(v). Structure of polymyxin C:

Nothing is known about the fatty acid content and detailed structure of polymyxin C.

B. CIRCULINS.

(1). Producing strain and properties of circulins:

Murray and Tetrault (1948) isolated a strain of B. circulans (Q-19) from a soil sample which produced an antibiotic they called "circulin". Circulin was more active against Gram-negative than Gram-positive microorganisms. Murray et al. (1949) noted that circulin sulphate was very soluble in water, less soluble in lower alcohols and insoluble in non-polar organic solvents. In acid solutions, it withstood autoclaving for 15 min. at 15 lbs. of pressure, but stability decreased if the pH of the solution increased above 7. It was not inactivated by pepsin but the activity was destroyed by trypsin within seven days. Circulin was dialysable, and it showed levorotation in aqueous solutions. The antibiotic gave positive biuret and ninhydrin tests and was toxic to mice, the LD50 being 23 mg. per kg. of body weight when injected intravenously. Peterson and Reineke (1949 a,b) found that circulin was inactivated by lipase. Howell (1949) found crystalline circulin sulphate to have a melting point of 235°C and absorption bands at 252, 258 and 264 nm. The isoelectric point of circulin in 0.02M citrate buffer was at pH 7.

(2). Isolation:

Murray et al. (1949) isolated circulin as the sulphate from clarified culture fluids by adsorption on active charcoal and elution with aqueous tertiary butanol acidified with H_2SO_4 . The eluate was concentrated in vacuo and neutralized with $Ba(OH)_2$. Peterson and Reineke (1949a,b) further puri-

fied circulin sulphate by a chromatographic method in which the antibiotic was subjected to chromatography on a column of a mixture of Darco-50 and Celite-545 and eluted with aqueous tertiary butanol acidified with ${\rm H_2SO_4}$. By these methods, they were able to separate circulin into two active components, circulins A and B.

Howell (1949) purified circulin by extraction with an acetone-H2SO4-ammonium sulphate mixture. The active principle was then precipitated from the acetone solution by the addition of chloroform. The precipitate was dissolved in water and reprecipitated with the addition of ammonium sulphate. Finally, the circulin sulphate was crystallized from a diluted ethanolic solution. Recrystallization could be performed in methanol, ethanol, isopropanol, acetone or molar sodium acetate solutions.

(3). Structural studies:

Peterson and Reineke (1949a,b) found that circulin contained five L-DAB residues, one L-threonine, one D-leucine and a fatty acid residue with a minimum molecular weight of 854. The carboxyl groups of all amino acid residues were bound, the only free groups in the molecule being the Γ -amino groups of DAB. It was believed that the fatty acid was attached to the hydroxyl group of threonine and this was the reason circulin was sensitive to lipase. Howell (1949) found that circulin sulphate had a molecular weight of 1050 and the empirical formula $C_{41}H_{55}O_{15}N_9SO_4$. Dowling et al. (1952) showed that both circulins A and B contained isoleucine in addition to the constituents reported by Peterson and Reineke.

Grady et al. (1958) showed that circulin A consisted of L-DAB,

L-threonine, D-leucine, L-isoleucine and MOA in the molar ratios 6:2:1:1:1. From the data obtained by partial acid hydrolysis, Koffler (1959) proposed a tentative formula for circulin A (32) which was a cyclodecapeptide with no side chain. He also believed that circulin B had an identical structure

to circulin A with the exception that the MOA in circulin B was attached to the Γ -amino group of DAB as marked by an asterisk in the formula (32).

Since circulins and polymyxins had close similarity in biological and chemical properties, the correctness of the structure of circulins A and B proposed by Koffler (1959) aroused the concern of Fujikawa et al. (1965). They confirmed the constituents of circulin A reported by Koffler (1959), but from their partial acid hydrolysis and enzymatic hydrolysis studies, they found that circulin had a different structure than that proposed by Koffler. The structure of circulin A was similar to polymyxin Bl, differing from Bl only in replacement of D-Phe and L-Leu of the Bl with D-Leu and L-Ileu in circulin A (33).

Hayashi <u>et al</u>. (1968) found that circulin B had a similar structure to circulin A and only differed from A in having IOA in place of MOA (see 33 above).

C. COLISTINS.

(1). Producing strain and properties of colistins:

Koyama et al. (1950) isolated colistin from cultures of B. colistins, which was believed to be closely related to B. polymyxa. Colistin also is known as colomycin, colimycine or colo-mycin but it differs from the Soviet antibiotic colimycin (Gause et al., 1956), which is produced by Streptomyces and is related to neomycin.

Wright and Welch (1960) reported that colistin sulphate absorbed only in the 210-250 nm region in the ultraviolet spectrum. Schwartz et al. (1960) noted that colistin was a basic peptide. The base itself was insoluble but the salt was soluble in water. Solutions of colistin were levorotatory and stable at pH 2 to 6 but the stability decreased above pH 6. The presence of serum in colistin solutions did not alter antibiotic activity, and it was active against Gram-negative but much less so against Gram-

positive bacteria and fungi.

(2). Isolation:

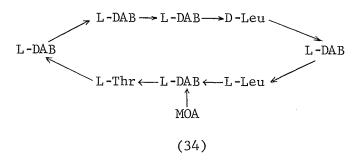
Koyama (1952) isolated colistin sulphate from broth by treatment with sulphuric acid and heat. Colistin could also be isolated as the picrate. Kurihara and Suzuki (1953) converted colistin picrate to hydrochloride by dissolving picrate in concentrated HCl with crystallization from acetone. Fujiko and Namiki (1957) obtained crystalline colistin phosphate from an alcoholic solution of colistin by mixing with concentrated $\rm H_2SO_4$.

Fujimasa (1956) absorbed colistin to a weak acidic cation exchanger and liberated it with acid solution with further purification by anion exchange. A similar procedure was used by Morito (1962a) in which he first acidified the culture fluid with HCl, adsorbed the colistin to a column of Amberlite TRC-50 (Na⁺ form) and then eluted it with HCl solution. The active principle was precipitated by adjusting the pH so that it was alkaline and the procedure was repeated until a pure substance was obtained.

(3). Structural studies:

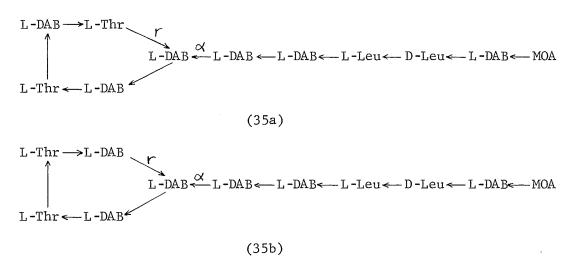
Oda et al. (1954) found that colistin could be separated into three active components, colistins A, B and C by paper chromatography using 0.2M glycine buffer (pH 2.5) as a developing fluid. Oda and Ueda (1954) showed that the hydrolysates of colistin contained leucine, threonine, DAB, and the fatty acid, MOA.

Suzuki (1956) noted that colistin had free OH and r-amino groups, the OH group of which was essential to the antibiotic activity. Suzuki (1957a) believed that colistin was composed of L-threonine, L-leucine, L-DAB and MOA in a molar ratio of 1:1:1:5:1. Its hydrochloride salt had a molecular weight of 1200 ± 50 and the empirical formula $C_{45}H_{85}O_{10}N_{13}$ -4HCl. Suzuki (1957b) further showed that colistin had a threonine OH group and four r-amino groups of DAB free, but there were no free α -amino or carboxyl groups in the molecule. From these data together with the information obtained from partial hydrolysis, Suzuki (1957c) proposed a tentative structure for colistin (34).



Biserte and Dautrevaux (1957b) confirmed that the colistin possessed neither terminal α -amino nor α -carboxyl groups but they found only one threonine, one leucine and four DAB residues in the colistin molecule. Dautrevaux and Biserte (1961) showed that colistin was an heterometric

decapeptide consisting of six L-DAB, two L-threonine, one L-leucine, one D-leucine and one MOA residue. It had the structure of a cyclopentapeptide with a side chain of five amino acids attached to a residue of L-DAB in the ring. The α -amino group of the DAB which terminated this side chain was bound to the carboxyl group of the fatty acid, MOA. Two possible arrangements of the cyclopentapeptide ring were proposed by them (35a and 35b).



In 1961, Suzuki et al. (cited by Suzuki et al., 1963a) found that commercial colistin could be separated into three components corresponding respectively to the colistins A, B and C designated by Oda et al. (1954). Colistins A and B had much stronger antibacterial activity than colistin C. The concentration of colistin C in commercial preparations was small and was frequently absent.

Morito (1962a) separated colistin A into colistins A_1 and A_2 by ion-exchange and countercurrent distribution methods. Colistins A_1 and A_2 were similar in all respects but differed in fatty acid content. Colistin A_1 contained MOA and colistin A_2 , IOA. Morito (1962b) further showed that

both colistins had two leucine, one threonine, and five DAB residues and he proposed an identical structure to that reported by Suzuki (1957c).

Suzuki et al. (1963a) showed that both colistins A and B contained six L-DAB, two L-threonine, one L-leucine and one D-leucine. Furthermore, colistin A contained MOA and colistin B, TOA. However, they could not separate colistin A into colistins A_1 and A_2 as claimed by Morito (1962a). The molecular weight of the hydrochloride of both colistins A and B was about 1360.

Suzuki et al. (1963b) confirmed that colistin A had no free α amino or carboxyl groups in its molecule. Based on the earlier data and on
the results from partial acid hydrolysis, he proposed two possible structures (36a and 36b). Later, from information obtained from enzymatic studies
on colistin A, the same authors (1963c) eliminated structure 36b.

$$rNH_{2}$$

$$rNH_{2}-L-DAB \longrightarrow L-DAB \longrightarrow L-Thr-OH$$

$$L-Leu \qquad \qquad \downarrow r$$

$$D-Leu \longleftarrow L-DAB \longleftarrow L-DAB \longleftarrow L-DAB \longleftarrow L-Thr \longleftarrow L-DAB \longleftarrow MOA$$

$$rNH_{2} \qquad rNH_{2} \qquad OH \qquad rNH_{2}$$

$$(36a)$$

$$rNH_{2}-L-DAB \longrightarrow L-DAB \longrightarrow L-Thr-OH$$

$$L-Leu \qquad \qquad \downarrow \alpha$$

$$D-Leu \longleftarrow L-DAB \longleftarrow L-DAB \longleftarrow L-DAB \longleftarrow L-Thr \longleftarrow L-DAB \longleftarrow MOA$$

$$rNH_{2} \qquad rNH_{2} \qquad OH \qquad rNH_{2}$$

$$(36b)$$

Suzuki and Fujikawa (1964) further proved that colistin B had an identical structure to colistin A except that colistin B contained IOA instead of MOA.

D. POLYMYXINS M.

From a soil sample obtained in the vicinity of Moscow, Ilinskoya and Rossovskaya (1958) isolated a strain of \underline{B} . $\underline{polymyxa}$ which produced an antibiotic substance similar to the polymyxins. This antibiotic was designated polymyxin M.

Khokhlov et al. (1960) noted that polymyxin M could be purified by means of ion-exchange methods and its properties were similar to those of other polymyxins. It melted with decomposition at 225 - 228°C, had a rotation power $\left[\alpha\right]_{D}^{25}=$ -48.1 (in water) and a molecular weight of 1185. The hydrolysates of polymyxin M contained DAB, threonine, leucine, and fatty acid residues, the fatty acid being identified as MOA. Stepanov et al. (1960) showed that polymyxin M contained five free amino groups. Khokhlov and Chih (1961) and Silaev et al. (1961a,b) showed that polymyxin M contained one leucine, three threonine, six DAB and one MOA residue. No free α -amino or α -carboxyl groups were detected.

Silaev et al. (1962) found that purified polymyxin M was homogeneous as judged by countercurrent extraction. Yulikova et al. (1965) and Silaev et al. (1965) proposed an identical structure for polymyxin M (37).

Leu
$$\rightarrow$$
 DAB \rightarrow Thr

DAB

Thr

DAB

Thr

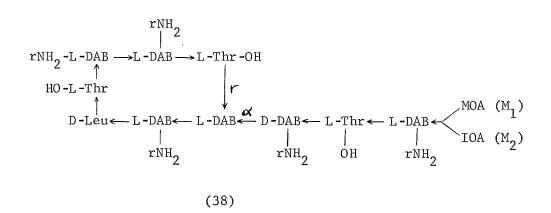
DAB

DAB

MOA

(37)

However, Wilkinson and Lowe (1966) found that purified polymyxin M, just like other polymyxins, was a mixture of closely related antibiotics and was separable into M_1 and M_2 by countercurrent distribution. Both had the same amino acid composition but differed from each other in fatty acid content. Polymyxin M_1 contained MOA and polymyxin M_2 , TOA. They also noted that the amino acid composition, electrophoretic and chromatographic behavior, optical rotation and nephrotoxicity of polymyxins M were paralleled by those of polymyxins M. They believed that polymyxins M were identical with polymyxins M and should have the structure shown below (38).



E. SUMMARY

All members of the polymyxin group of antibiotics are basic peptides. They can be classified into two groups according to the solubilities of their free bases in water: the water-soluble group containing polymyxins A, C, D and M; and the water-insoluble group, polymyxins B and E, colistins A and B, and circulins A and B.

Except for polymyxin C whose characterization is incomplete, each antibiotic consists essentially of two closely related peptides. Each member of the pair differs from the other only in the content of fatty acid, having either (+)-6-methyloctanoic acid (MOA) or an isooctanoic acid (IOA). All polymyxins share common amino acid residues, $L-\alpha, \Gamma$ -diaminobutyric acid (DAB) and L-threonine, but different individual pairs have their own specific amino acids (Table IV).

Furthermore, all polymyxins have a common type of structure (39) in which a chain of three amino acids is attached to a cyclic heptapeptide ring via the α -amino group of the DAB residue. The terminal α -amino group of the chain is acylated with one or the other of the two fatty acids (R). Differences in individual polymyxins reside in the nature of the three amino acid residues X, Y, and Z (Table V).

TABLE IV

SUMMARY OF THE AMINO ACID AND FATTY ACID COMPOSITION OF POLYMYXINS

polymyxin	DAB	Leu		Ileu	Thr	Ser	fatty acid	
WATER-SOLUBLE GROUP								
$A_1 = M_1$	5L & 1D*	1D		~	3L	-	MOA	
$A_2 = M_2$	5L & 1D	1D	_	-	3L		IOA	
С	+**	***	-	-	+	-	MOA	
D_1	5L	1D	-	-	3L	1D	MOA	
D_2	5L	1D	-	-	3L	1D	IOA	
WATER-INSOLUBLE GROUP								
B ₁	6L	1L	1D	-	2L	-	MOA	
B ₂	6L	1L	1D	-	2L	-	IOA	
E_1 = colistin A	6L	1L & 1D	-	-	2L	-	MOA	
$E_2 = colistin B$	6L	1L & 1D	-	-	2L	-	IOA	
circulin A	6L	1D	-	1L	2L	-	MOA	
circulin B	6L	1D	-	1L	2L	-	IOA	

 $[\]star$ 5L & 1D means five L-isomers and one D-isomer.

^{** +} signifies present, and -, absent.

 $\begin{tabular}{lllll} TABLE & V \\ STRUCTURE & OF THE & MEMBERS & OF THE & POLYMYXIN & GROUP & OF ANTIBIOTICS \\ \end{tabular}$

Polymyxin	R	X	Y	Z
$A_1 = M_1$	MOA	D-DAB	D-Leu	L-Thr
$A_2 = M_2$	IOA	D-DAB	D-Leu	L-Thr
B ₁	MOA	L-DAB	D-Phe	L <i>-</i> Leu
B ₂	IOA	L-DAB	D-Phe	L - Leu
D_1	MOA	D-Ser	D-Leu	L-Thr
D ₂	IOA	D-Ser	D-Leu	L-Thr
E_1 = colistin A	MOA	L-DAB	D - Leu	L-Leu
$E_2 = colistin B$	IOA	L-DAB	D-Leu	L-Leu
Circulin A	MOA	L-DAB	D-Leu	L-Ileu
Circulin B	IOA	L-DAB	D-Leu	L-Ileu

IX. POLYPEPTIN.

(1). Producing strain, nomenclature and properties of polypeptin:

McLeod (1948) isolated a bacterium, \underline{B} . $\underline{krzemieniewski}$ M-14 from soil, which produced an antibiotic. The antibiotic was named "circulin". Since this name was also applied to another antibiotic produced by the \underline{B} . $\underline{circulans}$ Q-19 strain discovered by Murray and Tatraut (1948), this antibiotic was renamed "polypeptin" (Garson \underline{et} \underline{al} ., 1949).

McLeod (1948) showed that polypeptin could be autoclaved for 30 min. in acid or neutral solutions but not in alkaline without denaturation. It was active against Gram-positive and Gram-negative bacteria as well as fungi and was extremely toxic to mice. Polypeptin also caused hemolysis of the erythrocytes of man, rabbit, sheep and mouse.

Howell (1950) noted that polypeptin sulphate was soluble in water, alcohols, and pyridine but insoluble in organic solvents, with polypeptin acetate having higher solubility than the sulphate. The sulphate melted at 230° C with decomposition, showed specific rotation $\left[\mathcal{A}\right]_{D}^{20} = -93.3^{\circ}$ (c, 3% in 70% isopropanol) and had an isoelectric point at pH 11. It was not inactivated by pepsin, trypsin, hydrogen sulfide or ferric chloride.

(2). Isolation and structural studies:

Howell (1950) isolated polypeptin by acetone extraction from acidified culture broth, removal of impurities from the extract by ammonium sulphate precipitation and reprecipitation by chloroform. This precipitate was dissolved in warm ethanol and crystalline polypeptin sulphate was obtained

from this solution when it cooled. Recrystallization was performed in either methanolic or ethanolic solutions. The crystalline polypeptin sulphate still appeared to be a mixture with the major component approaching 90%.

In countercurrent distribution studies, Hausmann and Craig (1952) found that crystalline polypeptin sulphate contained at least two components, the major one consisting of 80% of the mixture in contrast with the results of Howell (1950). The major component contained three L-DAB, one L-threonine, one D-valine, one L-isoleucine, two L-leucine, one L-phenylalanine and one unknown fatty acid with the formula $C_8H_{13}O_2$. The molecular weight of the free base was 1145 with the empirical formula $C_{56}H_{96}O_{13}N_{12}$.

The detailed structure of polypeptin still remains unknown.

X. SERRATAMOLIDE.

On media containing glycerol and peptone, Wasserman et al. (1961, 1962) noted that certain strains of <u>Serratia marcescens</u> produced a neutral colorless compound, which they named "serratamolide". The antibiotic activity of serratamolide against Gram-positive organisms was similar to that of depsipeptides isolated from <u>Fusarium</u>. Hydrolyzed under mild alkaline conditions, serratamolide converted to serratamic acid (40) which had been isolated from several members of the <u>Serratia</u> group by Cartwright (1955).

Serratamolide was isolated from liquid cultures by methylene chloride extraction or from solid media by acetone extraction. After the removal of the solvent by distillation <u>in vacuo</u>, the active residue was

$$_{\text{CH}_{3}(\text{CH}_{2})_{6}\text{CH-CH}_{2}\text{CONHCH}}^{\text{COOH}}$$
 $_{\text{CH}_{2}\text{OH}}^{\text{COOH}}$
(40)

extracted with boiling ethanol. By a process of fractional crystallization in hot and cold ethanol, crystalline serratamolide was obtained. Recrystallization was effected from absolute ethanol (Wasserman et al., 1961, 1962).

Wasserman et al. (1961, 1962) showed that serratamolide was optically active where $\left[\alpha\right]_D^{25}=+4.8$ (ethanol), containing two free hydroxyl and two C-methyl groups but no amino nitrogen or methoxyl. It had a melting point 159 - 160°C. No absorption above 200 nm was found except for endabsorption above 250 nm. Elementary analysis showed that serratamolide's molecular formula was $C_{26}H_{46}O_8N_2$. In acid hydrolysis, serine and an oily acid-insoluble component, 3-hydrodecanoic acid, were found.

Based on the information obtained from infrared spectrum analysis, and partial and total hydrolyses, Wasserman <u>et al</u>. (1962) suggested the structure of serratamolide was as shown below (41). Shemyakin <u>et al</u>. (1964) confirmed this by synthesis of the diacetyl derivative.

XI. SUBTILINS.

(1). Producing strain and properties of subtilins:

Jansen and Hirschmann (1944) found a strain of <u>B</u>. <u>subtilis</u> which produced a polypeptide antibacterial substance which they designated "subtilin". Subtilin was suspected to be a mixture of antibiotics rather than a single active entity. These authors showed that subtilin was stable in acid but easily inactivated by alkali. At pH 2.5, it withstood autoclaving at 115°C for 10 min. The antibiotic was sensitive to light and was freely dialysable.

Salle and Jann (1945) found that subtilin was active against Grampositive bacteria, fungi and Neisseria. Anderson et al. (1946) stated that subtilin had no immediate effect on erythrocytes but caused hemolysis after 24 hr. incubation at 4°C. However, Salle and Jann (1947) showed that subtilin was not toxic to experimental animals.

Dimick et al. (1947a,b) showed that subtilin was soluble in acid and wet alcohols but insoluble in alkali and all dry organic solvents. Its solubility in acid solutions decreased markedly in the presence of salts. Both trypsin and pepsin inactivated the antibiotic.

Hassell(1948) noted that subtilin gave positive responses to the ninhydrin reagent, Ehrlich's reagent for indole derivatives and Folin-Denis reagent for phenol. Brink et al. (1951) found that an aqueous solution of subtilin possessed no maximum absorption in the ultraviolet region but had a shoulder at 275 - 280 nm and an inflection point at 285 nm. Specific rotation was $\left[\mathcal{A}\right]_{\mathcal{D}}^{25} = -36^{\circ}$ (c, 0.865 in water).

(2). Isolation:

Jansen and Hirschmann (1944) acidified whole culture fluid with HCl and the resulting precipitate was ground and extracted with warm ethanol. The active principle was then salted out from ethanolic solution by the addition of NaCl. The antibiotic was crystallized from the ethanol and NaCl solution.

Dimick et al. (1947b) isolated subtilin through n-butanol extraction from acidified culture fluid. After the addition of petroleum ether, the n-butanolic solution was extracted with acetic acid. The active principle in the acetic acid was salted out by NaCl. Impurities present were removed by ethanol and the active residue left was dissolved in acetic acid repeatedly salted out by NaCl, deionized by ion-exchangers and finally dried. A similar but simplified method was used by Fevold et al. (1948) for the isolation of the antibiotic.

Brink et al. (1951) found that subtilin concentrates from the above methods were essentially homogeneous when they were subjected to countercurrent distribution. Stracher and Craig (1959), however, found subtilin to be a mixture of peptide antibiotics, and named the major component subtilin A. Alderton and Snell (1959) noted that subtilin contained at least six active components separable by electrophoretic methods. The major one was identical to Stracher and Craig's subtilin A.

(3). Structural studies:

Jansen and Hirschmann (1944) showed crystalline subtilin to have an elemental analysis of: C, 54.4; H, 7.7; and N, 14.5%. It was predicted

that tyrosine would be present. Dimick et al. (1947b) found that subtilin contained 15.8% total N or 11.0% amino-N and 4.2% sulphur. Titrating with lithium hydroxide, Brink et al. (1951) gave a value of 3340 for the molecular weight of subtilin.

Lewis and Snell (1951) showed subtilin was composed of two glycine, one alanine, one leucine, one isoleucine, one proline, one phenylalanine, one tryptophan, three lysine, three glutamic acid, three lanthionine-like substances, four unknown $C_7H_{12}O_3N_2S$, and five amide residues. The average minimum molecular weight was 3420 but might possibly be 7000. Aspartic acid and glycine were not in D-configuration and aliphatic acids were not present. Furthermore, the subtilin molecule might be a ring structure. By isolation, Alderton and Fevold (1951) showed the lanthionine-like substance reported by Lewis and Snell (1951) to be mesolanthionine. Carson (1952) noted that the unknown C_7 substance referred to above was an unknown diamino-dicarboxy1 sulfur acid with the formula ${\rm C_{5}H_{8}S(NH_{2})_{2}(COOH)_{2}}$. He also detected the presence of another unknown unnatural amino acid which contributed a free lpha-amino group to the molecule. Other free amino groups found in the subtilin molecule were contributed by the δ -amino group of lysine and one of the two amino groups of the diamino-dicarboxyl sulfur amino acids. Alderton (1953) identified this ${
m C_7}$ unknown compound as methy1-

(42)

lanthionine (42).

Stracher and Craig (1959) found that subtilin A contained all the amino acid residues reported by Lewis and Snell (1951) with an additional one discovered by Carson (1952) which was identified as sarcosine (N-methylglycine). Subtilin possessed three free lysine δ -amino groups and one sarcosine α -amino group. The subtilin A molecule contained rings consisting in part of five sulphur atoms with a side chain comprised of Sar-(Glu.Leu. Sar.Asp)-Lan-. Sarcosine was the N-terminal substance and lanthionine served as the bridge-head for attachment of the side chain. One of the five rings in the molecule must be completely peptidic where the rest might be peptide chains joined by the thioester linkages of the four β -methyl-lanthionines present. Subtilin A was believed to have an empirical formula $C_{144}H_{226}N_{38}O_{37}S_5$ and a molecular weight 3242. The detailed structure of subtilin A remains unknown and little information regarding other subtilins is available at the present time.

XII. TYROTHRICIN, TYROCIDINES AND GRAMICIDINS.

A. TYROTHRICIN.

(1). Producing strains:

Dubos (1939a,b) isolated a Gram-positive <u>Bacillus</u>, capable of lysing living staphylococci, from soil to which he had repeatedly added mineral media and suspensions of staphylococci, pneumococci and group A hemolytic streptococci over a period of two years. Dubos and Hotchkiss (1941) identified this organism as <u>B. brevis</u> BG strain. They also isolated several other strains of the same species from cheese, soil, manure and sewage all strains of which were capable of producing varying amounts of the same antibacterial agent.

Hoogerheide (1940a,b) as well as Strokes and Woodward (1942) also independently isolated from soil other strains of \underline{B} . \underline{brevis} which produced a similar substance.

(2). Isolation:

Dubos (1939b) found that the active principle in the culture medium was precipitable at pH 4.5 and the precipitate was soluble in neutral buffers. Dubos and Cattaneo (1939) noted that acidic acetone removed the impurities from the resulting solution. The active material left in the acetone solution was precipitable by the addition of a large volume of salt solution. This precipitate was no longer soluble in water but readily so in acetone or ethanol. Hotchkiss and Dubos (1940a) obtained three crystal-

line preparations from this precipitate with further treatment. Two acid substances were isolated from the alcohol solution of the precipitate by precipitation with ether and fractional crystallization of the dried precipitate from hot ethanol. One of these two acids which was least soluble in ethanol was designated graminic acid, and the other, larger in amount and more soluble in alcohol, was called gramidic acid. The third substance, named gramicidin, which was soluble in alcohol but insoluble in ether, was obtained by repeated precipitation from alcohol through the addition of ether. Later, however, Hotchkiss and Dubos (1940c) discovered that graminic acid was actually a hydrochloride salt of a weak base and renamed it tyrocidine hydrochloride. At the same time, they also noted that gramidic acid was a mixture of free tyrocidine and its hydrochloride salt. Therefore, the name gramidic acid was abandoned. They also used the name "tyrothricin" for the crude bactericidal agent (a mixture of tyrocidine and gramicidin) which had been isolated from B. brevis.

B. TYROCIDINES.

(1). Isolation:

Hotchkiss and Dubos (1940b) obtained a highly purified crystalline tyrocidine preparation by repeated recrystallization from acidified absolute methanol. In countercurrent distribution studies, Battersby and Craig (1952a) found that crystalline tyrocidine was a mixture of three active major components and a number of minor peptides. They named the three major ones tyrocidine A, B and C according to the order of their partition ratio in countercurrent distribution.

(2). Properties:

Hotchkiss and Dubos (1940c) showed that crystalline tyrocidine hydrochloride melted at 237 - 239°C with decomposition and had an optical rotation $\left[\alpha\right]_D^{25} = -102°$ (c, 1.00, 95% ethanol). Hotchkiss and Dubos (1941) noted that tyrocidine was resistant to the action of common proteolytic enzymes. It was soluble in methanol, ethanol, acetic acid and pyridine, sparingly soluble in water, acetone and dioxane, and insoluble in ether and hydrocarbon solvents. Aqueous solutions of tyrocidine had low surface tension and behaved as a detergent solution. Tyrocidine precipitated a number of soluble proteins as do some of the cationic detergents.

Hotchkiss (1941) noted tyrocidine reacted slowly with nitrous acid, and that it had a major dissociation point at pH 8.6 and a secondary one above pH 10.

Dubos (1941) found that tyrocidine was active against both Gram-positive and Gram-negative species, and that it lysed cells which were sensitive to it. Its action, however, was inhibited by many tissue constituents.

(3). Structural studies:

Hotchkiss (1941) found that the hydrolysates of tyrocidine contained tyrosine, tryptophan, aspartic acid and other dibasic amino acid residues. From determination of the chloride content, the minimal molecular weight for tyrocidine hydrochloride was 1285 ± 50 and the empirical formula might be ${}^{\rm C}_{63}{}^{\rm H}_{83}{}^{\rm N}_{13}{}^{\rm O}_{13}{}^{\rm HCl}$. He believed that tyrocidine was a peptide constructed in such a way that two basic amino, three amide and one

carboxyl or acidic phenolic group were free.

Christensen et al. (1941) reported that tyrocidine's elementary analysis was: C, 59.7; H, 6.9; N, 14.5; and C1, 2.52% with dissociating groups at pH 9.0 and above pH 11. Its minimum molecular weight was 2700 and it contained tryptophan, tyrosine, alanine, phenylalanine, ammonia and dibasic amino acid residues.

Gorden et al. (1943b) found phenylalanine, leucine, proline, valine, tyrosine, ornithine, glutamic acid, tryptophan and aspartic acid residues in acid hydrolysates of tyrocidine. The phenylalanine isolated from hydrolysates had mainly the D-configuration and the other amino acids were all L-isomers. Christensen et al. (1945) confirmed the presence of L-aspartic acid, L-valine, L-leucine, and L-tryptophan by microbiological determination assay.

(i). Structure of tyrocidine A:

Battersby and Craig (1952a) separated three major components of tyrocidine by countercurrent distribution and found that all three peptides contained phenylalanine, leucine, tyrosine, valine, proline, ornithine, glutamic acid, and aspartic acid as well as ammonia residues in their hydrolysates. In addition, tyrocidines B and C contained tryptophan. There were no free α -amino or α -carboxyl groups in any of the three components. The α -carboxyl group of aspartic acid and the α -carboxyl group of glutamic acid were conjugated with amide groups which converted to ammonia during acid hydrolysis. The only free functional groups in the molecule were the α -amino group of ornithine and the hydroxyl group of tyrosine.

In tyrocidine A, Battersby and Craig (1952a) found that all

amino acid residues were L-isomers except that of phenylalanine which appeared to be a mixture of two moles of the D- with one mole of the L-isomers. They believed that the amino acid residue formula of tyrocidine A could be written as:

 $(\text{D-Phe})_2(\text{L-Phe})(\text{L-Val})(\text{L-Tyr})(\text{L-Leu})(\text{L-Pro})(\text{L-Orn})(\text{L-Asp-NH}_2)(\text{L-Glu-NH}_2)$ which corresponded to the empirical formula $\text{C}_{66}\text{H}_{86}\text{O}_{13}\text{N}_{13}$. Battersby and Craig (1952b) found tyrocidine A to have a minimal molecular weight of 1270.

Paladini and Craig (1954) proposed a structural formula for tyrocidine A (43) which was confirmed by Ohno and Izumiya (1966) by synthesis.

(ii). Structure of tyrocidine B:

King and Craig (1955a) found that tyrocidine B was also a cyclopeptide having an amino acid formula:

(44)

(iii). Structure of tyrocidine C:

Ruttenberg <u>et al</u>. (1965a) noted that tyrocidine C was also a cyclic decapeptide with a structure similar to the other tyrocidines. Tyrocidine C differed from tyrocidine B by substitution of one of the D-phenylalanine residues with a D-tryptophan (45).

$$\begin{array}{c} \text{L-Val} \longrightarrow \text{L-Orn} \longrightarrow \text{L-Leu} \longrightarrow \text{D-Phe} \longrightarrow \text{L-Pro} \\ \uparrow & \downarrow \\ \text{L-Tyr} \longleftarrow \text{L-Glu} \longleftarrow \text{L-Asp} \longleftarrow \text{D-Try} \longleftarrow \text{L-Try} \\ \downarrow & \downarrow \\ \delta \text{NH}_2 & \text{rNH}_2 \end{array}$$

(45).

C. GRAMICIDINS.

(1). Purification:

Hotchkiss and Dubos (1940c) showed that gramicidin could be obtained directly by extraction of the alcoholic solution of tyrothricin with acetone. Further purification was effected by repeated crystallization from acetone.

Gregory and Craig (1948) found that crystalline gramicidin was a mixture of chemically related substances. They obtained two crystalline components, together with a mixture, after countercurrent distribution. The first component, which was less soluble in organic solvents, was named gramicidin A and the other, gramicidin B. Craig et al. (1949a) showed by countercurrent distribution that gramicidin contained at least three major components, gramicidin A, B and C. Ramachandran (1963) separated a new component, gramicidin D, from gramicidin A.

(2). Properties of gramicidins:

Christensen et al. (1941) showed that gramicidin lost no activity

during two hrs. of boiling in alcohol, little during 15 hrs. of standing in a 50% alcoholic solution of 1N NaOH. However, heat treatment in the presence of diluted HCl or NaOH alcoholic solutions completely destroyed its activity within two hrs.

Tishler et al.(1941) showed that gramicidin had principle absorption maxima at 281.5, 290 and 269 nm. It responded positively to common protein tests such as the biuret, xanthoproteic and the Hopkin-Cole reaction. Gramicidin was precipitated by some protein precipitants such as flavinic, sifiamic and picric acids.

Dubos (1941) showed that gramicidin was completely inactive against Gram-negative bacilli, moderately active against meningococci and gonococci, and highly inhibitory to all Gram-positive strains. It never caused lysis even in the most susceptible strains. The effect of gramicidin was slightly inhibited by serum, tissue extracts or peptone but the phospholipid, phosphatidyl serine was strongly inhibitory.

Dubos and Hotchkiss (1941) found that gramicidin caused a slow hemolysis of erythrocytes but small quantities of glucose prevented this action.

- (3). Structural studies:
- (i). Preliminary studies:

Hotchkiss and Dubos (1940b) showed that gramicidin consisted of: C, 62.7; H, 7.5; and N, 13.9% with an empirical formula $C_{74}H_{106}N_{14}O_{14}$. The molecular weight was about 1400. Gramicidin contained neither free basic nor acidic groups. However, after hydrolysis, it liberated a total of 11 moles non-volatile acid, 11 moles of basic groups, 10 moles of amino acids (including 2.4 moles of tryptophan) and a mole of 14-16 carbon-saturated aliphatic acid. Methoxyl and acetyl groups, histidine, arginine, tyrosine and ammonia were all absent in gramicidin. Furthermore, nearly one-half of the amino acid residues in gramicidin were D-isomers. Lipmann et al. (1941) indicated that 45% of the amino acids in gramicidin hydrolysates had the D-configuration.

Hotchkiss and Dubos (1941) further showed that gramicidin contained no sulphur, halogen or phosphorus in its molecule. Hotchkiss (1941) showed that gramicidin was a polypeptide containing 14.8% nitrogen. L-tryptophan, D-leucine, alanine, and an unknown hydroxyamino acid residue were present. The molecular weight of gramicidin was in the range of 1250 to 1550 and the empirical formula might either be $C_{55}H_{79}N_{11}O_{10}$ or $C_{74}H_{105}N_{15}O_{13}$. Independently, Christensen et al. (1941) showed that gramicidin's elementary analysis was C, 62.5; H, 7.5 and N, 14.6%, similar to the results of Hotchkiss and Dubos above. No sulphur or phosphorus was present and they showed that tryptophan, leucine, alanine and the unknown hydroxyl amino acid content of gramicidin had an approximate molecular ratio of 2:2; (2 or 3):1.

Christensen (1943) showed the presence of DL-valine residues in

all gramicidins. Gordon et al. (1943a) suggested that the gramicidin molecule contained 24 amino acid residues distributed as: six D-leucine, five L-tryptophan, five DL-valine, two L-alanine, two glycine and two of the unknown hydroxylamino residues. Synge (1944a) showed that the five DL-valine residues were distributed as two L-valine and three D-valine. Synge (1944b) identified the unknown hydroxylamino compound as 2-amino-ethan-1-ol,(NH2-CH2-CH2-OH).

Synge (1945a) believed that the gramicidin molecule contained six L-tryptophan, six D-leucine, three D-valine, three L-alanine, two L-valine, two glycine and two ethanolamine residues in contrast with the previous results. The ethanolamine residues were involved in a peptide linkage through their amino groups and their hydroxyl groups were free. However, James and Synge (1951) later suggested that the hydroxyl groups of ethanolamine might not be free. They also said that gramicidin contained neither volatile and non-volatile fatty acid nor ether-extractable carboxylic acid. The ureido structure was also thought to be absent.

Craig et al. (1949a) found that all three major components, gramicidins A, B and C contained glycine, alanine, leucine and tryptophan, but gramicidin B had phenylalanine and gramicidin C, tyrosine in addition.

Okuda et al. (1962) showed that gramicidin A contained one glycine, two L-alanine, four DL-valine, four D-leucine, four L-tryptophan and one ethanolamine. Gramicidins B and C differed from gramicidin A in containing L-phenylalanine and L-tyrosine respectively in place of one or more L-tryptophan.

Ramachandran (1963) showed that all gramicidins contained glycine,

alanine, valine, leucine, tryptophan, and ethanolamine residues. However, gramicidin A and gramicidin B differed from each other in tryptophan content. Gramicidin B contained additional tyrosine and gramicidin C, additional phenylalanine. Gramicidin D had one or two isoleucine residues which replaced one or two of four residues of valine present in gramicidin A (Table VI).

TABLE VI

AMINO ACID COMPOSITION OF GRAMICIDINS PROPOSED BY RAMACHANDRAN (1963)

Gramicidin	K*	G1y	Ala	Val	Leu	Try	Ileu	Phe	Tyr	Ethanolamine
	0.70						0			1
В	0.32	1	2	4	4	3 - 4	1	1	0	1
С	1.41	1	2	4	4	6	0	0	1	1
D	0.59	1	2	3	4	6	1	0	0	1

 $[\]boldsymbol{K}^{\star}$ value is the partition ratio in countercurrent distribution.

(ii). Present concepts of the structure of gramicidin A:

Ishii and Witkop (1963) showed that gramicidin A was heterogeneous by means of their isolation of valine-gramicidin A and isoleucine-gramicidin A. Valine-gramicidin A had four L-tryptophan, four D-leucine, two D-valine, two L-valine, one glycine and one ethanolamine residue.

Isoleucine-gramicidin A had similar constituents except that one of the two L-valines in valine-gramicidin A was substituted by one L-isoleucine.

Sarges and Witkop (1964a) discovered that the gramicidins A con-

tained an N-formyl group. They later showed (1964b) both gramicidins A to be linear N-acylated decapentapeptide ethanolamines. Sarges and Witkop (1965a) proposed the following structures for gramicidins A (46a,b) which were found to be correct by chemical synthesis (Sarges and Witkop, 1965b).

(46a valine-gramicidin A)

(46b isoleucine-gramicidin A)

(iii). Present concepts of structure of gramicidin B:

Sarges and Witkop (1965c) showed that gramicidin B, like gramicidin A, was mixture of valine- and isoleucine-gramicidins B. The N-formyl group was also present. Gramicidins B were linear N-acylated decapenta-peptide ethanolamines with similar amino acid compositions except that tryptophan at position 11 of gramicidin A was replaced by L-phenylalanine (47a,b).

(47b isoleucine-gramicidin B)

(iv). Structure of gramicidin C:

Sarges and Witkop (1965d) went on to show that gramicidin C was also a mixture of valine and isoleucine-gramicidins C. Gramicidins C were analogous to gramicidins A and B, except for the amino acid at position 11 being replaced by L-tyrosine instead of tryptophan or phenylalanine (48a,b).

(48a valine-gramicidin C)

(48b isoleucine-gramicidin C)

D. GRAMICIDIN S.

(1). Producing strain and properties of the antibiotic:

Gause and Brazhnikova (1944a) isolated a bacterium, <u>B. brevis</u> which they labelled the "Gause-Brazhnikova" strain, from Russian soil. It produced a bactericidal polypeptide which was called "Soviet gramicidin" or gramicidin S.

Gause and Brazhnikova (1944b) showed that gramicidin S was thermostable, withstanding heating to 160° C in dry crystalline form or autoclaving at 120° C for 30 min. in solution or boiling in 1% alcoholic HCl. Belozersky and Paschina (1944) noted that gramicidin was insoluble in water, acids, or alkali, but very soluble in alcohol or acetone. It was slowly dialyzable. The crystalline form of gramicidin S melted at $268 - 270^{\circ}$ C and contained 13% of nitrogen. The biuret reaction was positive but the xanthoproteic and Millon's reactions were negative. Its activity was directed against both Gram-positive and Gram-negative bacteria.

(2). Isolation:

Gause and Brazhnikova (1944a) showed that gramicidin S could be isolated by acidification of the culture fluid. The resulting precipitate was dissolved in ethanol and the impurities were removed by ether extraction. The alcoholic solution was then concentrated, mixed with activated charcoal, and filtered. The pure gramicidin S would crystallize from this filtrate in the cold. Recrystallization was effected in an acetone-water mixture in the presence of charcoal.

(3). Structural studies:

Belozersky and Paschina (1944) noted the presence of ornithine, proline, and leucine in the hydrolysates of gramicidin S. In the molecule, the free amino group was contributed by an α -amino residue and the δ -amino group of ornithine was bound.

Synge (1945b) showed that gramicidin S was a polypeptide compound with an equal molar ratio of L-valine, L-proline, L-leucine, L-ornithine and D-phenylalanine. It possessed only one basic amino group and no free carboxyl group. In light of the evidence of a high optical rotation value of the molecule, Synge (1945b) believed that gramicidin S was a cyclopeptide. Sanger (1946) also expressed the same view because he found only the 6-amino group of ornithine with the FDNB method.

Consden et al. (1946, 1947) found that gramicidin S had the sequence $-\alpha$ -L-valyl-L-ornithyl-L-leucyl-D-phenylalanyl-L-prolyl- which occurred once or repeatedly in a cyclic peptide chain. According to Crowfoet and Schmidt (cited by Consden et al., 1946), who examined a series

of derivatives of gramicidin S by X-ray crystallography, gramicidin S had either a simple pentapeptide structure or was a decapeptide which had crystallographic two-fold symmetry. The two-fold symmetry could arise as a result of the repetition of the peptide sequence in a cyclic decapeptide.

The cyclodecapeptide structure for gramicidin S (49) was established through molecular weight determination by the partition substitution method (Battersby and Craig, 1951), chemical synthesis (Schwyzer and Sieber, 1956) and X-ray studies (Schmidt \underline{et} \underline{al} ., 1957).

(49)

Since gramicidin S is a basic cyclodecapeptide as are the tyrocidines and has a pentapeptide sequence Val-Orn-Leu-Phe-Pro identical to them, and since the gramicidins are linear pentadecapeptides and structurally unrelated to gramicidin S, Ruttenberg $\underline{\text{et}}$ $\underline{\text{al}}$. (1965b) feel that the term gramicidin S is a misnomer.

E. GRAMICIDINS J_1 AND J_2 .

(1). Producing strains and properties of gramicidins J:

Otani and Saito (1954) isolated a strain of \underline{B} . \underline{brevis} from soil near Osaka, which produced an antibiotic related to gramicidin S. This antibiotic was named "gramicidin J". Several years later, another strain of \underline{B} . \underline{brevis} which also produced a similar substance was isolated in Japan by Okuda (1959). This antibiotic was named "gramicidin \underline{J}_2 ". For clarity, Okuda (1959) proposed renaming the former as gramicidin \underline{J}_1 .

Toki (1955) showed that gramicidin J_1 had absorption maxima at 264, 258, 252, and 250 nm in alcoholic solution. Otani <u>et al</u>. (1958) showed that crystalline gramicidin J_1 contained only one active entity judged by the countercurrent distribution method. It was very soluble in ethanol, methanol, and chloroform, slightly soluble in acetone and water, and insoluble in ether. Gramicidin J_1 melted at 292 - 293°C with decomposition. Its optical rotation was $\left[\alpha\right]_D^{18} = -308.9^{\circ}$ (96% ethanol), and it gave positive responses to biuret and ninhydrin tests. Gram-positive but not Gram-negative bacteria were sensitive to the antibiotic. It was hemolytic to goat erythrocytes and toxic to mice, having an intraperitoneal $LD_{50} = 12.5$ mg/kg of body weight.

Okuda (1959) noted that gramicidin J_2 had identical physico-chemical and biological activities to gramicidin J_1 but the two were distinguishable by countercurrent distribution. Gramicidin J_2 showed absorption maxima at 265, 258 and 251 nm.

(2). Isolation:

Otani (1957) purified gramicidin J_1 by acidification of the culture fluid with HCl and adsorption of the antibiotic with diatomaceous earth. The active principle was removed from the earth by extraction with warm methanol. Gramicidin J_1 was then salted out from the methanol by NaCl and further purification was effected by repeated crystallization from acidified methanol. Otani isolated gramicidin J_2 with similar treatment. The impurities left were further removed by precipitation with water and adsorption to Al_2O_3 . The purified antibiotic was then crystallized from methanolic solution.

(3). Structural studies:

Otani and Saito (1954) and Saito (1958a) showed that gramicidin J_1 contained one D-phenylalanine, one L-phenylalanine, one D-leucine, one L-ornithine, one D-ornithine, one L-valine and one L-proline residue. Elementary analysis showed its hydrochloride to have C, 58.12; H, 8.03; N, 13.7 and Cl, 5.4%. After reaction with FDNB reagent, the only DNP-derivative found in the hydrolysates of DNP-gramicidin J_1 was DNP-ornithine. Since it contained no free α -amino or α -carboxyl groups in the molecule, a cyclic peptide structure was proposed. The molecular weight would be about 800 as determined by the partial substitution method.

Based on the analyses of partial acid hydrolysates, Saito (1958b) showed gramicidin ${\bf J}_1$ to be a cycloheptapeptide with a structure as shown below (50).

(50)

Otani (1957) and Okuda (1959) showed that gramicidin J_2 contained one D-ornithine, one L-ornithine, one D-leucine, one L-valine, one D-phenylalanine and one L-proline residue. Elementary analysis showed it had C, 55.07; H, 8.17; and N, 14.54%.

Noda (1959) found that the synthetic cyclo-D-phenylalanyl-D-leucyl-L-ornithyl-L-valyl-D-ornithyl-L-prolyl.2HCl had the same antibiotic activity, paper chromatographic behavior and X-ray diffraction pattern as natural gramicidin J_2 . Therefore, gramicidin J_2 must have the structure shown in (51).

D-Phe
$$\longrightarrow$$
D-Leu \longrightarrow L-Orn
L-Pro \longleftarrow D-Orn \longleftarrow L-Val

(51)

XIII. STAPHYLOCOCCAL ANTIBIOTICS.

Over the years, various investigators have shown that both \underline{S} . aureus and \underline{S} . epidermidis produce antibacterial agents which appear to have spectra similar to peptide antibiotics produced by other bacteria. Apart from this, knowledge regarding the nature and properties of these antibiotics is rather fragmentary.

One of the earliest reports concerning antibiotics from staphylococci is that of Cornil and Babes (1885) who showed that a staphylococcal strain inhibited growth of the anthrax bacillus and other strains of Staphylococcus. The most recent reports are those of Lachowicz (1965) and Hsu and Wiseman (1967).

The major features of this poorly characterized group of anti-bacterial agents, so far as they are known, are summarized in Table VII.

Noteworthy characteristics of the group as a whole are that the agents are relatively stable over a wide range of pH, and are quite heat resistant.

Their sensitivity to trypsin and other proteolytic enzymes is variable.

Generally speaking, their inhibitory spectrum is restricted to Grampositive bacteria.

Little is known about the chemical nature of these antibiotics, but it does appear that those at least which are mentioned in the table are peptides, large and small.

TABLE VII

PROPERTIES OF STAPHYLOCOCCAL ANTIBIOTICS

authors	heat stable at	рН	effects of pH enzyme serum		dialy- zability	soluble in	inhibitory spectrum	chemical nature	
Jennings and Sharp (1947)	100°C for 5 min	stable at 4.5 - 8.0	?	?	no	water	Gram +	?	
Gardner (1949)	acid but not alkaline pH	stable in acid	inactivated by trypsin	?	yes	water and alcohol	Gram +	protein	
Loeb <u>et</u> <u>al</u> . (1950)	121°C for 20 min	stable at 2 - 12	inactivated by trypsin, but not by pepsin	partially affected	yes	water and hydrophilic solvents	Gram +	poly- peptide	
Fregnan and Smith (1962)	100°C for few min	stable at 2 - 8	inactivated by trypsin & α-amylase	?	no	water	mycoba- cteria	polypep- tide or glyco- protein	-92-
Barrow (1962, 1963)	83 ⁰ C for few min	in acid	inactivated by trypsin not by pep- sin	not affected	yes	water	Gram +	peptide	
Lachowicz (1965)	100°C for 1 hr	stable at 1 - 10	not affected by pepsin or trypsin	?	no	water	Gram +	poly- peptide	
Hsu and Wise- man (1967)	115°C for 10 min	stable at 2 - 11	partially inactivated by trypsin & chymotrypsin	not affected	yes	water	Gram + & myco- bacteria	peptide	

MATERIALS AND METHODS

MATERIALS AND METHODS

I. MATERIALS

(1). Strains of bacteria employed:

Two active antibiotic-producing strains, 29297 and 36534, isolated by Hsu and Wiseman (1967) were selected. Both strains were coagulase-negative staphylococci isolated from the cervix-uteri of two different patients. Their physiological characteristics (see Appendix I) fitted the description of the genus Staphylococcus in the 7th edition of Bergey's Manual of Determinative Bacteriology (Breed et al., 1957). Staphylococcus aureus Oxford 209P, which was used as the standard indicator strain, was originally obtained from Dr. A.C. Maniar of the Provincial Laboratories in Winnipeg.

All bacterial strains were kept in the lyophilized state at room temperature. Before use, the cells were revived by suspension in Brain-Heart Infusion (BHI) broth and 18-hr subculture on BHI agar slants at 37°C. The purity of the culture was checked by the Gram-staining reaction.

(2). Media and chemicals:

Proteose peptone, BHI broth and BHI agar media were obtained as the dehydrated form from Difco Laboratories, Detroit, Michigan. Whenever possible, all reagents used in this study were of the analytical grade. Unless otherwise indicated, buffers used were made up according to the instructions of Cruickshank (1965).

(3). Glassware:

The glassware used for chemical tests was first boiled with diluted HCl solution for two hr, washed with detergent, rinsed thoroughly with tap-water and then with distilled water.

II. METHODS

(1). Quantitative assay of antibiotic activity:

Fluids containing antibiotic were assayed by the methods of Hsu and Wiseman (1967). A series of two fold dilutions of antibiotic was made in three ml volumes of distilled water, starting at 1:2 in calibrated Klett tubes. The diluted antibiotic was sterilized by autoclaving at 10 lb pressure (110°C) for 10 min. After cooling, three ml of a standard suspension of the Oxford indicator strain in double strength BHI broth was added to each tube. The tubes were agitated and the optical density (0.D.) of each tube was recorded in a Klett colorimeter equipped with filter no. 69 (transmission 660 - 740 nm). The tubes were incubated at 37°C for 18 hr. At the end of the incubation, tubes were shaken on a Vortex Jr. Mixer (Scientific Industries Inc., New York) for 15 sec and the O.D. was again determined. The difference between the two O.D. readings was plotted on a graph paper against the reciprocal value of the \log_2 dilution of the antibiotic. The end point was taken as the reciprocal value of the \log_2 dilution of the antibiotic corresponding to the O.D. of the indicator strain equal to the $\operatorname{mid}\text{-point}$ of the linear portion of the growth curve. The \log_2 value was then treated as given in the following example:

10g₂ total units
antibiotic titre (reciprocal of antilog₂) units antibiotic/ml

4 16 5.3

The total antibiotic units were divided by three to give units/ml, since the volume of fluid in the titration was 3 ml.

(2). Production of crude antibiotic:

Dolman-Wilson liquid medium (Dolman and Wilson, 1940) supplemented with ferrous ammonium sulphate, manganese chloride and sodium citrate (see Appendix II) was employed in antibiotic production. The medium was divided into two parts and prepared as follows: Part I consisted of proteose peptone and 900 ml of distilled water. This solution was adjusted to pH 7.8 and autoclaved at 15 lb pressure (121°C) for 25 min. Part II was composed of the salt mixture and ammonium lactate which were dissolved in 100 ml of distilled water. The pH of this solution was adjusted to 5.5 and the fluid was sterilized by passage through a Millipore HA membrane (pore size = 450 mm). Part I was cooled to room temperature and added to Part II with thorough mixing. The pH of the mixture was 7.2. Five hundred ml of this medium was dispensed into a sterile one litre Erlenmeyer flask which was then plugged with cotton.

A heavy suspension of the antibiotic-producing strain adjusted to 0.D. = 0.500 was prepared in distilled water. Each flask was seeded with 0.5 ml of this suspension and then incubated at 32°C with constant shaking in a Controlled Environment Incubator Shaker (New Brunswick Scientific Co., New Brunswick, N.J.). The shaking speed was adjusted to 110 strokes per min;

the length of incubation period being three days for strain 29297 and four days for strain 36534. After incubation, the purity of the culture was checked by staining and the bacterial cells were removed by centrifugation at 10,000 g for 15 min in a refrigerated centrifuge. The active supernatant was referred to as crude antibiotic fluid.

Each operation produced about 7.5 litres of active liquid with a titre varying from three to six units per ml.

(3). Concentration of the antibiotic fluids:

Flash evaporation was used in the concentration of crude and purified antibiotic fluids. The flash-evaporator was obtained from the Buchler Instrument Co., Fort Lee, N.J. The temperature of the water bath in which the evaporating flask was kept, was $50 \pm 1^{\circ}\text{C}$, a temperature which did not affect antibiotic activity.

(4). Ion-exchange chromatography:

A strong cationic ion-exchanger, Dowex 50-X2 (H⁺ form, 50 - 100 mesh, J.T. Baker Chemical Co., Philipsburg, N.J.) was selected for chromatography. The resin was washed and converted to the Na⁺ form according to the procedure suggested by Moore and Stein (1951). After treatment, the resin was suspended in 0.1M NaCl solution, pH 7.0, poured into a 4.5 X 60cm column and packed by gravity. The column was equilibrated with a continuous flow of 0.1M NaCl solution, pH 7.0, at a rate of 200 ml/hr for two days. The material to be chromatographed was adjusted to pH 7.0 before application to the column and the sample size was limited to 100 ml per column per run.

Antibiotic was eluted in 100 ml volumes from the column with 0.1M NaCl at pH 7.0 at a rate of 200 ml/hr. At the end of each run, the resin was cleaned with 200 ml of 1N HCl and regenerated by addition of 400 ml of 2N NaOH solution. The excess NaOH was removed with 0.1M NaCl.

(5). Gel filtration:

Sephadex gels and columns (5 X 100 cm in size) were supplied by Pharmacia of Canada Ltd., Montreal. The procedures used for preparation of the gel and column packing were those recommended by the manufacturer (Pharmacia, 1963). After packing, distilled water at a rate of 160 ml/hr was passed through the columns from top to bottom for two days. The void volume (V_O) of each column was determined with blue dextran (Sigma Chemical Co., St. Louis, Mo.). Forty ml 0f 0.01% dye was passed through the column and V_O was taken as that volume which corresponded to elution of the dye from the column at maximum 0.D. 540 nm.

Samples of antibiotic, 40 ml in volume, were neutralized before being added to the columns, and the flow rate was adjusted to 160 ml/hr, distilled water being used as the eluent. Twenty-eight fractions of 40 ml each, commencing 120 ml before the appearance of $\rm V_{\rm O}$, were collected from the column.

After each use, columns were cleaned by the application of 3 - 4 litres of distilled water. Since the gel filtrations were performed at room temperature, growth of microorganisms could occasionally have been a problem. This was controlled by forcing 100 ml of 0.1% (w/v) sodium azide in water through the column from bottom to top. Azide was cleared from the column by the application of several void volumes of distilled water.

(6). Mobility of staphylococcal antibiotics in an electric field:

The mobility of the antibiotics produced by these two staphylococcal strains in an electric field at different pH values was detected by the following processes. Twenty-five ml of BHI broth with 2% Noble agar (Difco) added was poured onto a 102 X 83 mm glass plate which was placed in a large Petri-dish (14 cm in diameter). After the agar solidified, the plate was seeded with the producing strain by stabbing the centre of the plate with an end-sealed Pasteur pipette which had previously been dipped into the suspension of the producing strain. After being incubated at 37°C for two days, the plate was put into the electrophoresis chamber with filter paper wicks dipped into the buffer reservoirs. The plate was allowed to stand in such a manner for two hr at room temperature to facilitate equilibration of the buffer. The buffers used were 0.05M citrate-phosphate buffer (pH 5.0 - 5.5), phosphate buffer (pH 6.0 - 7.5), and barbitone buffer (pH 8.0 - 9.0). Then, electric current (20 v/cm and 50 mA/plate) was applied for various lengths of time. Immediately after the electrophoresis, the plate was sterilized with chloroform vapor for one hr at room temperature in a closed metal chamber and sprayed with the standard suspension of the indicator strain, S. aureus 209P, which was suspended in BHI broth concentrated four-fold. The sprayed plate was incubated at 37°C for 18 hr and the distance of the clear inhibition zone from the origin was determined in mm.

(7). Chemical analyses:

(a). Qualitative:

Qualitative chemical tests of antibiotic preparations were based on the methods outlined in Shriner et al. (1964), Oser (1965) or Kabat and Mayer (1961) except that phenolic groups were determined by the method of Inglett and Lodge (1959) and sulphur groups were assayed by the method of Klipp and Barney (1959).

(b). Quantitative determination:

Protein content was determined either by the method of Lowry $\underline{\text{et}}$ $\underline{\text{al}}$. (1951), with egg albumin as the standard, or by the quantitative ninhydrin method of Moore and Stein (1954) with leucine as the standard. Total nitrogen content was assayed by the modified micro-Kjeldahl technique of Markham (1942) with $(\text{NH}_4)_2\text{SO}_4$ as the standard.

(c). Amino acid analyses:

Amino acid content of the purified antibiotic products was assayed with Technicon Auto Analyzer (Technicon Corp., Ardsley, New York) through the courtesy of Mr. Yong-Soo Park of the Department of Pharmacology, University of Manitoba.

(d). N- and C-terminal amino acid determination:

The N-terminal amino acid groups of the highly purified materials were determined by Sanger's method (Sanger, 1945, 1949). One ml of highly purified antibiotic solution (about 10 mg in dry weight) was conjugated with an excess amount of Sanger's 1-fluoro-2,4-dinitro-benzene (FDNB) reagent (Sanger, 1949). After the conjugation reaction was complete, free FDNB reagent was removed by extraction with chloroform and the treated material

was treated with 6N HCl at 110°C for 12 hr in a sealed evacuated ampoule. This fluid, freed from the acid by flash-evaporation, was extracted three times with an equal volume of ether. The ether extracts were pooled and concentrated. Then, both the ether concentrate and the aqueous solution of the treated fluid, together with standard N-2,4-dinitrophenyl (DNP) amino acid (Sigma Chemical Co.), were applied to Whatman no. 1 filter paper which had previously been saturated in 0.1M phthalate buffer, pH 6.0 (Blackburn and Lowther, 1951). The paper was developed in a solvent system of tertiary amyl alcohol saturated with phthalate buffer, pH 6.0.

The C-terminal amino acid groups of the purified antibiotics were detected by the Dakin-West degradation as given by Vanderhaeghe and Parmentier (1960). One ml of highly purified antibiotic solution (about 10 mg dry weight) was heated with 0.5 ml of pyridine and 1.25 ml of acetic anhydride in a sealed evacuated tube at 130°C for 6 hr. The fluid was subjected to flash-evaporation to dryness and the residue was further hydrolyzed in 1.5 ml of 6N HCl at 110°C for 18 hr. After the acid was removed by further flash-evaporation, the residue was dissolved in distilled water and the solution was chromatographed on Whatman no. 1 paper in the solvent system n-butanol/acetic acid/water, 4:1:5 by volume.

(e). Determination of the amino acid sequence of the antibiotic peptide:

The highly purified antibiotic 29297 zinc-precipitable fraction was partially hydrolyzed by heating at 110°C for two hr with 6N HCl in a sealed evacuated tube. After the HCl was completely removed by flash-evaporation, the peptide fragments in the residue were conjugated with FDNB

reagent by Sanger's method as previously described. The resulting DNPpeptides were extracted by chloroform and the chloroform-extracted material
was concentrated by evaporation. This material was chromatographed as described previously except that it was applied as a band one cm in width to
Whatman no. 4 filter paper. The resulting separated bands were cut off and
the DNP-peptide on each band was eluted by the same solvent. The eluent was
concentrated and its purity was checked by thin-layer chromatography on
silica gel G (E. Merck Co., Darmstadt, Germany) plates with tertiary amy1
alcohol saturated with 0.1M phthalate buffer, pH 6.0, as the developing
solvent. The free amino acids left in the aqueous fraction were also identified on paper with n-butanol/acetic acid/water, 4:1:5 by volume, as the developing agent.

(8). Acid hydrolysis:

Hydrolysis of antibiotic peptide with acid was performed in the following manner: An equal volume (one ml) of concentrated HCl (22° Be', J.T. Baker Chemical Co., Philipsburg, N.J.) and aqueous antibiotic solution were mixed in a five ml ampoule. This was evacuated with a water-pump and the ampoule sealed. The sealed ampoule was autoclaved at 10 lb pressure (110°C) for 18 hr. After heating, the liquid was transferred to the flashevaporator and evaporated to dryness. The sample was freed of HCl by repeated dissolution in distilled water and evaporation to dryness.

(9). Enzymatic oxidative deaminations:

Deamination of the acid hydrolysates of highly purified antibiotics

by L-amino acid oxidase was investigated according to the method of Wellner and Meister (1960). The enzyme was purchased from Sigma Chemical Co. (St. Louis, Mo.), the source of which was <u>Crotalus</u> <u>adamanteus</u> venom.

Deamination by D-amino acid oxidase was performed by the method of Burton (1955). The enzyme, which was obtained from hog kidney, was purchased from Sigma. Catalase from beef liver and other co-factors were purchased from the same source.

Standards used with both methods were solutions which contained $100\ \text{mM}\ \text{L-leucine}$ and $300\ \text{mM}\ \text{D-alanine}$.

In both procedures, the Warburg flask was incubated at 37°C in a water bath and equilibrated in air for 15 min prior to the addition of enzyme. The manometric apparatus was supplied by Bronwill Scientific Inc. (Rochester, N.Y.). Readings were taken at 10 min intervals for 30 min and then at 30 min intervals for $5\frac{1}{2}$ hr. At the end of this time, total $0\frac{1}{2}$ uptake was calculated by the method of Umbreit et al. (1957).

EXPERIMENTAL RESULTS

RESULTS

PART I. PRODUCTION AND TITRATION OF THE ANTIBIOTICS

I. DEVELOPMENT OF LIQUID MEDIUM SUITABLE FOR ANTIBIOTIC PRODUCTION

Hsu and Wiseman (1967) had produced antibiotics 29297 and 36534 on solid media in large trays overlain with cellophane. While their media gave reasonably good yields, quantities obtained, however, were limited and handling of the large trays was awkward. It was therefore felt that development of a liquid medium ought to be investigated.

Hendlin (1949) had shown that ferrous and manganese ions were essential for good production of bacitracin. Other investigators have found this to apply to certain other peptide antibiotics. Consequently, 0.01 gm/L of ferrous ammonium sulphate and 0.2 gm/L of MnCl₂ were added to the basic Dolman-Wilson medium (Dolman and Wilson, 1940). Sodium citrate at a concentration of 0.2 gm/L was also added to prevent precipitation of salts. This medium was referred to as supplemented Dolman-Wilson medium. The preparation of the medium has been described in Materials and Methods as well as in Appendix II. After sterilization, the supplemented medium was dispensed in 100 ml volumes into 250 Erlenmeyer flasks. Each flask was inoculated with 0.1 ml of the producing strain suspended in distilled water to 0.D. = 0.500. Some flasks were shaken at 110 strokes/min and others remained stationary. Incubation proceeded for three days at 37°C at which time pH, growth and antibiotic activity were measured.

The results (Table VIII) showed that agitation of the cultures during the incubation period generally increased the growth in both supplemented and unsupplemented Dolman-Wilson media. As the result of abundant growth, the pH of the agitated cultures was much higher than that in stationary media. Under stationary conditions, both antibiotic-producing strains grew poorly and produced no detectable antibiotics regardless of the type of medium employed. With agitation, however, antibiotics were produced by both strains in the supplemented medium only, although the growth of either strain in the unsupplemented medium was very similar to the supplemented one. Therefore, it was concluded that suitable aeration and supplementation of the medium were both necessary for the facilitation of antibiotic production for strains 29297 and 36534. Subsequent experiments thus employed Dolman-Wilson medium supplemented with ferrous ammonium sulphate, MnCl₂, and sodium citrate.

An attempt was made to substitute the proteose-peptone of Dolman-Wilson medium with casamino acids (Difco) and growth factors, or with corn steep liquor obtained from the A.E. Staley Mfg. Co. of Illinois, in order to facilitate antibiotic production. The results (Table IX) indicated that although the growth of either strain was not affected by the substitution, antibiotic production was partially or completely eliminated.

TABLE VIII

EFFECT OF AGITATION AND SUPPLEMENTATION OF DOLMAN-WILSON MEDIUM ON ANTIBIOTIC PRODUCTION IN STAPHYLOCOCCI

	stra	strain 29297			strain 36534		
tre	eatment	growth*	рН	antibiotic activity (units/ml)	growth	рН	antibiotic activity (units/ml)
stationary	unsupplemented	0.100	7.1	0	0.090	7.1	0
	supplemented	0.100	6.5	0	0.100	6.5	0
shaken**	unsupplemented	0.760	8.3	0	0.750	8.4	0
	supplemented	0.800	8.7	3.9	0.800	8.7	4.0

* O.D. 660 nm

** shaken at 110 strokes/min

TABLE IX

EFFECT ON ANTIBIOTIC PRODUCTION OF PROTEOSE PEPTONE REPLACEMENT IN SUPPLEMENTED DOLMAN-WILSON MEDIUM BY CASAMINO ACIDS OR CORN STEEP LIQUOR

		<u>strain</u>	29297	strai	in 36534
proteose peptone subtituent	conc. (%)	growth*	antibiotic activity (units/ml)	growth	antibiotic activity (units/ml)
none (control)	-	0.600	4.2	0.500	4.1
casamino acids**	2	0.700	0	0.800	0
corn-steep liquor	1	0.400	0.7	0.400	0
	2	0.800	2.1	0.800	0
	5	1.250	0.7	0.900	0

^{* 0.}D. 660 nm

^{**} growth factors added as follows: nicotinic acid, 2 X 10^{-7} M; pyridine, 2 X 10^{-7} M; biotin, 2.5 X 10^{-6} M; thiamine, 2 X 10^{-7} M; and riboflavin 5 X 10^{-6} M

II. FACTORS INFLUENCING PRODUCTION OF THE ANTIBIOTICS

(1). Effect of temperature:

A 1000 ml Erlenmeyer flask which contained 500 ml of supplemented Dolman-Wilson medium was inoculated with 0.5 ml (0.1 ml/100 ml medium) of standardized culture where 0.D. = 0.500. Three flasks were incubated over a temperature range $24 - 40^{\circ}$ C for three days during which they were shaken at the rate of 110 strokes/min.

Results are shown in Fig. 1 in which it is observed that the optimal temperatures for growth and for production of antibiotics do not coincide. The highest titres of antibiotics 29297 and 36534 were attained at a temperature of 32°C whilst maximal growth in both cases took place at 37°C.

(2). Effect of incubation time:

Conditions of this experiment were similar to those given in (1) except that incubation proceeded at 32°C while incubation time was varied. Results are given in Fig. 2 and show that with strain 36534, maximal antibiotic production was attained after four days of incubation and with 29297, after three days. Differences in both cases over the three to five days range were not large. With both strains, the O.D. rose to a maximum at two to three days, falling off thereafter. In view of the small differences in antibiotic titre over the three to five days ranges, cultures were subsequently incubated for three to four days.

In summary, quantitative antibiotic production was facilitated

FIGURE 1

EFFECT OF TEMPERATURE OF INCUBATION ON THE ANTIBIOTIC PRODUCTION

(A). STRAIN 29297

(B). STRAIN 36534

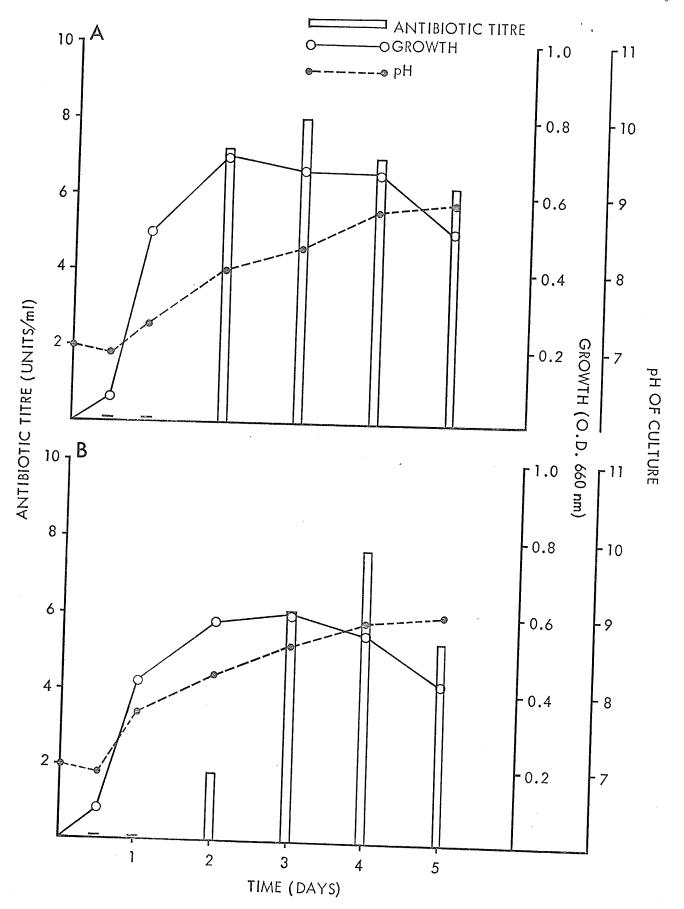
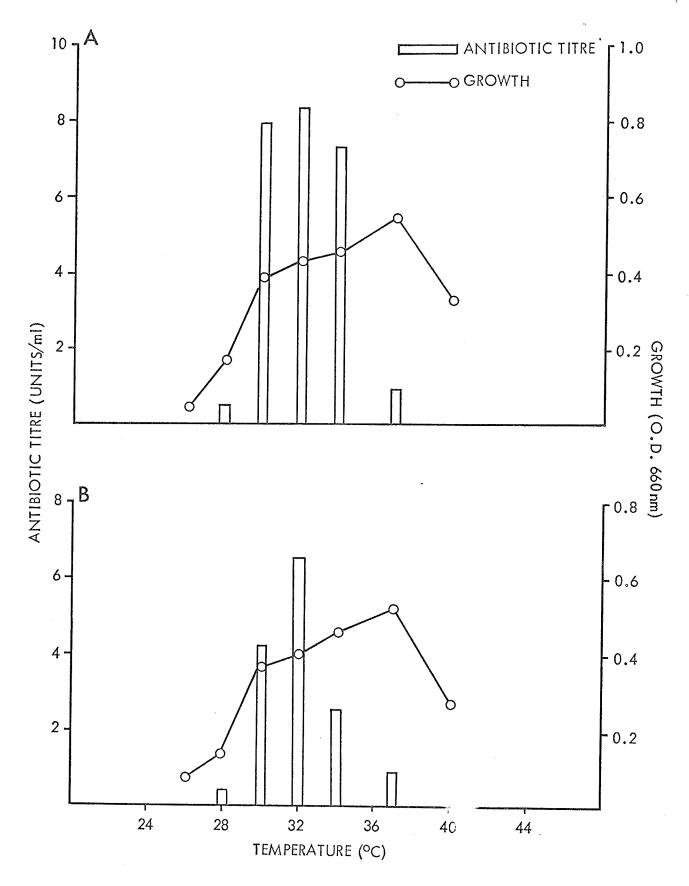


FIGURE 2

EFFECT OF LENGTH OF INCUBATION ON THE ANTIBIOTIC PRODUCTION

- (A). STRAIN 29297
- (B). STRAIN 36534



by the inoculation of flasks containing 500 ml volumes of supplemented Dolman-Wilson medium. Each flask received 0.1 ml inoculum/100 ml medium as described previously. Incubation proceeded at 32°C for three to four days in the Brunswick shaker with an agitation rate of 110 strokes/min.

III. FACTORS INFLUENCING ANTIBIOTIC ASSAY

(1). Sterilization of the antibiotics:

The stability of crude antibiotic fluids and solutions of highly purified product obtained after double crystallization and double methanol precipitation (ref. Part II) was tested. The antibiotic liquid was divided into two parts. One was sterilized by autoclaving at 10 lb pressure (110° C) for 10 min and the other was filtered through a Millipore HA membrane. Both parts were then titrated separately under the same conditions.

It was noted that both methods of sterilization gave identical results (Table X). Crude and highly purified materials resisted heat equally well. For the sake of convenience, autoclaving was the method of choice when sterile active fluids were required.

(2). <u>Medium</u>:

Antibiotics were titrated as described in Materials and Methods but it was decided to test the effect of the assay medium on antibiotic titres. Media tested were Brain Heart Infusion broth (Difco), Veal Infusion broth (BBL), Trypticase-Soy broth (Difco), and Nutrient broth (BBL).

TABLE X

COMPARISON OF ANTIBIOTIC TITRES OF ACTIVE FLUIDS STERILIZED BY TWO METHODS

		tre (units/ml)	
material	concentration	sterilized by	sterilized by
material	(mg N/m1)	filtration*	autoclaving**
produced by strain 29297			
crude fluid	1.98	4.2	4.1
highly purified zinc- precipitable fraction***	0.17	16.6	16.2
highly purified zinc- soluble fraction	0.20	8.0	8.0
produced by strain 36534			
crude fluid	5.11	4.4	4.5
highly purified zinc- precipitable fraction	0.05	7.5	7.6
highly purified zinc- soluble fraction	0.09	6.5	6.4

^{*} passage through a Millipore membrane (pore size = 450 nm)

^{**} autoclaved at 10 lb pressure (110 $^{\rm o}{\rm C})$ for 10 min

^{***} twice crystallized and twice methanol precipitated

As shown in Table XI, different end points were obtained with the various media. Brain Heart Infusion broth caused the least inhibition and was used subsequently.

(3). <u>Incubation period</u>:

The antibiotic titre, as affected by the length of incubation of the indicator strain, was also investigated. Antibiotic titrations of crude and concentrated, partially purified material (HCl-treated fraction, ref. Part II) were performed as described under Materials and Methods. Titres were read over the time interval 8 - 48 hr. Results (Table XII) showed that titres of a given antibiotic fluid remained approximately constant between eight and 24 hr with deterioration beyond 24 hr. This was particularly notable with the partially purified, concentrated materials. Subsequent titrations were incubated for 18 hr for the sake of convenience since titres were relatively stable during the 8 - 24 hr time interval.

TABLE XI

EFFECT OF ASSAY MEDIUM ON THE ANTIBIOTIC TITRES

	growth of indicator	antibiotic (unit	activity s/ml)
broth	strain*	29297	36534
Brain Heart Infusion	0.370	4.0	5.3
Veal Infusion	0.375	2.1	2.7
Trypticase-Soy	0.380	1.8	2.0
Nutrient	0.370	1.2	0

* O.D. 660 nm

TABLE XII

RELATIONSHIP BETWEEN ANTIBIOTIC TITRE AND LENGTH OF INCUBATION PERIOD OF THE INDICATOR STRAIN

length of incubation (hr)	growth of indicator strain*		ic titre s/ml) 36534
crude material			
8	0.300	3.5	4.0
12	0.340	3.3	3.2
24	0.370	3.2	3.2
48	0.370	2.9	2.1
partially purif	ied and concen	trated mate	<u>rial</u>
8	0.300	16.0	33.0
12	0.310	14.9	33.0
24	0.370	14.9	32.0
48	0.360	6.9	14.9

* O.D. 660 nm

PART II. PURIFICATION

I. EFFECT OF MINERAL ACIDS ON THE ANTIBIOTIC ACTIVITY

The use of hydrochloric acid in the purification of antibiotic was tested. Twenty-five ml of the crude antibiotic fluid was acidified to pH 2 with concentrated acid. After the acidified fluid had stood overnight at 4°C, considerable precipitation resulted which was separated from the fluid by centrifugation and then suspended in nine ml of distilled water. Both the suspension and supernatant fluid were neutralized with 4N NaOH and diluted to 10 and 30 ml respectively with distilled water. All original antibiotic activity was found in the supernatant fraction and none was associated with the precipitate (Table XIII). Specific activity of 29297 and 36534 preparations increased about 1.5 - 2-fold. Acid controls which were neutralized by the addition of alkali were not toxic to the indicator strain. Sulphuric, phosphoric and nitric acids were also tested but offered no advantages over hydrochloric acid.

II. FURTHER PURIFICATION OF THE HC1-TREATED ANTIBIOTICS

(1). Precipitation by metal ions:

(a). Preliminary studies:

The object of these studies was to see if metal ions would cause precipitation in the HCl-treated antibiotic fluid and whether the precipitate was soluble at acid and alkaline pH. It would then be possible to

TABLE XIII

EFFECT OF HYDROCHLORIC ACID ON THE ACTIVITY OF STAPHYLOCOCCAL ANTIBIOTICS

			ntibiotic 2	ibiotic 29297		antibiotic 36534		
treatment	fraction	activity (total units)	recovery (%)	specific activity*	activity (total units)	recovery (%)	specific activity	
crude		96	100	2.2	90	100	0.9	- -
crude with HCl	precipitate	0	0	-	0	0	-	
	supernatant	96	100	3.1	90	100	1.6	

^{*} units of antibiotic activity per mg of protein

select those ions which caused heavy precipitation and determine how they affected the antibiotic activity.

Sixteen mono-, di-, and tri-valent metal salts were tested. Each salt was added to 25 ml of the antibiotic fluid to give a final concentration of 0.1M. The resulting precipitate was suspended in distilled water and the suspension was equally divided into three parts. Part I, II, and III were carefully adjusted to pH 3, 7, and 10 respectively.

The results (Table XIV) showed that the metal ions could be classified into three groups according to the amount of precipitate formed. Group I, which included Al⁺⁺⁺, Ba⁺⁺, Fe⁺⁺⁺, Fe⁺⁺, Hg⁺⁺, Mg⁺⁺, Mn⁺⁺, Pb⁺⁺, and Zn⁺⁺, caused heavy precipitation in the HCl-treated antibiotic fluid. Group II consisted of Ca⁺⁺, Cd⁺⁺, Cu⁺⁺ and Ag⁺ ions which formed moderate amounts of precipitates. Little or no precipitation occurred in Group III which contained Mg⁺⁺, Co⁺⁺, Li⁺ and Ni⁺⁺. Most precipitates were soluble at pH 3 but became insoluble at pH 7 and 10. An exception was the precipitate caused by Pb⁺⁺ ions, which was insoluble at any pH.

With the exception of lead acetate, salts which caused moderate to heavy precipitation in the HCl-treated antibiotic fluids were further investigated for their effects on antibiotic activity. Except for Ba $^{++}$, Mn $^{++}$, Zn $^{++}$, Ca $^{++}$ and Ag $^{+}$, the other salts were too toxic for use as precipitants. Silver and calcium ions were not considered since it was found that they afforded low recoveries of the antibiotics.

(b). Effect of $Ba(OH)_2$ on the antibiotic activity:

After the removal of precipitate from the HCl-treated antibiotic fluid, the supernatant required neutralization before an assay could be

PRECIPITABILITY OF ANTIBIOTIC FLUIDS WITH METAL SALTS AT NEUTRAL pH AND SOLUBILITY OF THE RESULTING PRECIPITATE AT DIFFERENT pH LEVELS

metal salt		nt of oitate	solubility of precipitate			
	29297	36534	рН 3	рН 7	pH 10	
GROUP I						
A1 ₂ (SO ₄) ₃ (NH ₄) ₂ SO ₄	heavy	heavy	+*	-	•••	
BaCl ₂	11	11	+	-	-	
FeSO ₄	11	11	+	-		
FeCl ₃	11	11	+	-	-	
HgCl ₂	11	1.1	+	-	_	
MnCl ₂	11	11	+	-	-	
Pb-(CH ₃ COO) ₂	11	ti .	-	-	-	
ZnC1 ₂	11	11	+	-	-	
GROUP II						
CaCl ₂	moderate	moderate	+	-	-	
Cd(NO ₃) ₂	11	11	+	-	-	
CuSO ₄	11	11	+	-	-	
AgNO ₃	11	11	+	-	-	
GROUP III						
MgSO ₄	light	none				
Co(NO ₃) ₂	none	11				
LiC1	11	11				
NiC1 ₂	11	Ħ				

 $[\]star$ + indicates soluble, and - indicates insoluble

performed. Since Ba⁺⁺ ion was an excellent non-toxic precipitant, its use as a neutralization agent was considered. For this purpose, highly alkaline Ba(OH)₂ was investigated; the HCl-treated antibiotic fluid (pH 2) was mixed with 0.1M salt and the resulting precipitate from 30 ml of the antibiotic fluid was separated from the supernatant by centrifugation. The precipitate was dissolved in eight ml of 0.01N HCl solution, neutralized and clarified. The supernatant at pH 9.0 was neutralized to pH 7.0. In order to avoid the formation of metal-protein precipitates in the BHI titration medium, the antibiotic activity of the fluids, in this experiment only, was assayed in Dolman-Wilson medium. This medium did not precipitate in the presence of the metal ions as did BHI.

The results (Table XV) showed that the precipitate caused by Ba++ ions was completely inert whereas the total activity was preserved in the supernatant fraction. Specific activity of 36534 and 29297 increased three to eight fold respectively when compared with the control. The Ba(OH) $_2$ salt was used for further purification of the HCl-treated material.

(c). Effect of $MnCl_2$ and $ZnCl_2$ on the activity:

After the $\mathrm{Ba(OH)}_2$ -treated antibiotic fluid was clarified, the effect of further treatment with 0.1M MnCl_2 or ZnCl_2 was investigated. The resulting precipitates were dissolved in 0.01N HCl , neutralized with NaOH, clarified and tested. The supernatant which contained the soluble Mn^{++} or Zn^{++} ions was saturated with $\mathrm{H}_2\mathrm{S}$. The resulting precipitate was inert and was discarded before the supernatant was neutralized and tested.

The results (Table XVI) showed that both metal ions could precipitate certain amounts of antibiotic out of solution. However, Zn^{++} ions were

TABLE XV

EFFECT OF BARIUM HYDROXIDE ON THE ACTIVITY OF STAPHYLOCOCCAL ANTIBIOTICS

			ntibiotic 2	9297	antibiotic 36534		
treatment*	fraction	activity (total units)	recovery (%)	specific activity**	activity (total units)	recovery (%)	specific activity
none		3725	100	1.9	8093	100	1.3
treated with $Ba(OH)_2$	precipitate	0	0	-	0	0	~
	supernatant	3600	97	16.5	8008	99	3.7

 $[\]boldsymbol{*}$ antibiotic assays performed after neutralization to pH 7.0

 $[\]ensuremath{\mbox{\sc wnits}}$ units of antibiotic activity per mg of protein

			tibiotic 29	297	antibiotic 36534			
treatment	fraction	activity (total units)	recovery (%)	specific activity*	activity (total units)	recovery (%)	specific activity	
Ba(OH) ₂ -treated control		13254	100	15.5	13728	100	4.0	
further treated with MnCl ₂	precipitate**	2386	18	14.5	1922	14	12.0	
	supernatant***	5037	38	17.4	3569	26	7.8	
further treated with ZnCl ₂	precipitate	4374	33	23.4	4805	35	26.6	
	supernatant	7687	58	10.1	8374	61	11.2	

 $[\]ensuremath{\text{\#}}$ units of antibiotic activity per mg of protein

 $[\]ensuremath{^{\prime\prime\prime}}$ precipitate dissolved in 0.01N HCl, neutralized with NaOH and tested

^{***} supernatant treated with $\mathrm{H}_2\mathrm{S}$ and neutralized with NaOH before testing

superior to Mn $^{++}$ ions when percent recovery and specific activity were considered. Thus, the fraction was treated further with zinc and was referred to as the zinc-precipitable fraction. The remaining activity in the supernatant was referred to as the zinc-soluble fraction. Other zinc salts were as effective as ${\rm ZnCl}_2$ in precipitating the antibiotics, but the chloride was subsequently used.

(d). Influence of pH on precipitation of antibiotics by zinc ions:

Since zinc ions caused precipitation only in neutral and alkaline
conditions (see Table XIV), two conditions, pH 7 and 9, were selected for
an assessment of their effects on quantitative recovery of zinc-precipitated
antibiotics. Thirty-five ml of Ba(OH)₂-treated antibiotic fluid at pH 9.0
was adjusted to pH 7.0 with HCl. This was was then mixed with 5.0 ml of
aqueous zinc chloride solution to give a final concentration of the salt
from 0.01 to 0.2M. The precipitate was collected, dissolved and assayed as
described previously.

The results (Table XVII) showed that at pH 7 and 9 a 0.1M concentration of zinc ions was the most effective in precipitating antibiotic activity with slightly better recovery at pH 9.0. Under these conditions, precipitation was complete since additional zinc added to the clarified supernatant produced no further precipitate even though some activity still remained.

In summary then, HCl-treated antibiotic fluid was brought to pH $9.0 \text{ with } 0.1 \text{M Ba}(\text{OH})_2$. The precipitate was discarded and antibiotic in the supernatant was further precipitated by the addition of 0.1M ZnCl_2 .

TABLE XVII

RELATIONSHIP BETWEEN PH OF THE ANTIBIOTIC FLUIDS, CONCENTRATION OF ZINC IONS AND RECOVERY OF ZINC-PRECIPITATED ANTIBIOTICS

pH of the	concentration	antibiotic	29297	antibiotic	36534
$Ba(OH)_2$ -treated	of zinc ions	activity	recovery	activity	recovery
antibiotic fluid	(Moles)	(total units)	(%)	(total units)	(%)
7*	0	148	100	144	100
	0.01	0	0	0	0
	0.05	18	12	0	0
	0.10	54	37	34	24
	0.20	36	24	22	15
9	0	148	100	144	100
	0.01	0	0	0	0
	0.05	22	15	24	17
	0.10	62	42	48	33
	0.20	38	26	26	18

 $[\]boldsymbol{*}$ adjusted to this pH by the addition of HCl

(2). Precipitation by organic compounds:

Neutralized HC1-treated antibiotic fluids were treated with various organic compounds and the precipitation which occurred was noted as shown in Table XVIII. It was found that with the exception of urea, all substances added caused a moderate to heavy precipitation. Most precipitates were soluble in distilled water at neutral pH. An exception was the precipitate caused by tannic acid, which was insoluble in water between pH 3 - 11.

Four of the compounds, picric and trichloroacetic acids, methanol and ethanol, were further investigated since they appeared to be good precipitants. All permitted relatively good recoveries of antibiotics, but removal of picric and trichloroacetic acids became a problem when it was realized that the antibiotics were small dialyzable peptides. Recoveries with methanol were slightly better than with ethanol although results were similar. In Table XIX, it was shown that about 77% of the antibiotics was removed as a precipitate with a two fold increase in specific activity. Of interest here is the fact that methanol precipitations had to be performed at 4°C with subsequent removal of the alcohol at that temperature. Precipitations at room temperature destroyed the activity.

(3). Extraction with water immiscible organic solvents:

Water immiscible organic solvents such as benzene, chloroform, ethyl ether, ethyl acetate, hexane and petroleum ether were tested for their ability to extract the antibiotic activity from neutralized HCl-treated material. The ratio of solvent to the antibiotic fluid was 4:1. It was

TABLE XVIII

PRECIPITABILITY OF ANTIBIOTIC FLUID IN THE PRESENCE OF SOME ORGANIC COMPOUNDS

		amount of	precipitate	solubility
substance	amount added	29297	36534	at pH 7
picric acid	0.1M	heavy	heavy	soluble
tannic acid	0.01M	11	11	insoluble
methano1	4:1 (v/v)	11	11	soluble
ethanol	11	TT.	11	11
isopropanol	11	11	11	11
acetone	11	11	11	11
trichloroacetic acid	0.1M	moderate	11	11
n-butanol	4:1 (v/v)	**	moderate	11
tert-amyl alcohol	11	Ħ	11	11
propylene glycol	11	11	11	11
ethylene chloride	11	11	11	11
urea	0.1M	none	none	-

TABLE XIX

EFFECT OF METHANOL ON THE ACTIVITY OF STAPHYLOCOCCAL ANTIBIOTICS*

		an	tibiotic 29	297	antibiotic 36534		
treatment	fraction	activity (total units)	recovery (%)	specific activity**	activity (total units)	recovery (%)	specific activity
none		1660	100	4.9	3940	100	10.3
methanol	precipitate	927	56	8.0	3043	77	22.9
	supernatant	547	33	2.5	827	21	3.3

^{*} performed at 4°C

 $[\]ensuremath{\mbox{\sc w}}\xspace^*$ units of antibiotic activity per mg of protein

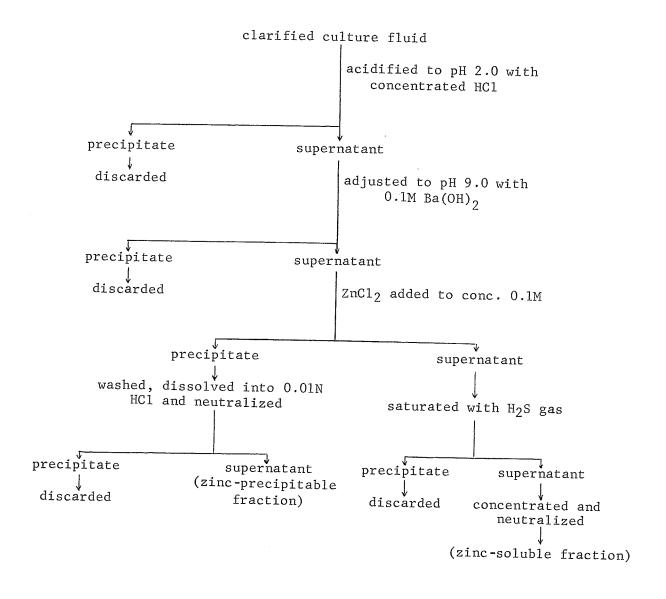
found that solvent extract, evaporated to dryness and resuspended in distilled water, contained no activity in contrast with the aqueous fraction which retained full activity.

III. OUTLINE OF INITIAL SCHEME FOR PARTIAL PURIFICATION

According to the evidence presented in these studies, an initial scheme (Table XX) suitable for partial purification of staphylococcal antibiotics was arranged. The clarified culture fluid, which was derived from the supplemented Dolman-Wilson liquid medium, was first acidified to pH 2 with concentrated HCl and then allowed to stand at 4°C overnight. The inert precipitate formed due to acidification was removed by centrifugation and discarded. The supernatant was adjusted to pH 9 by the direct addition of solid $Ba(OH)_2$ to the fluid, to a concentration of approximately 0.1M. This treatment had two purposes: These were the further removal of inert impurities as precipitate and provision of alkaline conditions for the ${\rm ZnC1}_2$ treatment. After the fluid was clarified, 0.1M ZnCl₂ was added. At this stage, a portion of the antibiotic from either strain precipitated out of the solution. These precipitates were soluble only in acid conditions. That portion precipitable by zinc is designated the zinc-precipitable fraction, and that in the supernatant, the zinc-soluble fraction. Since a portion of the antibiotic from both strains remained in the supernatant fluid, it was considered that the crude antibiotics were mixtures of closely related compounds.

TABLE XX

INITIAL SCHEME USED FOR PARTIAL PURIFICATION OF STAPHYLOCOCCAL ANTIBIOTICS



For the zinc-precipitable fraction, the precipitate was collected by centrifugation, resuspended in distilled water and recentrifuged. The latter processes were repeated twice. The washed precipitate was dissolved in 0.01M HCl, immediately neutralized and the insoluble material discarded. As to the zinc-soluble fraction, it is obvious that the supernatant fluid after treatment with 0.1M ZnCl, contains Zn $^{++}$ and Ba $^{++}$ salts. These were removed by precipitation with $\rm H_2S$ gas which was generated from HCl and $\rm Na_2S$ and bubbled through the fluid. It was noted after clarification and neutralization that the zinc-soluble and zinc-precipitable fractions had a yellow color.

Table XXI gives the percent recovery of antibiotics and specific activity at different stages in the initial scheme. As shown in the table, recoveries of zinc-precipitable and soluble fractions of 29297 were 33 and 41% respectively with about a 27 fold increase in specific activity. With respect to antibiotic 36534, percent recoveries were about the same, and specific activities showed an increase of 17 fold when compared to crude. If one assumes the total recovery in both cases from IV a and b to be about 75% (see Table XXI), it is evident that about 15 - 20% of the activity of the Ba⁺⁺-treated material is unrecoverable.

TABLE XXI

SPECIFIC ACTIVITY AND PERCENT RECOVERY OF STAPHYLOCOCCAL ANTIBIOTICS 29297

AND 36534 AT DIFFERENT PURIFICATION STAGES

-	stage of purification	amount (ml)	activity (total units)	recovery	total protein (mg)	specific activity*
ANTI	BIOTIC 29297					
I.	crude	940	3760	100	4559.0	0.8
II.	HC1-treatment	955	3725	96	1989.0	1.9
III.	Ba(OH) ₂ -treatment	900	3600	96	217.8	16.5
IV.	ZnC1 ₂ -treatment					
а.	Zn-precipitable fraction	150	1245	33	52.5	23.7
Ъ.	Zn-soluble fraction	850	1530	41	74.0	20.7
ANTI	BIOTIC 36534					
I.	crude	960	8373	100	13680.0	0.6
II.	HC1-treatment	975	8093	97	6332.5	1.3
III.	Ba(OH) ₂ -treatment	910	8008	96	2138.0	3.7
IV.	ZnC1 ₂ -treatment					
а.	Zn-precipitable fraction	150	2955	35	288.0	10.3
Ъ.	Zn-soluble fraction	390	3393	41	322.8	10.5

 $[\]boldsymbol{\ast}$ units of antibiotic activity per mg of protein

IV. FURTHER PURIFICATION OF ZINC-PRECIPITABLE AND ZINC-SOLUBLE FRACTIONS

Further purification was felt to be necessary since the specific activity of final products from fractions of both antibiotics showed no sign of reaching a plateau.

(1). <u>Ion-exchange chromatography</u>:

A cation-exchanger, Dowex 50-X2, was selected and was prepared and operated as described in Materials and Methods. Results are shown in Fig. 3. It was noted that all fractions showed only one antibiotic activity peak which came off the column about 100 to 200 ml after the void volume ($V_0 = 300 \text{ ml}$). The peak of activity, in all cases, was not coordinated with the peak absorption at 280 nm. Table XXII shows that activity levels for zinc-precipitable and zinc-soluble 29297 in the effluent were low, about 80% of the activity of both fractions being irretrievably lost on the column. Specific activity decreased with the zinc-precipitable fraction; the increase shown by the zinc-soluble fraction was negligible. Results obtained with 36534 were different. Only about 5 - 10 % of the antibiotic activity was lost on the column, and specific activity of both fractions increased about two to three fold.

(2). Gel filtration:

Gel filtration was conducted with Sephadex G-15 columns which were prepared and operated as described in Materials and Methods. The partially purified antibiotic fluid, after zinc treatment, was subjected

DOWEX 50-X2 ELUTION PATTERNS OF DIFFERENT FRACTIONS OF ANTIBIOTICS 29297 AND 36534

- (A). 29297 ZINC-PRECIPITABLE FRACTION
- (B). 29297 ZINC-SOLUBLE FRACTION
- (C). 36534 ZINC-PRECIPITABLE FRACTION
- (D). 36534 ZINC-SOLUBLE FRACTION

 $V_0 = \text{void volume}$

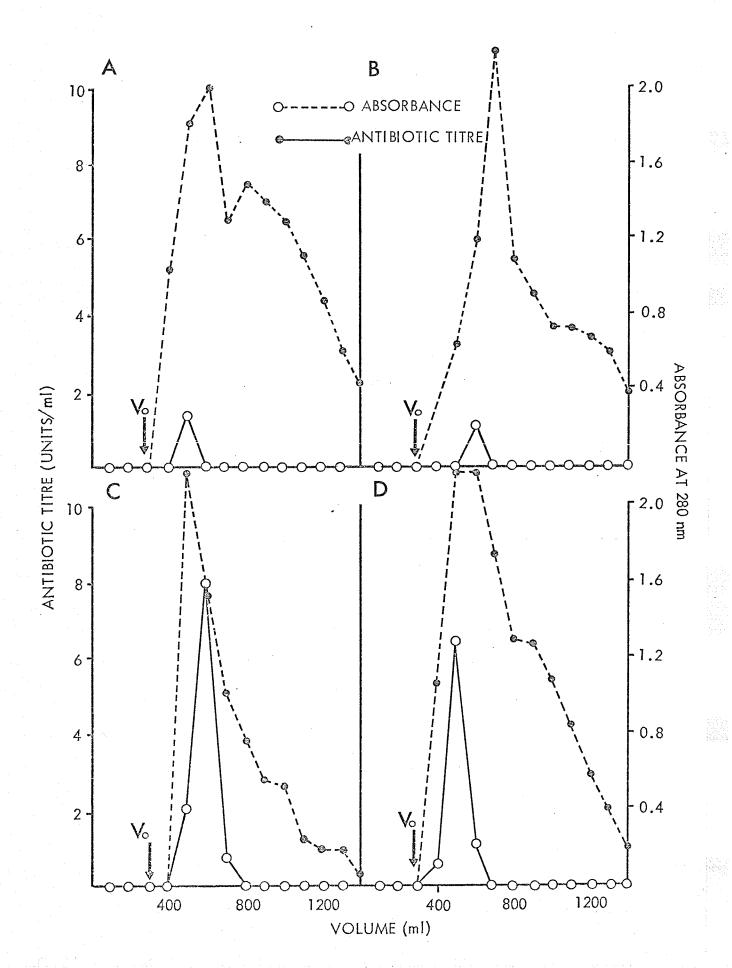


TABLE XXII

EFFECT OF DOWEX 50-X2 PASSAGE ON SPECIFIC ACTIVITY OF
ZINC-PRECIPITABLE AND SOLUBLE FRACTIONS OF ANTIBIOTICS 29297 AND 36534

		biotic 292	97	anti	biotic 365	34
fraction	activity (total units)	recovery (%)	specific activity*	activity (total units)	recovery (%)	specific activity
Zn-precipitable						
before	670	100	31.2	1330	100	32.4
after	130	19	18.1	1100	83	72.8
Zn-soluble				•		
before	730	100	18.7	900	100	25.0
after	.110	15	22.7	890	99	79.5

133.

^{*} units of antibiotic activity per mg of protein

to gel filtration on Sephadex G-15. The elution patterns from the G-15 columns are illustrated in Figs. 4 and 5. In all cases, antibiotic activity was partially or completely separable from material which absorbed at 280 nm. Antibiotic activity itself never showed more than one peak regardless of treatment.

Concentrated active effluents of antibiotic 29297 obtained from Sephadex G-15 were usually colorless. Similar fractions of antibiotic 36534 were light yellow in color. Rechromatography on Sephadex G-10 (data not shown) did not remove this color.

As indicated in Table XXIII, percent recoveries of all fractions were close to unity. Furthermore, specific activity was increased in all cases, the 29297 zinc-soluble fraction showing the largest increase and the 36534 zinc-soluble fraction the smallest.

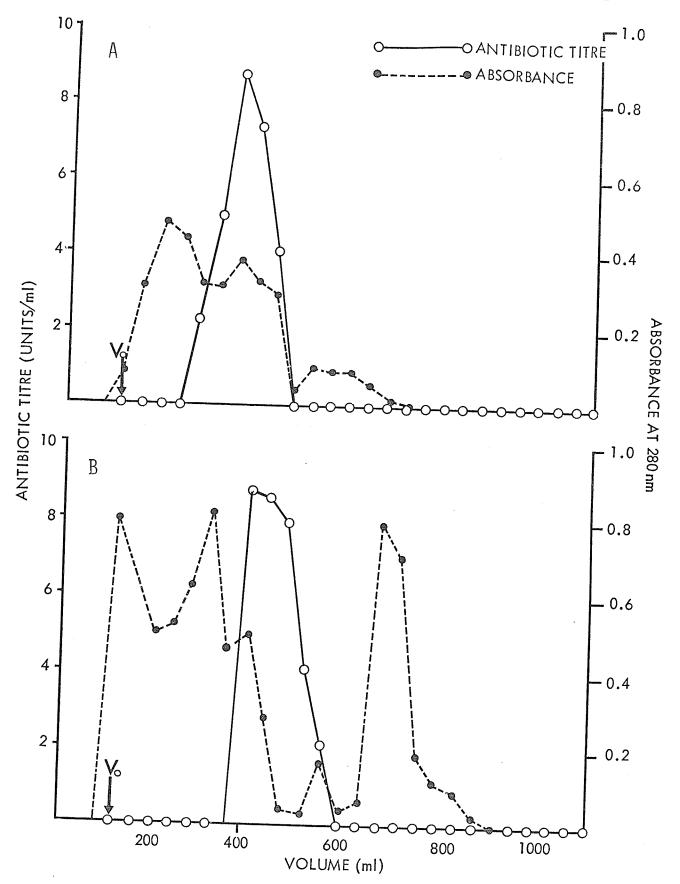
(3). Crystallization:

After Sephadex gel-filtration, both fractions of antibiotic 29297 could be crystallized at 4°C if the active fluids were previously concentrated at 55°C to a point of saturation or near saturation. However, antibiotic 36534 fractions could not be crystallized under the same conditions if only Sephadex gel-filtration had been previously used for further purification. It was found that the concentrated liquid of the zinc-precipitable and soluble fractions of antibiotic 36534 must be passed through Dowex 50-X2 and then desalted on Sephadex G-15 before crystallization could be effected. Recrystallization of both 29297 and 36534 fractions was performed by dissolving the crystals in distilled water at 55°C until

ELUTION PATTERNS OF ANTIBIOTIC 29297 FROM SEPHADEX G-15 COLUMNS

- (A). ZINC-PRECIPITABLE FRACTION
- (B). ZINC-SOLUBLE FRACTION

 V_{o} = void volume



ELUTION PATTERNS OF ANTIBIOTIC 36534 FROM SEPHADEX G-15 COLUMNS

- (A). ZINC-PRECIPITABLE FRACTION
- (B). ZINC-SOLUBLE FRACTION

 $V_o = void volume$

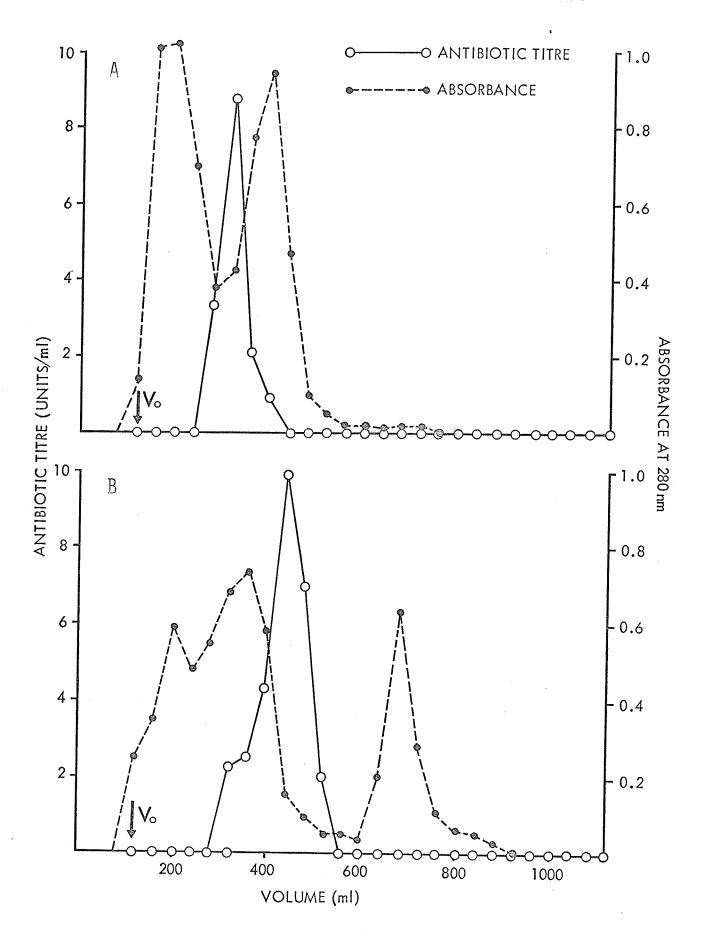


TABLE XXIII

EFFICIENCY OF SEPHADEX G-15 GEL FILTRATION IN THE FURTHER PURIFICATION OF ANTIBIOTICS 29297 AND 36534

	antibiotic	activity			
antibiotic	(total	units)	recovery	specific	activity*
_fraction	before	after	(%)	before	after
29297 zinc- precipitable	620	595	96	36.9	135.2
29297 zinc- soluble	210	205	98	16.8	117.1
36534 zinc- precipitable	190	187	98	20.7	33.4
36534 zinc- soluble	97	94	97	12.9	19.6

 $[\]boldsymbol{\ast}$ antibiotic units per mg of protein

the liquid was saturated by the antibiotic, then filtration through a Millipore HA membrane (pore size = 450 nm) and rapid cooling to 4°C. Little or no further increase in specific activity after recrystallization was noted in all fractions (see Tables XXVI and XXVII). Crystals of the fractions were colorless, odorless and octahedron-shaped, but after standing soon assumed an irregular appearance (Fig. 6). Loss of water may have contributed to this change.

V. FINAL PURIFICATION SCHEMES FOR STAPHYLOCOCCAL ANTIBIOTICS 29297 AND 36534

Final purification schemes for 29297 and 36534 are shown in Tables XXIV and XXV respectively. It will be noted that purification of 29297 (Table XXIV) does not require Dowex 50-X2. That given in Table XXV for 36534 requires that the material must be passed through Dowex 50-X2 followed by desalting on Sephadex G-15.

Recrystallized fractions of both antibiotics were occasionally weakly positive when tested by the Lowry and ninhydrin reagents. Since methanol was effective as a precipitant of antibiotics from partially purified material (see Table XIX), recrystallized fractions were subjected to methanol treatment at 4°C as described previously. It was found that the antibiotics, which were precipitated by this procedure, were generally freed from ninhydrin and Lowry positive material.

Since the antibiotics now contained no Lowry or ninhydrin-positive material, neither of these reagents was of value in specific activity determinations. It was therefore necessary that specific activity be

CRYSTAL FORMS OF STAPHYLOCOCCAL ANTIBIOTICS*

- (A). 29297 ZINC-PRECIPITABLE FRACTION
- (B). 29297 ZINC-SOLUBLE FRACTION
- (C). 36534 ZINC-PRECIPITABLE FRACTION
- (D). 36534 ZINC-SOLUBLE FRACTION

* Mag. = 400X

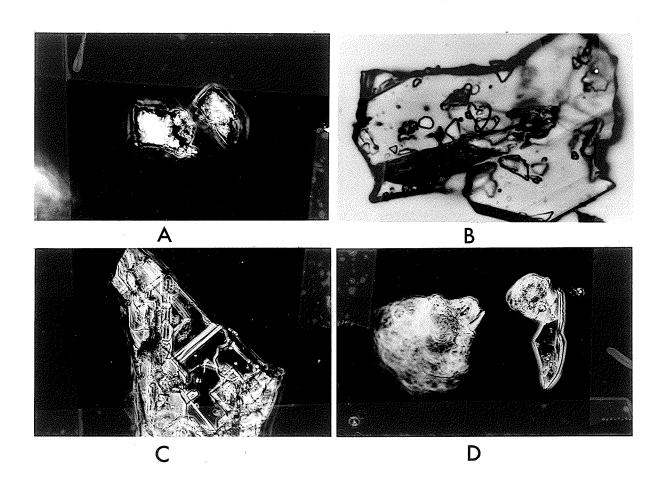


TABLE XXIV

PURIFICATION SCHEME OF STAPHYLOCOCCAL ANTIBIOTIC 29297

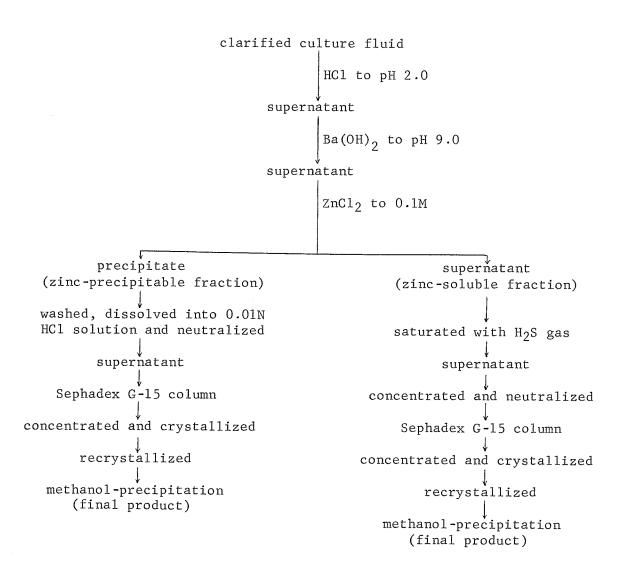
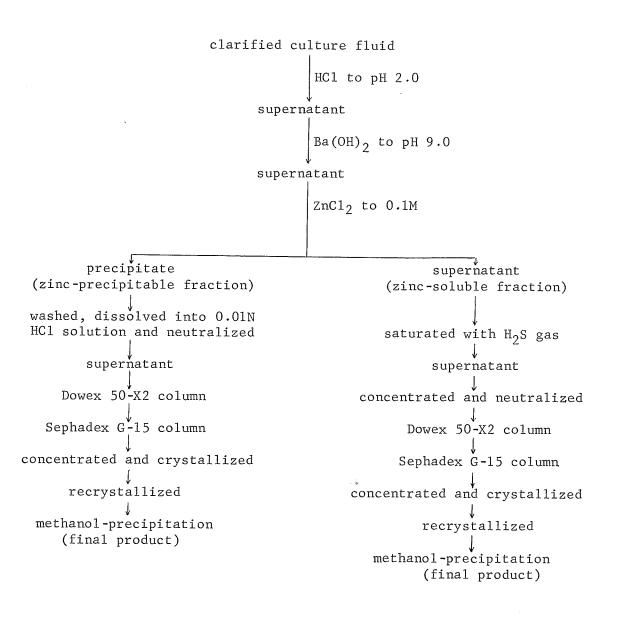


TABLE XXV

PURIFICATION SCHEME OF STAPHYLOCOCCAL ANTIBIOTIC 36534



redetermined by nitrogen analysis, as performed by Markham (1942) micro-Kjeldahl method (see Table XXVI and XXVII). Recovery of antibiotic 29297 zinc-precipitable fraction after the second methanol precipitation was 3%; that for the zinc-soluble fraction was 6%. Percent recoveries for the zinc-precipitable and soluble fractions of antibiotic 36534 were similar.

-143
TABLE XXVI

SPECIFIC ACTIVITY AND PERCENT RECOVERY OF STAPHYLOCOCCAL ANTIBIOTIC 29297 AT DIFFERENT STAGES OF PURIFICATION

stage of purification	total volume (ml)	total activity (units)	recovery (%)	total nitrogen (mg)	specific activity*
I. crude	955	13084	100	6178.9	2.2
II. HCl-treatment	900	12822	98	4220.0	3.1
III. Ba(OH) ₂ -treatment	770	12691	97	2641.1	4.8
IV. ZnCl ₂ -treatment					
a. zinc-precipitable fraction	520	4318	33	561.6	7.7
1. Sephadex G-15	320	4187	32	144.9	28.9
2. crystallization	55	2094	16	22.1	124.2
3. recrystallization	38	1047	8	12.9	114.2
4. methanol-precipitation	24	654	5	6.7	152.8
5. 2nd methanol- precipitation	25	390	. 3	2.5	156.0
b. zinc-soluble fraction	735	7850	60	917.5	7.4
1. Sephadex G-15	435	7720	59	440.4	17.5
2. crystallization	135	3664	28	87.0	42.2
3. recrystallization	65	1832	14	35.1	52.0
4. methanol-precipitation	47	1308	10	21.6	60.9
5. 2nd methanol- precipitation	40	785	6	12.8	61.3

^{*} units of antibiotic activity per mg of nitrogen

TABLE XXVII

SPECIFIC ACTIVITY AND PERCENT RECOVERY OF STAPHYLOCOCCAL ANTIBIOTIC 36534 AT DIFFERENT STAGES OF PURIFICATION

stage of purification	total volume (ml)	total activity (units)	recovery (%)	total nitrogen (mg)	specific activity*
I. crude	950	7600	100	8825.5	0.9
II. HCl-treatment	910	7372	97	5427.0	1.4
III. Ba(OH) ₂ -treatment	800	7370	97	3006.9	2.5
IV. ZnCl ₂ -treatment					
a. zinc-precipitable fraction	305	2660	35	408.7	6.5
1. Dowex 50-X2	165	2204	29	123.8	17.9
2. Sephadex G-15	125	2128	28	86.3	24.8
3. crystallization	60	1564	14	13.9	112.5
4. recrystallization	30	782	7	5.0	155.6
5. methanol-precipitation	17	456	6	2.7	165.6
6. 2nd methanol- precipitation	20	304	4	1.8	168.9
b. zinc-soluble fraction	400	3876	51	1328.0	2.9
1. Dowex 50-X2	495	3800	50	405.9	9.4
2. Sephadex G-15	450	3790	50	252.0	15.2
3. crystallization	60	1900	25	27.6	69.6
4. recrystallization	35	988	13	14.4	68.3
5. methanol-precipitation	27	760	10	10.0	76.0
6. 2nd methanol- precipitation	25	530	7	6.9	76.8

^{*} units of antibiotic activity per mg of nitrogen

PART III. CHARACTERIZATION OF ANTIBIOTIC FRACTIONS

I. BIOLOGICAL PROPERTIES

Effect of 29297 zinc-precipitable fraction on viability of S. aureus 209P:

The effect of highly purified $^{(4)}$ antibiotic preparations on the viability of indicator cells was studied by mixing equal volumes of antibiotic solution (85.4 units/ml) and a standardized suspension of the indicator strain, \underline{S} . \underline{aureus} 209P, (0.D. = 0.100) in double strength BHI broth. The mixture was incubated at 37°C. At different intervals, samples (0.5 ml each) were taken and viable counts were made according to the technique of Miles and Misra (1938). Results were expressed as the mean of 10 counts.

Table XXVIII shows that the antibiotic had a bactericidal effect upon the indicator strain, about 5% of the initial inoculum alive after 16 hr incubation. Most of the cells were killed in the first hour with the rate of killing decreased thereafter.

Some observations were made on the appearance of treated indicator strain under the microscope. No evidence of unusual shape or form was observed in Gram-stained cells, but it was noted that many cells became Gram-negative after exposure to the antibiotic. The antibiotic did not cause lysis of the cells as reflected in the absence of a reduction in optical density (660 nm) of a test suspension.

^{(4).} twice crystallized and twice methanol precipitated.

TABLE XXVIII

EFFECT OF ANTIBIOTIC 29297 ZINC-PRECIPITABLE FRACTION ON VIABILITY OF INDICATOR STRAIN OF STAPHYLOCOCCUS AUREUS 209P

time (hr)		(X10 ⁸ cells/ml)
(1117)	control	antibiotic*
0	1.16	1.16
1/4	0.87	0.44
1/2	1.02	0.51
1	1.47	0.19
2	2.34	0.19
4	3.79	0.19
8	11.20	0.18
16	19.50	0.06

^{*} antibiotic concentration = 42.7 units/ml

II. NATURE OF THE ANTIBIOTICS

(1). Stability of antibiotic fluids under ultraviolet light irradiation:

Stability of antibiotic under ultraviolet light irradiation was studied with both partially (HCl-treated) and highly purified (twice crystallized and twice methanol-precipitated) materials. Ten ml of the antibiotic fluid was placed in a disposable plastic Petri-dish, 8.5 cm in diameter. The thickness of the liquid layer in the dish was about 1 mm. The plate was placed under an ultraviolet light lamp (General Electric Co., TB tube, 30 watts, 115 V, 91.5 cm in length) and was irradiated for various lengths of time at room temperature. The distance from the lamp to the center of the plate was 20 cm. After irradiation, the liquid was sterilized by filtration and then assayed for activity.

The results are shown in Table XXIX. It was noted that both the partially and highly purified antibiotic fluids were equally resistant to the irradiation. After 10 min of irradiation, the loss of activity was never higher than 10% of the original in all cases.

(2). Absorption spectra in ultraviolet and visible light:

Aqueous solutions of highly purified material which contained about 2 mg of ninhydrin-positive material⁽⁵⁾ per ml were scanned in the Unicam SP-800B spectrophotometer from 200 to 800 nm. It was found that the antibiotics did not show any absorption in the visible light region (350 -

^{(5).} determined after hydrolysis. Unhydrolyzed material is usually ninhydrin-negative

TABLE XXIX

STABILITY OF PARTIALLY AND HIGHLY PURIFIED STAPHYLOCOCCAL ANTIBIOTICS UNDER ULTRAVIOLET LIGHT IRRADIATION

	irradiation	antibio activity	tic 29297	antibio activity	tic 36534
material	time (min)	(total units)	recovery (%)	(total units)	recovery (%)
partially					
purified*	0	170	100	190	100
	1	160	94	170	90
	5	165	97	180	94
	10	165	97	170	90
highly purified**					
a. zinc-precipitable					
fraction	0	400	100	730	100
	1	400	100	720	98
	5	390	98	730	100
	10	400	100	720	98
b. zinc-soluble					
fraction	0	450	100	870	100
	1	440	98	860	99
	5	440	98	850	98
	10	430	96	850	98

 $[\]mbox{\ensuremath{\,^\star}}$ HCl-treated antibiotic fluids

^{**} Twice crystallized and twice methanol precipitated preparations

800 nm). In the ultraviolet region (200 - 350 nm), however, a small shoulder at about 270 - 280 nm was observed with the 29297 zinc-precipitable fraction (Fig. 7). A similar shoulder at 255 - 265 nm was observed with the 29297 zinc-soluble fraction. Shoulders were observed in the same wavelength regions for the fractions of the antibiotic 36534 but they were very much flattened.

(3). Mobility of crude antibiotics in an electric field at various pH values:

The mobility of antibiotics 29297 and 36534 in an electric field at different pH values was investigated as reported in Materials and Methods. It was found that antibiotic 36534 showed slight movement towards the anode if the pH of the buffer was above 5.5 and the duration of electrophoresis was longer than 45 min. Antibiotic 29297 on the other hand did not move at any pH regardless of the length of time applied.

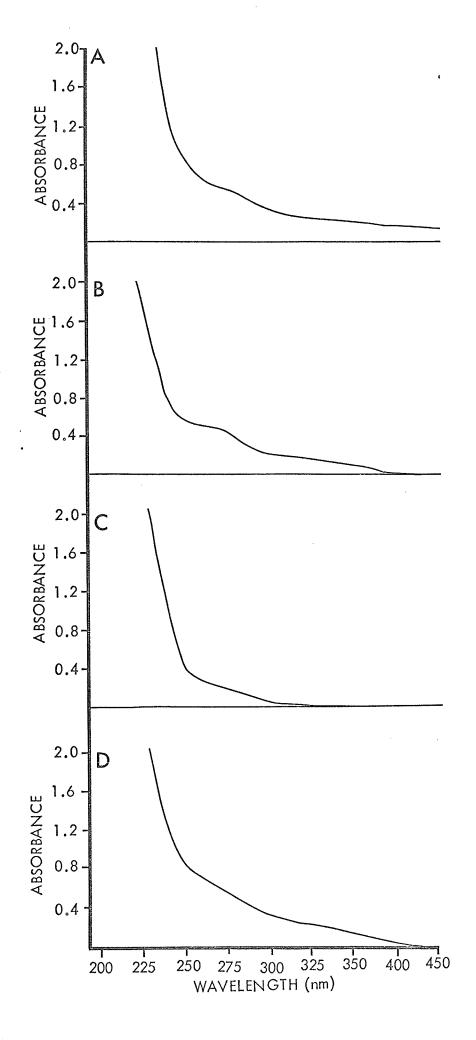
(4). Melting points:

The melting point of all four highly purified antibiotic preparations was determined by the method of Shriner et al. (1964). Twice crystallized and twice methanol-precipitated material was first dried at 37°C and further dried at 160°C for two hr. The dried material was immediately ground to a fine powder. The experiment was conducted in a concentrated sulphuric acid bath heated such that the temperature rose at the rate of 1°C per min. It was noted that all fractions tested did not show any sign of melting up to 320°C. Rather, the antibiotics decomposed with charring

THE ULTRAVIOLET LIGHT ABSORPTION SPECTRA OF STAPHYLOCOCCAL ANTIBIOTICS

- (A). 29297 ZINC-PRECIPITABLE FRACTION
- (B). 29297 ZINC-SOLUBLE FRACTION
- (C). 36534 ZINC-PRECIPITABLE FRACTION
- (D). 36534 ZINC-SOLUBLE FRACTION





when the temperature reached 278 - 280°C.

III. CHEMICAL ANALYSES

(1). Qualitative:

A number of qualitative chemical analyses was performed on all four highly purified preparations to assess their degree of purity and to help determine their chemical nature. For comparison, a pure substance known to give a positive reaction with the reagent in question was used as a reference. Reagent blanks were also included as negative controls and all work was done in duplicate.

The antibiotics gave positive results with the biuret, periodic acid oxidation, ferrous chloride and Dubois' tests (Table XXX). All other chemical tests conducted (Table XXXI) were negative. The exceptions were Lowry and ninhydrin tests which occasionally showed a weakly positive result with some batches of purified material. These results were thought to be caused by traces of contamination rather than the antibiotics themselves. Such material was further treated with methanol at 4°C until all ninhydrin-positive and Lowry-positive substances were removed.

These analyses clearly indicate that the four purified antibiotics are free of carbohydrates, proteins, lipids, and nucleic acids. The nature of the positive reactions indicates that they may be peptides with some hydroxyl functional groups.

TABLE XXX

POSITIVE CHEMICAL TESTS ON ANTIBIOTICS 29297 AND 36534*

name of test	reference chemical	responsible groups
Biuret	urea	RCONH ₂ , RCSNH ₂ , RCH ₂ NH ₂ or
		RCH(NH)NH ₂
Periodic acid oxidation	hydroxyamine-HC1	RCH(OH)-(OH)CHR', RCH(OH)-COR',
		RCO-COR' or RCH(OH)-CH(NH ₂)R'
Ferric chloride	phenol	enols
Dubois	glucose	reducing groups

 $[\]ensuremath{\star}$ zinc-precipitable and zinc-soluble fractions from each antibiotic

-153-TABLE XXXI NEGATIVE CHEMICAL TESTS ON ANTIBIOTICS 29297 AND 36534*

	reference	
name of test	chemical	responsible groups
Molisch	glucose	carbohydrates
Benedict	glucose	reducing sugars
Fehling	glucose	reducing sugars
Silver nitrate	NaC1	halogens
Sodium iodide	NaC1	chlorides
Millon-Nasse	phenol	tyrosine or 3,5- unsaturated phenol
Sulphur	cystine	cysteine or cystine
Barium chloride	cystine	sulphur
Diazotized sulfanilic acid	phenol	phenolic
Formaldehyde-sulphuric acid	phenol	phenolic
Sodium bisulfite	formaldehyde	aldehyde
Tollen	glucose	aldehyde
Potassium permanganate	toluene	unsaturated aliphatic
Fiske-Subbarow	KH ₂ PO ₄	phosphorus
Ninhydrin**	egg albumin	α -NH ₂
Lowry**	egg albumin	aromatic amino acid
Xanthoproteic	egg albumin	aromatic

^{*} zinc-precipitable and zinc-soluble fractions from each antibiotic
** occasionally weakly positive

(2). Combustion:

It was felt necessary to ensure that the antibiotic activity of the preparations was not due to the presence of a toxic undetected inorganic compound or metal ion. Solutions of the highly purified materials were first gently heated to dryness in crucibles and then strongly heated until all organic substances in the residues were completely vapourized. The ash left was dissolved in distilled water and the liquid was assayed.

Only a trace of ash was left after burning. This was white in color and showed a yellowish flame in the Bunsen burner. The ash could be dissolved in distilled water and when tested this solution was alkaline (about pH 9). The solution showed no toxic effects on the indicator strain, although the original before burning was highly active.

(3). Pronase hydrolysis:

Since the qualitative chemical analyses led one to believe that these antibiotics were peptide in nature, highly purified antibiotics were incubated with the non-specific proteolytic enzyme, pronase. The experiment was performed as follows: Antibiotic solution was mixed with pronase in a ratio of substrate to enzyme = 1:2 (w/w). The mixture was incubated at 37° C for various lengths of time. After incubation was complete, the reaction was stopped by autoclaving at 10 lb pressure (110° C) for 10 min and the antibiotic activity of this heated solution was assayed. Also, pronase-hydrolyzed material was applied to Whatman filter paper no. 1 together with the untreated solution. The paper was developed by a solvent system which contained n-butanol/acetic acid/water, 4:1:5 by volume.

Distilled water in the presence and absence of pronase was tested along with the samples as controls.

The results (Table XXXII) showed that the activity of antibiotic 29297 was completely destroyed after it had been incubated with pronase for 24 hr. In the same length of time, an average of 90% of the activity of antibiotic 36534 was diminished. A longer incubation period with the enzyme up to four days had little effect on the remaining activity of antibiotic 36534. Pronase itself did not have any toxic effects on the indicator strain.

Paper chromatograms revealed that although the untreated material did not show any ninhydrin-positive spots, those treated with pronase had six to seven ninhydrin-positive spots. One of these spots had an identical $R_{\rm f}$ value with the pronase which had been incubated under the same conditions.

(4). Oxidation by nitrous acid:

Since both qualitative chemical analyses and pronase hydrolysis had demonstrated that the antibiotics likely were peptides, the presence of free α -amino groups and their relationship to antibiotic activity were investigated. Oxidation of the antibiotics with nitrous acid was performed since it is known that nitrous acid reacts specifically with free amino groups by converting these groups to hydroxyl groups with the liberation of nitrogen gas (Oser et al., 1965). Nitrous acid was prepared according to the method of Shriner et al. (1964). Three ml of highly purified antibiotic fluid was mixed with three ml of freshly prepared HNO₂ solution. The mixture was incubated at 55°C for one hr. Then the reaction was

TABLE XXXII

THE EFFECT OF PRONASE ON HIGHLY PURIFIED ANTIBIOTIC PREPARATIONS

material	incubation (days)	antibiotic activ without pronase	ity (units/ml) with pronase	activity lost(%)
29297 zinc-				
precipitable	0	6.9	-	0
	1	3.2	0	100
29297 zinc- soluble	0	10.5	-	0
	1	7.2	0	100
36534 zinc- precipitable	0	10.7		0
Freezpreadre			-	0
	1	9.5	0.5	95
	4	9.4	0.4	96
36534 zinc-				
soluble	0	15.5	-	0
	1	14.4	2.3	84
	4	10.7	1.0	91
water	0	0	0	-
	1	0	0	-
	4	0	0	-

stopped by neutralization of the mixture with 4N NaOH. The neutralized fluid was sterilized by filtration and assayed for antibiotic activity.

It was observed that under the conditions used, the controls which consisted of a mixture of cysteine and tyrosine, reacted vigorously with the nitrous acid. On the other hand, little or no reaction was observed in the mixture of antibiotic fluid and acid.

The results of antibiotic assay (Table XXXIII) showed that after nitrous acid treatment, antibiotic solutions increased their activity greatly. Since sodium nitrite (a product of neutralization of nitrous acid with NaOH) itself had a toxic effect on the growth of the indicator strain as shown in the controls, the increase in activity was interpreted as evidence of a synergistic reaction between antibiotic and sodium nitrite.

(5). Amino acid content:

The amino acid content of highly purified antibiotic preparations was assayed in the Technicon Auto Analyzer (Technicon Corp.). Before assay, the material was hydrolyzed by 6N HCl and the acid removed by flash-eva-poration. Results of the assays (Table XXXIV) revealed that the four fractions of the two staphylococcal antibiotics had an identical numbers of amino acid residues. Each fraction contained 11 amino acid residues, eight of which were commonly shared and the remaining three of which were different in each of the four fractions. Those shared in common were two glycine, one aspartic acid (or asparagine), one glutamic acid (or glutamine), one alanine, one arginine, one lysine and one serine. In addition, the 29297 zinc-precipitable fraction contained one threonine, one valine and one

TABLE XXXIII

EFFECT OF NITROUS ACID OXIDATION ON THE TITRE OF HIGHLY PURIFIED ANTIBIOTICS

	antibiotic acti	vity (units/ml)
material	untreated	treated
29297 zinc-precipitable	4.8	8.0
29297 zinc-soluble	7.0	12.0
36534 zinc-precipitable	1.9	2.7
36534 zinc-soluble	5.0	8.0
cysteine and tyrosine mixture (control 1)	0	1.6
water (control 2)	0	0.7

TABLE XXXIV

AMINO ACID COMPOSITION OF STAPHYLOCOCCAL ANTIBIOTICS

	minimal number of residues				
	<u>2</u> 9297		<u>36534</u>		
	zinc-	zinc-	zinc-	zinc-	
amino acid	precipitable	soluble	precipitable	soluble	
Glycine	2	2	3	2	
Aspartic acid	1	2	1	2	
Glutamic acid	1	2	1	1	
Alanine	1	1	1	1	
Arginine	1	1	1	1	
Lysine	1	1	1	1	
Serine	1	1	1	1	
Threonine	1	0	1	1	
Proline	0	1	1	0	
Valine	1	0	0	0	
Leucine	1	0	0	0	
Histidine	0	0	0	1	
Ammonia	2	4.	2	2	
Total amino acid residues	11	11	11	11	
Minimal molecular weight	1147	1206	1088	1186	

leucine; the 29297 zinc-soluble fraction contained one aspartic acid (or asparagine), one glutamic acid (or glutamine) and one proline; the 36534 zinc-precipitable fraction had one glycine, one threonine and one proline; and the 36534 zinc-soluble fraction possessed one aspartic acid (or asparagine), one threonine and one histidine. Based on the sum of the molecular weight of the amino acid residues, the minimal molecular weight of these antibiotics would be approximately 1200. This figure coincided with the elution pattern of Sephadex G-15.

(6). Analyses of terminal amino acid residues:

Although the experiment on oxidation with nitrous acid had revealed that these peptide antibiotics contained no free α -amino groups, further evidence was sought to support this finding by means of the analysis of terminal amino acid residues. The N-terminal residues in the highly purified antibiotics were determined by Sanger's method (Sanger, 1945, 1949) and the C-terminal by the Dakin-West degradation (Vanderhaeghe and Parmentier, 1960). Detailed procedures are given in Materials and Methods.

(a). N-terminal residues:

It was found that either extracts of the FDNB-treated hydrolysates of the four antibiotic fractions were colorless and showed no yellow spot on paper chromatograms. The only DNP-amino acid found in the acid hydrolysates of the four antibiotic fractions was water soluble ℓ -DNP-lysine. Based on this evidence, it was concluded that these peptides had no free α -amino groups in their molecules.

(b). C-terminal residues:

The material treated with acetic anhydride gave the same number

of ninhydrin-positive spots as the untreated control. Also, there were no apparent differences in the color density of the spots when treated as compared to the untreated material. The acetic anhydride would react with any free C-terminal amino acid and convert it to the corresponding amino alcohol which would not give a positive ninhydrin test. Failure to change the number of ninhydrin-positive spots meant that there were no free C-terminal groups present in the antibiotic fractions.

(7). Oxidative deamination of antibiotics by L- and D-amino acid oxidases:

Information on L- and D-amino acid residues and their ratio to one another in the antibiotic peptides was provided by oxidative deamination in the presence of L- and D-amino oxidases. The experiments were performed as described in Materials and Methods. Results were expressed as the total 0_2 uptake after incubation for six hr at 37°C which was calculated according to the formula given by Umbreit et al. (1957).

In Table XXXV, oxygen uptake in μ l is expressed as an equivalent to L-leucine and D-alanine. It is evident from the table that L- and D-amino acid oxidases deaminated the antibiotic hydrolysates in all cases, as reflected by 0_2 uptake. From the data presented, it has been determined that some of the amino acids are in the D-form. With respect to 29297 zinc-soluble and 36534 zinc-precipitable fractions, four of the 11 amino acids are D-form. In the case of 29297 zinc-precipitable and 36534 zinc-soluble fractions, six of the 11 amino acids occur as the D-isomer.

OXIDATIVE DEAMINATION OF ACID HYDROLYSATES OF PURIFIED ANTIBIOTICS BY L AND D-AMINO ACID OXIDASES

substrate	O ₂ uptake in presence of L-amino acid oxidase (μ1)	equivalent to L-leucine (mM)	O ₂ uptake in presence of D-amino acid oxidase (μ1)	equivalent to D-alanine (mM)	ratio (L/D)
L-leucine standard	/ 296.38	100.00	-	-	
D-alanine standard	-	-	116.18	300.00	
29297 zinc-soluble	23.04	7.77	16.05	4.60	7/4
29297 zinc- precipitable	16.15	5.44	20.40	5.85	5/6
36534 zinc-soluble	40.71	13.73	54.67	15.68	5/6
36534 zinc- precipitable	28.50	9.61	20.16	5.78	7/4

st the ratio of equivalents to L-leucine and D-alanine in the same antibiotic preparation

707

IV. STRUCTURAL STUDIES

Highly purified 29297 zinc-precipitable fraction was used for structural studies. The material was first subjected to partial acid hydrolysis which was conducted as described in Materials and Methods. After completion of hydrolysis, peptide fragments were conjugated with Sanger's FDNB reagent. Nine DNP-peptides were thus isolated and analyzed. The results (Table XXXVI) showed that four contained lysine, two contained valine and the rest leucine, serine or aspartic acid (or asparagine) as the N-terminal amino acid residues. The amino acid content of each peptide fragment is also given in the Table. From these results, a tentative sequence for each peptide fragment was deduced and these are compiled in Table XXXVII.

Since this antibiotic fraction contained two glycine residues per molecule of the antibiotic, and since glycine would only show one ninhydrin-positive spot on paper chromatograms, two alternative sequences are possible for fragments 4 - 8. All the peptide sequence overlapped one another, the overall arrangement of these fragments giving

Lys-Ala-Asp-Glu-Ser-Leu-Thr-Gly-Val-Gly-Arg-Lys-Ala

or

Lys-Ala-Asp-Glu-Ser-Leu-Thr-Val-Gly-Gly-Arg-Lys-Ala

TABLE XXXVI

AMINO ACID CONTENT OF PEPTIDE FRAGMENTS ISOLATED FROM PARTIAL ACID HYDROLYSATES OF THE 29297 ZINC-PRECIPITABLE FRACTION

peptide <u>frag</u> ment	DNP-amino acid	fine and a di
TIASINGIL	DMI -amilio acid	free amino acid content
1	di-DNP-Lysine	Ala, Asp, Glu
2	di-DNP-Lysine	Ala, Asp, Glu, Ser
3	di-DNP-Lysine	Ala, Asp, Glu, Ser, Leu, Thr
4	di-DNP-Lysine	Ala, Asp, Glu, Ser, Leu, Thr, Gly, Val
5	DNP-Valine	Gly
6	DNP-Valine	Gly, Arg, Lys, Ala
7	DNP-Leucine	Thr, Val, Gly, Arg, Lys, Ala
8	DNP-Serine	Leu, Thr, Val, Gly, Arg
9	DNP-Aspartic acid	Glu, Ser

TABLE XXXVII

TENTATIVE PEPTIDE SEQUENCES OF FRAGMENTS ISOLATED FROM PARTIAL ACID HYDROLYSATES OF ANTIBIOTIC 29297 ZINC-PRECIPITABLE FRACTION

peptide fragment	tentative peptide sequence
1	Lys-Ala-Asp-Glu
2	Lys-Ala-Asp-Glu-Ser
3	Lys-Ala-Asp-Glu-Ser-Leu-Thr
4	Lys-Ala-Asp-Glu-Ser-Leu-Thr- <u>Gly-Val-Gly</u>
	Lys-Ala-Asp-Glu-Ser-Leu-Thr- <u>Val-Gly-Gly</u>
5	<u>Val-Gly</u> or <u>Val-Gly-Gly</u>
6	<u>Val-Gly</u> -Arg-Lys-Ala or <u>Val-Gly-Gly</u> -Arg-Lys-Ala
7	Leu-Thr- <u>Gly-Val-Gly</u> -Arg-Lys-Ala or Leu-Thr- <u>Val-Gly-Gly</u> -Arg-Lys-Ala
8	Ser -Leu -Thr - <u>Gly -Val -Gly</u> -Arg or Ser -Leu -Thr - <u>Val -Gly -</u> Gl <u>y</u> -Arg
9	Asp-Glu-Ser
overall	Lys-Ala-Asp-Glu-Ser-Leu-Thr- <u>Gly-Val-Gly</u> -Arg-Lys-Ala
	Lys-Ala-Asp-Glu-Ser-Leu-Thr- <u>Val-Gly-Gly</u> -Arg-Lys-Ala

Because there were 11 amino acid residues, this sequence should be

Cyclo-Lys-Ala-Asp-Glu-Ser-Leu-Thr-Gly-Val-Gly-Arg

or

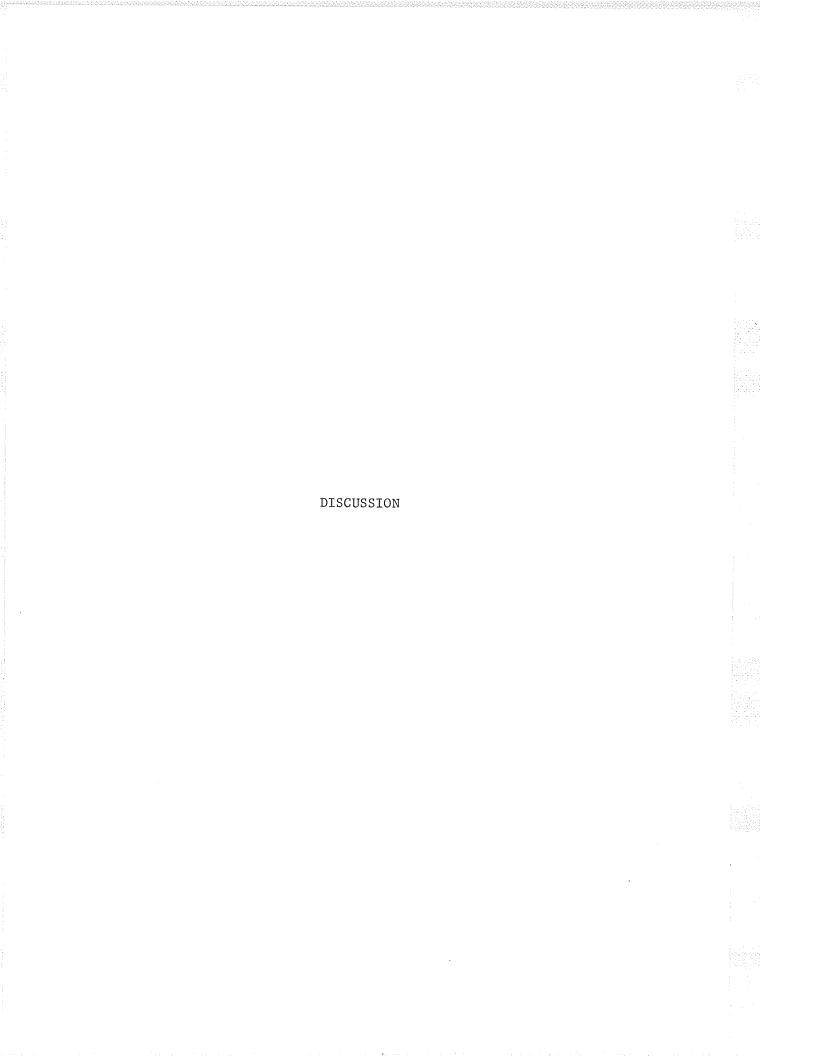
Cyclo-Lys-Ala-Asp-Glu-Ser-Leu-Thr-Val-Gly-Gly-Arg.

The aspartic and glutamic acid residues might be present as asparagine and glutamine respectively.

A tentative structural formula for 29297 zinc-precipitable fraction is given in Fig. $8.\,$

FIGURE 8

TENTATIVE STRUCTURE OF 29297 ZINC-PRECIPITABLE FRACTION



DISCUSSION

A method has been developed which permits production of staphylococcal antibiotics in a liquid medium. Quantities of antibiotics produced in the supplemented Dolman-Wilson medium match those produced on solid media. Adequate oxygen tension and the presence of Fe⁺⁺⁺ and Mn⁺⁺ ions were both necessary for antibiotic production. Other investigators (Dujardin-Beaumetz, 1932; Duliscouet, 1939, 1945; Jennings and Sharp, 1949) claimed that their strains of Staphylococcus would produce antibiotics only upon solid media. It is difficult to compare their results with those presented here in view of the facts that different strains and different media were used by these investigators. Furthermore, the genus Staphylococcus appears to produce a large family of closely related antibacterial agents, many of which might conceivably require different conditions for production. Evidence has been put forward in this investigation that several fractions with antibacterial activity are produced by Staphylococcus strains 29297 and 36534.

Optimal antibiotic production by both strains in the supplemented liquid medium required an incubation temperature of 32°C. A temperature of 37°C, however, was required for maximal growth. The appearance of antibiotic coincided with commencement of the stationary phase of growth with respect to strain 36534, but Fig. 2 indicates that for strain 29297, maximum titres were reached at the end of the logarithmic phase of growth. No data are available which would indicate unequivocally that the antibiotics are truly extracellular products, but the results of Fig. 3 are not incon-

sistent with this. In view of the amino acid composition of the antibiotics, it is unlikely that they would be a component of the cell wall of the producing strain.

Initial observations of Hsu and Wiseman (1967) indicated that antibiotics of both strains 29297 and 36534 remained in the supernatant fluid after precipitation of macromolecular impurities by HCl. This has been confirmed and extended to include precipitation of additional impurities with Ba(OH)₂. The resulting precipitate was inert, the activity being found entirely in the supernatant solution. The presence of Ba(OH)₂ created optimal conditions for zinc treatment. It is obvious that antibiotic activity precipitated directly from crude material by zinc would be heavily contaminated with proteins, polysaccharides and possibly nucleic acids. Thus it was felt that use of a heavy metal salt in purification must be preceded by removal of such substances by acid or other treatment.

The addition of $ZnCl_2$ to $Ba(OH)_2$ -treated antibiotics separated the material into two active fractions. Since a part of the activity is precipitable by zinc ions, it seems feasible to suggest that Zn^{++} combines with one of the components of the mixture. The zinc-antibiotic complex is soluble at pH 2 or lower, which indicates that dissociation of the complex has probably taken place. Since it is impossible to test the antibiotic activity of this solution at such low pH, it is necessary to neutralize with NaOH. It was observed that a precipitate was formed after the pH of the solution was brought to 7. It is very likely that this precipitate is $Zn(OH)_2$ since Na^+ ions are higher in the electromotive series than Zn^{++} . Consequently, Na^+ would replace Zn^{++} in the zinc-antibiotic complex. The

overall reaction which taken place is thought to be represented by the following equations:

(1)
$$Zn^{++} + AB^{--} \xrightarrow{pH 9} ZnAB \downarrow \text{ (precipitation)}$$

(2) ZnAB
$$\xrightarrow{\text{pH 2}}$$
 Zn $^{++}$ + AB $^{--}$ (dissociation)

(3)
$$Zn^{++} + AB^{--} + 2NaOH \xrightarrow{pH 7} Zn(OH)_{2} + Na_2AB$$
 (replacement)
 $AB = antibiotic$

With regard to the supernatant fraction of the zinc-treated antibiotics, soluble Ba $^{++}$ and Zn $^{++}$ ions were removed by the application of H₂S gas. Hydrogen sulphide will precipitate these ions as the insoluble sulphides. The solution at this point can be neutralized and concentrated without loss of activity.

Anker et al. (1948) reported that bacitracin could be precipitated with inactivation by heavy metal ions low in the electromotive series. However, they found that heavy metals high in the series precipitated the antibiotic without loss of activity. With regard to staphylococcal antibiotics 29297 and 36534, the opposite situation applies. As already mentioned Ca^{++} and Mn^{++} , in contrast with Zn^{++} ions afford low recovery of activity.

Precipitation of 29297 and 36534 by Zn⁺⁺ separates the antibiotics into a zinc-precipitable and a zinc-soluble fraction. As already stated, the addition of extra Zn⁺⁺ to supernatant permits no further recovery from that source. It is not, therefore, correct to state that the precipitation caused by Zn⁺⁺ ions is incomplete. Rather it suggests that

 ${\rm Zn}^{++}$ has precipitated one of two antibiotics present in crude culture.

In connection with the further purification of these antibiotic fractions, Sephadex G-15 was used to remove impurities from both zinc-precipitable and zinc-soluble components of 29297 and 36534. However, as Table XXIII shows, this treatment increased the specific activity of the two components of 29297 four to seven-fold. With regard to 36534, the increase was much less, but Sephadex G-15 was nevertheless of value in desalting the solutions. Passage of the components of 36534 through Dowex 50-X2 also increased specific activity two to three-fold with good recoveries. Its use with 29297 caused little or no increase in specific activity withlow recovery. Consequently it was felt that Dowex was of no value in the purification of 29297.

The evidence presented in this study strongly indicates that the zinc-precipitable and zinc-soluble antibiotic fractions of strains 29297 and 36534 are low molecular weight peptides. The positive periodic acid oxidation test suggests that these fractions do contain free hydroxyl groups. These are characteristic of the amino acids threonine and serine, either of which or both are found in all fractions. Aromatic amino acids are not present in any fraction as indicated by amino acid analysis, negative Lowry and xanthoproteic tests. However, a small shoulder was observed in the ultraviolet light absorption spectra of all fractions. This would indicate that the antibiotic molecules probably possess a ring structure. The fractions did not give a color with ninhydrin reagent and little or no reaction was observed with nitrous acid. These responses indicate that the antibiotics contain no free α -amino groups as do normal peptides or proteins.

This strongly suggests that the antibiotics are cyclic like numerous other microbial peptide antibiotics, or that the α -amino groups are masked by acidic groups as one finds in the polymyxins and gramicidins A, B, and C. Furthermore, no C- or N-terminal amino groups were detected in any of the antibiotic fractions. Masking of these groups by fatty acids seemed unlikely in view of the fact that none were detected in the hydrolysates of the antibiotics. By contrast, N-terminal amino acid residues are not found in polymyxins. It has been shown that their N-terminal groups are masked by linkage with 6-methyl-octan-l-oic acid (MOA) or isooctanoic acid (IOA) as mentioned in the Review of the Literature. The N- and C-terminal groups of gramicidins A, B, and C are conjugated with formic acid and ethanolamine respectively.

In summary, evidence which indicates cyclization of the four antibiotic fractions is listed as follows:

- (1) ninhydrin test and nitrous acid oxidation negative
- (2) no detectable C- and N-terminal amino groups
- (3) small shoulder at 260 280 nm in UV spectra
- (4) no oily (fatty acid) substances detected in acid hydrolysates

 All fractions are very soluble in water but insoluble in the
 usual organic solvents. According to the amino acid analyses, none of the

None of the fractions proved to be particularly mobile in an electric field. The isoelectric point (pI) depends upon the pK_a values of

amino acids found in the fractions contain hydrophobic side chains.

the ionic groups of the side chains. The average of the total pK values should give an approximate value of the pI. Ionic groups found in the

antibiotic fractions are β -carboxyl of aspartic acid (pK_a = 3.0 - 4.7), Y-carboxyl of glutamic acid (pK_a = 4.4), ϵ -amino of lysine (pK_a = 9.4 - 10.6), guanidinium of arginine (pK_a = 11.6 - 12.6) and imidazolium of histidine (pK_a = 5.6 - 7.0). The numbers of acidic and basic groups in the antibiotic molecules are roughly the same. Therefore, the pI of the antibiotics should approximate 7.

The structure of the 29297 zinc-precipitable fraction has been tentatively determined as shown below:

$$\begin{array}{c} \text{Lys} \longrightarrow \text{Ala} \longrightarrow \text{Asp} \longrightarrow \text{Glu} \longrightarrow \text{Ser} \longrightarrow \text{Leu} \\ \\ & \stackrel{\frown}{\text{Arg}} \longleftarrow \text{Gly} \longleftarrow \text{Val} \longleftarrow \text{Gly} \longleftarrow \text{Thr} \longleftarrow \end{array}$$

However, the region $-Gly \longrightarrow Val \longrightarrow Gly$ is in dispute. Reference to Table XXXVII of the Results indicates that this region of peptide fragments 4 - 8 may possibly be $-Val \longrightarrow Gly \longrightarrow Gly$. The problem here is reflected in the fact that two glycine have been detected in each mole of the antibiotic. Also, no peptide fragments have been isolated which contain only glycine or valine. Two peptide fragments isolated contained the repeating units $-Lys \longrightarrow Ala$. The same repeating unit is found in fragments 1 - 4. This provides further strong evidence of cyclization.

Although the structure of the other three antibiotic peptides was not determined, it is very likely, in view of their chemical similarities, that they are also cyclic in structure. Eight amino acids are shared in common by all fractions, the exceptions being valine, leucine and serine. If these amino acids are absent, they may be replaced by others such as

aspartic and glutamic acids, proline or histidine. In the polymyxins, tyrocidines and gramicidins, a number of amino acids likewise are shared in common by members of the groups, and certain individual amino acids may or may not be present and therefore substituted by others.

The staphylococcal antibiotics show some of the specific features of peptide antibiotics as compiled by Bodanszky and Perlman (1969). These are (1) the occurrence of D-amino acids, (2) the existence of proline and imino acid, (3) the formation of small cyclic areas within the macrocyclic structure of the peptide molecule, and (4) stability to heat and relative insensitivity to the action of proteolytic enzymes (see Hsu and Wiseman, 1967). However, they felt that antibiotics which contain arginine or arginine and histidine are relatively uncommon.

The unique features of the staphylococcal antibiotics investigated in this study are that they do not contain sulphur, aromatic or unusual amino acids and they have a high ratio of D- to L-amino acids. Non-amino acid moieties are also not found in their molecules.

The relationship between other staphylococcal antibiotics and the antibacterial peptides investigated in this study is unclear. However, it is evident that 29297 and 36534 peptides are not enzymes in contrast with the lysostaphin group of Schindler and Schuhardt (1964). None of the 29297 and 36534 peptides causes lysis of sensitive strains at any concentration and they cannot therefore be identical with lysostaphins or with the staphylolytic agent described by Suginaka et al. (1967). Since so little is known of the antibacterial substances isolated from staphylococci by Myers (1946), Jennings and Sharp (1947), Gardner (1949) and Loeb et al. (1950), it is

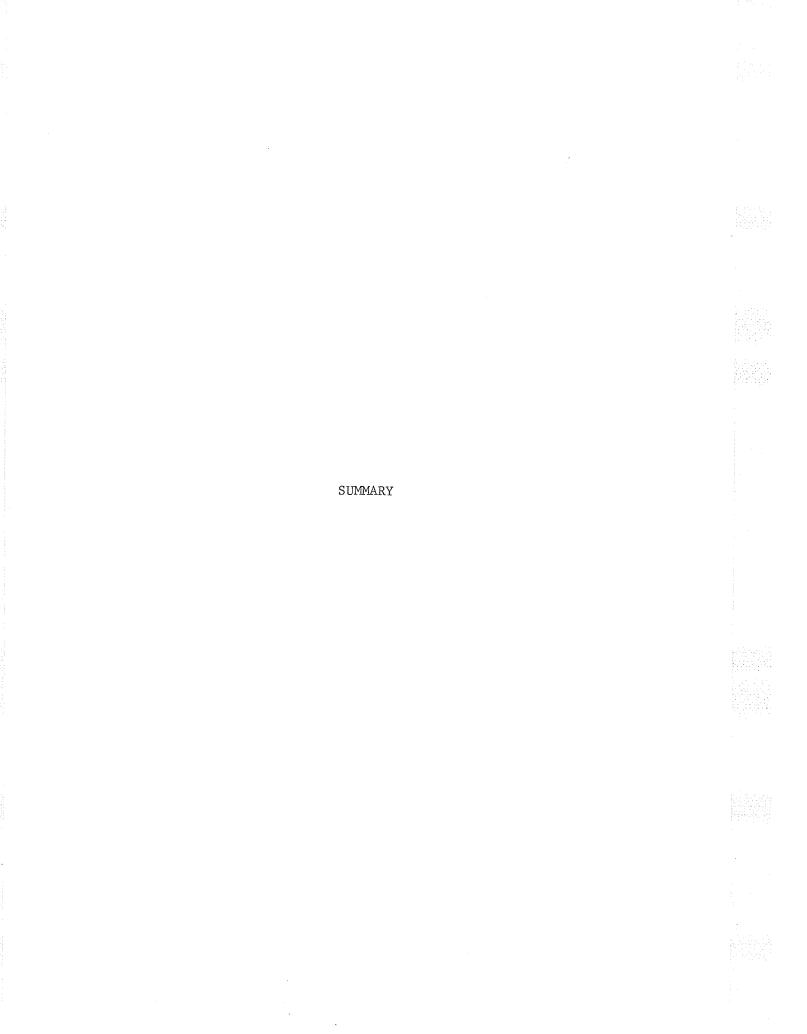
impossible to compare the preparations with those described by these investigators. It is likely, however, that the agents described are peptides. Fregnan and Smith (1962), Barrow (1962, 1963) and Lachowicz (1965) described staphylcoccal antibacterial agents which probably were peptides, as well, but again, too little is known of these substances to make a proper comparison of them with the 29297 and 36534 peptides.

Another group of antibacterial agents of interest is that described by Fredericq (1946) which he called "staphylococcin". Fredericq thought that such substances should be classified as bacteriocins. Hamon and Peron (1963) studied 20 staphylococcins and found that <u>Listeria</u>, <u>Bacillus</u> and <u>Corynebacterium</u> were often sensitive to the agents. Obviously the staphylococcins described are not true bacteriocins as defined by Jacob <u>et al</u>. (1953), nor are the 29297 and 36534 peptides properly called bacteriocins, sincetheir inhibitory spectrum extends through the range of Gram-positive species.

Another antibiotic isolated from Gram-positive cocci worthy of mention is micrococcin, from Micrococcus spp. It has been investigated by Su (1948a,b) and by Heatley and Doery (1951). They have shown that it is a polythiazole which has arisen from cyclization of polycysteine. It is a close relative of micrococcin P isolated from Bacillus pumilus by Fuller (1955). Peptides 29297 and 36534 are unrelated to micrococcin in that they contain no cysteine, or sulphur for that matter. Nisins of streptococci (Mattick and Hirsch, 1944) also contain sulphur amino acids in contrast with the antibiotics described in this study.

Nothing is known of the mode of action of the antibiotics 29297

and 36534. It is known that they are bactericidal (see Part III of Results), and that they are not lytic. Earlier observations by Hsu and Wiseman (1967) indicate that Gram-positive bacteria are sensitive to the agents. Gramnegative species were generally resistant, the only exception being Brucella abortus. The major differences between Gram-positive and Gram-negative bacteria reside in the cell wall structure. It thus seems reasonable to propose that peptides 29297 and 36534 act by blocking cell wall synthesis. Speculation beyond this is not possible at the present time.



SUMMARY

- (1) Antibiotics from <u>Staphylococcus</u> <u>epidermidis</u> 29297 and 36534 were produced in supplemented Dolman-Wilson medium in the absence of agar. Aeration (as reflected by agitation) and temperature were important in the production of maximum amounts of antibiotics. Length of incubation was also a factor.
- (2) Antibiotic assays were affected by the nature of the suspending broth and length of incubation.
- (3) Initial purification of crude antibiotics involved treatment with HCl to pH 2.0. The supernatant fluid, which contained the activity, was adjusted to pH 9.0 with $Ba(OH)_2$. The Ba^{++} ions precipitated further impurities and brought the pH to optimal conditions for treatment with $ZnCl_2$.
- (4) Precipitation of the active principles with $\rm Zn^{++}$ ions separated the 29297 and 36534 antibiotics into two fractions designated zinc-precipitable and zinc-soluble.

The zinc-precipitable and zinc-soluble fractions of 36534 were further purified on columns of Dowex 50-X2 and Sephadex G-15. The two fractions of 29297 were subjected to Sephadex G-15 gel filtration only, since low recoveries were obtained with Dowex 50-X2.

(5) All fractions of antibiotics were twice crystallized from aqueous solutions. Traces of ninhydrin-positive or Lowry-positive material in the crystallized fractions were removed by precipitation with methanol at 4°C . The final products decomposéd without melting when heated to 278

- 280°C to leave a trace of non-toxic white ash.
- (6) Recrystallized and twice methanol-precipitated fractions of the antibiotics did not absorb in the visible spectrum (350 800 nm) and showed only a small shoulder at 260 280 nm in the UV region. The antibiotics were immobile in an electric field.
- (7) Qualitative tests showed that the antibiotics were free of carbohydrates, lipids, proteins and nucleic acids. They were sensitive to pronase and could be autoclaved without loss of activity. No N- or C-terminal amino acid residues were detected. The fractions were ninhydrinnegative and did not react with nitrous acid.
- (8) Amino acid analyses of the highly purified fractions showed that they contained 11 amino acids, eight of which they shared in common. The three remaining residues varied from fraction to fraction. The minimal molecular weights were approximately 1200 in each case.
- (9) The evidence suggests that the 29297 and 36534 zinc-soluble and zinc-precipitable fractions are cyclic peptides, about half of their amino acids occurring as the D-isomers.
- (10) Sequence studies of the 29297 zinc-precipitable fraction showed that it probably had the structure:

$$\begin{array}{c} \text{Lys} \longrightarrow \text{Ala} \longrightarrow \text{Asp} \longrightarrow \text{Glu} \longrightarrow \text{Ser} \longrightarrow \text{Leu} \\ \\ \stackrel{} \triangle \text{Arg} \longleftarrow \text{Gly} \longleftarrow \text{Val} \longleftarrow \text{Gly} \longleftarrow \text{Thr} \longleftarrow \end{array}$$

The -Gly \longrightarrow Val \longrightarrow Gly - sequence is in dispute and could be -Val \longrightarrow Gly -.

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APPENDICES

APPENDIX I

MORPHOLOGICAL AND PHYSIOLOGICAL CHARACTERISTICS OF THE ANTIBIOTIC-PRODUCING STAPHYLOCOCCAL STRAINS 29297 AND 36534

characteristics		
colonial characters	circular, smooth, glistening, with entire margin, and of butyrous consistency	
color of colony	yellowish white	
oxygen requirement	aerobic, facultatively anaerobic	
growth in 10% NaCl	positive	
H ₂ S production	negative	
coagulase-activity*	negative	
fermentation		
inulin	N**	
raffinose	N	
salicin	N	
glucose	Ag	
maltose	Ag	
mannitol	Ag	
sucrose	Ag	

^{*} tube and slide test

^{**} N = no fermentation

Ag = acid with small quantity gas after 24 hr incubation at 37° C

APPENDIX II

CONSTITUENTS OF SUPPLEMENTED DOLMAN-WILSON LIQUID MEDIUM USED FOR ANTIBIOTIC PRODUCTION

PART I:	
Difco proteose peptone	20.0 gm
Distilled water	900 m1
Part I is adjusted to pH 7.8 and autoclaved at 15 lb pressur	e for 25 min.
PART II:	
NaCl	5.0 gm
Ammonium lactate (80% syrup)	8.0 ml
к ₂ нро ₄	1.0 gm
NaH ₂ PO ₄ ·H ₂ O	1.0 gm
MgSO ₄ ·7H ₂ O	0.2 gm
CaCl ₂	0.1 gm
Ferrous ammonium sulphate (1% solution in 0.1N HC1)	1.0 m1
MnCl ₂ ·4H ₂ O	0.2 gm
Sodium citrate	0.2 gm
Distilled water	100 ml
Part II is sterilized by passage through a Millipore filter.	pH is
adjusted to 5.5.	
After Part I is cooled to room temperature, Part II is added	to Part I

and mixed well. Final pH is 7.2.