

MINUTES

5th Annual International *Burkholderia cepacia* Working Group Meeting

Bethesda, Maryland

April 7th-9th, 2000

Meeting Organizers & Co-chairs: John J. LiPuma, Jane L. Burns, Paul W. Whitby

Minutes prepared by Jane L. Burns

The meeting began with an introduction of those in attendance. Dr. LiPuma acknowledged the support of the Cystic Fibrosis Foundation (US) and the Canadian Cystic Fibrosis Foundation. AstraZeneca Pharmaceuticals, USA and the Merrem Product Group, AstraZeneca Canada Inc were also thanked for providing significant financial support for the meeting through the provision of unrestricted educational grants. Caroline McPherson and Cynthia Adams from the Cystic Fibrosis Foundation were acknowledged for their assistance in arranging the meeting.

A list was circulated for attendees to note their contact information. Abstracts from the meeting will be available on the IBCWG web site.

David Speert led a discussion of the rights and responsibilities of members of the working group. This primarily focussed on the goal of collaboration. The responsibility of group members to share intellectual property and techniques and to decrease the sense of secrecy was stressed.

John LiPuma presented data on the US referral laboratory now located at the University of Michigan in Ann Arbor. As of 4/00 1932 isolates had been received. These were from 935 individuals at 138 CF centers in 111 US cities. Analysis is complete on 1912. 1416 were identified as *B. cepacia* by the referring lab; 1271 were confirmed to be *B. cepacia* and 145 (10%) were not *B. cepacia*. This percentage has been constant over the past 2 ½ years. Among isolates misidentified as *B. cepacia* by referring labs, approx. 30% were *B. gladioli*, 25% were not classifiable, and the remainder were scattered among other species. Of the 496 strains sent with no identification or as not *B. cepacia*, 319 were confirmed as not *B. cepacia* and 177 (35%) were *B. cepacia* complex. 1051 isolates were looked at to compare identification techniques used in 108 referring labs. Nine commercial systems were used as the primary identification method. 76 labs also used a secondary method of identification. Overall, the positive predictive value of an identification of *B. cepacia* was 71-98% and the negative predictive value was 50-82%. Most commercial systems do not appear to be adequate as the sole method to identify *B. cepacia* complex.

The epidemiology of strains from 642 *B. cepacia* complex-infected patients was also examined: Approximately 50% were genomovar III, 35% *B. multivorans* (GII), 5% *B. vietnamiensis* (GV), 10% were genomovars I, VI, *B. stabilis* (G IV), and recA group C (GVII). Thus all genomovars are seen in CF patients in the US. 43% of GIII strains were BCESM +; only ET-12 clone isolates were cblA+. Examination of a major Philadelphia/Washington, DC clone showed that it lacked BCESM.

Deb Henry from David Speert's lab at the University of British Columbia in Vancouver presented data from the Canadian Referral Laboratory. Recent data looking at regional distribution of all Canadian isolates showed that genomovar III is the most common overall and that RAPD group 002 (ET-12) strains are the dominant isolates from Ontario, Quebec and the Maritime Provinces. In fact, all British Columbia patients with RAPD type 002 have had contact with Toronto. RAPD group 006, on the other hand, is only found in British Columbia. Genomovar II was the second most common genomovar seen. Different clinical severity has been ascribed to different RAPD groups. In the past 15 months, there have been 50 isolates typed including 14 GIII, 11 *B. multivorans*, 1 GI, 2 *B. vietnamiensis*, and 1 other *B. cepacia* complex. Incidence data in British Columbia from the past 20 years has shown: 1980-85: 3 GIII strains, 1 *B. multivorans*; 1985-90: 5 GIII, 5 *B. multivorans*, 1 other; 1990-95: 30 GIII, 8 *B. multivorans*, 2 other; 1995-April 2000: 8 GIII, 9 *B. multivorans*, 5 other.

Infection control issues were also discussed by Dr. Speert who provided a copy of the recent Canadian recommendations. *Pseudomonas aeruginosa* has not been identified as being nosocomially acquired and no segregation is recommended. Control of *B. cepacia*, which has been demonstrated to be transmitted from person to person, requires different recommendations including minimizing contact in the hospital and clinics, recognizing that some social contacts may still continue. The question of transmissibility and virulence of GII vs. GIII strains was also discussed. In Canada, there has only been evidence for spread of GIII strains; no spread of GII has been documented. The Canadian document advises against interaction between patients who are colonized with *B. cepacia* and those who are culture-negative. Whereas there has been no evidence for spread of GII among CF patients, no genomovar-specific recommendations have been made. A discussion ensued regarding the advisability of making recommendations that are based upon specific genomovars. In the US, *B. multivorans* clones involving multiple patients have been detected. The Glasgow outbreak and an outbreak in Cardiff involved *B. multivorans* as well. In France, two of the five main epidemic clones are *B. multivorans*. Thus, it was suggested that infection control recommendations be made on a center-by-center basis with full knowledge of local epidemiology. The need for an infection control consensus was stressed. Jane Burns related plans for an American CF Foundation consensus conference on infection control to complement those in the UK and Canada.

Tom Coenye discussed updates in the taxonomy of *B. cepacia* complex and related organisms. Eight species have now been identified in the complex, all of which have 98-99% similarity of 16s rRNA and 30 to 50% DNA-DNA hybridization. GI contains the type strain and, when ultimate speciation is performed, will carry the name *B. cepacia*. GII has been named *B. multivorans*. GIII cannot be readily distinguished from GI. GIV has been recently named *B. stabilis*. GV is named *B. vietnamiensis*. GVI is a new genomovar that is similar to *B. multivorans* and has only been isolated from CF patients. GVII is also a new genomovar. *B. pyrocinia* should also be included as part of the *B. cepacia* complex and has only been identified in the natural environment. *Pandoraea* strains, which may be mistaken for *B. cepacia* complex, include *P. pulmonicola*, *P. apista* and *P. sputorum* and are only found in CF. "Group 11" strains include multiple novel species including *B. caledonica* (found in the rhizosphere in Scotland) and *B. fungorum* (found in fungi, root nodules, and as animal and human clinical isolates including CF). Multiple novel species of *Ralstonia spp.* including *R. basiliensis*, *R. metallidurans*, and *R. campinensis* have been identified for bioremediation, but no human isolates have been seen.

Group 35 isolates have been found in root nodules and *R. thomasi* has been isolated from CF patients.

The source of GIII strains was discussed. Patient to patient transmission has been previously demonstrated, but acquisition from the environment has not been suggested until recently. This may be because isolates in the natural environment are more antibiotic susceptible and standard clinical isolation medium will not recover them. Viillard et al Int J Syst Bacteriol, 48:549, 1998 in a survey in France and Southern Australia, using PCAT medium has identified two “phenons” from soil, phenon B was recently found to represent multiple GIII isolates. Other studies supporting this include a study of rice seeds from the Philippines with isolation of *B. glumae* (70 isolates), *B. gladioli* (50 isolates), *B. cepacia* complex (30 isolates: 12 GI, 1 GII, 9 GIII, 2 GV and 4 others). This suggests the need to use special isolation media (that does not contain a lot of antibiotics) to obtain isolates from soil.

An ongoing study by John LiPuma and Jennifer Parke is looking at isolates from the soil and rhizosphere in Corvallis, Philadelphia, and Cleveland using two different media. They have identified different numbers of organisms and different phenotypes from the same sample dependent upon the media used and have also identified lower optimal incubation temperatures. Carlos Gonzales also described GIII strains from onion fields containing BCESM and lytic phages.

Susanna McColley described the CF clinician’s perspective of *B. cepacia* and expressed both local and national concerns. She described *B. cepacia* as having the greatest psychological effect on CF patients and caregivers of any organism. Issues she highlighted include: optimum microbiology laboratory identification, infection control, and strategies to manage patients. Locally, she expressed a sense of relief that her own center has instituted strict infection control guidelines for CF. The need for a national consensus in the US was also stressed. With regard to clinical microbiology she questioned whether the current type and frequency of culture is adequate (specifically, if OP cultures are adequate in young children who do not expectorate or if bronchoalveolar lavage should be routinely performed), whether laboratories that process CF samples have the optimum techniques for identification and susceptibility testing, and whether referral laboratories for confirmation of identification of *B. cepacia* and for susceptibility testing of resistant isolates are being underutilized. She requested that the IBCWG put together a protocol with universal laboratory techniques for *B. cepacia*. When told that these techniques had been developed by the IBCWG, she requested that this be published in more accessible sites. Suggestions were made (in addition to the IBCWG web site) that ASM News might be a possible venue as well as dissemination by the CF Foundation to all CF centers in the US. Other issues of clinical importance that were discussed included the need for studies to investigate the management of initial colonization with *B. cepacia* and optimal strategies to prevent development of antibiotic resistance.

Bruce Marshall described a new statistical model of 5 year survival in transplant patients to help determine those variables that confer a survival advantage. CF registry data was used, ½ to develop the model and ½ to validate it (4860 patients in the development group, 4898 in the validation group). Groups were similar with regard to clinical criteria and microbiology. Twenty one variables were selected and numerous were found to have an insignificant effect on survival

including age, height, genotype, *P. aeruginosa*, *Stenotrophomonas maltophilia*, *Haemophilus influenzae*, pregnancy and FEV₁ slope. Negative factors included: female gender (-6), diabetes mellitus (-13), *B. cepacia* (-40) and number of acute pulmonary exacerbations in the past year (-10 per PE, up to 5 per year). When the model was validated with the second group of patients, it was found to be highly predictive, especially in the patients with > 50% predicted mortality. Kaplan-Meier plots of transplant survival vs. non-transplant survival were shown for the groups with: 10 to 30% predicted survival where there is an ~1 year survival advantage with transplant; 30 to 50% predicted survival where there is an ~2 year survival advantage with transplant; 50 to 70% survival where there is no survival advantage or disadvantage; and 70 to 90% predicted survival where there is a survival disadvantage with transplant. Two case vignettes were demonstrated.

Mary Corey presented her abstract entitled: “Short and long term mortality risks of *B. cepacia* and *P. aeruginosa*” (see abstracts).

George Mallory presented his abstract entitled: “Prevalence of *B. cepacia* in US CF centers 1989-98: Revised questionnaire to assess pathogenic significance of *B. cepacia* in US lung transplant candidates and recipients with CF” (see abstracts).

Jonathan Collins presented his abstract entitled: “Determining the prevalence of *B. cepacia* complex in the Republic of Ireland” (see abstracts).

Kerstin Dunbar presented her abstract entitled: “Molecular epidemiology of *B. cepacia* complex infection in Northern Ireland CF patients by RAPD” (see abstracts).

Andrew McDowell presented his abstract entitled: “Molecular speciation of *B. cepacia* complex pathogens in CF sputum” (see abstracts).

Catherine Doherty presented her abstract entitled: “Use of pulsed-field gel electrophoresis for typing isolates of *B. cepacia*” (see abstracts).

Kevin Markey presented his abstract entitled: “*B. cepacia* complex—potential virulence factors” (see abstracts).

Bindu Nair presented her abstract entitled: “Induction of antibiotic resistance in *B. cepacia*” (see abstracts).

Chris Mohr presented his abstract entitled: “Invasion and intracellular survival of *B. cepacia*” (see abstracts).

Ute Schwab presented her abstract entitled: “Localization of *B. cepacia* in well-differentiated human tracheobronchial epithelial cultures” (see abstracts).

Philip Sayre from the EPA presented information on commercial uses of *B. cepacia* and related organisms and their regulation. He identified 12 potential uses of bacteria: bioremediation, waste water treatment, biomining/bioleaching, desulfurization of coal and oil, oil recovery, biomass conversion, drain cleaner, turf builder, biofertilizer, specialty chemical production and biosensor. Of these, 4 categories of use have been found for *B. cepacia* including bioremediation (4), specialty chemical production (6), biosensor (1), and biomass conversion (1). Possible pathways to control these include: voluntary submission of information, preparation of facts sheets, targeting relevant industries and trade organizations, and TSCA (Toxic Substances Control Act) options for information gathering and control by the EPA. Some of these, such as bans, are tough because they require a causal link. Specific protocols to help identify *B. cepacia* in other potential commercial uses were suggested, since many companies may not even be aware that their products contain this organism (see abstracts for additional details).

Kevin Kerr presented his abstract entitled: “Susceptibility of *B. cepacia* to ultraviolet light” (see abstracts).

Ananda Chakrabarty presented his abstract entitled: “Clinical and environmental isolates of *B. cepacia* exhibit differential cytotoxicity towards macrophages” (see abstracts).

Gino Medrano presented his abstract entitled: “Genetic characterization of the plant watersoaking phenotype expressed by plant and clinical *B. cepacia*” (see abstracts).

The working group then broke into discussion groups around 3 topics: *Group A*: Management, Infection Control, Outcomes, moderated by George Mallory; *Group B*: Microbiology, Taxonomy, Ecology, Molecular epidemiology, moderated by Esh Mahenthiralingam; *Group C*: Virulence, Pathogenesis, Animal models, moderated by David Speert. The goal of the groups was to **identify priorities for investigation**. The group moderators presented their reports the following morning.

Group A: Management, Infection Control, Outcomes
Priority Recommendations

1. The use of up-to-date laboratory techniques for the proper identification of *B. cepacia* in respiratory cultures of CF patients should be the expected standard of care in every accredited CF center worldwide. This improvement should benefit patients and centers, enhance the accuracy of national CF registries and provide the opportunity for broad-based epidemiologic studies of *B. cepacia* complex and, eventually, *B. cepacia* genomovars/species.
2. National CF registries and *B. cepacia* laboratory repositories should be encouraged worldwide. There should be annual reports of incidence and prevalence of *B. cepacia*, nationwide and by region. Center-specific data (with information with regard to lab

techniques) should be available to serious investigators. Public dissemination of center-specific *B. cepacia* incidence and prevalence should be avoided at the present time.

3. There should be strong support with Canada and from outside Canada for the multicenter controlled trial at the University of Ottawa of individually-tailored antibiotic therapy (MCBT) of *B. cepacia*. Extension of the study to other countries should be encouraged.
4. The IBCWG should support the CFF consensus conference on infection control policies. We believe that the following should come out of the conference:
 - a. succinct, universally-applicable recommendations for infection control in light of the potential contagion of *B. cepacia*
 - b. consider “separation” of individual patients in health care settings, in lieu of the previous recommendations for cohorting
 - c. specific, legally-defensive recommendations regarding the employment of health care workers with CF
5. Resources need to be invested to correlate clinical outcomes data with the increasingly sophisticated and accurate data on individual *B. cepacia* complex isolates processed in the *B. cepacia* repository laboratories
6. Because CF lung transplant recipients may be at particularly high risk for infectious disease complications due to *B. cepacia*, there should be a concerted effort to correlate clinical outcomes and microbial data (including speciation) in a retrospective (and potentially prospective) multi-center study.
7. Strong guidelines for the priority of communication in the event of geographic relocation of CF patients with established *B. cepacia* infection should be developed. We believe that the patient and family, referring center and receiving center all have practical and ethical duties in this regard.

Group B: Microbiology, Taxonomy, Ecology, Molecular epidemiology
Priority recommendations

1. Microbiology
 - a. Diagnosis of *B. cepacia* complex at the microbiology bench—what is currently feasible? *B. multivorans* (genomovar II) and *B. stabilis* (genomovar IV) are currently the only two species which may be distinguished at the bench using thorough biochemical analysis and growth temperature requirements. It must be noted that phenotypically, genomovar VI cannot be distinguished from *B. multivorans*. Differentiation of the remaining genomovars within the *B. cepacia* complex requires a polyphasic approach or recently developed PCR-based assays (see 1b) which may not be possible in all diagnostic microbiology laboratories.

- b. What are the current minimum criteria for correct identification of the *B. cepacia* complex? Biochemical testing as described by Vandamme et al., 1997, Vandamme et al. 2000 and Henry et al 1997 & 1999 have been well established. These basic criteria must now be supplemented by several molecular assays:
- i. **LiPuma et al. 1999, J. Clin. Microbiol, 37:3167-70:** This paper describes PCR assays based on the 16S rRNA gene. The method and primers represent a significant advance in specificity over those developed earlier by Campbell *et al.* (1995) and Bauernfeind *et al.* (1999). *Burkholderia* genus specific, *B. vietnamiensis* and *B. multivorans* specific PCR tests are described. Genomovars I, III and IV isolates are identified collectively as a group by another PCR described in the report.
 - ii. **Segonds et al. 1999, J. Clin. Microbiol, 37: 2201-08:** This paper describes PCR assays based on the 16S rRNA gene and identifies genus/species/ genomovar specific restriction fragment length polymorphism (RFLP). It is applicable to all bacterial species since it is based on universal primers. Identification of the *B. cepacia* complex is straightforward, however, differentiation of genomovars I, III and IV is not possible by this method.
 - iii. **Whitby et al., 2000, J. Clin. Microbiol, 38:282-85:** This paper describes PCR assays for the identification of *Burkholderia gladioli* based on the 23S rRNA gene. These methods enable *B. cepacia* and *B. gladioli* to be easily distinguished.
 - iii. **Mahenthiralingam et al, 2000 submitted:** Assays based on the 16S rRNA gene RFLP and the *recA* gene are described. Sequence polymorphism in the *B. cepacia recA* gene is capable of differentiating all the current genomovars and identifying novel genomovars. Information on the method may be obtained by emailing: Mahenthiralingame@cardiff.ac.uk

2. Taxonomy

- a. Maintain educational effort on the *B. cepacia* complex and its epidemiology: It was felt that education to the CF healthcare community was still required on basic terms such as genus, species, genomovar, strain (clone), and isolate as they applied to the *B. cepacia* complex. Some basic definitions may be placed on the web site or written into a review directed at the CF medical community.
- b. Clinical Outcome versus Genomovar: More data and the publication of detailed studies are urgently required on the role played by the strain genomovar in clinical outcome. Difficulties in obtaining patient data and ethical considerations make such studies hard to carry out, but the research community should strive to carry them out.
- c. How should *B. cepacia* identification be reported: As with previous minutes of the IBCWG it was still felt that all detail should be included to assist with education of the health care community. Minimum identification should include the following: (i) *B. cepacia* complex; (ii) genomovar number (if known); (iii) new species name (if known). In addition, extra effort should be made to differentiate the current *B. cepacia* complex from other new *Burkholderia* species.

- d. Phenotypic differentiation of genomovar I from genomovar III: This is still not possible with simple biochemical or phenotypic criteria (no 100% differences exist). While molecular methods are starting to make this possible, they would not be incorporated into routine diagnostic testing. Tom Lessie suggested examining whether differences exist in the ability of these genomovars to metabolise D-serine in a dissimilation assay. Deb Henry will analyze this. (NOTE: Deb has subsequently examined this in 47 isolates (8 genomovar I, 22 genomovar IIIa and 17 genomovars IIIb) and serine utilization as a sole source of carbon is not useful to differentiate between *B. cepacia* complex isolates.
- e. New genomovars: Genomovar VI and Genomovar VII: The description of genomovar VI has been accepted with revision and will be published this year; this new species cannot be phenotypically distinguished from *B. multivorans*. Genomovar VII is now well characterized and demonstrates very characteristic fatty acid profiles that enable a species name to be proposed immediately. The description of genomovar VII will be submitted for publication this year.
- f. Taxonomy and virulence studies: In order to clarify and determine the pathogenic potential of each genomovar it was felt that ALL new studies characterizing virulence traits within the *B. cepacia* complex should strive to systematically compare genomovars. Comparison of uncharacterized ENVIRONMENTAL versus CLINICAL “ISOLATES” should cease and not be tolerated in the submission of data for publication. This should be replaced by systematic evaluation between genomovars and comparison of characterized environmental and clinical strains within a single genomovar.

3. Ecology

- a. Define the source and diversity of the *B. cepacia* complex within the rhizosphere and other natural environments: Systematic studies should be performed to examine aquatic, soil, rhizosphere, leaf surface and other potential natural environments for the presence of the *B. cepacia* complex. The source and geographical location should be highly defined in these studies.
- b. Include genomovar III strains recovered from the natural environment within the experimental strain panel to stimulate further analysis.
- c. Re-evaluate previously published literature on the prevalence of *B. cepacia* complex in the natural environment: Due to the taxonomic complexity of this species group, several strains from previously published studies of the natural environment have been found not to be members of the *B. cepacia* complex. (see abstract by Mahenthiralingam, et al) Interpretation of the data from such publications is therefore not possible. Old data should be re-evaluated and new systematic studies with minimum identification criteria listed above performed.
- d. Define the extent and frequency of genetic exchange which occurs with *B. cepacia* complex isolates in the natural environment: Typing techniques such as Multilocus

Sequence Typing may enable these studies to be performed and are being pursued by members of the IBCWG. It will be very valuable to understand gene flow and evolution of the *B. cepacia* complex. These studies will also shed light on why some genomovars such as *B. stabilis* (genomovar IV) are genetically stable while others such as *B. multivorans* (genomovar II) appear highly unstable.

- e. Define better methods for the recovery of *B. cepacia* complex isolates from the natural environment: Highly selective media with multiple antibiotics may lead to poor recovery of the *B. cepacia* complex, since natural isolates appear to initially possess lower resistance than clinical strains. The growth temperature for recovery of strains from the natural environment should not be above 30°C.

Group C: Virulence, Pathogenesis, Animal models
Priority recommendations

1. Challenges include:
 - a. to identify “virulent” strains
 - b. to identify “valid” in vitro screens
 - c. to identify “valid” animal models
 - d. to identify virulence determinants
2. In vitro models:
 - a. A549 (respiratory epithelial cell line) invasion: two points of view were expressed: that all genomovars invade in the model and that differential invasion can be demonstrated. These need to be reconciled.
 - b. U937 uptake and survival
 - c. NHBE (1° culture of human bronchial epithelium): differential toxicity
 - d. Type II pneumocytes in 1° culture: differential toxicity
 - e. Neutrophil-mediated killing: all genomovars behave the same
3. Ex vivo models:
 - a. human tracheobronchial culture at the air-liquid interface: examined with one strain, one non-CF donor
 - b. human tracheal rings: examined with one strain, one non-CF donor
 - c. onion toxicity: watersoaking and maceration: some difference among the genomovars
4. Animal models:
 - a. Sajjan: CF mice vs. wild-type, multiple intranasal instillations, two strains: difference seen between strains and between mouse lines
 - b. Burns: agar bead mouse: genomovar differences
 - c. Sokol: agar bead rat: several GIII strains, virulence differences correlate with bacterial phenotypes
 - d. Speert: mildly neutropenic mouse, intranasal instillation, differential toxicity among genotypes
 - e. Valvano/Kerr: amoebae: most invasive also was the most virulent in Speert model

5. Future directions:
 - a. Validation of animal models
 - b. Selective expression of bacterial genes in the CF lung
 - c. Probe genome arrays with bacterial RNA from sputum
 - d. Develop quantitative methods to investigate type III secretion
 - e. *B. cepacia* genome project may help identify candidate virulence determinants
6. Immediate plans:
 - a. Compare and contrast the 5 animal models, using the same strains from the experimental panel. This will be expensive and is likely to require a group grant to fund.
 - b. Expand the phenotype/genotype catalog on the IBCWG web page to include all known genetic and phenotypic characteristics of each strains

Shawn Aaron reported on the multiple combination bactericidal antibiotic testing (MCBT) study being performed at 5 Canadian CF centers. This is a prospective, randomized, double-blind study of the efficacy of MCBT-guided therapy vs. conventional therapy in patients with *B. cepacia*. The primary outcome measure is the time to the next pulmonary exacerbation. Secondary outcome measures are sputum bacterial density, change in PFT's, treatment failure and hospital length of stay (see abstract for further details).

Philip Murphy presented a proposal for a PFGE standardization project. This was developed by him and John Moore to help standardize conditions for the performance of PFGE to enable comparison among laboratories. Conditions to be standardized would include DNA extraction technique, agarose gel electrophoresis conditions, molecular weight and internal standards, hardware and software. A multi-center ring trial is proposed with 17 blinded centers (6 in the US, 5 in Canada, 6 in the UK) using 35 isolates (the experimental panel plus additional GVI and GVII strains), standardized protocols and analysis criteria, visual vs. computer analysis. The proposal is for John LiPuma to coordinate the study and to use a standard protocol. It would also be possible for each center to add in a comparison of their own methodology. Costs were expected to be 2000 per center and it was proposed that each country submit a full proposal to their own funding agencies. The goals would be to establish an IBCWG PFGE scheme, with the method and results published and on the web site. A lively discussion ensued at which time numerous opinions were expressed about whether this study would be as useful as developing a typing scheme that might utilize techniques that are all being performed in different labs. Because the method from John Govan is already published including what the panel strains look like using this method (published and on the web site) it is not clear that this would add significantly given the costs. It was also felt that the costs were underestimated. An alternative proposal was that a harmonization of current schemes with coordination of nomenclature and a panel of control strains for QC might be of further benefit.

Esh Mahenthiralingam presented the latest information on the sequencing of *B. cepacia* to be funded by the Wellcome Trust and performed at the Sanger Sequencing Center. A meeting held in London on April 5th determined (with significant input from members of the IBCWG) that genomovar III was the most appropriate type of strain because the clinical significance of this

genomovar in CF. J2315 was selected as the best characterized and most appropriately archived genomovar III strain. It is BCESM and *cblA* pilus positive. An official application will be submitted to the Wellcome Trust on July 1st, but that is a formality, the commitment for the study is there. The plan is for construction of an M13 library of 200,000 shotgun clones as well as a bacterial artificial chromosome (BAC) library and a λ library. Unassembled sequence will be available on the Sanger Center web site and clones will also be available, once sequenced. It is expected that it will take 2 years to complete the sequence.

Uma Sajjan presented her abstract entitled “A promising animal model of *B. cepacia* lung infection in CF” (see abstracts).

David Speert presented his abstract entitled “Differential pathogenicity of genomovars of *Burkholderia cepacia* in a murine intranasal infection model” (see abstracts).

Tom Lessie presented his abstract entitled “N-acyl homoserine lactone formation by *Burkholderia multivorans* and *B. vietnamiensis* isolates” (see abstracts).

Pam Sokol presented her abstract entitled “N-acyl homoserine lactone-mediated interspecies communication between *Burkholderia cepacia* and *Pseudomonas aeruginosa*” (see abstracts).

Esh Mahenthiralingam presented his abstract entitled “*recA* based identification of *B. cepacia* complex species” (see abstracts).

To conclude the meeting, Jane Burns led a discussion of a mission statement developed by the organizing committee (below) and announced plans for next year’s meeting. It will be held in Canada and will be organized by Miguel Valvano and Mary Corey with the assistance of David Speert. Issues related to funding of the meeting were discussed and possible solutions proposed. Tentative dates for the meeting were March 23rd-25th, March 31st-April 2nd, or April 6th-8th. These dates will be checked with possible venues and hopefully plans can be begun in sufficient time to meet grant application timetables for funding (up to 6 months before the meeting).

IBCWG Mission Statement

4/9/00

The IBCWG is an international group whose goals are:

1. To share new clinical and research information in an interdisciplinary fashion among CF clinicians, clinical and research microbiologists, plant pathologists and others with an interest in *Burkholderia cepacia*.
2. To share bacterial strains, molecular biology techniques and model systems among those in the group.
3. To foster collaborative research interactions among members so that there is a coordinated approach and redundant efforts are avoided.
4. To provide informed opinions in an advisory capacity to parties with an interest in *B. cepacia* (e.g. the CF community, regulatory agencies, etc).