

COMMENTS

Comment on “Structural and Vibrational Assignment of *p*-Methoxyphenethylamine Conformers”

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Assignment of molecular conformers is difficult when the evidence is incomplete. In the past this has led to mistaken assignments, which have subsequently been corrected in the light of additional, firmer evidence: See, for example, 3-(4-hydroxyphenyl)propionic acid,¹ 2-phenylethylamine (PEA),² 2-phenylethanol,³ and benzyl alcohol.⁴ Unfortunately, a recent study of *p*-methoxyphenylethylamine (MPEA)⁵ has provided another example. The implicit starting point for these assignments was the early work of Martinez et al.,⁶ in which origin bands in the LIF spectrum of MPEA (and tyramine) were assigned to gauche or anti conformers on the assumption that pairs of gauche conformers which vary only in the orientation of the methoxy (or hydroxy) group on the ring have their band origins split by a constant amount. Data obtained subsequently, and compiled in Table 1, show this assumption to be false: the splitting of gauche conformer band origins varies considerably with the group terminating the side chain.

The reported conformational analysis of MPEA⁵ also conflicts with the well established conformational assignments of the origin bands in PEA^{2,7} (see Figure 1a,b):

(1) Bands ascribed to the symmetric and nonsymmetric anti conformers in MPEA are apparently separated by just 19 cm⁻¹, but in PEA the separation is 91 cm⁻¹ (cf. amphetamine 80 cm⁻¹,⁸ *p*-aminophenylethylamine, 90 cm⁻¹⁹).

(2) The strongest band in MPEA, E, is assigned to the symmetric anti conformer, **1**, but in PEA (and amphetamine and *p*-aminophenylethylamine) the equivalent conformer (V) is only weakly populated. On the other hand, the relatively weak band, A, of MPEA is assigned to structure **8** corresponding to the most stable conformer of PEA. This argument is quite independent of the *calculated* relative energies for MPEA in ref 5, although it is consistent with them—bearing in mind that the B3LYP method seriously underestimates the conformational preference for NH $\cdots\pi$ gauche conformers due to a lack of dispersion.¹⁰

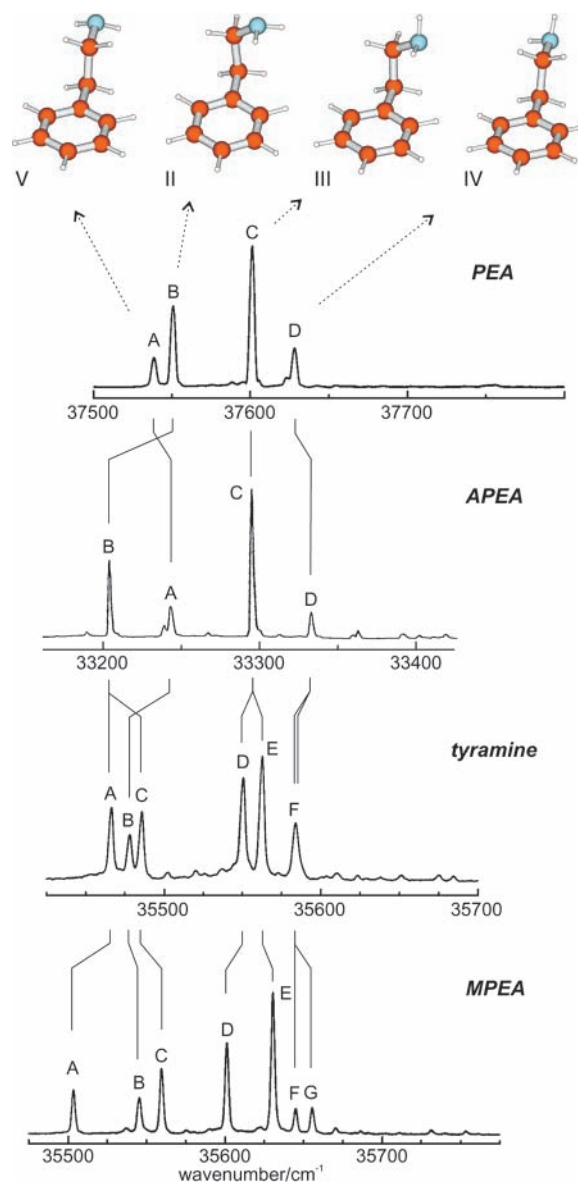


Figure 1. (top) Molecular conformers of 2-phenethylamine (PEA).^{2,7} (bottom): Fluorescence excitation spectra showing the relationship between band origins of PEA, *p*-aminophenylethylamine (APEA), tyramine, and *p*-methoxyphenylethylamine (MPEA). (Spectra are adapted from refs 6 and 9.)

(3) There is no apparent correlation between the overall appearance of the dispersed emission spectra of MPEA and the side chain conformation. Emission spectra of the anti and gauche conformers of PEA are quite distinct, despite the fact that most of the vibrational activity is in the ring modes.⁶

Comparison of the fluorescence excitation spectra of PEA and its ring-substituted analogues, *p*-aminophenylethylamine (APEA), tyramine, and MPEA, provides a straightforward relationship between their conformer origins, see Figure 1. APEA has the same number of origins as PEA: the symmetric

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TABLE 1: Band Origins of gauche Conformer Pairs Distinguished by the cis or trans Arrangement of R₁ and R₂ Groups in Parasubstituted Molecules R₁-CH₂CH₂C₆H₄O-R₂

name	R ₁	R ₂	gauche origins/cm ⁻¹	splitting/cm ⁻¹
4-propylphenol	CH ₃	H	35444, 35456 ^a	12
3-(4-hydroxyphenyl)propionic acid	COOH	H	35703, 35722 ^{b,c}	19
tyrosol	OH	H	35531, 35560 ^d	29
4-propylanisole	CH ₃	CH ₃	35496, 35537 ^a	41
3-(4-methoxyphenyl)propionic acid	COOH	CH ₃	35750, 35768 ^e	18
2-(4-methoxyphenyl)ethanol	OH	CH ₃	35549, 35609 ^e	60

^a Reference 14. ^b Reference 1. ^c Reference 15. ^d Reference 16. ^e Reference 9.

TABLE 2: Conformational Assignments of 2-Phenethylamine (PEA), Amphetamine (AMP), *p*-Aminophenylethylamine (APEA), Tyramine, and Revised Assignments of *p*-Methoxyphenylethylamine (MPEA)

conformer ^a	PEA ^b		AMP ^d		APEA ^e		tyramine		MPEA	
	band	cm ⁻¹ ^c	band	cm ⁻¹	band	cm ⁻¹	band	cm ⁻¹ ^c	band	cm ⁻¹ ^c
V	A	37538	A	37559	A	33243	B	35479	B	35546
II	B	37551	B	37551	B	33204	A	35467	A	35505
II'							C	35486	C	35559
III	C	37602	C	37612	C	33296	D	35551	D	35601
III'							E	35563	E	35631
IV	D	37629	D	37639	D	33333	F	35585	F	35645
IV'							F	35585	G	35655
splittings										
IV - V		91		80		90		106 ^f		104 ^f
III - II		51		61		92		81 ^f		84 ^f
II' - II								19		54
III' - III								12		30
IV' - IV								<2		10

^a Structures II-V: refer to Figure 1. For tyramine and MPEA, (II,II'), (III,III'), and (IV,IV') are the pairs of alternative conformers generated by flipping the ring OH or OCH₃. ^b Assignments from refs 2 and 7. ^c Band positions from ref 6. ^d Band positions and assignments from ref 8. ^e Band positions and partial assignments from ref 9. ^f Calculated using the center of each pair (II, II'), (III, III'), and (IV, IV').

nature of the aniline-like NH₂ group means that they are not split. The assignments to anti or gauche conformers have been unambiguously confirmed by analysis of its partially resolved rotational band contours. (These are predominantly B-type, with Q-subband spacing corresponding to $\{A'' - \frac{1}{2}(B'' + C'')\}$ values of 0.124 cm⁻¹ for bands A and D and 0.084 cm⁻¹ for bands B and C.)⁹ When the *p*-NH₂ substituent is replaced by an -OH or -OCH₃ group to give tyramine or MPEA, the origins of conformers II, III, and IV split, but their relative positions (and relative intensities) remain very similar. A key point is that for all five phenethylamine derivatives listed in Table 2, as well as tryptamine¹¹ and histamine,¹² the dominant spectral features are associated with gauche conformers stabilized by an NH $\cdots\pi$ interaction.

In the case of tyramine, our assignments are largely consistent with those proposed earlier by Levy,⁶ with the minor revision of swapping bands B and C. The choice of band B for the symmetric anti conformer origin of MPEA and tyramine, in preference to A or C, is based upon the following observations. (i) The ionization potentials of the MPEA conformers A and C are within 30 cm⁻¹ of each other, while that of B is 300 cm⁻¹ lower, making it the "odd-one-out". (ii) In tyramine, band B is weaker than the A/C pair, particularly in its R2PI spectrum.¹³ (iii) The dispersed emission spectrum of band B in tyramine is very similar to that of anti conformer origin F, while those of A and C, are like gauche conformer bands D and E.⁶ Likewise, the dispersed emission spectra of MPEA also divide into two distinct groups: B, F, G (anti) and A, C, D, E (gauche).⁵ The revised conformational assignments of MPEA (and tyramine) are summarized in Table 2, along with the deduced splittings.

For MPEA, there remains only the task of distinguishing the cis/trans methoxy arrangement within each pair of conformers: (A, C), (D, E), and (F, G). *Speculative* assignments A = **4**, C = **7**, D = **5**, E = **8** (referring to the conformer labels of ref 5) are consistent with the observed and calculated vibrational frequencies for the S₀ state (e.g., ν_{15}), the lower energy conformer of each pair having the more intense origin band and the cis origin being found at higher wavenumber than the trans origin for both sets.

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