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APPENDIX A

KANOKSILAPATHAM'S (2005) FRAMEWORK

Introduction

Move 1: Announcing the importance of the field

Step 1:Claiming the centrality of the topic

e.g.: Protein degradation plays an important role in a wide array of cellular events.

Step 2: Making topic generalizations

e.g.: Protein export pathways are less well characterized, although. . .

Step 3: Reviewing previous research

e.g.: Double-stranded RNA (dsRNA) induces potent cellular responses in diverse biological systems (R).4

Move 2: Preparing for the present study

Step 1:Indicating a gap

e.g.: The mechanism of processing the nature, 184nt 6S RNA from its precursor has not been characterized.

Step 2: Raising a question

e.g.: Is conformational stability a determinant of rebonuclease cytotoxicity?

Move 3: Introducing the present study

Step 1: Stating purpose(s)

e.g.: The present study was designed to evaluate whether the efficiency and carrier ligand specificity of replicative by pass past Pt-DNA abducts by Pob could be determined by the mode of translesion synthesis and whether. . .

Step 2: Describing procedures

e.g.: Wetherefore investigatedAJformation in primary keratinocytes, which has led us to novel insights. When perfectly contact-inhibited primary cells are stimulated, they form intercellular junctions by an active and dynamic process, driven by actin filament polymerization. This remarkable mechanism involves the calcium-activated production of filopodia, which penetrate and embed into neighboring cells. . .

Step 3: Presenting findings

e.g.: Our results show that U2snRNP is functionally associated with the E complex and is also required for its assembly.

Methods

Move 4: Describing materials

Step 1: Listing materials

e.g. Bacterial strains used in this study and their origin are listed in Table 3.

Step 2: Detailing the source of the materials

e.g. COS-7 cells were obtained form S.Brandt (Vanderbilt University, Nashville, Tenn).

Step 3: Providing the background of the materials

e.g. The fun 12 strains J130 and J133 were described previously.

Move 5: Describing experimental procedures

Step 1: Documenting established procedures

e.g.: Detection employed the ECL kit (American Pharmacia Biotech) according to the manufacture's specification.

Step 2: Detailing procedures

e.g.: Proteins in both fractions were precipitated by the addition of 4 volumes of cold acetone, collected by centrifugation, and resuspended in electrophoresis sample buffer.

Step 3: Providing the background of the procedures

e.g.: Complete details of all constructions will be provided upon request.

Move 6: Detailing equipment (optional)

e.g.: Images were recorded through a Hamamatsu C-2400 New vicon camera using a 10 x objective and brightfield optics. Video images were digitized at a rate of 6 frames/min as described above.

Move 7: Describing statistical procedures (optional)

e.g.: The t-test was used to statistically compare the individual ratios from two given strains.

Results

Move 8: Stating procedures

Step 1: Describing aims and purposes

Step 2: Stating research questions

Step 3: Making hypotheses

Step 4: Listing procedures or methodological techniques

Move 8, Step 1: Describing aims and purposes and Step 4: Listing procedures or methodological techniques

e.g.: To determine whether these GTPases participate in the phagocytosis of P. aeruginosa, we expressed guanine nucleotide binding-deficient alleles of Rac1 or Cdc42, or a GAP for both proteins, in RAW LRFMLPR.2 cells, and performed association and phagocytosis assays.

Move 8, Step 3: Making hypotheses, Step 1: Describing aims and purposes, and Step 4: Listing procedures or methodological techniques

e.g.: Mondo A and Mlx heterodimerize are predicted, based on primary amino acid sequences, to bind CACGTG E-box sequences. To determine whether p19 cells

contained E-box binding activity associated with MondoA-Mlx heterodimers, P19 cytoplasmic extracts were incubated with double-stranded CACGTG oligonucleotides immobilized on beads and following extensive washing, retention of MondoA Mlx heterodimers on the DNA beads was determined by Western blotting.

Move 9: Justifying procedures or methodology

Step 1: Citing established knowledge of the procedure

e.g.: (We chose the more precisely defined LSTer region over the RSTer region for analysis.) LSTer region contains two approximately equivalent arrest sites, LSTer 2, separated by about 27 kbp (R). . .

Step 2: Referring to previous research

e.g.: . . .However, both identified murine GBPs had C20-type Cax motifs, and the mGBP1 protein appeared to be successfully C20 modified (R). (Therefore, mGBP1 was examined to determine if it would also be C20 modified or might instead be farnesylated.)

Move 10: Stating results

Step 1: Substantiating results

e.g.: Full length VASP-GFP localized to adhesion zippers and cell–cell borders with no obvious deleterious effects (Figs. 6A–D). This was true in the majority (>90%) of transfected cells, even those that fluoresced highly with GFP (examples shown).

Step 2: Invalidating results

e.g.: In contrast, TD-GFP interfered with formation of adhesion zippers and epithelial sheets (Figs. 6E–H)

Move 11: Stating comments on the results

Step 1: Explaining the results

Step 2: Making generalizations or interpretations of the results

Step 3: Evaluating the current findings

Step 4: Stating limitations

Step 5: Summarizing

Move 10 and Move 11, Step 2:Making generalizations or interpretations of the results

Move 10. . .. . .an inhibitor of lysosomal cysteine proteases (R), had a significant effect on c-Myc degradation (Fig. 1B).

Move 11, Step 2 These results suggest that proteolysis of c-Myc is proteasome dependent. [MCB4]

Move 10 and Move 11, Step 5: Summarizing

Move 10. . .. . .exhibited more frequent lateral pseudopod activity and more frequent changes in direction (see arrows, Fig. 7B).

Move 10 and Move 11, Step 1: Explaining the results

Move 10 Our results determine localization of these mutants in vivo using GFPtaggedSte18p.

Move 11, Step 1 We presume that the localization of GFP-tagged Ste18p is representative of native Ste18p because the wild-type fusion protein rescues mating in a ste18 strain.

Discussion

Move 12: Contextualizing the study

Step 1: Describing established knowledge

e.g.: Type III secretion systems translocate proteins out of cells and often require chaperones specific for each of the secreted substrates. Chaperones were thought to prevent internal degradation of the secretion substrate and to deliver that protein to the secretion apparatus

Step 2: Presenting generalizations, claims, deductions, or research gaps

e.g.: (S1) A detailed understanding of the catalytic mechanisms and substrate selectivity of HAT enzymes is an important component of defining the molecular basis of their biological functions. (S2) Furthermore, such understanding is likely to enhance the design of potent and selective HAT inhibitors. (S3) Prior to this investigation, a preliminary mechanistic analysis on the HAT enzyme GCN-5 was reported. (S4)In this study, mixed histone substrates were used as the acetyl- CoA acceptor (R). (S5) Whereas this study revealed an intersecting line pattern for GCN-5 suggestive of a ternary complex mechanism, more detailed studies investigating order of substrate binding were not described. (S6) The complexity of the mixed histone substrate may have made detailed mechanistic studies difficult.

Move 13: Consolidating results

Step 1: Restating methodology (purposes, research questions, hypotheses restated, and procedures)

e.g.: To identify the mechanism by which kinesin-I binds axonal cargo, we screened for novel axonal transport mutants in Drosophila.

Step 2: Stating selected findings

e.g.: We show that the essential Gpi11 and Gpi13 proteins are involved in late stages in the formation of the yeast GPIs, and we identify and characterize three new candidates GPI precursors.

Step 3: Referring to previous literature

e.g.: Here we report the characterization of purified functional spliceosomal complex E. In contrast to the current model of spliceosome assembly, which proposes that U2 snRNP first binds in the A complex, our data indicate that U2 snRNP first associates with pre-mRNA during E complex formation. [MC5] The experiments presented here confirm the previously reported data (R), showing that polb can catalyze extensive bypass of platinum-DNA adducts in a single-stranded region of DNA.

Step 4: Explaining differences in findings

e.g.: . . .they were not easily distinguished in centroid tracks of regA_ cells (Fig. 4D–F), primarily because the peak velocities of regA_ cells were in many cases depressed

and the tracks were not as persistent and directional during period of increased velocity.

Step 5: Making overt claims or generalizations

e.g.: . . .Simply changing the CaaX motif of mGBP1 to a form recognized by Ftase significantly improved mGBP1 modification. This result also indicates that the CaaX motif of mGBP1 is not likely to be buried within the structure of the protein, because such masking would presumably impede interaction with either Ftase or GGTase I.

Step 6: Exemplifying

e.g.: This is not meant to imply that protein substrate recognition by PCAF would not be influenced by the non-catalytic domains of PCAF. For example, a 25-amino acid peptide derived from the known acytelation site of p53 is a very weak PCAF (full-length). . .

Move 14: Stating limitations of the study

Step 1: Limitations about the findings

e.g.: As yet, we have not detected 6S RNA-dependent differences in the recovery of growth after stationary phase (R).

Step 2: Limitations about the methodology

e.g.: Additionally, some interactions may be too transient for detection by FRET.

Step 3: Limitations about the claims made

e.g.: Our cystallographic results also do not rule out a proposed mechanism in which the phosphates together coordinate a single metal ion (R).

Move 15: Suggesting further research (optional)

e.g.: In the future, it will be challenging to assess what contribution DNA unwinding makes to the distribution of replication start sites in vivo.

Note: the examples illustrated in this framework are cited from Kanosilapatham's (2005) study

APPENDIX B

TEXTS

Food Technology

F1 Narasimhanaidu Kamalakkannan & Khalid S. Alnumair. (2009). Rutin alters fatty acid composition in diabetic tissues. *Nutrition & Food Science, 39(6),* 655 - 662

F2 Ayantunji Gbadamosi, Ojo Olukayode Iwaloye & David Bamber. (2009). An exploratory study of students' consumption of non-alcoholic beverages in Nigeria: A qualitative perspective. *Nutrition & Food Science, 39(6),* 609 - 618

F3 Fredriksson-Ahomaa, M., Wacheck, S., Koenig, M., Stolle, A. & Stephan, R. (2009). Prevalence of pathogenic Yersinia enterocolitica and Yersinai pseudotuberculosis in wild boars in Switzerland. *International Journal of Food Microbiology, (135),* 199-202

F4 Kelly, L., Murchie, L., Xia, B., Whyte, P., & Madden, RH. (2009). Probabilistic model for contamination of egg dishes with Salmonella spp. made from shell eggs produced on the island of Ireland. *International Journal of Food Microbiology, (135),* 187-192

F5 Horacek, M., E. Eisinger & W. Papesch. (2009). Reliability of stable isotope values from meat juice for the determination of the meat origin. *Food Chemistry, (118),* 910-914

F6 Bounaix MS, Gabriel V, Morel S, Robert H, Rabier P, Remaud-Siméon M, Gabriel B & Fontagné-Faucher C.(2009).Biodiversity of Exopolysaccharides Produced from Sucrose by Sourdough Lactic Acid Bacteria. *Journal of Agricultural and Food Chemistry.* 57 (22), 10889-10897

F7 Huang, Q., Fu, X., He, XW., Luo, FX., Yu, SJ., & Li, L. (2009). The effect of enzymatic pretreatments on subsequent octenyl succinic anhydride modifications of cornstarch. *Food Hydrocolloids*, (24), 60-65

F8 Gonipeta, B., Parvataneni, S., Tempelman, RJ. & Gangur, V. (2009). An adjuvant-free mouse model to evaluate the allergenicity of milk whey protein. *Journal of Diary, 92(10)*

F9 Stanic, D., Radosavljevic, J., Polovic, N., Jadranin, M., Popovic, M., Vuckovic, O., Burazer, L., Jankov, R. & Cirkovic Velickovic, T. (2009). Removal of N-terminal peptides from B-lactoglobulin by proteolytic contaminants in a commercial phenol oxidase preparation. *International Dairy Journal, (19),* 746-752

F10 Joshi,R., Banwet,DK. & Shankar, R. (2009). Indian cold chain: modeling the inhibitors", *British Food Journal, 111(11),*1260 - 1283

Crop & Plant

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C2 Tenea,GN. , Spantzel, J., Lee, LY., Zhu, Y., Lin, K., Johnson, SJ. & Gelvin, SB. (2009). Overexpression of several arabidopsis histone genes increases agrobacterium-mediated transformation and transgene expression in plants. *Plant Cell* **21**: 3350–3367

C3 Zhang, X.G & Oppenheimer, D. G. (2009) IRREGULAR TRICHOME BRANCH 2 (ITB2) encodes a putative aminophospholipid translocase that regulates trichome branch elongation in Arabidopsis. *Plant J. 60,* 195–206

C4 Mayer, KFX., Taudien, S., Martis, M., Simkova, H,, Suchankova, P., Gundlach ,H., Wicker, T., Petzold, A., Felder, M., Steuernagel, B., Scholz, U., Graner, A., Platzer, M., Dolezel, J. & Stein, N. (2009). Gene content and virtual gene order of barley chromosome 1H. *Plant Physiol 151*:496–505

C5 Fernández-Marín, B., Balaguer, L., Esteban, R., Becerril, JM.& García-Plazaola, JI. (2009). Dark induction of the photoprotective xanthophylls cycle in response to dehydration. *J Plant Physiol, 166*:1734–1744

C6 Vandekinderen, I., Devlieghere, F., Van Camp, J., Denon, Q., Sánchez- Alarcon, S., Ragaert, P. & De Meulenaer, B. (2009). Impact of a decontamination step with peroxyacetic acid on the shelf-life, sensory quality and nutrient content of grated carrots packed under equilibrium modified atmosphere and stored at 7^{0}C. *Postharvest Biology and Technology, (54),* 141-152

C7 Winkler, JB., Lang, H., Graf, W. & Munch, JC. (2009). Experimental setup of field lysimeters for studying effects of elevated ozone and below-ground

pathogen infection on a plant-soil-system of juvenile beech (Fagus sylvatica L.). *Plant Soil, (323),* 7-19

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C9 Cha, J.Y., Jung, M. H., Ermawati, N., Su'udi, M., Rho, G. J., Han, C. D., Lee, K. H. & Son, D. (2009). Functional characterization of orchardgrass endoplasmic reticulum-resident Hspn90 (DgHsp90) as a chaperone and an ATPase. *Plant Physiology and Biochemistry, (47),* 859-866

C10 Farooq, M., Basra,S. M. A., Wahid, A., Ahmad, N., & Saleem, B. A,.(2009). Improving the drought tolerance in rice (Oryza sativa L.) by exogenous application of salicylic acid. *J. Agron. Crop Sci*. *195*, 237–246.

Animal Science

A1 Giesecke, K., Hamann, H., Stock, K. F., Woehlke, A., Sieme, H. & Distl. O. (2009). Evaluation of SPATA1-associated markers for stallion fertility. *Animal Genetics, (40),* 359-365

A2 Ji, R., Cui, P., Ding, F., Geng, J., Gao, H., Zhang, H., Yu, J., Hu, S. & Meng, H. (2009). Monophyletic origin of domestic bactrian camel (Camelus bactrianus) and its evolutionary relationship with the extant wild camel (Camelus bactrianus ferus). *Animal Genetics, (40),* 377-382

A3 Fields, S.D., Perry, B.L. & Perry, G. A. (2009). Effects of GnRH treatment on initiation of pulses of LH, LH release, and subsequent concentrations of progesterone. *Domestic Animal Endocrinology, (37),* 189-195

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A5 Hoque, M. A., Katoh, K. & Suzuki, K. (2009).Genetic associations of residual feed intake with serum IGF-I and leptin concentrations, meat quality, and carcass cross sectional fat area ratios in Duroc pigs J. *Anim Sci.*0: jas.2008-1268

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A8 Dawson, L.E.R., Fearon, A.M., Moss, B.W., & Woods, V.B (2010). Effects of substitution of a proportion of the concentrate in grass silage/concentrate-based diets with extruded linseed on performance and meat quality of dairy bulls. *Animal Feed Science and Technology, (156),* 10-18

A9 Nishio, M., Kahi, A.K. & Hirooka, H. (2010). Optimization of mate selection based on genotypic information with overlapping generations. *Journal of Animal Breed Genetics,* (127), 34-41

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CURRICULUM VITA

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