PIGS IN SPACE: EFFECT OF ZERO GRAVITY AND AD LIBITUM FEEDING ON WEIGHT GAIN IN CAVIA PORCELLUS

Colin B. Purrington
6673 College Avenue, Swarthmore, PA 19081 USA

ABSTRACT:

One ignored benefit of space travel is a potential elimination of obesity, a chronic problem for a growing majority in many parts of the world. In theory, when an individual is in a condition of zero gravity, weight is eliminated. Indeed, in space one could conceivably follow ad libitum feeding and never even gain an gram, and the only side effect would be the need to upgrade one's stretchy pants("exercise pants"). But because many diet schemes start as very good theories only to be found to be rather harmful, we tested our predictions with a long-term experiment in a colony of Guinea pigs (Cavia porcellus) maintained on the International Space Station. Individuals were housed separately and given unlimited amounts of high-calorie food pellets. Fresh fruits and vegetables were not available in space so were not offered. Every 30 days, each Guinea pig was weighed. After 5 years, we found that individuals, on average, weighed nothing. In addition to weighing nothing, no weight appeared to be gained over the duration of the protocol. If space continues to be gravity-free, and we believe that assumption is sound, we believe that sending the overweight — and those at risk for overweight — to space would be a lasting cure.

INTRODUCTION:

The current obesity epidemic started in the early 1960s with the invention and proliferation of elastane and related stretchy fibers, which released wearers from the rigid constraints of clothes and permitted monthly weight gain without the need to buy new outfits. Indeed, exercise today for hundreds of million people involve only the act of wearing stretchy pants in public, presumably because the constrictive pressure forces fat molecules to adopt a more compact tertiary structure (Xavier 1965).

Luckily, at the same time that fabrics became stretchy, the race to the moon between the United States and Russia yielded a useful fact: gravity in outer space is minimal to nonexistent. When gravity is zero, objects cease to have weight. Indeed, early astronauts and cosmonauts had to secure themselves to their ships with seat belts and sticky boots. The potential application to weight loss was noted immediately, but at the time travel to space was prohibitively expensive and thus the issue was not seriously pursued. Now, however, multiple companies are developing cheap extra-orbital travel options for normal consumers, and potential travelers are also creating news ways to pay for products and services that they cannot actually afford. Together, these factors open the possibility that moving to space could cure overweight syndrome quickly and permanently for a large number of humans.

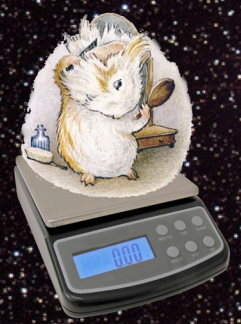
We studied this potential by following weight gain in Guinea pigs, known on Earth as fond of ad libitum feeding. Guinea pigs were long envisioned to be the "Guinea pigs" of space research, too, so they seemed like the obvious choice. Studies on humans are of course desirable, but we feel this current study will be critical in acquiring the attention of granting agencies.

MATERIALS AND METHODS:

One hundred male and one hundred female Guinea pigs (Cavia porcellus) were transported to the International Space Laboratory in 2010. Each pig was housed separately and deprived of exercise wheels and fresh fruits and vegetables for 48 months. Each month, pigs were individually weighed by duct-taping them to an electronic balance sensitive to 0.0001 grams. Back on Earth, an identical cohort was similarly maintained and weighed. Data was analyzed by statistics.

RESULTS:

Mean weight of pigs in space was 0.0000 +/- 0.0002 g. Some individuals weighed less than zero, some more, but these variations were due to reaction to the duct tape, we believe, which caused them to be alarmed push briefly against the force plate in the balance. Individuals on the Earth, the control cohort, gained about 240 g/month ($p = 0.0002$). Males and females gained a similar amount of weight on Earth (no main of effect of sex), and size at any point during the study was related to starting size (which was used as a covariate in the ANCOVA). Both Earth and space pigs developed substantial dewlaps (double chins) and were lethargic at the conclusion of the study.



CONCLUSIONS:

Our view that weight and weight gain would be zero in space was confirmed. Although we have not replicated this experiment on larger animals or primates, we are confident that our result would be mirrored in other model organisms. We are currently in the process of obtaining necessary human trial permissions, and should have our planned experiment initiated within 80 years, pending expedited review by local and Federal IRBs.

ACKNOWLEDGEMENTS:

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Natural Killer Cells Disintegrates In Vitro Model Tumors but not Intravital Tumors

Per Albertsson[1*] MD PhD, Ulf Nannmark[1] LDS PhD, Myoung H Kim[2] PhD, Richard P Kitson[2] PhD., Per Basse[3] MD PhD, Ronald H Goldfarb[2] PhD and Bengt R Johansson[1] MD PhD
1) Institute of Anatomy and Cell Biology University of Göteborg, Sweden; 2) University of North Texas HSC, Fort Worth, TX; 3) University of Pittsburgh Cancer Institute
*Dept of Oncology Sahlgren University Hospital Göteborg, Sweden

INTRODUCTION

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ABSTRACT

We have re-evaluated the morphology of the infiltration process of A-NK cells into melanoma cell colonies. Increasingly simplified experimental *in vitro* and *intra vital* models were evaluated by electron microscopy. Firstly, studying tumours grown intraperitoneally abolished the influence of distribution, arrest and the transvascular migration process. Secondly, in tumour cell colonies formed in vitro the infiltration was assumed to depend on cell-to-cell and cell-to-matrix contacts due to the lack of contribution by preformed tissue components, influencing the shape and extension of the tumour growth. Thirdly, A-NK cells and tumour cells were separated with the matrix equivalent (Matrigel®) in where the ability of the A-NK cells to affect the integrity of matrix components during formation of target cell contacts could be examined. The Matrigel® co-incubation experiments revealed that A-NK cells pre-cultured for 5 days altered generally the initial homogeneous texture of the Matrigel®. A microporous appearance by 6 h became a loose filamentous meshwork by 24 h. On the other hand, long-termed cultured (more than 5 days) A-NK cells, instead formed large excavations in the Matrigel, that seemed to contain an expanding material. Also was the remaining matrix less affected with the long-term cultured A-NK cells. The melanoma cell colonies formed *in vitro* were disintegrated during the A-NK cell infiltration process and in analogy with Matrigel® experiments, long-termed cultured A-NK cells were located in wide spaces between tumour cells. After adoptive intra peritoneal injection, isolated A-NK cells had infiltrated the tumour mass and were generally surrounded by a slightly wider intercellular space than the adjacent tumour cells.

It is suggested that the conspicuous capacity of A-NK cells to disintegrate extracellular matrix, and dissolve tumour equivalents in vitro, tallies with effects by proteases. Similar effects was not confirmed in the more complex intra peritoneal model, possibly due to presence of protease inhibitors or restrains by endogenous extracellular matrix components.

RESULTS

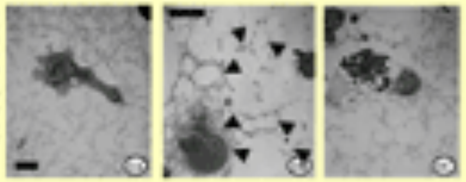

Fig 1. [illegible]

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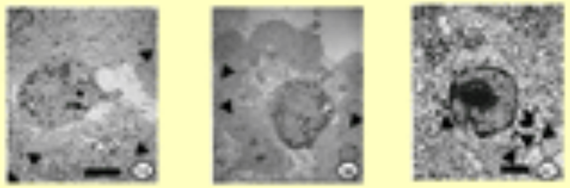

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DISCUSSION

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MATERIAL and METHODS

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Automatic paralogous gene detection and structural annotation of multigene families: application to the MYB family of transcription factors in *Arabidopsis thaliana*.

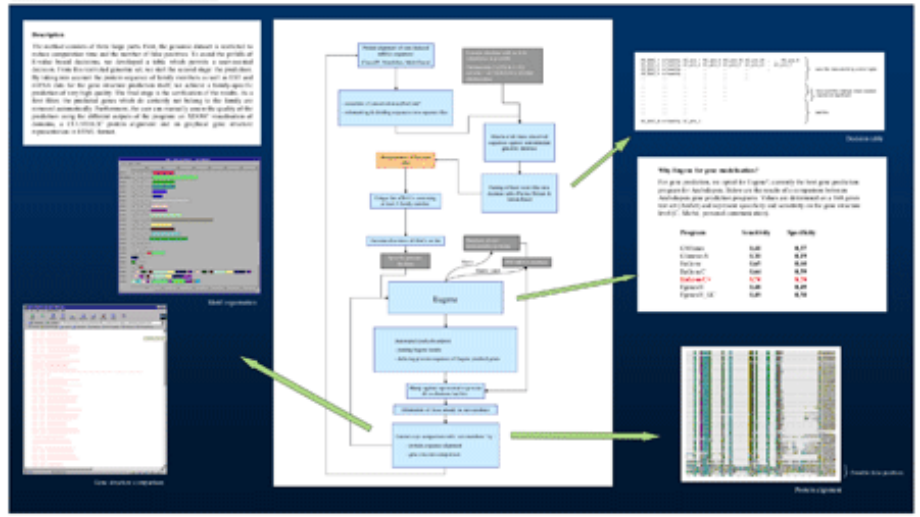
Jeroen Raes[1,2], Sébastien Aubourg[3], Patrice Dehais[1] and Pierre Rouzé[1,2]

[1] Department of Plant Genetics, Flanders Interuniversity Institute for Biotechnology (VIB), University of Ghent, Ghent, Belgium
[2] Laboratoire associé de l'INRA, University of Ghent , Ghent, Belgium
[3] Current affiliation: Unité de Recherche en Génomique Végétale, INRA, Evry, France

Introduction

Now that more and more full genome sequences become available, the possibilities for evolutionary research seem endless: one can collect all members of a gene family, without missing the low or conditionally expressed ones, which was often the case in cDNA-library based family studies. Unfortunately, having the complete genome is only the beginning: the automatic annotation done by the large sequencing consortia is often of poor quality[1]. As such, it is very unlikely that a perfect and exhaustive set of family members can be collected just by using the family name as query in a search engine (e.g. SRS).
To avoid the tedious task of manually correcting structural and functional annotation, we developed a method that allows us to retrieve exhaustively all family members given a representative set (e.g. of experimental origin) and a set of genomic (e.g. BAC) sequences. The final result of this routine consists of the gene structure, position and mRNA/protein sequence of all the family members.
This method was applied to the Myb family of transcription factors in the *Arabidopsis thaliana* genome.

Methodology



Application

The Myb family of transcription factors is one of the largest families in *Arabidopsis thaliana*. They are implicated in various processes, such as secondary metabolism, cellular morphogenesis, growth regulator response signalling, etc[5]. This diversity of functions, combined with an explosive expansion of this family in comparison to animals (e.g. Humans have only 3 known Mybs), make this family very interesting for gene family evolution studies. As a family, it is not of the easiest to detect: the only conserved area is a 50aa sequence which is repeated (degenerately) up to three times. At the genomic level, the repeats are usually interrupted by an intron, which increases the detection difficulty even further.
From a set of 24 representative R2-R3 Myb subfamily members, ±140 R2-R3 Mybs were found in the Arabidopsis genome, which is in agreement with a recent study done on Arabidopsis transcription factors[6]. In more than 90% of the cases, the comparison to the other family members allowed us to decide that the automated gene structure prediction was correct.

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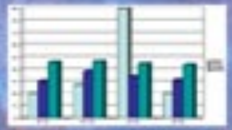

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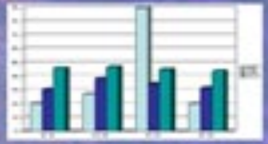

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