plasmodia in repeated tests. This suggests, as could be expected, that inherent factors other than mating-type may affect mating and plasmodium formation. While the results are consistent with a two-type mating system, they are not consistent with any of the multifactorial mating-type systems well known in other micro-organisms.

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[1] Skupienski, M. F. X., *C.R. Acad. Sci., Paris*, **167**, 81 (1918); **182**, 150 (1926).

MICROBIOLOGY

Mode of Action of Hair-loosening Organisms

CONSIDERABLE research has been devoted to the development of enzymes for replacing the normal putrefactive techniques for the loosening of wool and hair fibres on animal pelts. Detailed knowledge of the tissues responsible for anchoring the fibre in the skin is therefore essential.

Examination of fibres obtained from skins which have been exposed to bacterial attack shows that the follicle bulb has been completely digested, leaving a tapered root of exposed cortical cells. It is considered that digestion of the root bulb permits the fibre to be readily withdrawn from the skin and that the organisms responsible penetrate down the follicle to attack the soft keratin.

In recent work, however, we have related the appearance of the follicle to the force necessary to withdraw fibres from pelts and have observed that, when the depilation load has fallen to the level at which the fleece is normally pulled from the skin, the whole follicle is removed intact with the fibre. At a later stage of putrefaction, although the depilation load is virtually unchanged, the follicle is rapidly digested to give the typical tapered appearance.

Fig. 1 shows a bundle of intact follicles on fibres pulled as soon as the depilation load had fallen to a level suitable for pulling.

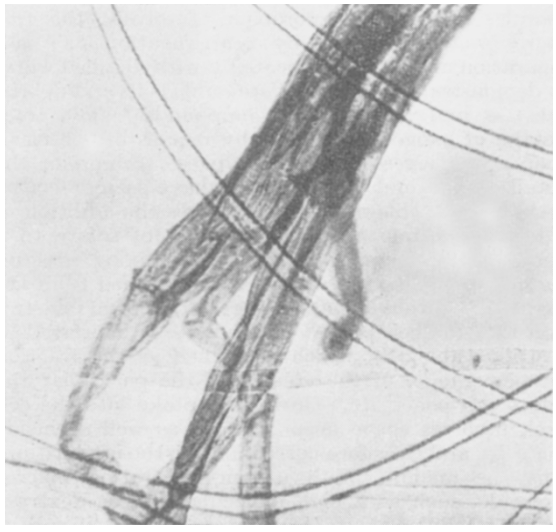

Fig. 1

It seems, therefore, that the bacteria penetrate from the flesh side of the skin to proliferate around the follicles, and that the most significant feature of fibre loosening is the digestion of material in these regions. Whereas efforts have, in the past, been concentrated on the degradation of the soft keratin, the production of an enzyme designed to digest the dermal material immediately adjacent to the follicle would seem likely to result in a greater yield of undamaged fibre.

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Taxonomy of Yeasts

ON different occasions, when studying the classification of yeasts, I have been able to appreciate how little consistency there is in the taxonomic characters in use. Recently, I have met with fresh anomalies which, in my opinion, make a complete revision of the present system of classification of yeasts unavoidable.

(*a*) From the aqueous solution separated from oil during the manufacture of olive oil, in Spain named 'alpechín', a yeast culture was isolated, *Ac* 11, which is a characteristic *Zygosaccharomyces*, able to produce vigorous alcoholic fermentation and which ferments glucose, galactose, saccharose, melibiose and raffinose completely, and does not ferment or assimilate maltose or lactose. In accordance with the classification of Lodder and Kreger-van Rij[1], this yeast could be considered as a *Sacch. microellipsodes*; however, as to the organism described by Lodder and Kreger-van Rij as a *Sacch. microellipsodes*, is it truly a *Saccharomyces*? The Dutch authors admit that they have not been able to observe spores in the strain under study, and neither could Stelling-Dekker in 1931; moreover, Kudriavtzev[2] categorically denies that the organism is a *Saccharomyces*, not because of its inability to sporulate, but because of its morphology, its weak fermentation of the carbohydrates, etc.; and states that, in his opinion, its place in the classification system is not yet sufficiently clear. Therefore, it is possible that our organism *Ac* 11 corresponds to a *Saccharomyces* species which has not yet been described, for which I propose the name of *Sacch. malacitensis* (from Málaga, the province from which I received the sample of 'alpechín').

Moreover, I had earlier obtained a hybrid[3] crossing *Sacch. oxidans* (ferments glucose, saccharose and raffinose 1/3) and *Sacch. oleaceus* (ferments glucose, galactose, melibiose and raffinose 1/3), to which I gave the symbol *H* 7–4–1; this has a fermentation spectrum identical with that of *Sacch. malacitensis*. Though there are notable differences between the morphology of *H* 7–4–1 and *Sacch. malacitensis*, it would be reasonable to suppose that, were the origin of *H* 7–4–1 unknown, it would be classified as a *Sacch. malacitensis* strain. However, in biology it is inconsistent to consider as a new species an organism obtained by hybridation with other diverse organisms, since a species includes all the potentially interbreeding individuals, the descendants of which are also potentially interbreeding. Therefore the doubt arises whether the present separation of species in the genus *Saccharomyces* is admissible, based as it is fundamentally on the simple difference of fermentation of only one carbohydrate.