chloroplasts, have shown that this D-penicillamine copper chelate (PA-Cu) has an action similar to the Cu-Zn and Mn superoxide dismutase enzymes in a range of reactions involving superoxide[10].

Flax cotyledon leaves were floated on solutions of paraquat and PA-Cu and the herbicidal effect was initially followed by assessing the breakdown of chlorophyll, the most obvious phytotoxic symptom. The table shows that after 72 h illumination, the breakdown of chlorophyll in paraquat treated leaves was significantly retarded by the additional presence of PA-Cu.

Previous work has shown that disruption of the tonoplast and plasmalemma were the earliest structural changes observed in leaf cells following paraquat treatment[11]. This is brought about by various reactions generally known as lipid peroxidation which are initiated by free radicals. It is unlikely that superoxide possesses the necessary reactivity to abstract protons from unsaturated fatty acids in the membrane to instigate this deteriorative chain reaction, it is more probable that initiation is by a more reactive species derived from superoxide, such as singlet oxygen[12] or .OH radicals[13]. The process of lipid peroxidation can be monitored by the release of ethane from the damaged tissue[14–16]. The figure shows that the release of this simple hydrocarbon from flax cotyledon leaves was considerably promoted by paraquat treatment, however this was minimised when PA-Cu was also present. Although PA-Cu has a high superoxide dismutating capability ($K = 10^9\ M^{-1}\ S^{-1}$)[17], it failed to completely prevent paraquat induced damage.

Chlorophyll levels in treated flax cotyledons

Treatment	Chlorophyll content (µg/g fresh weight)
Control	540
Paraquat (10^{-6} M)	300
Paraquat + PA-Cu	430

20 cotyledon leaves from 7-day-old flax seedlings were used for each treatment and were incubated in 70-ml screw top flasks fitted with serum rubber material to allow sampling of the flask atmosphere. The addition of paraquat was delayed for 24 h to allow PA-Cu to penetrate the leaf tissue. A concentration of 50 nmoles of PA-Cu in 3 ml was equivalent to 50 superoxide dismutase units, as determined by the ability to inhibit nitrite formation from hydroxylamine[10]. Chlorophyll was determined upon conclusion of the experiment (72 h illumination with 5500 lux), according to the method of Arnon[19].

This can be explained by the fact that only a very small proportion of the superoxide produced need escape dismutation for the damage process to assume a more complex nature which is then more difficult to control.

These experiments have provided good evidence for the actual generation of superoxide in vivo in paraquat treated leaves. They also demonstrate that PA-Cu, which is already in pharmaceutical use in the nonchelated form[18], might be efficacious in the reduction of paraquat poisoning in humans.

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Genetic changes of pupa weight in *Tribolium castaneum* under domestication[1]

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Summary. The evolution of the genetic and phenotypic parameters of pupa weight in 6 wild populations of *Tribolium castaneum* under domestication was studied. A gradual increase of the phenotypic and additive genetic variances of the populations was detected accompanied by small or non-significant changes of the mean. These results are interpreted as short-term consequences of the relaxation of centripetal (stabilizing) selection forces under laboratory conditions.

Natural selection is considered to be the main process responsible for the adaptation of populations to their particular environments. The action of natural selection is directly exerted on fitness and indirectly on any other trait genetically correlated with it. A consequence of this indirect selective action is the temporal change of the genetic and phenotypic distributions of quantitative traits[2]. It is of interest to study these changes in populations subject to a given environmental stimulus over a number of generations. These changes can be more easily observed when the

stimulus is a drastic one; e.g. when a population captured in nature is subsequently maintained under laboratory conditions. In the present work the evolution of the genetic and phenotypic parameters of pupa weight of 6 natural populations of *Tribolium castaneum* is studied over the 1st 4 generations of life in the laboratory. Comparisons are made between these wild populations and other populations kept in the laboratory for several years.

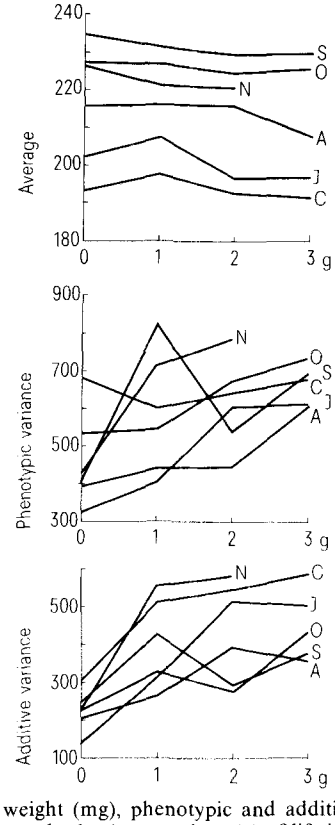
Material and methods. 6 wild populations of *T. castaneum* – Andújar (A), Carpio (C), Jerez (J), Navalmoral (N), Osuna (O) and Sevilla (S) – were collected from granaries in Southern Spain. Initial sample sizes were 240 individuals. The Consejo[3] and Purdue[4] populations have been maintained in the laboratory for more than 10 years. Generation 0 refers either to the offspring of the wild females or to the contemporary generation in the laboratory populations.

The trait considered is individual 21-day pupa weight. The culture medium consists of 95% whole wheat flour and 5% dried brewer's yeast. All populations are kept at 70% relative humidity and 33 °C.

Each wild population is maintained in the laboratory in 3 different ways: 1. By single-pair random matings in separate vials with 100 males and 100 females per generation. Each mating is represented in the next generation by 1 male and 1 female offspring. Pupa weight is scored on 3 males and 3 females per family in each population in each of the 1st 4 generations of life in the laboratory. 2. In population cages without overlapping generations. 100 males and 100 virgin females are sampled from each cage every generation and placed in a new cage to be parents of the next generation. 3. In population cages with overlapping of generations. These cages are kept during the same period of time as populations 1 and 2, with culture medium added at regular intervals. The precise number of generations elapsed during this period cannot be known for populations 3. In the populations maintained in cages, pupa weight was only scored at the end of the period of stay in the laboratory on 300 individuals of each sex per population.

Results. Mean pupa weight, phenotypic variance (V_P) and heritability (h^2), estimated by full-sib correlation analysis, are shown in the table, both for the wild populations at generation 0 and for the contemporary laboratory populations. The mean pupa weights of the laboratory populations are significantly higher that those of the wild populations which in turn are phenotypically and genetically more variable. The evolution of the mean, phenotypic, and additive genetic variances (this latter estimated as $V_{Ai} = h_i^2 V_{Pi}$ in the ith generation) over the 1st 4 generations of life in the laboratory is shown in the figure for the populations 1. The population means did not significantly change with time and the phenotypic and additive variances increased gradually. Cage populations 2 behaved in a similar manner (table), the average difference between the means in generations 0 and 3 being 0.6 ± 2 mg. By generation 3 the phenotypic variance of the populations 2 showed a 72% increase, from an initial value of 463 to 797. On the other hand, the mean of the cage populations 3 (table) showed a significant average increase of 9 ± 2 mg from generation 0 to the end of the experiment. This change was also accompanied by an average 44% increase in the phenotypic variance, from an initial value of 463 to 667.

Discussion. Wild populations of *T. castaneum* appear to be genetically and phenotypically more variable for pupa weight than laboratory populations. Similar results have been reported for other quantitative traits in *T. castaneum*[5] and *Drosophila melanogaster*[6]. Genetic variation for enzyme polymorphisms has been found to be positively correlated with environmental diversity in *D. pseudoobscura*[7]. The smaller heritability of our laboratory populations



Average pupa weight (mg), phenotypic and additive variances of populations 1 over the 1st 4 generations (g) of life in the laboratory (sexes pooled, 600 individuals scored per locality and generation).

Mean ($\bar{x}$, mg), phenotypic variance (V_P) and heritability (h^2) of pupa weight for the base populations (generation 0) and, at generation 3 for the populations maintained in cages with (3) and without (2) overlapping of generations

Locality	Generation 0			Generation 3 Populations 2		Populations 3	
	$\bar{x}$	V_P	h^2 (%)	$\bar{x}$	V_P	$\bar{x}$	V_P
Andújar	216	396	52	224	746	233	601
Carpio	193	688	45	193	808	193	974
Jerez	202	327	44	204	681	213	545
Navalmoral	226	427	56	213	548	235	528
Osuna	227	538	42	228	1111	237	622
Sevilla	235	404	61	241	886	241	733
Consejo	273	865	38				
Purdue	253	583	20				

Sexes pooled. 600 individuals scored per locality, generation, and population. $0.7 \leq SE(\bar{x}) \leq 1.4$. $SE(h^2) = 9$ for all localities.

may also be interpreted as an adaptation to the highly specific and homogeneous laboratory habitat.

Natural selection forces can be assumed to be smallest in populations 1, at least with respect to fertility and mating success, and largest in populations 3, where opportunity is given for natural selection to act on all fitness components; populations 2 represent an intermediate situation. It has been proposed[8] that pupa weight of natural populations of *T. castaneum* is subject to centripetal (stabilizing) selection, the genes controlling the expression of the trait acting in an essentially additive manner and showing overdominance for fitness. Under this model, a relaxation of natural selection forces in the short term should occur when transferring wild populations to the laboratory. Consequently, an increase of the genetic and phenotypic variances should follow without necessarily implying a change of the mean. This is in agreement with our results. On the other hand, it has also been proposed[9] that fitness may be determined by the trait itself; our observations are also consistent with the consequences of this alternative model. It seems difficult to discriminate experimentally between both models although they are conceptually very different[10,11]. In the long term, the domestication process may result in an increase of the mean pupa weight, as suggested by the estimates found for our laboratory populations. This increase can be interpreted as the consequence of directional selection towards a new optimum which is subsequently maintained by centripetal selection. This process is better observed in our populations 3 where the action of natural selection should be more intense.

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Prostaglandin-like substances in *Propionibacterium acnes*. III. Differential contractile effects on smooth muscle layers of the human utero-tubal junction[1]

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Summary. The biological activity of a lipid fraction extracted from *P. acnes* was tested on isolated smooth muscle strips from the human utero-tubal junction. The bioassay experiments support the concept that prostaglandin-like substances (PLS) occur in *P. acnes*. However, in the bioassay system used, the effect of PLS was different from that of $PGF_{2\alpha}$ and PGI_2 but similar, although not identical, to that of arachidonic acid and PGE_2.

Acne vulgaris is prerequised by the presence of sebum and *Propionibacterium acnes*. The relationship between sebum excretion rate and clinical severity of the disease is now well established[2]. However, the exact mechanism by which androgens enhance sebum excretion rate, and the further development of an inflammatory acne lesion, is still not fully understood. The fatty acids produced by microbial lipolysis of sebaceous triglycerides have been suggested as initiators of a toxic inflammatory reaction[3]. Recent investigations claim that these fatty acids are only mildly inflammatory when injected in physiological concentrations into human skin[4]. With guinea-pig sensitization tests it has been shown that especially the short and middle-chain fatty acids may act as potent allergens[5]. The precise role of *P. acnes* as a trigger factor in the development of the initial inflammatory lesions is yet to be determined. Deleterious bacterial products are probably not only lipase, but might also be other enzymes, antigens or hitherto unidentified metabolites acting as terminal inflammatory mediators.

At the beginning of 1977, prostaglandin-like substances (PLS) of the E-type were isolated from the lipid fraction of *P. acnes*[6]. Recently it has also been demonstrated that these substances stimulate the formation of cyclic AMP in rat ovaries[7]. In addition, bioassay experiments on gerbil colon[8], as well as on human umbilical artery[9], verify that the PLS from *P. acnes* mimic the effects of prostaglandins of the E-type. Likewise, in an in vivo study (hamster cheek pouch) these compounds induced a PGE-like response[10].

Natural prostaglandins such as PGE_2 and $PGF_{2\alpha}$ may be bioassayed by studying their contractile effects on 3 different animal muscle tissues: the rat stomach, the chicken rectum and the rat colon[11]. The 3 muscle layers of the human utero-tubal junction (UTJ) react differently to diverse prostaglandins and may offer an alternative possibility for detection of specific prostaglandin compounds[12].

The aim of this investigation was to elucidate the biological activity of PLS from *P. acnes* by comparing the contractile effects with those of arachidonic acid (AA), PGE_2, $PGF_{2\alpha}$ and PGI_2. The in vitro technique utilized is a modification of a method which was originally developed to elucidate the effect of various biologically active substances on isolated circular and longitudinal smooth muscle at the ampullary-isthmic junction of the human Fallopian tube[13].

Material and methods. The spontaneous contractile activity of small strips from the external (uterine) and the inner (longitudinal) smooth muscle layers of the human UTJ was recorded as described earlier[12]. Tissue specimens were obtained from cycling women undergoing sterilization or hysterectomy. The strips were approx. 4 mm long with a cross sectional area of about 1.0 mm^2. 1 'uterine' and 1 'longitudinal' strip was mounted in each organ chamber, which was filled with 50 ml of Krebs bicarbonate buffer