

Applicant: Bahler
Attachment No: SCaRF01
Ref No: 18

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Referee's Comment on Fellowship Application

Overall assessment

If you feel these comments are confidential and you do NOT want these comments passed to the applicant please tick here ☐

the insight displayed by Dr. Bahler is excellent and reflects the fact that he is at the forefront of the field of post-genomic studies exploiting unicellular model genetic organisms and microarray technology. There are many arguments that underpin the importance of understanding fission yeast biology, the major one being that mitosis in this yeast more closely resembles vertebrate cells than does *S.cerevisiae*, another one is that heterochromatin metabolism and the involvement of RNA in these processes is absent in the other yeast.

The principal investigator has an impressive track record and the 5 year plan is very well formulated. Although the breadth of the experiments may seem daunting and although the diversity of molecular processes that are targeted may appear too large, the fact that a unicellular organism will be employed makes these objectives attainable. In order to integrate data from these diverse experiments it is crucial that the experiments be performed in parallel in the same lab so as to reduce noise in the datasets that is invariably caused by laboratory specific idiosyncrasies. The breadth of experiments can thus be seen as a great advantage rather than intellectual dilution.

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This page WILL be passed on to the applicant.

We would appreciate your comments on: the importance of the project and its relevance to cancer research; the originality of the project; the quality of the plan of investigation; the likelihood of its successful conclusion within the time specified; and whether the level of support requested is appropriate.

With reference to the information about the Fellowship please comment on the suitability of the candidate to this level of Fellowship at this point in their career.

Cancer is a multi-factorial disease with many different incarnations. Although key signal transduction and metabolic pathways that are affected in cancer cells have been identified, it is only since the last 5 years that global approaches can be applied to understand the integration of every physiological pathway in cellular proliferation and growth. To date, curing cancer with generic drugs has involved targeting mitosis and replication, in that order. A full understanding of gene expression programs in the course of the cell cycle under a large set of conditions will permit the identification of factors that play pivotal roles in the control of gene expression as a function of cellular growth. However, prior to choosing new drug targets, it is crucial to understand the role of these factors in the wild type situation, so as to be able to profile individual patients for prognosis. Generation of a body of knowledge to allow such sophisticated medicinal strategies is exactly what Dr. Bahler proposes to achieve.

Dr. Bahler is strategically positioned at the EBI where he oversees genomic data acquisition and interpretation pipelines. Whenever, detailed phenotypes of individual cancers will be available, the results obtained by Dr. Bahler will be of great import. Furthermore, it is very likely that the researchers studying cancers by means of microarrays will be employing tools (software, databases) that have been optimised, based on the working experience accumulated by Dr. Bahler and colleagues. Finally, Dr. Bahler appears to be integrated in a very high calibre fundamental research network that involves the major players of the fission yeast community.

It is of utmost importance to cancer research that Dr. Bahler be given the means to pursue the research goals that are outlined in the present proposal. Of particular interest are the studies on mRNA incorporation into polysomes (translated mRNAs), because that aspect of post transcriptional gene expression control has been understudied.

The suitability of the candidate to this level of fellowship at this point in his career is perfect. Dr. Bahler is ready to accurately and effectively describe the cell cycle of *S.pombe* in a definitive fashion and, in the course of this exercise to lay foundations for similar analyses in man. Furthermore, he has demonstrated a high level of collaborative skills that will permit a seamless integration of data mining and hypothesis testing pipeline in the course of the next decade.