Late Ar-O_2 afterglow for amino acids treatment

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Ar-O_2 afterglows are very efficient media to inactivate bacteria [1]. Yet, little is known on the way active species of these media interact with basic chemical functional groups that take part in the composition of living materials. In Ar-O_2 afterglows, one finds at relatively high concentration ground state molecular oxygen $O_2(X^3\Sigma_g^-)$, vibrationally excited states of $O_2(X, v \geq 1)$, the singlet state $O_2(a^1\Delta_g)$ which is metastable and oxygen atoms. If the pressure is high enough, ozone O_3 must be included. Other species like $O_2(b^1\Sigma_g^+)$, $O(^1S)$ or $O(^1D)$ can be found but at much lower concentrations. These active species may react or not with given chemical functional groups. If we can determine the way they do, we might expect to predict how the simplest components of life, the amino acids are modified when they are treated by an Ar-O_2 afterglow. Amino acids contain various groups like C-C- and C-H simple bonds, saturated or unsaturated rings, the -COOH acid, -OH alcohol, -SH thiol functions and the -NH_2 amine group. Knowing which active species reacts with which functional group, one could predict the way amino acids would react in an Ar-O_2 afterglow. In recent works [2-4], we used model molecules (hexatriacontane $C_{36}H_{74}$, stearic acid ($C_{18}H_{36}O_2$), and biphenyl $C_{12}H_{10}$). We could draw the following conclusions:

- non linear effects occur: if the initial temperature varies from *e.g.* 333 K to 353 K, chemical modifications undergone by materials can be very different,
- O_2 is not inert and can react with radicals formed by other processes,
- consequently, O is not always responsible for material modifications,
- $O_2(a^1\Delta_g)$ does react with rings,
- chain mobility plays an important role: thick or thin films can behave very differently,
- crystallinity matters: depending on the chains orientation, etching rate may change.

These first studies will be continued with $-NH_2$ containing molecules before testing given amino acids and comparing predictions from the matrix data thus obtained.

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