

An indoor air model

Paul Comtois* and Nancy Marcoux

Laboratoire d'aérobiologie, département de géographie, Université de Montréal, CP 6128, Montréal, H3C 3J7, Canada

(*author for correspondence, e-mail: comtoisp@ere.umontreal.ca; fax: +1 514 3438008)

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Abstract

Indoor aerobiological data sets are often difficult to handle because they are not easily related to climatic parameters similar to those found outdoors. However, in large buildings, where ventilation systems allow a systematic knowledge of air flows, the transfer of a power distribution model to airborne spore concentration can simplify the task of reaching a decision on contamination presence. The use of the absorption percentage of each component of the ventilation system (air intake, filters, cooling, humidification, air return) can identify abnormalities (i.e. concentrations not following the general expected model, which could mean contamination requiring action), permit direct cleaning, and allow the restoration of a normal state after a short period of time.

...If you would not bring infection and diseases upon
yourselves, change the air you breathe, change it many times
in a day by opening the windows.

Erasmus Darwin

1. Introduction

Indoor air quality has recently been a very active field of research. Abundant information is now becoming available to the scientist and the general public on its main causes and consequences. It is not, however, a recent problem. From the neolithic period through the middle ages, men were confronted with indoor pollution, merely due to heating and cooking in enclosed areas. It is with the erection of chimneys in residential areas that this problem was transferred to the outdoors.

For most people, and up to the end of the XIXth century, indoor air quality and diseases were often linked (Brimblecome, 1987). This was largely forgotten with the generalized use of electricity and natural gas, and pollution became an outdoor problem. In the 1970's, however, the energy crisis and "tighter", more efficient, buildings have shifted our concerns about pollutants back to indoors, where problems

can surpass those caused by outdoor pollution. This phenomena is highly visible in indoor microbial contamination (Kay et al., 1991). But, it is much more difficult to set up exposure guidelines for airborne biological contamination – which are, and will always be, part of the human atmospheric environment – than for man-made chemical pollutants.

The aerobiology sampling protocol was recently standardized with a view to adequately compare different sites (Macher et al., 1995). As a result, we have reached a stage where we can gain a certain control over these problems. But there are still difficulties in making accurate assessments in complex situations where gross contamination is not present. The question that remains to be answered is whether modelisation of indoor fungal spores and CFUs in building ventilation systems can help to identify "abnormalities" in biological concentrations in such a way that precise interventions could be planned.

2. Rationale

Many models have been proposed for the dispersal of outdoor pathogens. However, there are important

differences between the outdoor and indoor situations. In the former, most parameters that have an effect on the aerobiological pathway are known (e.g. temperature, precipitation, wind speed, etc.). For we have a “moving box” of air that collects, then dilutes concentrations; and we reach very quickly a homogeneous situation. These concentrations will of course be site to site and season to season specific, but for a given place and period, they will be a recognizable pattern. Indoors, by contrast, we have an immobile “black box” where air travels, according to external influences and accumulates contamination of anthropic origin, thus creating heterogeneous situations. Indoors, it is almost like a Maxwellian model of aerobiology, where trapdoors are open or closed to contamination.

Therefore, the aerobiological analysis of domestic interiors requires a lot of data and, as a result, need careful understanding of the spatial and temporal framing of samplings. However, the situation is totally different in mechanically ventilated rooms. Indeed, a ventilation system acts like a bottleneck where all available air to the rooms has to move in a relatively short period of time. This, however, generates another problem. Since there is always an outdoor component, and since local contamination is not always negligible, what type of methodology should be used to determine contamination presence? Do we apply a threshold rule (v.g. 1000 CFU/m³) (Morey et al., 1984)? Do we specify an indoor/outdoor ratio (v.g. 1/3) (Brooks and Davis, 1992)? Do we consider the correlation of species presence indoors and outdoors? (see Rao and Burge, 1996 for a review).

This paper proposes a model that reduces large tables of airborne spore data to simple indices, thus allowing the objective discernment of contamination presence.

3. Sampling

All 22 ventilation systems of a 9 story building of an university campus in Montréal were sampled exhaustively and systematically in fall 1990. Samples of total spores were taken, in pair, with Burkard personal samplers (Burkard Manufacturing, Inc., Rickmansworth, U.K.) at a flow rate of 11 litres of air/minute on a gelatine (30%)/glycerine (70%) coated 75 × 25 mm microscopic slide. Samples of viable spores were taken, in pair, with Burkard portable air samplers for agar plates, drawing 15 litres of air/minute on 100

mm Petri dishes, one containing 35 ml of a Sabouraud medium (peptone, glucose, agar), the other 35 ml of a malt 2% medium (malt extract, peptone, agar). Sample exposure times varied from 3 to 4 minutes and were taken while the ventilation systems were in operation. Flow rates (which are fixed on these instruments) were checked before and after each set of samples were taken (i.e. after 20 minutes of operation).

In each system, samples were taken at five different sites (Figure 1): at the fresh air intake (1); after the filters (2); after the humidifier (of the water jet type) (3); after the coils (4); and in the air return ducts from the rooms (5). From a total of 110 sites, 440 samples were taken. All samples were taken during the same week (October 29th to November 2nd), between 10:00 AM and 15:00 PM. In this period, mean air temperature was 5.02 °C and mean relative humidity level was of 80.8%. Therefore, humidification was not needed and 100% fresh air was admitted. Outdoor “control” air was sampled twice on each day, at ground level, near the entrance of the building, on the same side of the building as the fresh air intake.

4. The model

From outdoors to the rooms, we hypothesize the following behavior of spores concentration: a sharp decline after the filters, a small increase either after humidification or after cooling, or both (due to microbial contamination associated with high moisture levels), and another decline in the rooms (because of mixing with “uncontaminated” air).

In order to locate abnormalities from this simple model (in fact, an inverted exponential distribution, characteristic of a constant death rate), we can calculate the efficiency of any part of the system as:

$$\text{Efficiency ("E")}: \frac{\text{exhaust} - \text{supply}}{\text{return} - \text{supply}}$$

v.g. for the filters, “EF”: (site 2 – site 1)/(site 5 – site 1).

However, the application of this simple index to our data set has generated a lot of negative values. This error is the result of using a closed system model, while, in reality, the sampled sites mimic an open model, i.e. are influenced by the outdoor air. Indeed, the value of the numerator (site 2 – site 1) for filters was expected to be negative by our model (see also Figure 2 in the results). At this point, we decided to use only the output of each component (yield or “Y”)

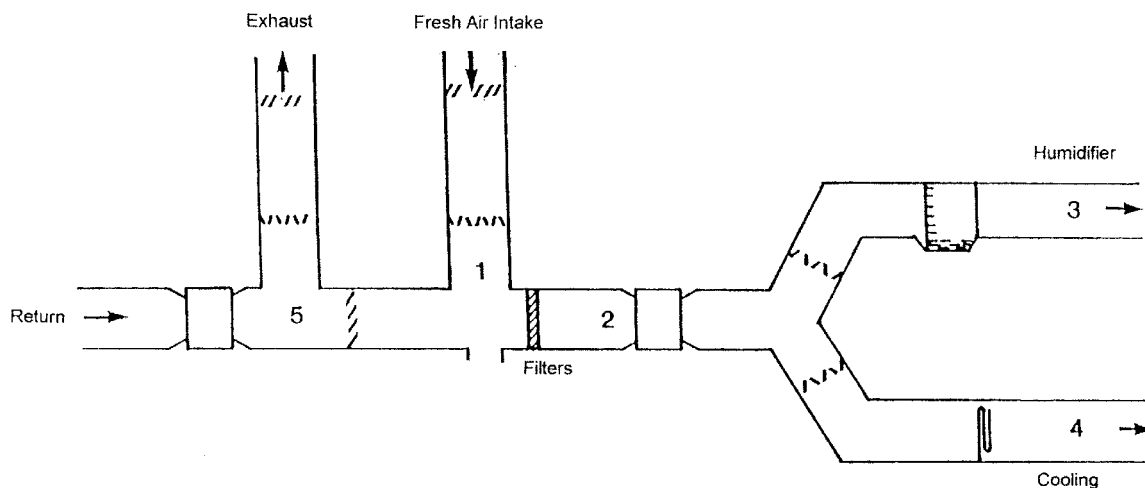


Figure 1. Diagram of air flux in each ventilation system and localisation of sampling sites.

and to integer all the elements for each system (for filters, “FY”: site 1/site 2; for humidifier, “HY”: site 3/site 2; and for cooling, “CY”: site 4/site 2).

Since our system is partially serial and partially parallel (graphically Y shaped, see Figure 1), we apply to the rooms the power distribution model of electrical circuits¹, so that:

Room yield or “RY” : (site 5/site 1)/(FY*(HY + CY)).

Yield (“Y”) can also be expressed as the capability of absorbing the external contamination, i.e.

$$\text{Absorption (“A”) : } (1 - Y) * 100,$$

which will be expressed as percentages.

5. Results

Overall, 67 different taxa were identified indoors and 23 outdoors. This difference can be related to the number of sites sampled: the ratio species/sites being respectively of 3.04 and 3.83.

Species composition will not be discussed here, but it can be said that, as expected for fall outdoors samples, *Cladosporium* dominates total spores (60%) and CFUs (71%). The other genera, in rank order, include: *Penicillium* spp., *Aspergillus* spp., and *Alternaria* spp. Indoors, *Cladosporium* spp. dominate the viable recoveries, but *Cladosporium* spore counts were similar to those of the *Aspergillus/Penicillium* type.

Results from each of the ventilation systems are presented in Tables 1, 2 and 3, showing viable units

(CFUs) on Sabouraud and on Malt, and total spores respectively. Mean concentration outdoors was 140 CFU/m³ or 1120 spores/m³. Indoor, we found 100 CFU/m³ or 1830 spores/m³. There was no statistical difference between the use of the Sabouraud or the Malt medium, the mean difference was 11 CFU/m³ (Kendall Tau of 0.333; p of 0.034).

6. Discussion

The average situation found in the systems corresponds exactly to the general behavior hypothesized in our model: an inverted exponential distribution (Figure 2). From a statistical point of view, only the presence of filters (between sites 1 and 2) is significant (t: 2.56; p: 0.007). While the net contribution of the humidifier site (the 2/3 ratio) or cooling site (the 3/4 ratio) were generally positive, they were not significant ($-0.26 > t > -0.81$; $0.60 < p < 0.79$). Of course, operating humidifier or cooling systems could totally change this result.

Mean absorption for the studied systems was 67%, which is exactly what the theory was predicting for a “normal” behavior (i.e. 66%, or an indoor/outdoor ratio of 1/3). Our model seems, therefore, to adequately represent the airborne situation of fungal spores, even if sampling was limited to specific (but systematic) sites.

The use of our absorption coefficient (“A”) (Table 4) allows the visualisation of the situation at each system. It can also be seen from this table that room absorption was well correlated with the average

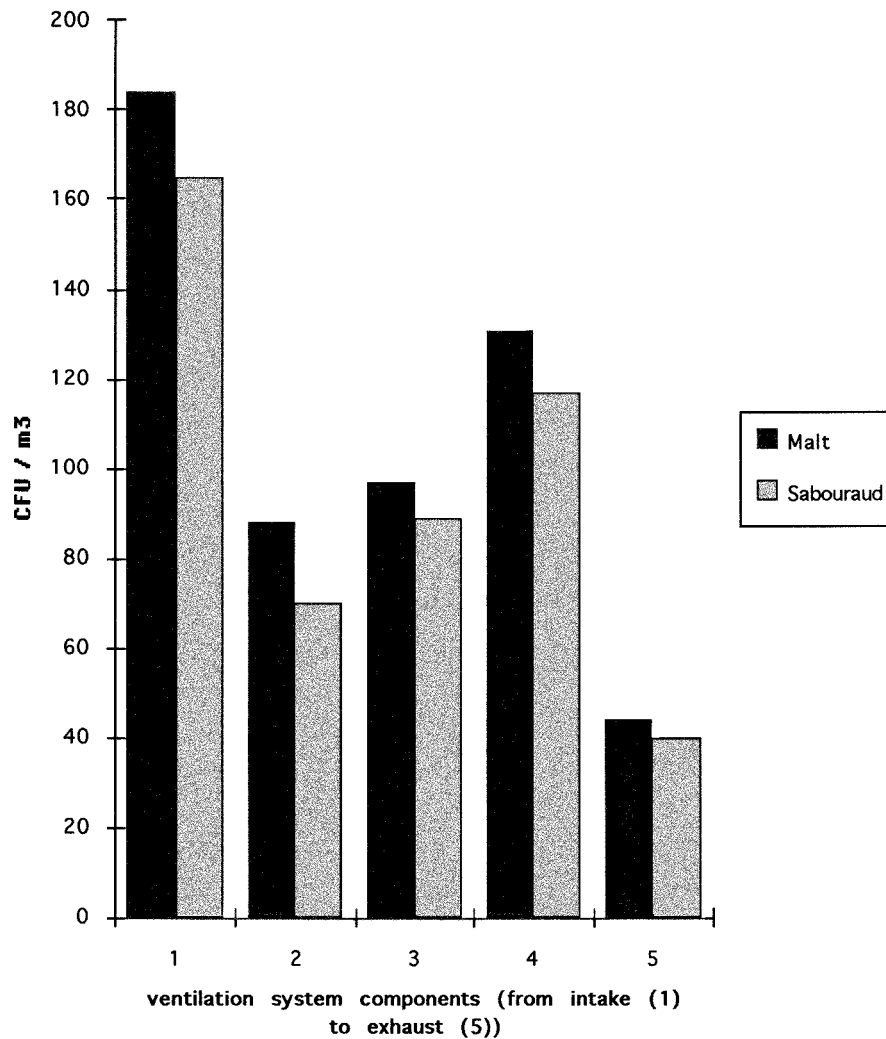


Figure 2. Mean frequencies distribution of airborne colonies forming units (CFU) in the studied ventilation system components (see Figure 1).

absorption level of each system (Figure 3) (Pearson's r of 0.987, p of 0.0001).

Moreover, there was a large agreement between a low indoor/outdoor ratio and a high absorption percentage (Pearson's r of 0.91). All negative "A" correspond to an indoor/outdoor ratio <1 . The net advantage of our model upon a simple indoor/outdoor ratio is that it allows the precise localisation of the contamination. It is, therefore, a significant addition to the indoor/outdoor comparison (which is still necessary).

Possible individual absorption percentage range from 17% (#C4) to 99% (#C3). However, two systems (B2 and C5) present negative absorption. This suggests that these systems disperse more fungal

particles than they receive from the outside. We therefore recommended that these two systems be cleaned.

After cleaning, the 2 systems presenting an abnormal behavior were re-sampled (after 3 months, i.e. February 1991) with the same methodology. This second sampling showed that the situation has again become normal, with a mean indoor/outdoor ratio of 37% (instead of -3034%), or a mean decrease of concentrations of 96%.

7. Conclusion

The use of a simple index of absorption has allowed us to handle a large data set of airborne spores and

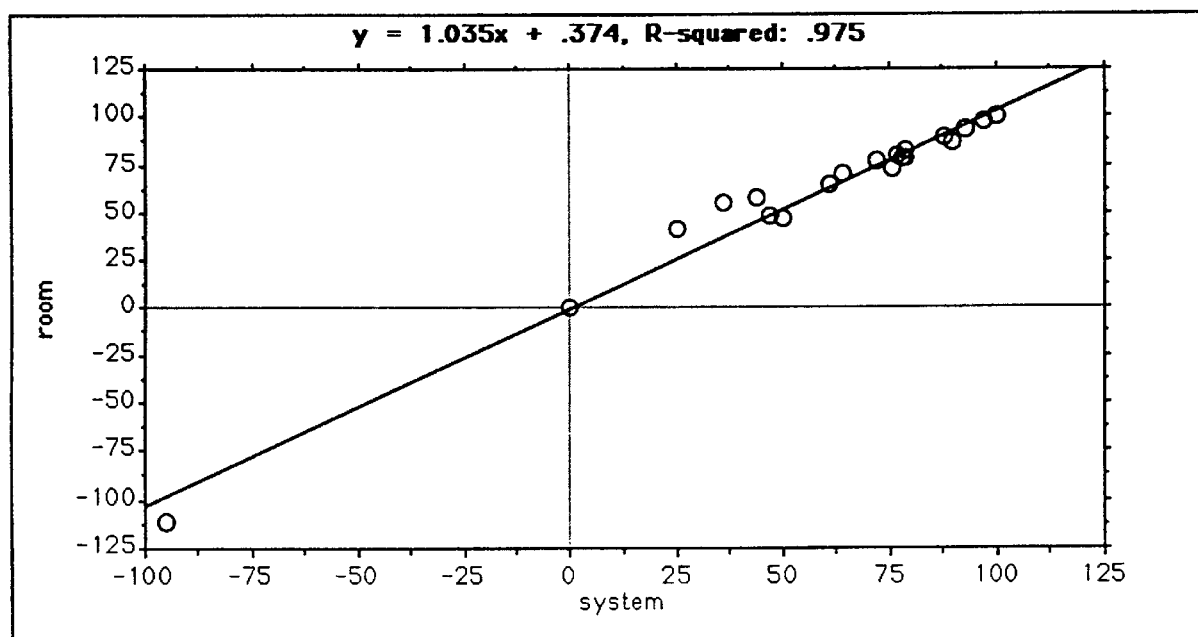


Figure 3. Simple Linear Regression model between room and ventilation system absorption levels.

Table 1. Fungal colonies forming units (CFU) concentrations per cubic meter of air on Sabouraud media, at each site (see Figure 1) of each 22 ventilation systems.

Systems	CFU/m ³					Mean[]	St. dev.
	Site 1	Site 2	Site 3	Site 4	Site 5		
A1	97	20	24	250	22	83	99
A2	97	82	91	45	20	67	33
A3	93	71	130	49	40	77	36
A4	93	10	66	44	11	45	36
A5	21	40	53	72	20	41	22
A9	64	112	56	63	24	64	31
B1	89	136	151	117	67	112	34
B2	87	118	92	207	79	117	53
B3	62	156	80	171	103	114	47
B4	44	95	103	132	23	79	45
B7	96	88	268	250	48	150	101
B8	108	171	155	81	58	115	48
B9	58	78	430	120	40	145	162
B10	–	57	140	106	–	101	42
C1	152	56	21	33	48	62	52
C2	353	1	51	9	63	95	146
C3	639	63	7	656	0	273	343
C4	727	8	21	61	14	166	314
C5	44	54	32	39	45	43	8
C6	99	81	12	7	9	42	45
C7	420	29	0	59	38	109	175
C8	20	30	18	13	21	20	6
Mean[]	165	71	91	117	38	96	48

Table 2. Fungal colonies forming units (CFU) concentrations per cubic meter of air on Malt media, at each site (see Figure 1) of each 22 ventilation systems.

Systems	CFU/m ³					Mean[]	St. dev.
	Site 1	Site 2	Site 3	Site 4	Site 5		
A1	76	71	80	326	11	113	122
A2	40	40	108	115	50	71	38
A3	134	93	110	10	55	80	49
A4	134	10	102	52	44	68	49
A5	141	70	63	99	0	75	52
A9	80	152	90	75	48	89	38
B1	114	240	138	249	66	161	80
B2	54	139	77	287	70	125	96
B3	104	228	96	234	103	153	71
B4	51	101	112	141	63	94	37
B7	80	176	188	235	16	139	89
B8	162	135	232	81	67	135	66
B9	156	201	534	335	50	255	186
B10	–	50	84	92	–	75	22
C1	318	24	7	87	56	98	127
C2	524	10	37	0	18	118	227
C3	624	50	20	350	0	209	272
C4	410	32	21	23	7	99	174
C5	43	36	8	16	63	33	22
C6	90	36	32	62	18	48	29
C7	475	48	10	29	39	120	199
C8	40	20	37	25	21	29	3
Mean[]	183	89	99	133	41	109	53

Table 3. Fungal spores concentrations per cubic meter of air at each site (see Figure 1) of each 22 ventilation systems.

Systems	Spores/m ³					Mean[]	St. dev.
	Site 1	Site 2	Site 3	Site 4	Site 5		
A1	1037	471	565	1415	346	767	447
A2	2991	1038	—	1227	94	1338	1209
A3	2799	1038	1037	1006	1635	1503	771
A4	1352	659	1036	910	125	816	460
A5	2234	188	1635	943	440	1088	846
A9	1227	2201	1098	816	565	1181	625
B1	879	1383	1100	785	124	1854	469
B2	157	407	596	943	18774	4175	8166
B3	912	1384	471	188	126	616	530
B4	345	1384	1131	1352	93	861	601
B7	1604	1824	1887	2295	378	1598	726
B8	2360	533	849	628	343	943	813
B9	1132	1195	1574	28092	157	1372	955
B10	—	1354	2266	1353	—	1658	527
C1	1417	407	535	1228	975	912	435
C2	1171	723	1572	849	377	938	454
C3	25638	282	723	1321	189	5631	11193
C4	23244	283	503	535	943	5102	10145
C5	219	313	345	754	534	433	213
C6	2297	439	439	597	502	855	809
C7	8439	755	—	314	503	2503	3962
C8	722	219	281	408	189	364	217
Mean[]	3913	840	982	1030	1305	1614	1296

Table 4. Mean absorption percentage of outdoor concentrations in each 22 ventilation systems and for the ventilated rooms, for colonies on Sabouraud media, colonies on Malt media, and spores.

Systems	Mean absorption %				
	Sabouraud	Malt	Spores	System mean	Room
A1	77.32	85.53	66.63	76.49	90.60
A2	79.38	—25.00	96.86	50.41	# Value!
A3	56.99	58.96	41.59	52.51	50.60
A4	88.17	67.16	90.75	82.03	85.00
A5	4.79	100.00	80.30	61.69	88.98
A9	62.50	40.00	53.95	52.15	73.74
B1	24.72	42.11	85.89	50.91	83.79
B2	9.20	—29.63	—11859.96	—3959.47	—321.85
B3	—66.13	0.96	86.18	7.01	69.54
B4	47.73	—23.53	73.04	32.41	87.19
B7	50.00	80.00	76.43	68.81	92.64
B9	46.30	58.64	85.47	63.47	76.93
B10	# Value!	# Value!	# Value!	# Value!	# Value!
C1	68.42	82.39	93.12	81.31	32.08
C2	82.15	96.56	96.78	91.83	43.59
C3	100.00	100.00	99.26	99.75	96.92
C4	98.07	98.29	95.94	97.44	58.72
C5	—2.27	—46.51	—143.84	—64.21	—24.82
C6	90.91	80.00	78.15	83.02	61.68
C7	90.95	80.00	78.15	83.02	61.68
C8	—5.00	47.50	73.82	38.77	56.99

colonies concentrations (more than 15,000 identifications were done) from a single building. Contamination, defined as “abnormalities” in concentrations and not necessarily as health hazards, were easily detected. Cleaning of only 4% of the ventilation systems components has allowed the restoration of a normal state in a very short period of time.

Aerobiological models are, therefore, a very useful tool in locating contamination and in testing the efficiency of cleaning, but it does requires thoroughly planned samplings. However, it must be stated clearly that application of this or similar models will not replace the aerobiological expertise of the investigator. It is a tool, not a panacea.

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Note

1. This model was applied, even if it refers to equal resistance on each side, which is not necessary true in our case.

References

- Brimblecome P.: 1987, *The Big Smoke*. Methuen, London, 185 pp.
- Brooks B.O. and Davis W.F.: 1992, *Understanding Indoor Air Quality*. CRC press, Boca Raton, 189 pp.
- Kay J.G., Keller G.E. and Miller J.F.: 1991, *Indoor Air Pollution*. Lewis publishers, Chelsea, 259 pp.
- Macher J.M., Chatigny M.A. and Burge H.: 1995, Sampling airborne micro-organisms and aeroallergens. In: *Air Sampling Instruments for Evaluation of Atmospheric Contaminants*. ACGHI, 8th edition, Cincinnati.
- Morey P.R., Hodgson M.J., Sorenson W.G., Kullman G.J., Rhodes W.W. and Visvesvara G.S.: 1984, Environmental studies in moldy office buildings: Biological agents, sources and preventive measures. *Annual American Conference of Governmental Industrial Hygienists* **10**, 21–35.
- Rao C.Y. and Burge H.: 1996, Review of quantitative standards and guidelines for fungi in indoor air. *J. Air & Waste Managt. Ass.* **46**, 899–908.